



Ph.D Thesis

**FUNCTIONAL DIVERSITY AND TROPHIC
RELATIONSHIPS IN BENTHIC
COMMUNITIES: A MULTI-SCALE SPATIAL
APPROACH IN NEOTROPICAL SAVANNA
STREAMS**

DIEGO MARCEL PARREIRA DE CASTRO

**BELO HORIZONTE, BRAZIL
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INTERNATIONAL CO-TUTELAGE THESIS



FUNCTIONAL DIVERSITY AND TROPHIC RELATIONSHIPS IN BENTHIC COMMUNITIES: A MULTI-SCALE SPATIAL APPROACH IN NEOTROPICAL SAVANNA STREAMS

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Thesis presented in co-supervision to obtain the degree of Doctor as a co-tutelage program between the Postgraduate Program in Ecology, Conservation, and Management of Wildlife (Universidade Federal de Minas Gerais, Brazil) and the Ecole Doctorale E2M2 (Université Claude Bernard Lyon 1, France).

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*Dedico este trabalho aos meus pais,
Tarlei e Celina, pelo exemplo e
determinação, e à minha esposa
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*“The love for all living creatures is the
most noble attribute of man”*

Charles Darwin

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RESUMO

Mudanças nos usos da terra e degradação ambiental devido a atividades humanas têm resultado em extremas alterações em ecossistemas tropicais, especialmente em riachos de cabeceira e suas bacias hidrográficas no Cerrado. Pressões humanas relacionadas à expansão agrícola e urbanização têm levado à redução drástica da cobertura vegetal nativa, comprometendo zonas ripárias, afetando e degradando ecossistemas aquáticos. Há uma necessidade urgente em quantificar e prever como as comunidades aquáticas respondem às mudanças nos usos do solo para orientar os esforços de conservação e manejo de recursos naturais. Esta tese teve como objetivo avaliar quais escalas espaciais mais influenciam as comunidades de macroinvertebrados bentônicos e como os usos da terra influenciam as relações tróficas e atributos biológicos de macroinvertebrados. O capítulo 1 avaliou como os usos da terra (representados por riachos em regiões de pastagem, plantação de cana de açúcar e vegetação nativa) influenciam o fluxo de energia e os nichos tróficos de macroinvertebrados. Em seguida foi avaliada qual escala espacial exerce maior influência na composição taxonômica e funcional de assembleias de macroinvertebrados (Capítulo 2). Por último, verificou-se a influência de um gradiente de distúrbios antrópicos sobre a diversidade funcional de assembleias de macroinvertebrados (Capítulo 3). Os resultados aqui apresentados demonstram que alterações nos usos do solo levam a comunidades de macroinvertebrados bentônicos em direção a comportamentos de alimentação mais generalistas e com maior sobreposição de nichos tróficos (Capítulo 1). Além disso, variáveis ambientais nas escalas local e regional explicaram significativamente variações na composição taxonômica e funcional de assembleias de Ephemeroptera, Plecoptera e Trichoptera, mas as métricas de uso do solo foram as que melhor explicaram as diferenças na composição funcional entre diferentes locais (Capítulo 2). E, por fim, foi observado que os sítios menos impactados (em condições de referência) têm assembleias de macroinvertebrados mais especializadas e mais diversas funcionalmente em comparação a locais perturbados (Capítulo 3). Os resultados encontrados corroboram que a biodiversidade deve ser avaliada em múltiplas escalas espaciais e que sejam considerados os elementos funcionais de comunidades biológicas, visando conservação e desenvolvimento de ferramentas preditivas. Este estudo contribui para uma melhor compreensão da estrutura e funcionamento de riachos na savana neotropical no contexto de subsidiar o desenvolvimento de instrumentos de avaliação ambiental. Tais abordagens contribuirão para o desenvolvimento de medidas mais adequadas de gestão e conservação que impeçam um avanço ainda maior da degradação de condições ecológicas de riachos tropicais.

Palavras-chave: escala espacial, uso da terra, atributos funcionais, fluxo de energia

ABSTRACT

Changes in land cover and use and the associated environmental degradation due to human activities have resulted in extreme alterations of tropical ecosystems, especially in headwater streams and their watersheds in the neotropical savanna. Human pressures related to agricultural expansion and urbanization have led to drastic reductions in native vegetation cover, affecting riparian zones and degrading aquatic ecosystem functioning. There is an urgent need to quantify and predict how aquatic communities respond to different intensities of land use to guide conservation and natural resource management efforts. This thesis aims to evaluate how spatial scales influence the relationship between habitat and benthic macroinvertebrate communities and how land use intensity affects the trophic relationships and biological traits of macroinvertebrates. In Chapter 1, we evaluated how the intensity of land use (represented by a gradient moving from native vegetation toward pasture and sugar cane plantations) influences the energy flow and trophic niches of macroinvertebrates. In Chapter 2, we investigated the spatial scales (e.g., catchment, local) that most influence the taxonomic and functional composition of macroinvertebrate assemblages. Finally, in Chapter 3, we examined the impacts of human pressures on the functional diversity of macroinvertebrate assemblages. we showed that the intensity of land use affects benthic macroinvertebrate assemblages, yielding more generalist feeding behaviors with greater overlap of trophic niches (Chapter 1). In addition, environmental variables at the local and catchment scales significantly explained the variations in the taxonomic and functional composition of Ephemeroptera, Plecoptera and Trichoptera assemblages, but land use variables best explained the differences in functional composition among sites (Chapter 2). Finally, we showed that less impacted sites (under reference conditions) had more specialized and more functional diverse macroinvertebrate assemblages compared to disturbed sites (Chapter 3). These results corroborate the idea that biodiversity should be evaluated at multiple spatial scales and that the functional elements of biological communities should be considered when aiming for conservation and the development of predictive tools. This study contributes to a better understanding of the structure and functioning of streams in the neotropical savanna by subsidizing the development of environmental assessment tools. Such approaches will contribute to the development of more appropriate management and conservation measures that will allow for evaluation of the impacts on biota of further degradation of the ecological conditions in tropical streams.

Key-words: spatial scale, catchment, land use intensity, functional traits, energy flow

RÉSUMÉ

Les changements d'intensité dans l'utilisation des sols et la dégradation de l'environnement en raison de activités humaines ont entraîné une forte altération des écosystèmes tropicaux, en particulier dans les cours d'eau de tête de bassin de la savane néotropicale. Les pressions humaines liées à l'expansion agricole et à l'urbanisation ont conduit à une réduction drastique de la couverture végétale indigène, affectant les zones riveraines et altérant le fonctionnement des écosystèmes aquatiques. Il est urgent de quantifier et de prévoir comment les communautés aquatiques répondent aux changements de l'utilisation des sols pour guider les efforts de conservation et de gestion des ressources naturelles. Dans ce contexte, cette thèse visait à évaluer à quelles échelles spatiales la relation entre habitat et communautés de macroinvertébrés benthiques s'exprimait le plus fortement et comment l'intensité d'utilisation des sols affectait les relations trophiques et la composition en traits biologiques des communautés de macroinvertébrés benthiques. Dans le chapitre 1, j'évalue comment l'intensité d'utilisation des sols (représentée par un gradient depuis la végétation autochtone, au pâturage, et à la plantation de canne à sucre et la végétation indigène) influe sur les flux d'énergie et les niches trophiques des macroinvertébrés benthiques. Ensuite, j'ai évalué à quelle échelle spatiale (bassin versant, localité) et pour quelles variables, le lien entre la composition taxonomique et fonctionnelle des assemblages de macroinvertébrés benthiques était le mieux exprimé (chapitre 2). Enfin, j'ai montré que les perturbations anthropiques avait un impact sur la diversité fonctionnelle des assemblages de macroinvertébrés benthiques (chapitre 3). Les résultats présentés ici montrent que les changements d'intensité de l'utilisation des sols conduisent les assemblages de macroinvertébrés benthiques vers des comportements d'alimentation plus généralistes avec un chevauchement des niches trophiques (chapitre 1). De plus, les variables environnementales à l'échelle locale et du bassin versant expliquent de façon significative les variations de la composition taxonomique et fonctionnelle des assemblages d'Ephéméroptères, Plécoptères et Trichoptères, mais les variables décrivant l'intensité d'utilisation des sols expliquent le mieux les différences de composition fonctionnelle entre les différents sites (chapitre 2). Enfin, J'ai montré que les sites quasi-naturels (dans des conditions de référence) ont des assemblages de macroinvertébrés plus spécialisés comparés aux sites perturbés (chapitre 3). Les résultats corroborent le fait que la biodiversité doit être évaluée en tenant compte de variables agissant à de multiples échelles spatiales et que les éléments fonctionnels des communautés biologiques doivent être considérés, en vue de la conservation et du développement d'outils prédictifs. Cette étude contribue à une meilleure compréhension de la structure et du fonctionnement des cours d'eau dans la savane néotropicale dans le contexte du développement d'outils d'évaluation environnementale. Ces approches contribueront à l'élaboration de mesures de gestion et de conservation plus appropriées et permettront d'examiner les conséquences futures d'une poursuite de la dégradation des conditions écologiques dans les cours d'eau tropicaux.

Mots clés: échelle spatiale, bassin versant, intensité d'utilisation des sols, traits fonctionnels, flux d'énergie

RÉSUMÉ ETENDU

L'intensité d'utilisation des terres et le couvert végétal des bassins versants influencent grandement l'habitat physique et, par voie de conséquence, les assemblages aquatiques qui vivent dans les cours d'eau ainsi que les flux d'énergie au sein de ces écosystèmes. Depuis longtemps, les écosystèmes d'eau douce subissent de nombreuses pressions liées aux activités anthropiques, notamment l'agriculture et l'urbanisation, qui réduisent le couvert de la végétation autochtone, y compris la végétation des zones riveraines, ce qui affecte et induit la dégradation des écosystèmes aquatiques. De ce fait, les activités anthropiques conduisent à la simplification des habitats et à une réduction la diversité des communautés aquatiques, mettant en péril l'intégrité écologique et la soutenabilité des processus écologiques dans ces écosystèmes. Les cours d'eau tropicaux sont parmi les écosystèmes les plus menacés au monde, notamment ceux situés dans les pays en développement. Dans les cours d'eau néotropicaux, il est ainsi urgent de quantifier et de prévoir comment les communautés aquatiques répondent aux changements dans l'utilisation des terres pour guider les efforts de conservation et la gestion des ressources aquatiques.

Depuis plus de 100 ans, les macroinvertébrés aquatiques sont utilisés comme bio-indicateurs de la qualité de l'eau et leur utilisation dans l'évaluation de l'intégrité écologique des cours d'eau tropicaux s'est accrue ces dernières années. Les approches traditionnelles pour évaluer les effets des perturbations anthropiques portent généralement sur la structure taxonomique des communautés (ex. richesse, abondance, diversité) et des indices multimétriques ont été proposés pour évaluer l'état de santé des cours d'eau. Cependant, ces indices basés sur la composition et l'abondance des organismes sont limités à la région dans laquelle ils ont été développés, car il existe une variation considérable de la distribution des espèces due à leur répartition biogéographique. L'utilisation d'approches prenant en compte les différences évolutives ou fonctionnelles entre les espèces peut améliorer les indicateurs standard pour évaluer l'état écologique des écosystèmes aquatiques. Depuis une vingtaine d'années, les traits d'espèces sont suggérés comme une approche alternative et

complémentaire des approches taxonomiques traditionnelles pour élucider les changements dans les communautés aquatiques liés à des perturbations naturelles ou anthropiques. Cette approche fondée initialement sur le concept théorique d'habitat templet a fourni de nombreuses applications pratiques dans l'évaluation écologique de la santé des cours d'eau.

Les évaluations écologiques utilisant les traits d'espèces offrent plusieurs avantages par rapport aux évaluations taxonomiques, telles que: (i) une plus grande stabilité de réponse de la composition en traits des communautés à large échelle spatiale par rapport à la composition taxonomique, ce qui permet d'étendre l'approche à différentes régions biogéographiques; (ii) un très large éventail de réponses aux facteurs de stress multiples; et (iii) la possibilité d'une compréhension plus mécanistes des phénomènes en jeu dans la relation espèces-environnement.

La plupart des études portant sur l'importance relative des échelles locales et régionales sur la composition en traits et taxonomique des assemblages dans les écosystèmes d'eau douce est limitée aux régions tempérées et boréales. L'identification du mode d'action des pressions anthropiques sur la composition en traits des communautés est susceptible d'améliorer notre capacité prédictive dans les modèles liant habitat et communautés biologiques, d'améliorer notre connaissance des processus en jeu dans les écosystèmes d'eau douce et d'aider au développement d'outils plus spécifiques que les évaluations traditionnelles pour les actions de gestion et les initiatives de conservation.

Dans cette thèse, mon objectif était d'étudier et de comprendre comment le couvert végétal et l'intensité d'utilisation des terres affectent la composition taxonomique et en traits des assemblages aquatiques ainsi que les relations trophiques dans les cours d'eau de tête de bassin en savane néotropicale. J'ai acquis des données sur les isotopes stables, des données sur les habitats et les paysages issues d'analyse d'imagerie satellitaire et des données sur la composition en taxons et en traits de assemblages d'insectes aquatiques pour étudier trois ensembles d'objectifs interdépendants correspondant à trois chapitres de la thèse.

Dans le premier chapitre (Castro et al., 2016, PloS One 11, e0150527), j'ai utilisé la technique des isotopes stables pour évaluer comment l'intensité d'utilisation des terres (représentée par un gradient depuis la végétation autochtone vers les pâturages et les plantations de canne à sucre) influence les flux énergétiques et les niches trophiques dans les assemblages aquatiques des cours d'eau néotropicaux. Les macroinvertébrés ont été échantillonnés et classés en groupes fonctionnels d'alimentation et les ressources trophiques disponibles ont été échantillonnées et leur composition isotopique en ^{13}C et ^{15}N a été identifiée le long de cours d'eau situés dans le biome du Cerrado (savane néotropicale). Les résultats montrent que les cours d'eau sous influence de pâturages ou de plantations de canne à sucre ont des niches trophiques plus larges et plus chevauchantes, ce qui correspond à des habitudes alimentaires plus généralistes de la part des invertébrés présents. En revanche, les groupes trophiques des cours d'eau traversant la végétation autochtone ont des niches trophiques plus étroites avec peu de chevauchements suggérant une plus grande spécialisation. Les sites sous influence de pâturages ont une plus grande gamme de ressources exploitées, ce qui indique une plus grande diversité trophique que les sites à couvert végétal naturel et la plantation de canne à sucre. Nous pouvons conclure que l'augmentation de l'intensité d'utilisation des terres modifient les réseaux trophiques et déplacent les assemblages de macroinvertébrés vers des comportements alimentaire plus généralistes et un chevauchement plus important des niches trophiques.

Dans le deuxième chapitre, j'ai évalué l'importance de la localisation géographique, du couvert végétal et de l'utilisation des bassins versants (décrit par 20 variables) et l'habitat physico-chimique local (décrit par 55 variables: hydromorphologie, substrat, écoulement, forêt ripariale et qualité de l'eau) dans les modifications de la composition taxonomique et fonctionnelle des assemblages d'Ephéméroptères, de Plécoptères et Trichoptères (EPT). Les traits des taxons EPT ont été quantifiés en utilisant 28 catégories de 7 traits biologiques, ce qui représente les meilleures connaissances actuellement disponibles pour les taxons EPT dans les cours d'eau néotropicaux de savane. Nous avons ensuite analysé les relations entre les variables définie à l'échelle des bassins versants et celles définies au niveau de l'habitat local

(site) et la composition taxonomique et en traits des assemblages d'insectes recueillis dans 160 sites. Les variables définies à l'échelle des bassins versants et de l'échelle locale du site contribuent à la variation significative de la composition taxonomique et en traits des taxons EPT. Le substrat et l'hydromorphologie locale ainsi que l'intensité d'utilisation des terres dans les bassins versants influencent le plus fortement la composition taxonomique alors que la composition des assemblages en traits est essentiellement liée à l'intensité d'utilisation des terres. La position géographique représente une plus faible part explicative de la variation des assemblages d'EPT, du fait d'une combinaison de l'histoire évolutive des genres d'EPT et de leurs capacités de dispersion variable.

Dans le troisième chapitre, j'ai étudié les changements dans la composition des assemblages d'EPT le long d'un gradient de perturbation anthropique séparant des cours d'eau de tête de bassin de référence, de cours d'eau moyennement ou fortement perturbés par les activités anthropiques. Alors que la richesse des genres d'EPT ne diffère pas entre niveaux de perturbation, la richesse et la diversité fonctionnelle montrent une diminution significative avec l'augmentation du niveau de perturbation. Nos résultats sur la réponse aux perturbations de la taille, la forme et la flexibilité du corps des organismes, de leur nombre de cycles de reproduction par an, de leur locomotion, et la relation au substrat avec les hypothèses faites a priori du substrat sur la réponse des traits aux changements d'intensité dans l'utilisation des terres des bassins versants, l'habitat physique et la qualité de l'eau. En combinant les analyses RLQ et dite "quatrième coin", nous montrons que 12 des 28 catégories de traits disponibles sont significativement associées à des changements d'intensité de l'utilisation des terres des bassins versants, de l'habitat physique et de la qualité de l'eau, le long du gradient de perturbation. La proportion d'individus ayant une grande taille corporelle, peu flexible, <1 cycle de reproduction par an, constructeur d'étui nymphaux (Trichoptères) et se déplaçant comme "climber" caractérisent les assemblages d'EPT des cours d'eau les moins perturbés. Enfin, les assemblages d'EPT des cours d'eau les moins perturbés montrent une spécialisation des traits beaucoup plus élevée par rapport aux cours d'eau perturbés contenant plus de taxons généralistes..

Cette thèse est une première évaluation quantitative et multi-échelle des conséquences des perturbations anthropiques sur les compositions taxonomiques et en traits des taxons EPT et sur les relations trophiques dans les cours d'eau de tête de savane néotropicale. En premier lieu je contribue à un accroissement des connaissances à travers l'élaboration d'une base de données de traits EPT spécifique, élaborée après une étude robuste et exhaustive de la littérature néotropicale exclusivement. J'ai sélectionné six traits (parmi ~ 15 possibles) possédant suffisamment d'informations fiables. En second lieu, j'ai pu identifier quelle échelle spatiale et quelles variables de perturbation anthropogéniques influencent le plus la composition taxonomique et les traits des assemblages d'EPT dans les cours d'eau de tête de bassin. Enfin, j'ai observé que les changements dans l'utilisation des terres conduisent à l'homogénéisation des communautés en termes de composition fonctionnelle. Cette étude contribue à une meilleure compréhension de la structure et du fonctionnement des cours d'eau néotropicaux de savane dans le contexte de la conception future d'outils d'évaluation pour la définition des aires de conservation prioritaires et l'élaboration d'indices d'intégrité biologique et fonctionnelle. De telles approches permettront d'élaborer des mesures de gestion et de conservation appropriées pour prévenir la dégradation des conditions écologiques.

GENERAL CONTEXT



Word cloud showing the main words and concepts used in this PhD. thesis.

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INTRODUCTION

The growth of the human population, rising consumption and the overexploitation of natural resources have caused the widespread alteration and disruption of natural systems, especially in freshwater ecosystems (Abell et al. 2008). These ecosystems have lost a great proportion of their species and habitat, and tropical biomes are at the forefront of these environmental problems (Laurance and Peres 2006). The loss of biodiversity in rivers, including the diversity of benthic organisms, is occurring at an alarming and increasing rate (Allan and Castillo 2007). This is because rivers have experienced many influences from human activities, such as sewage release, the destruction and degradation of habitats, the introduction of exotic species, and flow regulation (Dudgeon et al. 2006). These changes have generally led to the simplification of habitats and have reduced the diversity of aquatic communities, imperiling the ecological integrity and sustainability of ecological processes in these ecosystems (Cardinale et al. 2012). Tropical streams are among the most threatened ecosystems in the world (Dudgeon et al. 2006), but the pace of stream deterioration exceeds the pace of scientific research aimed at understanding ecosystem responses (Ramírez et al. 2008). In Brazil, all of these problems have affected the quality of water bodies, especially near urban centers and industrial development areas (Tejerina-Garro et al. 2005, Hepp et al. 2010).

The intensity of land use and the type of land cover in the catchments of aquatic systems greatly influence the physical habitat and, consequently, the aquatic communities and energy flow (Allan 2004, di Lascio et al. 2013). Agriculture and urbanization tend to reduce the coverage of native vegetation, including vegetation in the riparian zone, affecting and degrading aquatic ecosystems (Dudgeon et al. 2006). The resulting changes in physical habitat include increases in the sedimentation rate, changes in the hydrological regime, and increased water temperature and nutrient concentrations, which in combination, significantly impact aquatic biodiversity (Bryce et al. 2010, Hughes et al. 2010, Woodward et al. 2012) and ecosystem functioning (De Laender et al. 2016). In neotropical streams in particular, there is an urgent need to quantify and understand how aquatic communities respond to changes in land use to guide conservation efforts and the management of ecological resources.

Aquatic macroinvertebrates are widely used as bio-indicators of water quality (Rosenberg and Resh 1993, Bonada et al. 2006), and their usage in assessing the biotic integrity of tropical streams has increased in recent years (Ferreira et al. 2011, Oliveira et al. 2011, Ligeiro et al. 2013, Dedieu et al. 2016). Among macroinvertebrates, Ephemeroptera, Plecoptera and Trichoptera (EPT) comprise highly diverse aquatic assemblages in headwater streams (Bispo et al. 2006) and have important roles in nutrient cycling and energy transfer (Ferreira et al. 2014). In addition, EPT richness, for example, is a common metric for assessing the biological conditions of stream ecosystems (Stoddard et al. 2008). Traditional approaches to assessing anthropogenic disturbance have usually focused on the taxonomic structure of biological communities (e.g., species richness, abundance/density, and diversity, although some have used traits, such as feeding groups), and multimetric indices have recently been proposed to assess environmental conditions (Moya et al. 2011, Couceiro et al. 2012, Macedo et al. 2016). However, the use of indices based on the composition and abundance of organisms is restricted to the region in which these indices were developed because there is considerable ecological variation due to the biogeographic distribution of species, which changes over large spatial scales (Heino 2001, Bonada et al. 2007). Thus, the observed patterns may result from natural stochastic variations, which are independent of the changes associated with human disturbance (Dolédéc et al. 2011). In that respect, the use of approaches that account for the evolutionary, biological, ecological, or functional differences between species allows for the improvement of the standard indices developed to assess the environmental conditions of rivers (Petchey and Gaston 2002, McGill et al. 2006, Villéger et al. 2008).

To augment the conservation and management of tropical freshwater ecosystems, it is essential to develop biological tools that incorporate ecological information such as biological traits (Usseglio-Polatera et al. 2000b, DeLong and Thorp 2006, Tomanova et al. 2008). Furthermore, it is fundamental to understand at what spatial scale and under which types of human impact the differences in aquatic assemblages occur.

Spatial scales as environmental filters

Environmental patterns within a watershed directly affect the structure of biological communities in a hierarchically nested manner (Vannote et al. 1980, Frissell et al. 1986, Leps et al. 2015, Wojciechowski et al. 2017). At a large spatial scale, climate, geology and topography influence the geomorphic processes that govern smaller-scale energy inputs and local habitats (for example, determining the shape of river channels and network connectivity) for aquatic communities (Frissell et al. 1986, Allan 2004, Goldstein et al. 2007). Local physical and chemical habitats are thus determined by larger-scale processes (Leal et al. 2016), which makes it even more difficult to disentangle the role of the different environmental drivers acting on aquatic communities (Frissell et al. 1986, Allan 2004). Therefore, considering spatial scale in freshwater ecology studies is essential for a comprehensive understanding of the drivers that determine the structural and functional diversity of stream communities (Heino et al. 2003, Sandin and Johnson 2004, Hoeinghaus et al. 2007, Macedo et al. 2014, Liu et al. 2016).

The multiple spatial scales (e.g., region, river catchment, channel unit, and microhabitat) that structure biological communities are related to the idea of environmental filters. Each species possesses a specific set of traits that allows them to withstand habitat filters acting over multiple spatial scales, thereby determining their distribution pattern (Townsend and Hildrew 1994, Poff 1997). Considering the selective action of habitat filters at multiple scales can increase our understanding and predictive ability in ecology. Accordingly, identifying species traits that are sensitive to habitat characteristics at different spatial levels will likely enhance our ability to predict how species distributions are regulated across the landscape.

Human disturbances

Human disturbances are widely recognized as major threats to terrestrial and aquatic biodiversity worldwide (Vörösmarty et al. 2010, Carpenter et al. 2011, Dirzo et al. 2014). Freshwater ecosystems are especially vulnerable to anthropogenic disturbances because human populations generally settle close to rivers or in their surrounding catchment areas. Human activities can alter the balance of the natural forcing factors in aquatic ecosystems, for

example, by changing the relative abundance of different substratum types or altering the mean annual temperature regime. Such impacts can cause changes that are beyond the normal conditions expected for a given lotic ecosystem and affect ecosystem structure and function (Malmqvist and Rundle 2002). Moreover, multiple stressor effects associated with human activities also cause declines in freshwater biodiversity (Dudgeon et al. 2006, Vörösmarty et al. 2010).

The major human-induced drivers of change in freshwater ecosystems include hydrological regime modification, land use intensity, chemical inputs, exotic species, and harvesting. All drivers play a role, but some of them have substantial effects on freshwater systems (Carpenter et al. 2011). In particular, the intensity of land use, the amount of conversion of natural lands to human use and the alteration of management practices in human-dominated lands are major drivers of ecosystem change (Foley et al. 2005). Land use intensity affects geomorphological processes, causing channel hydromorphological changes, bottom siltation, substrate homogenization, decreases in flow variability (Allan, 2004), reduced litter input from riparian vegetation (Boyero et al. 2016), and water quality alteration (Woodward et al. 2012, Taylor et al. 2014). Such human-induced ecosystem changes are observed at multiple spatial scales (global, regional, local), constituting a complex and interconnected system (Rockström et al. 2009).

Energy flow and trophic relationships

In freshwater ecosystems, aquatic invertebrates are the main link between primary producers (e.g., periphyton and aquatic macrophytes) and higher trophic levels (e.g., vertebrates). By breaking down organic matter, these invertebrates contribute to litter decomposition and nutrient availability for other organisms (Wallace and Webster 1996, Covich et al. 1999, Jardine et al. 2005). Aquatic macroinvertebrates have been classified according to their feeding habits into functional feeding groups (FFG) based on morphological and behavioral characteristics (Cummins 1973, Merritt et al. 2008). Each of these groups relies on specific food resources, which are in turn influenced by different habitat characteristics. These groups include (i) scrapers that feed on organic matter bound to organic and inorganic substrates (e.g.,

periphyton, algae and their associated microbiota); (ii) shredders that feed directly on coarse particulate organic matter (CPOM); (iii) gathering-collectors that feed mainly on deposited fine particulate organic matter (FPOM); (iv) filtering-collectors that filter fine suspended organic matter; and (v) predators that feed on whole animals or their parts (Wallace and Webster 1996, Merritt et al. 2008).

Identifying and quantifying the trophic relationships between aquatic macroinvertebrates are essential to a better understanding of the functional relationships between organisms and the environment (Cardinale 2011, Thompson et al. 2012, Rooney and McCann 2012). Therefore, analyzing the trophic relationships among macroinvertebrates and the energy flow in aquatic ecosystems is required to understand community structures and dynamics and ecosystem functioning (Polis et al. 1997, Perkins et al. 2014).

To improve environmental assessments and inform the management of aquatic ecosystems, it is essential to understand how the intensity of land use influences the energy flow and trophic relationships in aquatic environments (DeLong and Thorp 2006). Changes in vegetation cover affect the nutrient input, food resource quality, and energy flow, which can lead to the simplification of food webs and a loss of biodiversity (Lorion and Kennedy 2009, Ferreira et al. 2012). The replacement of native vegetation by monocultures (e.g., pasture, sugarcane) disturbs ecosystem function and the sources that supply aquatic environments (Leberfinger et al. 2011) by modifying the structure and dynamics of aquatic communities that are dependent on allochthonous material provided by the surrounding vegetation and canopy cover (Ormerod et al. 1993, Dudgeon 1994, Ferreira et al. 2012).

Assessments of the energy flow, trophic structure, and trophic relationships between organisms can be obtained using stable isotopes (Post 2002, Layman et al. 2007, Boecklen et al. 2011, Perkins et al. 2014). The information yielded by isotopic signals allows us to (i) know the origin of organic matter (Post 2002), (ii) examine resource partitioning (Young et al. 2010), (iii) map the ecosystem fluxes of carbon and nitrogen (Peterson & Fry, 1987), (iv) characterize niche properties (Newsome et al. 2007) and (v) compare the ecological processes of riparian areas in different regions (Carvalho et al. 2017). The use of the stable isotope ratios of carbon ($\delta^{13}\text{C}$) and nitrogen ($\delta^{15}\text{N}$) as indicators of anthropogenic disturbances was first proposed by

Peterson and Fry (1987). The use of this method in trophic ecology has intensified in recent years (Medeiros and Arthington 2011, Blanchette et al. 2014, Rigolet et al. 2015, Bentivoglio et al. 2016, Greaver et al. 2016, Jackson et al. 2016), mainly for the purpose of describing the relationships between sources of organic matter, food chains and sources of pollution (Davis et al. 2012, Turner and Edwards 2012, Morrissey et al. 2013), contributing to the understanding of ecological processes in streams (di Lascio et al. 2013).

In δ -space (a bi-plot where each axis is defined by the isotopic values, i.e., $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$), the isotopic values define an area called the isotopic niche (Bearhop et al. 2004). As the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of a species are the result of all trophic pathways, the position in δ -space is one representation of the species' trophic niche (Layman et al. 2007). Trophic niche is a part of the ecological niche that uses a subset of dimensions related to trophic resources. The isotopic niche space is defined as the range of stable isotope values and provides insight into resource partitioning. In a coarse analogy with Hutchinson's (1957) n-dimensional niches, the isotopic niche is a subset of a multivariate space (Newsome et al. 2007). Although the isotopic niche is likely to be tightly correlated with the trophic niche, it is important to highlight that these are two different concepts that should not be mixed together. Nevertheless, the information contained within stable isotope ratios can be considered to be a descriptor of the key axes in Hutchinson's hypervolume, thus providing ecologically relevant information about the biological assemblages they represent (Bearhop et al. 2004, Jackson et al. 2011). An overlap in the isotopic niches of two consumers indicates the use of the same primary resources, whereas isotopic niche segregation demonstrates that the consumers use different resources. Human activities can alter the trophic niche of macroinvertebrates and their degree of overlap (Bearhop et al. 2004, Layman et al. 2007), potentially leading to communities with more generalist species.

Community specialization

Ecological specialization refers to the area in ecological niche space used by a species due to its specific traits (Futuyma and Moreno 1988). In freshwater systems, the replacement of habitat specialists by generalist species has been suggested to occur as a response of

assemblages to human activities, such as habitat degradation and land use intensity (Olden et al. 2004, Petsch 2016). Functional homogenization at the community level can alter ecosystem functioning and productivity and can result in the deterioration of ecosystem services (Clavel et al. 2011). At the community level, specialization can be estimated as the mean specialization of the species present in that community and can be used to develop indicators of conservation interest (Devictor et al. 2010).

The ecologically significant functional changes that can occur in homogenized communities are largely independent of taxonomic identities. Thus, a more subtle ecological examination of homogenization is required (Olden et al. 2004). In freshwater ecosystems, the replacement of habitat specialists by habitat generalists has been shown to occur as a response of assemblages to habitat degradation and land cover alteration (Petsch, 2016, Siqueira et al., 2015). This replacement may lead to a functional homogenization (i.e., increasing species' feature similarities) (Mondy and Usseglio-Polatera 2014), which may, in turn, increase species' vulnerability to environmental changes and decrease resilience and/or resistance to disturbances (Olden et al., 2004). Therefore, understanding the consequences of community homogenization due to human activities and identifying the main drivers causing these changes are critical for basic science and conservation.

Biological traits and ecological requirements

A trait is defined as any morphological, physiological or phenological feature measurable at the individual level (Violle et al. 2007). These features are measurable properties of an organism and are divided into biological (e.g., life cycle, maximum body size, mobility, reproduction) and ecological (related to habitat preference, such as temperature and organic pollution tolerances) features, reflecting the adaptations of organisms to environmental conditions (Menezes et al. 2010). Functional traits can be defined as traits that influence organismal fitness (via their effects on growth, reproduction and survival) and the functioning of ecosystems (Violle et al. 2007) and can be used to assess community functional diversity (Petchey and Gaston 2006). Species traits have been suggested as an alternative or complementary approach to the more traditional taxonomic approaches used to elucidate

community changes in freshwater ecosystems and have provided numerous practical applications in river assessment (Statzner and Bêche 2010, Culp et al. 2011, Mondy et al. 2012). Moreover, functional traits have been proven to serve as a promising proxy for community or ecosystem function in response to various types of disturbance (Tilman et al. 1997, Verberk et al. 2013, Enquist et al. 2015, Gagic et al. 2015), such as changes in land use (Vandewalle et al. 2010, Dolédec et al. 2011). However, our understanding of the way in which the functional diversity of macroinvertebrate communities influences patterns and processes in freshwater ecosystems needs to be broadened (Schmera et al. 2017).

From an ecosystem management perspective, trait-based assessments are expected to offer several advantages and practical applications over taxonomy-based assessments (Culp et al. 2011). The linkage of trait responses to disturbance offer the following advantages: (i) The trait composition of assemblages is more spatially stable than the taxonomic composition, allowing for comparisons between different biogeographic regions, overcoming variations in site-specific taxonomic composition (Statzner et al. 2001, 2004); (ii) traits cover a broad range of responses to multiple stressors (Dolédec et al. 1999; Mondy et al. 2016); and (iii) traits allow a more mechanistic understanding that can give access to the causes of change (Culp et al. 2011, Verberk et al. 2013). Many studies, especially in Europe, (e.g., Usseglio-Polatera and Beisel 2002, Statzner et al. 2005, Dolédec et al. 2006, 2011, Archaimbault et al. 2010) have demonstrated that the multiple trait-based approach can better detect the impact of human activities on aquatic ecosystems compared to traditional methods (e.g., diversity indices or chemical analysis).

The processes driving the relationships between biological assemblages and their environment have been described using ecological theories. The 'Habitat Templet' (Southwood 1977) and its riverine adaptation, the 'River Habitat Templet' (RHT; Townsend and Hildrew (1994)), have emphasized that specific combinations of traits determine the ability of individuals to coexist in a local community under specific environmental conditions. Derived from these theories, the habitat-filtering hypothesis (Poff 1997) postulates that the least suitable sets of biological traits are eliminated in a given environment and that only taxa possessing traits that pass through the habitat filter will be present in the community. There is thus a higher correspondence between environmental conditions and trait composition than between

environmental conditions and species composition due to a filtering of traits. In this context, human disturbances represent additional environmental filters that can change the expected trait composition of assemblages in natural conditions (Floury et al. 2017).

Using a functional trait approach thus allows for assessments of the extent of niche occupation, the regularity of species traits within the assemblage, the level of functional specialization and redundancy, and the individual trait contribution to the assemblage structure (Villéger et al. 2008, Mouillot et al. 2013). Identifying how human pressures modify the trait composition of assemblages can improve our ability to predict patterns and processes in freshwater ecosystems and aid in the development of tools that complement traditional assessments for management actions and conservation initiatives (Jonsson et al. 2016; Pallottini et al. 2016).

GENERAL METHODOLOGY

This chapter is dedicated to the overall methodology used in this thesis. First, I give a short description of neotropical savannas and the procedures used to select the sampling sites. Then, I describe the laboratory activities, macroinvertebrate sampling and identification, and isotope analysis procedures. Finally, I explain how the environmental variables were quantified and how I built the trait database used in the analysis. The statistical analyses are further presented in the respective chapters.

Study area

Neotropical savanna

The neotropical region is one of the eight biogeographic realms constituting the Earth's regions and covers South and Central America and the Caribbean (Udvardy 1975). The Neotropics contain significant areas of tropical rainforests (e.g., the Amazon and Atlantic Forests), seasonally dry forests (e.g., Caatinga) and savannas (e.g., Cerrado) (Pennington et al. 2006).

The Cerrado biome (neotropical savanna) is the second largest in South America (after the Amazon). This biodiversity hotspot is one of the most threatened biomes in the world (Myers et al. 2000). The Brazilian Cerrado has been the object of increasing anthropic pressure for many years, but the effects of land cover and land use changes in this ecosystem have been largely overlooked, with very few research and conservation efforts (Beuchle et al. 2015).

Since the 1970s, this region has suffered heavy losses of natural vegetation due to agricultural expansion, with natural vegetation being replaced with pasture and row crop agriculture (Hunke et al. 2015). According to Pennington et al. (2006), the areas cleared in the Brazilian Cerrado greatly exceed those cleared in the Amazon rainforest (Figure 1). Such agricultural activities have altered 40% of the native terrestrial plant cover (Foley et al. 2005) and have reduced or removed the native riparian vegetation, thereby degrading the ecological integrity of aquatic ecosystems (Macedo et al. 2014).

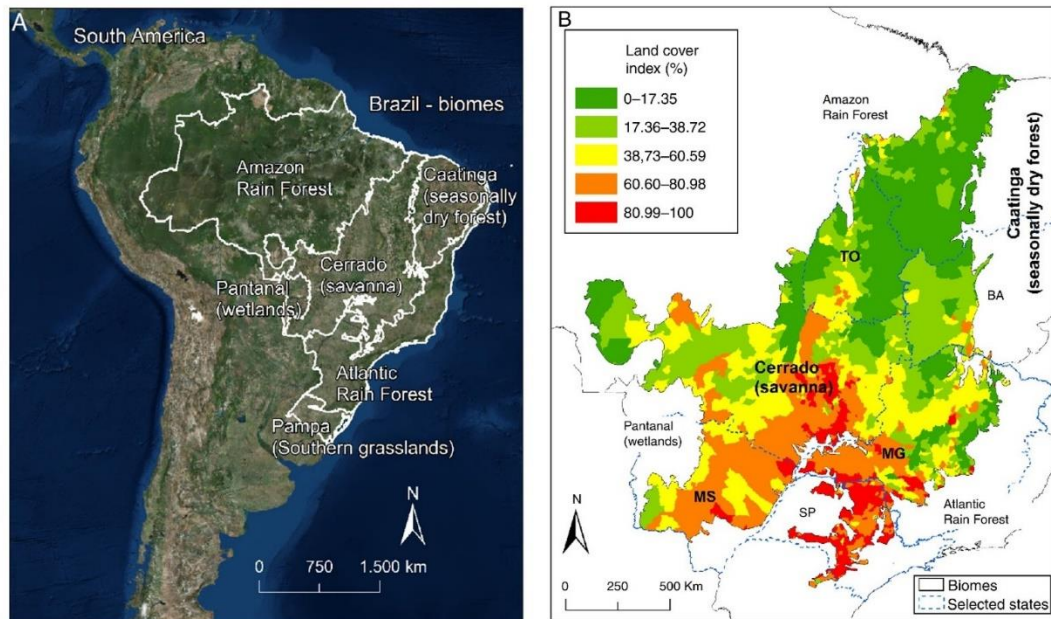


Figure 1: Original distribution of the Cerrado biome (Neotropical savanna) in South America (A) and the remnant area of Cerrado (year 2008) (B). In the land cover index, the lower the percentage value, the less human land conversion. Image adapted from Fernandes et al. (2016).

Hydrological units

Sampling campaigns were carried out in “wadeable streams” (rivers that can be crossed by feet for an average adult) of orders and dimensions of similar width and depth (Peck et al. 2006). Four sub-basins were selected in the Cerrado biome of the Minas Gerais state, upstream reservoirs of Nova Ponte (Araguari River Basin), Volta Grande (Grande River Basin), Três Marias (São Francisco River Basin) and São Simão (Paranaíba River Basin) (Figure 2). The four hydrological units were defined as the contributing drainage areas within 35 km upstream of each of four major hydropower reservoirs.

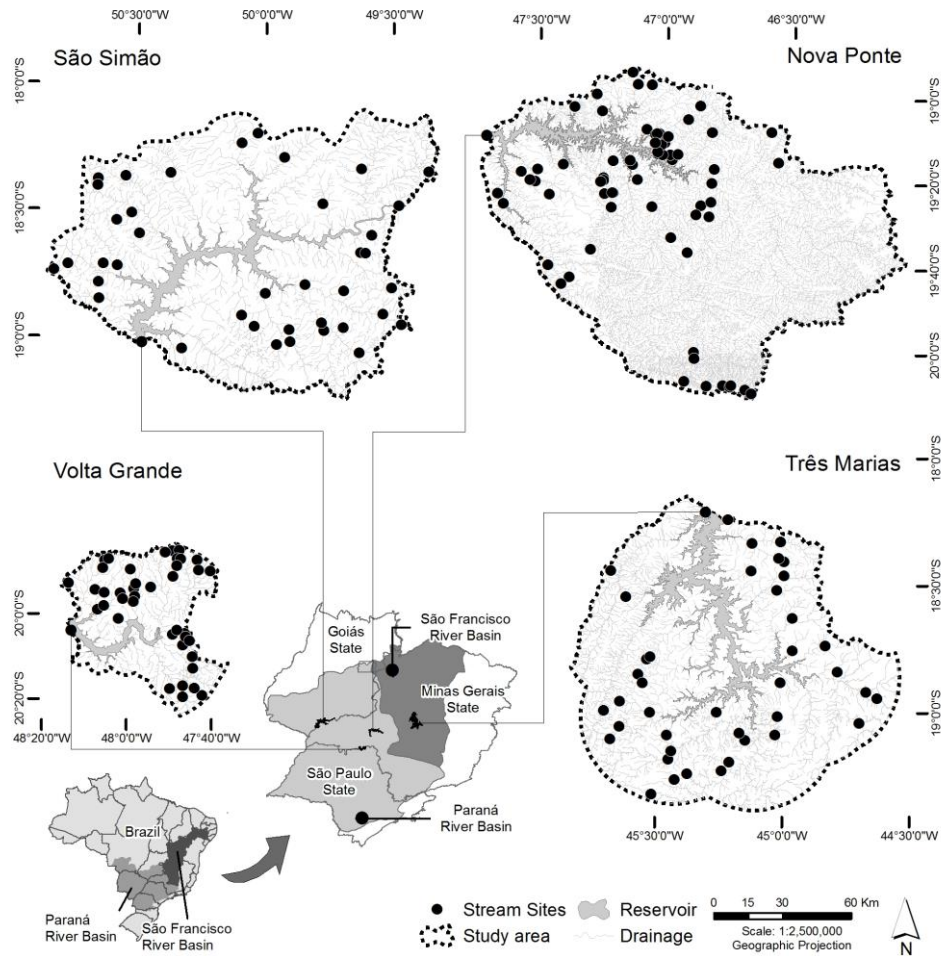


Figure 2: Locations of hydrological units and streams sites sampled in the Brazilian Neotropical savanna.

Sampling design

The site selection employed a spatially balanced probabilistic survey (Stevens and Olsen 2004) used by the U.S. Environmental Protection Agency (US-EPA) in its regional and national biomonitoring programs (Olsen and Peck 2008). In each of these hydrological units, 40 wadeable stream sites ranging from 1st to 3rd order were selected, totaling 160 randomly selected sites. In this approach, a master sample frame was first established using a digital hydrographical map (1:100,000 scale), and the sample sites were selected using a hierarchical, spatially weighted criterion (Stevens and Olsen 2004). We also included a set of 26 handpicked reference sites, considered to be the least-disturbed, located in Serra da Canastra National Park and the Serra do Salitre region in the Paraná River Basin (Nova Ponte hydrologic unit).

We sampled in September from 2010 to 2013, one year for each of the aforementioned hydrological units, ensuring that samples were all taken in the low flow season.



Figure 3: Some examples of headwater streams in the Cerrado biome showing different types of land use. Left side: least disturbed sites. Right side: disturbed sites. Image source: Laboratório de Ecologia de Bentos.

Stable isotope sampling

Within the São Simão hydrological unit, we selected 9 streams out of the 40 that were randomly selected for the collection of additional qualitative samples of macroinvertebrates and organic matter for stable isotopic analyses. We selected 3 streams in least-disturbed settings, 3 in pasture areas, and 3 in sugarcane areas. In those 9 streams, we considered the following: macroinvertebrates classified in different trophic functional groups (predators, scrapers, shredders, and filtering and gathering collectors), coarse particulate organic matter (CPOM), fine particulate organic matter (FPOM), periphyton, macrophytes, leaves from the riparian vegetation, and suspended particulate organic matter.

Invertebrate sampling and laboratory activities

We sampled aquatic insects at all 186 sites with a D-frame kick-net (30 cm aperture, 500 μ m mesh, and 0.09 m² area) for a total of 0.99 m² per site. Samples were collected along 11 equidistant transects on a systematic zigzag path throughout each site (minimum length of 150 m), as described in Hughes and Peck (2008), and samples were fixed in 4% formalin. We grouped all subsamples into a single pooled sample for each site. In the laboratory, the samples were sorted in different trays, and the organisms were identified at the family level under a stereoscopic microscope (Zeiss 32x) using taxonomic keys (Róldan-Pérez 1988, Merritt et al. 2008, Mugnai et al. 2010). The EPT individuals were identified at the genus level (Pes et al. 2005, Dominguez et al. 2006, Salles 2006, Mugnai et al. 2010) (Appendix 3).

Catchment land use and cover

We classified land use and cover within the upstream catchment of each site by interpreting a combination of high-resolution satellite images (0.6–5.0 m spatial resolution, Google Earth data: Google 2014) and Landsat multispectral satellite images (R4G3B2 false color band combination). The high-resolution images provided information about the shape and texture of the elements, and the multispectral images allowed for the distinction of vegetation

leaf structure. We identified four natural savanna cover types (woodland savanna, grassy-woody savanna, parkland savanna, and wetland palm swamp) (IBGE 2012) and four human-influenced land use (pasture, agriculture, eucalyptus forest, and urban areas) in the 186 sites (Appendix 2).

Physical habitat structure and water quality

At each site, the physical habitat was characterized using the standardized U.S. EPA field methods (Peck et al. 2006, Hughes and Peck 2008) adapted to neotropical savanna headwater streams by Callisto et al. (2014). At each site, we characterized the channel morphology, riparian structure, flow type, substrate type, and in-stream habitat cover (Kaufmann et al. 1999, 2009). The catchment and local scale were initially described by ~250 variables. We further eliminated those variables that had more than 90% zero values, low variability and high correlation with each other ($r > |0.8|$). These steps yielded a final set of 75 variables (Macedo et al. 2014). To assess the physical and chemical parameters of the water, we measured the temperature ($^{\circ}\text{C}$), electrical conductivity ($\mu\text{S cm}^{-1}$), pH, turbidity (NTU), and total dissolved solids (mg L^{-1}) in situ with a multi-probe (YSI, 650 MDS, model 6920). The total nitrogen (mg L^{-1}) and dissolved oxygen concentrations (mg L^{-1}) were determined from preserved water samples in the lab following Standard Methods (APHA 2005) (Appendix 2).

Isotopes analysis

All samples collected in the field were packed in a cooler with ice and subsequently frozen. At the laboratory, the samples of leaves, CPOM, FPOM, and macrophytes were dried at 60°C , ground, and stored in Eppendorf tubes. Periphyton and organic matter in suspension were filtered through glass fiber filters that had been calcined. Filters were dried, ground, and stored in Eppendorf tubes. Macroinvertebrate samples were washed and sorted. The organisms were then identified and classified according to their trophic functional groups and dried at 60°C for 48 h. The organisms were ground with the aid of a mortar and pestle and then stored in Eppendorf tubes.

Samples were sent to the Laboratório de Ecologia Isotópica in Centro de Energia Nuclear na Agricultura (CENA) of Escola Superior de Agricultura “Luiz de Queiroz” (ESALQ-USP), in Piracicaba, São Paulo. Isotopic analyses were performed (using a Thermo Finnigan Delta Plus mass spectrometer) by combusting samples under a continuous flow of helium in an elemental analyzer (Carlo Erba, CHN 1110). Ratios were expressed using the standard delta (δ) per mil notation:

$$\delta X = [(R_{\text{sample}}/R_{\text{standard}}) - 1] \times 10^3$$

where X is ^{13}C or ^{15}N and R are the $^{13}\text{C}:^{12}\text{C}$ or $^{15}\text{N}:^{14}\text{N}$ ratios of the samples and the standard.

Biological trait database

Neotropical literature

In the Neotropics, knowledge about the ecology and biological traits of tropical aquatic invertebrates is very scarce, despite some recent studies (Tomanova and Usseglio-Polatera 2007, Tomanova et al. 2008, Reynaga and Santos 2013, Dedieu et al. 2015, Milesi et al. 2016). In Brazil, few studies have considered multiple trait-based approaches (e.g., Colzani et al. 2013, Saito et al. 2015b, 2015a). However, these studies have generally used trait databases designed for temperate regions (e.g., Poff et al. 2006, Vieira et al. 2006), even though the characteristics of taxa may greatly differ between regions.

I carried out an intensive survey of the literature, and the biological trait structure of the invertebrate assemblage was described using 28 categories of 7 biological traits (Table 1). I used trait information that was available exclusively for neotropical macroinvertebrates (Baptista et al. 2006, Tomanova and Usseglio-Polatera 2007, Reynaga and Santos 2012, Dedieu et al. 2015). Biological traits and their respective trait categories described the EPT genus profile in terms of its morphology, life-cycle features, resilience, resistance to disturbance and feeding behavior (Appendix 1). This database represents the best available trait knowledge on Brazilian EPT.

Table 1. Traits and their categories used for 73 EPT genera collected in Neotropical savanna streams.

Trait	Category
Body size (mm)	<1.5
	1.5 - 2.5
	2.5 - 3.5
	3.5 - 5.0
	5.0 - 10.0
	>10
Potential number of reproductive cycles per year	< or = 1
	> 1
Feeding habits	Collector-Gatherer
	Shredder
	Scraper
	Collector-Filterer
	Predator
Locomotion	Burrower
	Climber
	Sprawler
	Clinger
	Swimmer
Body flexibility (°)	<10
	>10-45
	>45
Body form	Streamlined
	Flattened
	Cylindrical
	Spherical
Relation to substrate	Free living
	Silk net builders
	Case builder

Fuzzy coding

The affinity of each taxon for each trait category was described using a fuzzy coding approach (Chevenet et al. 1994). In this method, a score from 0 to 3 is assigned to each taxon in the categories as follows: 0 – no taxon affinity for the category; 1 – weak affinity; 2 – moderate affinity; and 3 – high affinity. This technique helps to compensate for different levels of information coming from diverse sources and variations that may exist within species due to the variable requirements of different developmental stages (Chevenet et al. 1994).

To determine the body size of each EPT genus, measurements were taken of the invertebrate linear body lengths (from the head to the end of the abdomen) using a stereomicroscope of ~10% of all EPT organisms sampled from the four HUs studied. Such measurements were then classified into 6 categories (Table 1) (Appendix 4).

OBJECTIVES AND STRUCTURE OF THE THESIS

From a macroecological perspective, specific evidence of how trait patterns vary along different environmental gradients in different geographical regions would provide useful knowledge about the overall patterns of trait response (Heino et al. 2013). Most past studies of trait-environmental and trait-spatial relationships have focused on streams in different regions and biomes around the world, such as in temperate (e.g., Bêche et al. 2006, Göthe et al. 2017), boreal (e.g., Heino 2005), and tropical forests in Asia (Ding et al. 2017) and South America (e.g., Colzani et al. 2013), but no studies have yet been undertaken in the neotropical savanna region, which is both a biodiversity hotspot and poorly studied region. The characteristics of similar taxa have been shown to differ between different continents (Serra et al. 2017).

The main objective of this thesis was to assess how land cover and land use in natural and human-impacted situations affected the taxonomic and trait compositions of aquatic invertebrate assemblages and trophic relationships and whether neotropical savanna headwater streams behave differently from other streams worldwide. I used stable isotopes, in-stream habitat and landscape data from analyses of satellite imagery, and the taxonomic and trait composition of EPT assemblages to investigate three interrelated sets of questions (Figure 3):

(1) How do the intensity of land use and the associated changes in land cover affect the energy flow and the trophic relationships among benthic macroinvertebrate communities? (Chapter 1).

(2) How do the catchment and local-scale variables contribute to shaping the EPT taxonomic and trait composition? (Chapter 2).

(3) How do EPT assemblages change with human impairment in terms of taxonomic composition, diversity and functional traits? (Chapter 3).

Chapter 1 was published in PlosOne, Chapter 2 was published in Freshwater Biology and the third chapter is under review in an international journal.

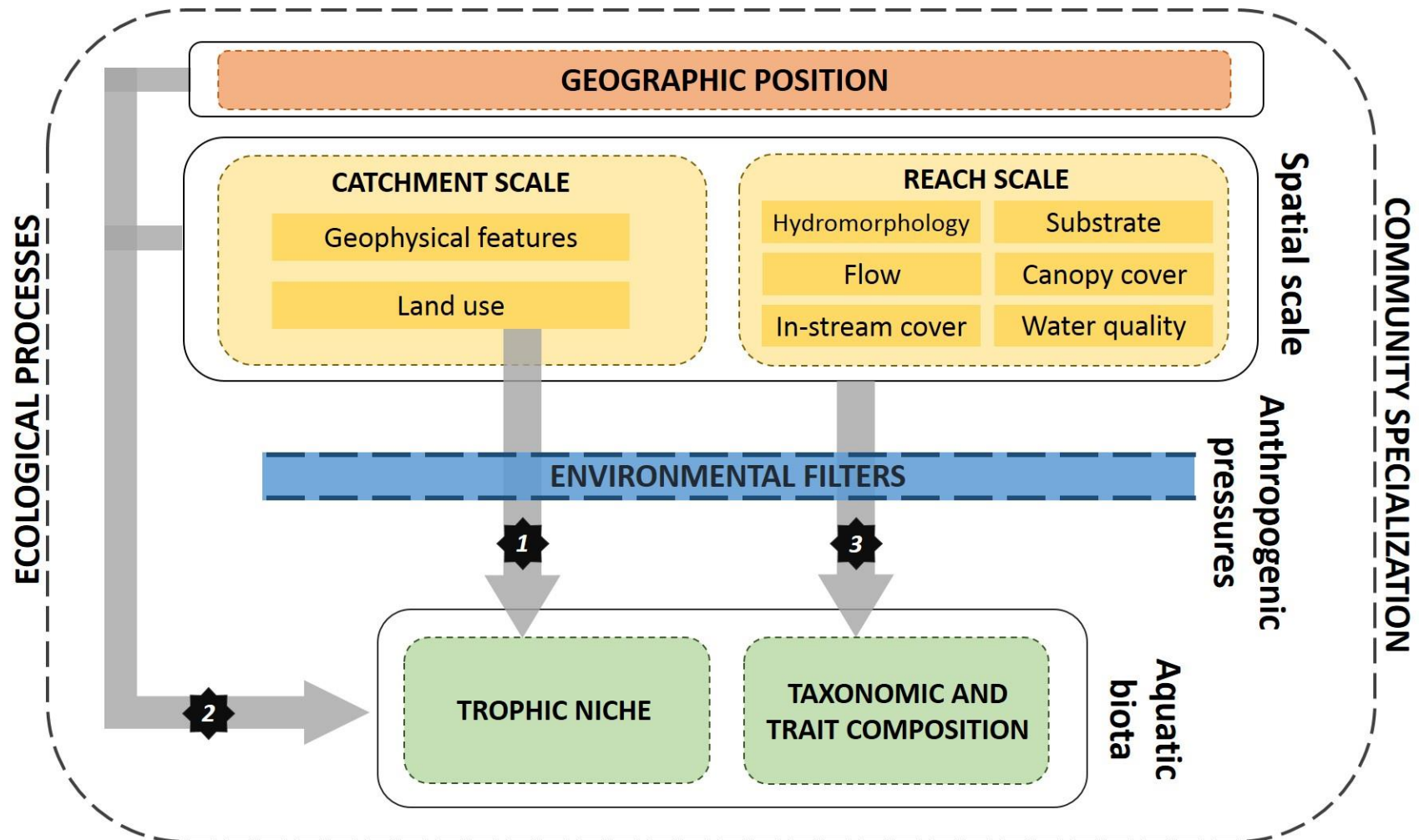


Figure 3: Methodological framework representing the overall thesis structure and links among chapters. The numbers 1-3 are related to each chapter of the thesis.

Chapter I

Land use influences niche size and the assimilation of resources by benthic macroinvertebrates in tropical headwater streams

Chapter 1 is a version of the following paper: Castro, DMP., Carvalho, DR., Pompeu, PS., Moreira, MZ., Nardoto., Callisto, M. (2016) Land use influences niche size and the assimilation of resources by benthic macroinvertebrates in tropical headwater streams. PLoS ONE 11(3):e0150527. doi: 10.1371/journal.pone.0150527

RESEARCH ARTICLE

Land Use Influences Niche Size and the Assimilation of Resources by Benthic Macroinvertebrates in Tropical Headwater Streams

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Abstract

It is well recognized that assemblage structure of stream macroinvertebrates changes with alterations in catchment or local land use. Our objective was to understand how the trophic ecology of benthic macroinvertebrate assemblages responds to land use changes in tropical streams. We used the isotope methodology to assess how energy flow and trophic relations among macroinvertebrates were affected in environments affected by different land uses (natural cover, pasture, sugar cane plantation). Macroinvertebrates were sampled and categorized into functional feeding groups, and available trophic resources were sampled and evaluated for the isotopic composition of ^{13}C and ^{15}N along streams located in the Cerrado (neotropical savanna). Streams altered by pasture or sugar cane had wider and more overlapped trophic niches, which corresponded to more generalist feeding habits. In contrast, trophic groups in streams with native vegetation had narrower trophic niches with smaller overlaps, suggesting greater specialization. Pasture sites had greater ranges of resources exploited, indicating higher trophic diversity than sites with natural cover and sugar cane plantation. We conclude that agricultural land uses appears to alter the food base and shift macroinvertebrate assemblages towards more generalist feeding behaviors and greater overlap of the trophic niches.

Introduction

Tropical streams are among the most threatened ecosystems in the world [1], especially in developing countries [2]. In recent decades, these environments have been experiencing substantial changes in land use and occupation. Such changes include replacing native vegetation with large-scale agricultural activities and poorly planned urban expansion.

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Those changes in turn have resulted in alarming losses of biodiversity in aquatic ecosystems, especially in tropical streams [1,3]. The Cerrado (neotropical savanna) is the second largest biome in South America (after the Amazon), a biodiversity hotspot [4] and one of the most threatened biomes in the world, mainly because of the replacement of natural vegetation with pasture and row crop agriculture [5,6]. Those agricultural activities currently alter 40% of the native terrestrial plant cover [7] and have reduced or removed the native riparian vegetation, thereby degrading aquatic ecosystem ecological integrity [8].

The replacement, reduction or removal of vegetation cover, especially in riparian areas, leads to the degradation of physical habitat structure, increased sedimentation rates, hydrological changes, and water temperature oscillations [9,10]. These changes directly influence the input of nutrients, allochthonous resources, autochthonous production [10], the quantity and quality of available food resources [9], and may simplify trophic structure and reduce biological diversity [11,12]. Therefore, studies addressing the impacts of changes in vegetation cover on the energy flow and trophic relations in aquatic environments are essential to an understanding of the mechanisms that regulate the ecological integrity of those environments.

In freshwater ecosystems, aquatic invertebrates are the main link between primary producers (e.g., periphyton and aquatic macrophytes) and higher trophic levels (e.g., aquatic vertebrates). By breaking down organic matter, they contribute to litter decomposition and nutrient availability for other organisms [13,14]. Aquatic macroinvertebrates may be classified according to their feeding habits into functional feeding groups (FFG) [15] based on morphological and behavioral characteristics [16]. Those groups include the following: (i) scrapers that feed on organic matter adhered to organic and inorganic substrates (e.g., periphyton, algae and their associated microbiota); (ii) shredders that feed directly on coarse particulate organic matter (CPOM); (iii) gathering-collectors that feed mainly on deposited fine particulate organic matter (FPOM); (iv) filtering-collectors that filter fine suspended organic matter; and (v) predators that feed on whole animals or their parts [14,16].

Macroinvertebrate assemblages are sensitive to environmental conditions and reflect the physical and chemical conditions of the ecosystem [17]. Therefore, analyzing trophic relationships among macroinvertebrates and the energy flow in aquatic ecosystems is required to understand assemblage structure and dynamics and ecosystem functioning [18].

The energy flow and trophic relationships among the organisms in an ecosystem may be assessed using stable isotope analysis (SIA) of carbon (C) and nitrogen (N) [19]. The ratios between stable isotopes of ^{13}C and ^{12}C (expressed relative to a standard and called $\delta^{13}\text{C}$) and of ^{15}N and ^{14}N (expressed relative to a standard and called $\delta^{15}\text{N}$) provide information that incorporates spatio-temporal scales and facilitates the analysis of food assimilation by consumers [20] and the definition of their trophic niches [21,22]. Stable isotope analysis has been an important and advantageous tool in trophic ecology studies [23] to examine resource partitioning [24], ecosystem fluxes of carbon and nitrogen [25], to reconstruct diets [26,27] and to characterize niche properties [22,28].

The $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values in consumers reflect the C and N stable isotope ratios of the food sources [20]. The ^{13}C enrichment between food sources and consumers is usually low (0–1‰) [29,30]. Because $\delta^{13}\text{C}$ values typically differ among basal sources (e.g., plant material from C3 and C4 plants), $\delta^{13}\text{C}$ is used as an indicator of C sources for certain consumers along food chains [18,20]. In contrast, the trophic fractionation of $\delta^{15}\text{N}$ usually varies from 2 to 4‰ at each trophic level [29,30], facilitating definition of the total length of the food chain and the position of an organism within it [18,31]. Therefore, the isotopic ratios of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ in animal tissues reflect information on their use of physical habitats and trophic characteristics and are currently used to determine organic matter origin, trophic relationships and niche size and overlap [22,28].

The relative contributions of food resources to the diet of an animal may be calculated using isotope mixing models [32]. However, most of food webs are too complex and the number of food sources exceeds the number of useful isotope tracers by more than one. In this case, the model does not generate exact values for proportional contributions of each source, but instead provides a range of possible contributions or feasible solutions [19]. Recently Bayesian mixing models have been proposed to assess stable isotope data (e.g., [33–36]) through the use of statistical distributions to characterize the uncertainties in food sources, consumer isotopic values, and estimated source contributions [19].

The isotopic C and N signatures of consumers in aquatic ecosystems may vary because of changes in riparian zones, which provide most of the organic matter used by aquatic communities [27]. In addition, riparian vegetation stabilizes stream banks and filters excessive inputs of materials (e.g., fine sediments) and nutrients (e.g., manure and fertilizers used in surrounding plantations) to the waterbodies [9,37]. Therefore, variations in riparian vegetation cover influence the dynamics and structure of aquatic communities (e.g. [38,39]), changing the isotopic composition of resources and consumers. In turn, those isotopic signatures aid comparisons of the ecological processes in riparian zones, identification of the effects of agriculture and deforestation on assemblages, and assessments of the interactions between riparian land cover and water bodies [20,40].

In this study, we evaluated how the energy flow and the trophic relationships among benthic macroinvertebrates were influenced by riparian land uses (natural vegetation, pasture, sugar cane plantation). Based on C and N stable isotope analyses, we compared isotopic niche breadth and the degree of niche overlap among macroinvertebrate trophic groups. We first tested whether anthropogenic activities in areas adjacent to streams can expand the trophic niche of macroinvertebrates and their degree of overlap. Then, we assessed whether anthropogenic land uses in riparian zones were associated with more generalist trophic groups and less specialized trophic groups compared with streams with native riparian vegetation.

Materials and Methods

Study area

We studied sites in tributaries of the São Simão Hydroelectric Power Plant Reservoir, located in the sub-basin of the Paranaíba River, southeastern Brazil (Fig 1). The Paranaíba River basin is the second largest drainage basin of the Paraná River basin, corresponding to a drainage area of 223 km² (25.4% of its area) [27].

Nine 2nd- and 3rd-order streams (on a 1:100,000 scale map) located in the states of Minas Gerais and Goiás were selected from 110 previously investigated streams [41]. We used a hierarchical and spatially balanced sampling algorithm (e.g., [8]) proposed by Olsen & Peck [42] to select those 110 sampling sites. The nine streams were selected according to their land use, where three were located in pasture areas, three were located in sugar cane plantation areas, and three were representative of natural riparian vegetation. A continuous segment proportional to the width of the stream (defined as 40 times the mean stream width, minimum of 150 meters) was sampled in each stream. We sampled available trophic resources and aquatic macroinvertebrates during the dry season (September) of 2012. We evaluated the land use of the riparian zones of the sites through use of satellite images [43]. For the nine sites, we determined the percentages of natural cover, pasture, and sugar cane plantations in a 150 m radius buffer around the upstream limit of each site [27]. To illustrate the variation in the physical habitat structure of streams with different land uses, environmental characteristics of each site were quantified (S1 Table) and are detailed in Carvalho et al. [27].

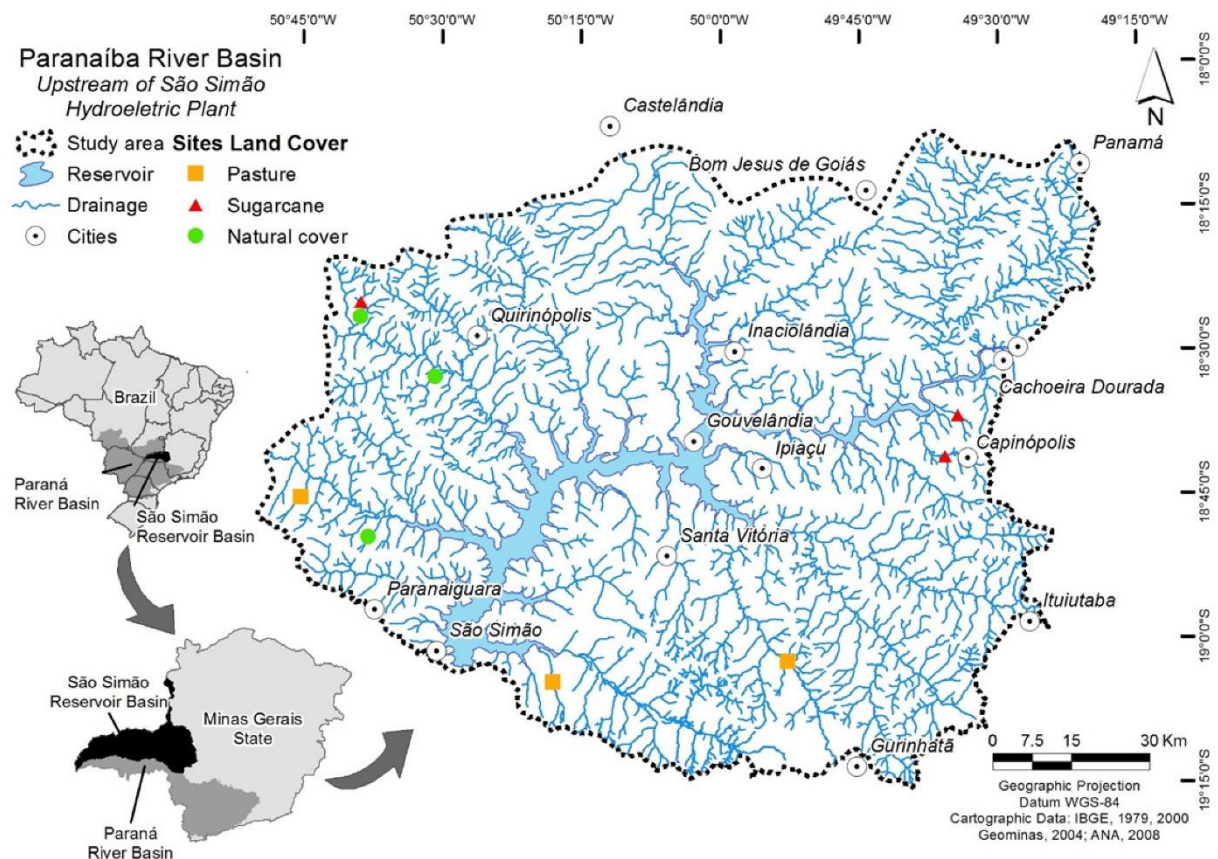


Fig 1. Locations of the nine stream sites selected according to their land use and study area in the states of Minas Gerais and Goiás, Brazil.

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Sample collection and processing

Each stream was subdivided into five equally sections. We collected five independent samples (one per section) of benthic macroinvertebrates from each site, along with five independent samples of food resources: CPOM, FPOM, filamentous algae, periphyton, leaves of the riparian vegetation (forest, pasture, sugar cane) and suspended particulate organic matter (seston). Only one site had aquatic macrophytes; therefore, macrophytes were not considered as resources in the analyses. We collected algae, CPOM, periphyton, FPOM, leaves of native riparian vegetation and seston from sites in all three types of riparian environments, whereas pasture grasses were collected only in the pasture environment and sugar cane leaves only in the sugar cane environments (S2 Table).

We collected benthic macroinvertebrates assemblages through use of D-frame kick-nets (30 cm aperture, 500 mm mesh), following a systematic zig-zag pattern along the segments defined [44], covering all different substrates and habitats in each site. Five sample units (0.09 m² each) were taken per stream, one per section, totaling 0.45 m² per site. All invertebrates sampled were stored on ice and after 2 days processed in laboratory. In the laboratory, the organisms collected were washed in distilled water, taxonomically identified [16,45,46] and classified into

Table 1. Taxa used in each trophic group analyzed. The letter “n” indicates the number of samples. Different numbers of invertebrates were used for each sample to reach a minimal amount of material for isotope analysis.

Consumers	Natural cover	(n)	Pasture	(n)	Sugar cane	(n)
Collectors	Chironomidae	4	Baetidae	2	Chironomidae	4
	Elmidae (larvae)	9	Chironomidae	3	Elmidae (larvae)	10
	Leptohyphidae	2	Elmidae (larvae)	6	Leptohyphidae	1
			Leptohyphidae	1		
Filter-feeders	Hydropsychidae	11	Hydropsychidae	11	Hydropsychidae	11
	Philopotamidae	3	Leptoceridae	3	Simuliidae	4
	Simuliidae	1	Simuliidae	1		
Shrimp-shredders	Palaemonidae	13	Palaemonidae	7	–	
Insect-shredders			Calamoceratidae	2	Calamoceratidae	1
	–		Odontoceridae	1	Odontoceridae	1
			Pyralidae	3	Pyralidae	1
Scrapers	Elmidae (adult)	6	Ampullariidae	2	Elmidae (adult)	6
	Leptophlebiidae	7	Elmidae (adult)	7	Leptophlebiidae	4
	Psephenidae	2	Leptophlebiidae	3	Planorbidae	4
Predators	Megaloptera	6	Megaloptera	3	Belastomatidae	1
	Naucoridae	2	Naucoridae	3	Megaloptera	3
	Odonata	6	Odonata	8	Naucoridae	2
	Perlidae	1	Perlidae	1	Odonata	8
					Perlidae	1

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functional feeding groups: predators, scrapers, shredders, gathering-collectors (hereafter “collectors”) and filtering-collectors (hereafter “filter-feeders”) [47–49]. Shredders were divided into insect-shredders (Insecta) and shrimp-shredders (Crustacea) because shrimp-shredders may have a generalist omnivore behavior, feeding on multiple resources [50]. Each macroinvertebrate functional feeding group was considered a consumer, whereas the periphyton, filamentous algae, seston, FPOM, CPOM and vegetation leaves were considered resources. The other macroinvertebrate functional feeding groups were considered as resources for predators. It was not always possible to obtain five samples of each functional feeding group or food resources in each site (e.g. just three samples of insect-shredders in the pasture areas), therefore, a total 232 food resource samples and 202 macroinvertebrate samples (among 270 possible: 9 sites x 5 samples x 6 resources / FFG) were obtained and analyzed. The last author, MC, has a permanent license to collect aquatic invertebrates (10365–2) in the entire Brazilian territory provided by IBAMA/Sisbio, in accordance with federal law and the regulations of the Brazilian Environmental Ministry. The sampling sites were private, and permission from the owner or manager was obtained prior to sampling. None of the sampled species was protected by Brazilian law or red-listed.

After identifying and classifying in functional feeding groups, organisms were then oven-dried at 60° for 48 h, ground to a fine and homogeneous powder using a mortar and pestle and then stored in Eppendorf tubes for subsequent analysis of their isotopic compositions. Collector, filter-feeder, predator and scraper consumers were found at sites in all three types of riparian environments, whereas shrimp-shredders were not found in the sugar cane sites and insect-shredders were not found in natural cover sites. Each FFG sample was composed of only one specific family and different numbers of invertebrates were used for each sample to reach a minimal amount of material for isotope analysis (Table 1).

Sampling of resources was carried out in parallel to macroinvertebrates collecting along the segments defined in each site. Periphyton was collected by scraping rocks with a brush (three rocks per segment) and placing the material in a plastic container with distilled water [44]. Seston was collected with a phytoplankton net (0.45 mm) set for 1 min upstream of each site. The samples were stored in coolers with ice after sampling and then transported to the laboratory, where they were kept frozen until processing. In the laboratory, the samples were filtered using a filtration apparatus coupled to a vacuum pump with calcined glass fiber filters (Millipore 45 μm). Filamentous algae was collected manually in each segment, stored in plastic containers in ice coolers and then frozen. The FPOM samples were collected from sediment deposits revolving the sediment and passing a phytoplankton net (0.45 mm) in the material in suspension. After the material was stored in plastic containers and then frozen. Pasture leaves, sugar cane leaves, and leaves of the natural riparian vegetation were manually collected along the segments delimited in each sampled stream, with the most common species being prioritized at the site. Species prioritization was made in compliance with the most common and abundant species in each segment. Five leaves were then collected from each of the five most common plants. We obtained samples of native riparian vegetation even at sugar cane and pasture sites. The CPOM was randomly collected from leaf litter deposits in the streams. All leaves were then stored in paper bags and kept in plant presses until processing in the laboratory. In the laboratory, all resource samples were dried in an oven at 60°C for 48 h and then ground with a mortar and pestle and stored in Eppendorf tubes. Approximately 2–5 mg of dried animal tissue and 5–10 mg of resources were used for the isotopic analysis.

All samples were sent to the Laboratory of Isotope Ecology of the Center for Nuclear Energy in Agriculture (Centro de Energia Nuclear na Agricultura—CENA), University of São Paulo (Universidade de São Paulo), Piracicaba, Brazil, for determination of the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values. Analyses of isotopic ratios were processed through sample combustion under a continuous flow of ultrapure helium in an elemental analyzer (Carlo Erba, CHN-1110) that was coupled to a Thermo Finnigan Delta Plus mass spectrometer for isotopic ratios. The results were expressed in delta notation (δ), in parts per thousand (‰), relative to standard international references (V-PDB—Vienna Pee Dee Belemnite for C and atmospheric air for N), and were calculated using the following equation:

$$\delta X = [(R_{\text{Sample}}/R_{\text{Standard}}) - 1] \times 10^3$$

where X is ^{13}C or ^{15}N and R represents the isotopic ratios $^{13}\text{C}/^{12}\text{C}$ or $^{15}\text{N}/^{14}\text{N}$ [25]. The analytical precision values estimated by replicates of the working standards of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ were ± 0.10 and ± 0.11 ‰, respectively.

When using stable isotope data to reconstruct animal diets, the resources must have isotopically distinct signatures to ensure a sensitive interpretation of the results. If they are not significantly different and are somehow logically related (e.g., same taxon or trophic group), the resources may be combined and represented in the mixing model by a single set of isotopic values [51]. The $\delta^{13}\text{C}$ values of samples of the riparian vegetation and CPOM deposited in the streams were very similar among the environments; therefore, the values of the riparian vegetation samples were excluded from the analyses. The FPOM and the seston samples also had similar $\delta^{13}\text{C}$ values and were grouped; hereafter, those groups are called fine particulate organic matter (FPOM).

Data analysis

We used the SIAR package for the analysis of stable isotopes [34,52] in R [53], to determine the relative contribution of each food resource available for the macroinvertebrates. Differences in the isotopic ratios of the food resources and consumers among environments were tested using

one-way analyses of variance (ANOVAs) when the normality and homoscedasticity assumptions were met. The nonparametric Kruskal-Wallis test was used for data with non-normal distribution.

In the partition analysis, the food resources of each land use category were considered separately to determine the contribution of each resource for the consumers. The mean value of the food resources in all categories was used to visually represent the spatial distribution of the taxa according to their $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values. The fractionation values used were $0.5 \pm 0.13\text{‰}$ for C and $2.3 \pm 0.18\text{‰}$ for N [29]. The trophic structure of the benthic macroinvertebrate assemblage was described for each land use using the metrics proposed by Layman et al. [21]. Those metrics use the stable isotope ratios of the different components of the food chain to describe the niche and trophic structure of the assemblage, providing information on the trophic diversity and redundancy within a food chain [54]. However, one of the limitations of using the metrics originally proposed by Layman et al. [21] is that those metrics are sensitive to the sample size and may not be comparable between studies and different sites. A second limitation is that the metrics, when applied to an assemblage, do not incorporate any natural variability within the system and, thus, provide only a point estimate of each metric [55].

A Bayesian approach recently developed for the aforementioned metrics enables the distribution of the sampling errors of the means estimated for the members of the assemblage. Using that approach, we generated a posterior distribution of the estimates of those metrics, providing a measure of uncertainty and allowing statistical comparisons among assemblages [54,55]. Thus, we calculated the five macroinvertebrate assemblage metrics through use of the Stable Isotope Bayesian Ellipses package in R (SIBER; [55]): 1) $\delta^{13}\text{C}$ range (CR_b) and $\delta^{15}\text{N}$ range (NR_b), which together indicate the variety of resources exploited by the assemblage. 2) The mean distance to centroid (CD_b), which is the mean Euclidian distance of each assemblage component to the centroid, indicating the trophic diversity within the food chain. 3) The mean nearest neighbor distance (MNND_b), which is the mean Euclidean distance from each group to its nearest neighbor in the $\delta^{13}\text{C}$ - $\delta^{15}\text{N}$ bi-plot space (plotted based on their mean stable isotope signatures), an estimate of the total density and clustering within the assemblage. Low MNND values indicate an increase in trophic redundancy, i.e., the occurrence of many groups with similar trophic levels. 4) The standard deviation of the nearest neighbor distance (SDNND), which measures the uniformity of the groups in bi-plot space, where lower SDNND values suggest a more uniform trophic niche distribution [21]. We calculated the metrics originally proposed by Layman et al. [21] and reformulated in a Bayesian framework by Jackson et al. [55] for each site, enabling a comparison of the structure and trophic ecology of each land use. Results were then compared between land uses based on the visual analysis of the credible intervals (CIs) of the Bayesian implementation of the Layman metrics. We estimated the standard ellipse area (SEA_c , in ‰^2) as a bivariate measure of the central mean of the isotopic niche [55]. The SEA_c enables calculating the degree of niche overlap of the assemblage (in %, where 100% indicates total overlap) and may be used as a quantitative measure of diet similarity among the different groups [56]. All measures were bootstrapped ($n = 10,000$, indicated by the letter “b”) to compare groups with different sample sizes. A small sample size correction (indicated by the subscript letter “c”) was applied to increase the accuracy of the comparisons, enabling the comparison of niches of groups with different sample sizes [55].

Results

Differences in the isotopic signatures of resources and consumers among land uses

The isotopic signatures of the food resources studied varied widely among and within land use types (Fig 2). In the natural cover sites, the periphyton and FPOM exhibited the highest $\delta^{13}\text{C}$

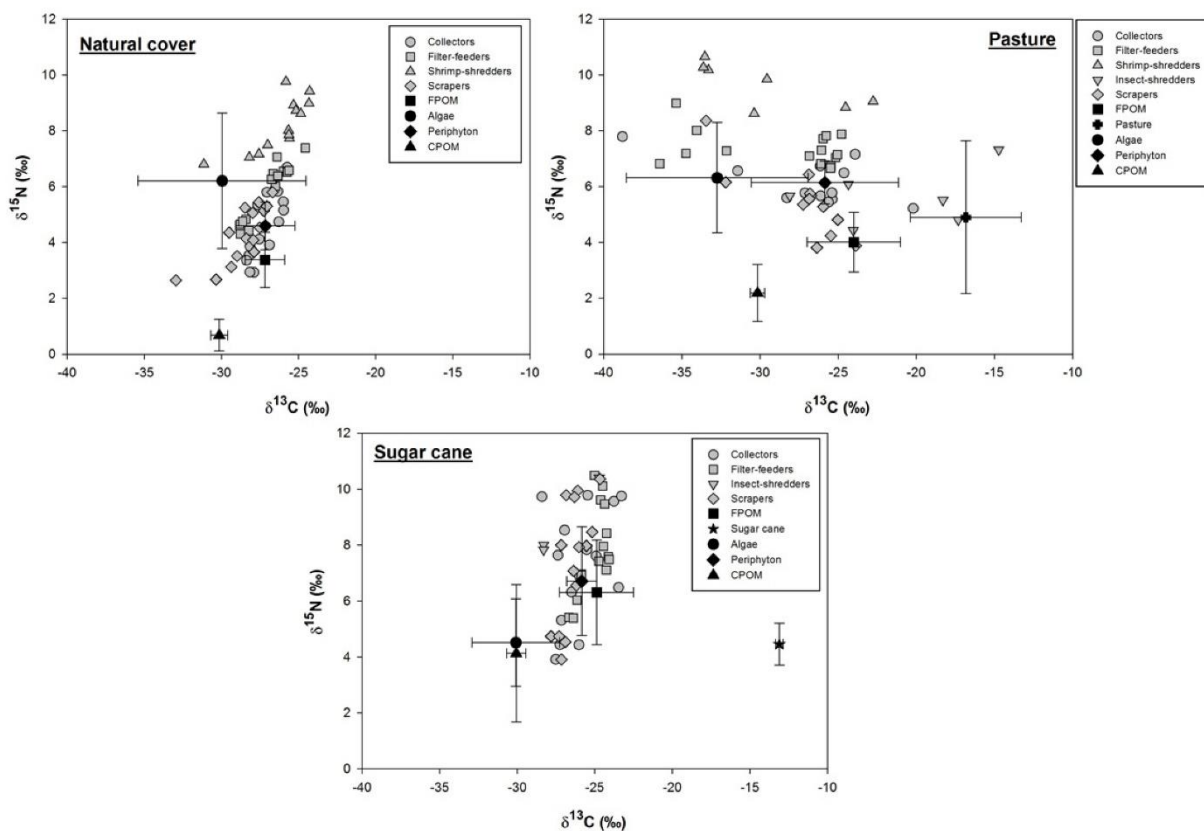


Fig 2. Representation of the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of food resources (mean $\pm$ SD) and consumers in sites with different riparian land uses.

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values, whereas CPOM had the lowest values. The pasture and sugar cane plants exhibited the highest $\delta^{13}\text{C}$ values, whereas CPOM and algae had the lowest $\delta^{13}\text{C}$ values (Fig 2). CPOM had the lowest $\delta^{15}\text{N}$ values in all land uses, algae exhibited the highest $\delta^{15}\text{N}$ values in the natural cover and pasture sites, and periphyton had the highest $\delta^{15}\text{N}$ values in sugar cane sites (Fig 2).

The consumers also exhibited wide variations in isotopic composition among land uses and functional feeding groups (Figs 2 and 3). In the natural cover sites, shrimp-shredders had the highest $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values, whereas scrapers had the lowest $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values. In pasture sites, insect-shredders had the highest $\delta^{13}\text{C}$ values, whereas shrimp-shredders and filter-feeders had the lowest $\delta^{13}\text{C}$ values. Also shrimp-shredders exhibited the highest $\delta^{15}\text{N}$ values, whereas scrapers and insect-shredders had the lowest $\delta^{15}\text{N}$ values (Figs 2 and 3). In sugar cane sites, predators (on average) exhibited the highest $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values (Fig 3, S2 Table), whereas the lowest $\delta^{13}\text{C}$ values were recorded for insect-shredders, and the lowest $\delta^{15}\text{N}$ values were recorded for collectors and scrapers (Fig 3).

Feeding contribution in each stream category

There was wide variation in the proportion of items assimilated by the functional feeding groups among the three land uses assessed. Sites with natural vegetation cover supported

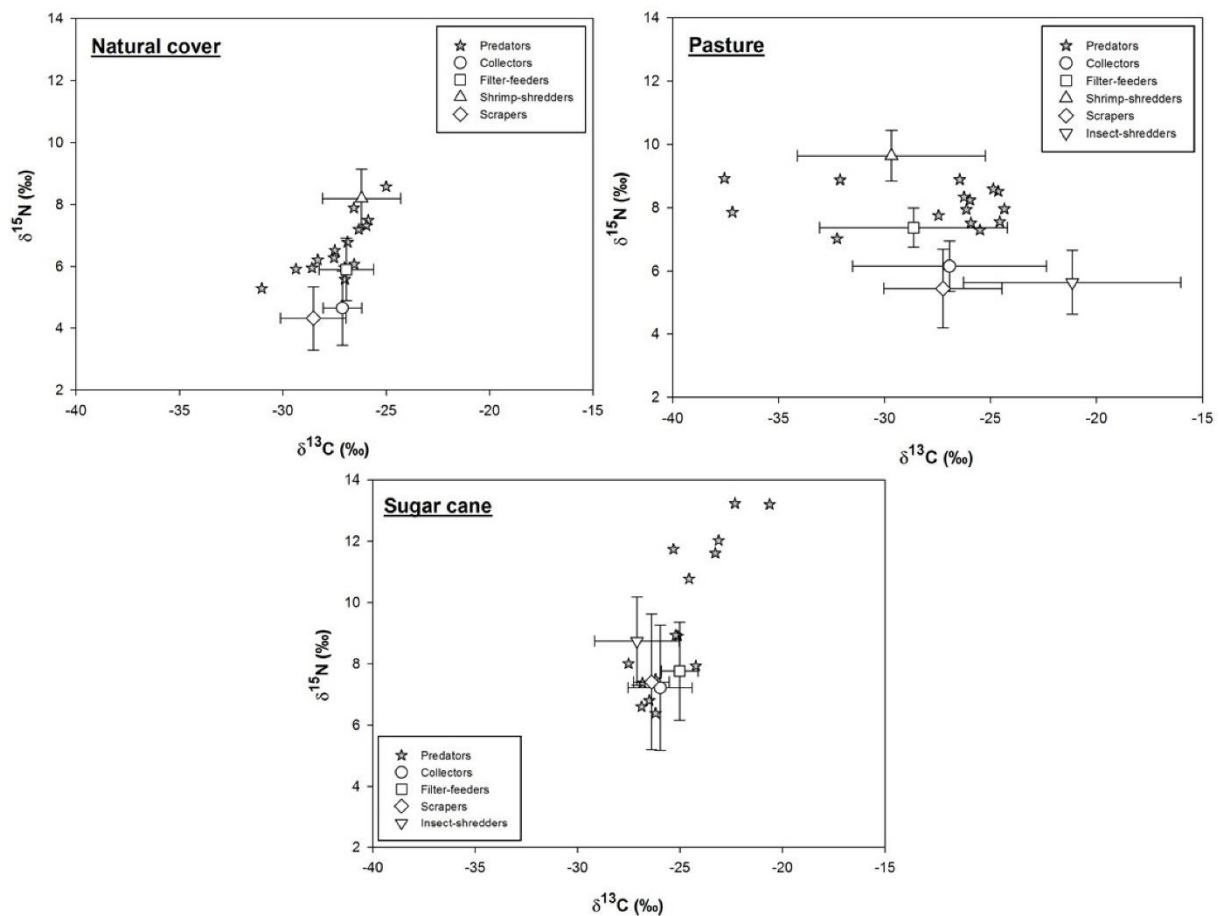


Fig 3. Representation of the $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of prey (mean $\pm$ SD) and predators in sites with different riparian land uses.

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macroinvertebrate assemblages with more specialist trophic habits. Collectors and filter-feeders assimilated 44–49% FPOM, scrapers assimilated 57% CPOM, and shrimp-shredders assimilated 83% algae and periphyton as opposed to CPOM (Fig 4A, S3 Table).

Some functional groups showed greater specificity for certain food resources in pasture streams. Collectors and scrapers assimilated 38–49% CPOM, whereas the filter-feeders assimilated 58% algae and periphyton. The insect-shredders assimilated nearly equal amounts of CPOM, FPOM, and pasture grasses. However, the shrimp-shredders continued assimilating mainly algae and periphyton (Fig 4B, S3 Table).

All functional feeding groups had more generalist trophic habits in the sugar cane sites, and none assimilated a single resource in particular. In addition, the sugar cane leaves contributed only 7–15% to the diets of macroinvertebrates (Fig 4C, S3 Table).

Predators had a pattern similar to that of the other trophic groups in the sugar cane sites, with no preferentially assimilated resource. Predators assimilated 40% and 53% scrapers in pasture sites and sites with natural cover, respectively (Fig 5, S4 Table).

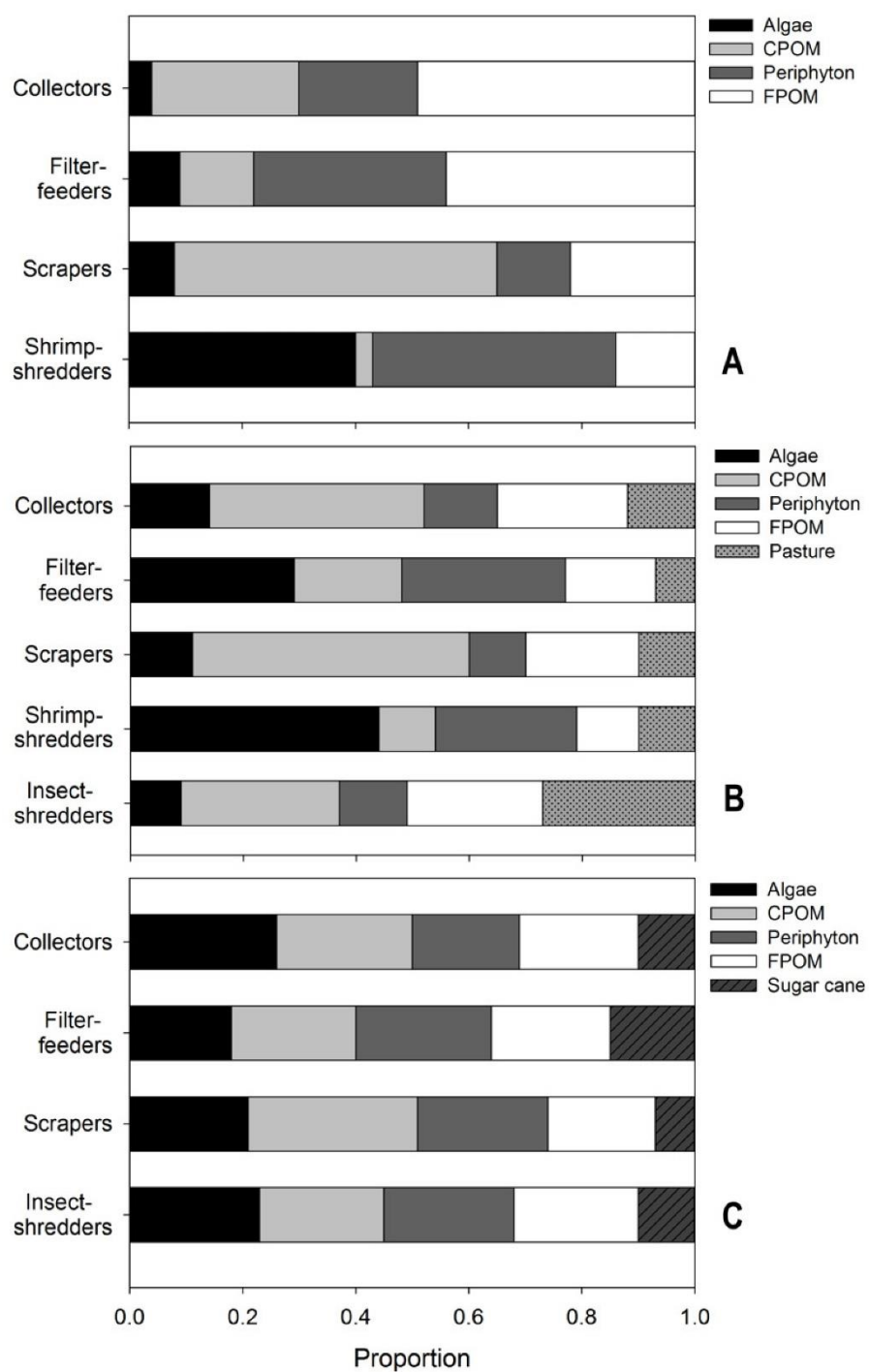


Fig 4. Means of the proportions of food resources used by each trophic group in each land use category based on stable isotopes analysis in R (SIAR) output: (A) natural cover, (B) pasture, and (C) sugar cane.

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Spatial differences in trophic structure

The standard ellipses (SEA_c) based on the isotope ratio of trophic groups of macroinvertebrates differed in size, shape and position in the $\delta^{13}C$ vs $\delta^{15}N$ bi-plot space (Fig 6). The groups with the lowest SEA_c values occurred in the sites with natural vegetation, followed by the sugar cane and pasture sites, which exhibited the highest SEA_c values.

Sites with natural riparian vegetation cover exhibited very little overlap of isotopic niches (i.e., overlap of standard ellipse areas) of the macroinvertebrate feeding groups (Fig 6A). Small overlaps were observed between the collectors, scrapers and filter-feeders. The shrimp-shredders exhibited the largest SEA_c (3.83‰^2), followed by scrapers (3.29‰^2), predators (3.01‰^2), collectors (2.26‰^2) and filter-feeders (1.42‰^2).

Considerable niche overlapping was observed among feeding groups in pasture sites (Fig 6B), especially between collectors and insect-shredders (30.7%) and scrapers (29.3%), and between filter-feeders and predators (25.4%). The other groups exhibited little or no niche overlap. The greatest SEA_c values were observed for the insect-shredders (19.2‰^2), followed by the collectors (9.67‰^2), predators (9.04‰^2), shrimp-shredders (8.89‰^2), filter-feeders (8.8‰^2) and scrapers (6.9‰^2).

The greatest niche overlaps among groups were observed in sugar cane sites (Fig 6C). In those sites, the niches of all feeding groups evaluated overlapped, with the highest overlap

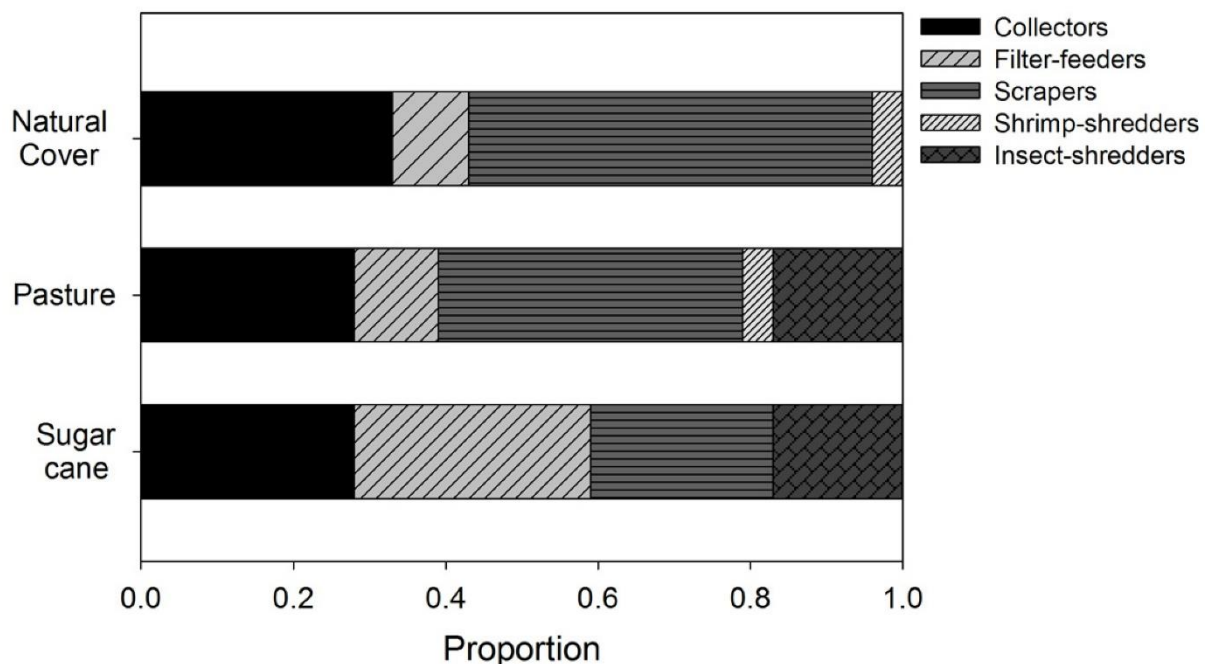


Fig 5. Means of the proportions of macroinvertebrate prey consumed by predators in each land use category based on stable isotopes analysis in R (SIAR) output.

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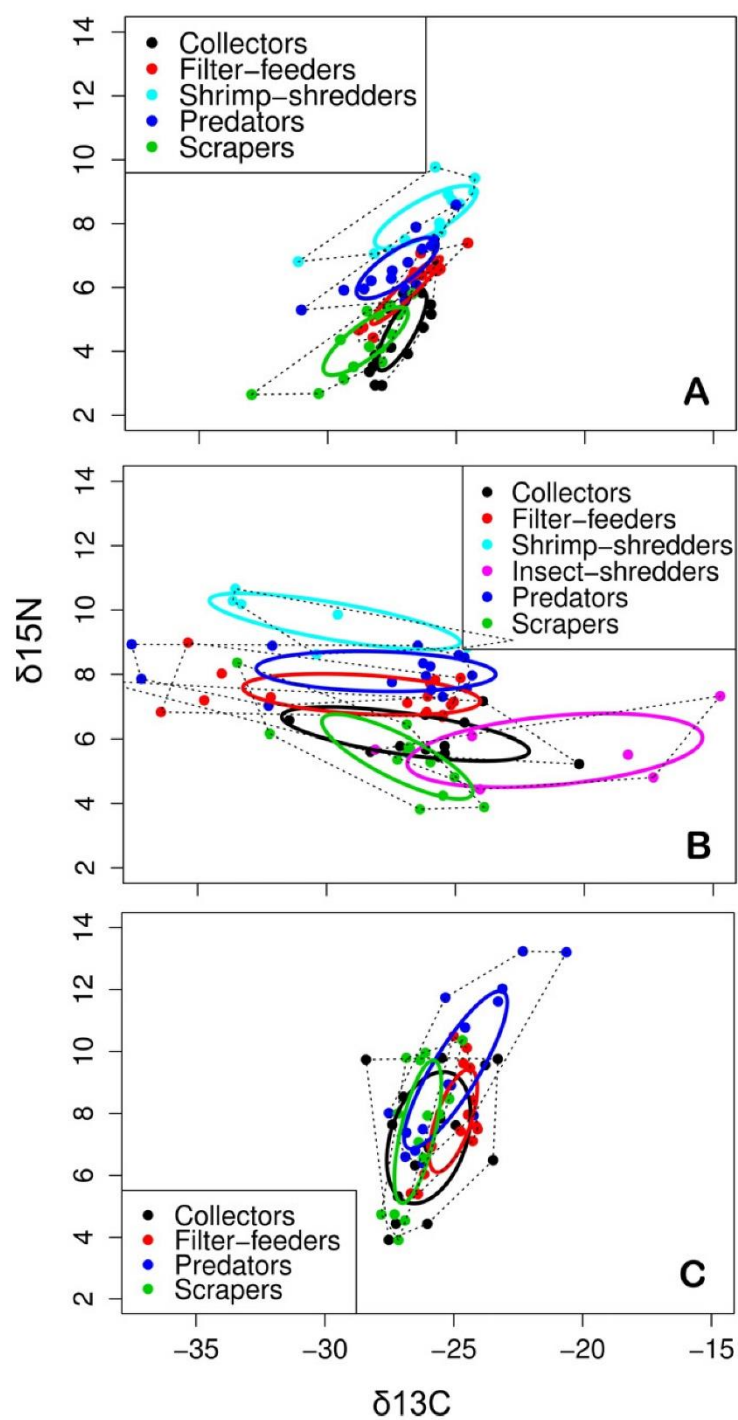


Fig 6. Standard ellipse areas (SEA, solid lines), representing the core isotopic niche space of the macroinvertebrate feeding groups, as determined through SIBER models for the three land use categories: (A) natural cover, (B) pasture and (C) sugar cane. The dashed lines delimit the total area of the macroinvertebrate assemblages of each land use category.

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values observed between collectors and scrapers (45.9%) and collectors and filter-feeders (31.4%). The niches of predators overlapped with the niches of all other groups, whereas the filter-feeders and scrapers exhibited the least niche overlap (24.7%). The collectors had the largest SEA_c (10.19‰^2), followed by predators (8.23‰^2), scrapers (4.96‰^2) and filter-feeders (3.71‰^2). Calculation of the SEA_c for insect-shredders in sugar cane sites was not possible because we obtained only three samples of this group.

The trophic niche metrics of the macroinvertebrate communities varied among land uses. Pasture sites had significantly greater ranges of resources exploited (NR_b and CR_b), trophic diversity (CD_b), and trophic redundancy ($MNND_b$) and showed significantly lower group uniformity ($SDNND_b$) (Table 2). In contrast, sugar cane sites exhibited the lowest values for all metrics and sites with natural cover had intermediate values that did not overlap with sugar cane sites except for $SDNND_b$ (Table 2).

Discussion

The use of stable isotopes along with analytical techniques, such as the Bayesian approach, allowed (1) identification of the main resources consumed by benthic macroinvertebrates and (2) assessment of how the different land uses affected resource availability and trophic dynamics in tropical streams. Our hypotheses were corroborated because we observed macroinvertebrate assemblages with wider trophic niches and greater niche overlap in altered sites and greater resource specialization in sites with natural vegetation.

All trophic groups and virtually all resources evaluated had higher $\delta^{15}\text{N}$ values in sugar cane and pasture sites. Nutrients from agriculture and cattle strongly affect the waterbodies and may have been responsible for the high $\delta^{15}\text{N}$ values found in those streams. On sugar cane plantations, vinasse, a byproduct of ethanol distillation, is the main fertilizer used, whereas chemical fertilizers and livestock manure are the main sources of residues and nutrients in pastures [27]. Fertilizers increase nitrification, leading to soil ^{15}N enrichment [57]. Agricultural residues usually have high $\delta^{15}\text{N}$ ratios [58], and most are carried into waterbodies and incorporated into food webs, thus changing the $\delta^{15}\text{N}$ available in food resources and consumers [59,60].

Although we categorized the groups *a priori*, macroinvertebrates had more generalist feeding habits at pasture and sugar cane sites, whereas more specialization occurred in macroinvertebrate assemblages of sites with natural riparian vegetation. Benstead & Pringle [61] reported similar results in a comparison of sites with preserved and deforested vegetation in Madagascar. They observed a simplification of the aquatic macroinvertebrate assemblages associated with a loss of specialist taxa associated with changes in the relative importance of the basal food resources. Therefore, we believe that land use changes lead to the selection of more generalist organisms and the elimination of more specialized organisms.

Table 2. Layman stable isotope metrics (mean and 95% credible intervals) for each land use category: NR_b = $\delta^{15}\text{N}$ range; CR_b = $\delta^{13}\text{C}$ range; CD_b = mean distance to centroid; $MNND_b$ = mean nearest neighbor distance; and $SDNND_b$ = standard deviation of mean distance to centroid.

Land use	NR_b	CR_b	CD_b	$MNND_b$	$SDNND_b$
Natural cover	3.93 (3.68–4.19)	2.39 (1.96–2.79)	1.42 (1.33–1.53)	1.28 (1.15–1.40)	0.54 (0.37–0.69)
Pasture	4.35 (4.01–4.67)	9.05 (7.47–10.5)	2.79 (2.46–3.09)	2.21 (1.92–2.49)	1.75 (1.16–2.25)
Sugar cane	2.45 (0.89–2.95)	1.70 (1.41–1.97)	1.08 (0.90–1.25)	1.07 (0.89–1.25)	0.52 (0.26–0.73)

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We found some unexpected results in our study; for example, scrapers assimilated more CPOM than periphyton, a result found in pasture and natural vegetation sites. According to Marchese et al. [62], who observed a high contribution of CPOM to chironomids and oligochaetes, this resource is highly colonized by bacteria, protozoa and algae, which may explain the preference for it. However, it is important to highlight that the classification of organisms into functional feeding groups is primarily related to morphology, feeding habits, or food acquisition and not to the food type per se [14]. Future studies should assess whether macroinvertebrate groups/guilds with wider trophic niches contain more generalists consuming a wide variety of food types or whether the organisms specialize in a different but narrower ranges of food resources [28].

In contrast with observations made for some fish species in the same region [27] and in other sites [10], in which was observed assimilation of sugar cane and grasses, these food resources were barely assimilated by the trophic groups evaluated. Although the FPOM was slightly richer in ^{13}C in pasture and sugar cane sites, its contribution to the trophic chain was very low. The C4 plants (grasses in general, such as pasture and sugar cane) are considered to have low nutritional quality compared with C3 plants and are little used by aquatic consumers in many cases, either because of their physical or chemical characteristics that reduce consumption or because consumers are able to select other higher-quality resources [63]. Although present in large amounts at the pasture and sugar cane sites, little C4 plant material entered the food chain through aquatic macroinvertebrates. Bunn et al. [64] and Martinelli et al. [65] also found that few C4 resources were incorporated into the trophic chain in anthropogenically altered sites, despite representing >50% of the detritus in the systems. This reduced contribution of C4 resources into aquatic trophic chains shows how the conversion of natural riparian vegetation into sugar cane plantations and pastures has the potential to alter the trophic dynamics and functional organization of aquatic communities, leading to substantial changes in stream ecosystem functions.

Pasture sites had autochthonous resources (algae and periphyton) with the widest $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ ranges. This wider range may result from reduced riparian canopy cover and, consequently, higher light input, promoting higher diversity and abundance of algae and periphyton species. Similar results have been reported by Turner & Edwards [66], where the producers (algae) had more widely dispersed $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values. They argued that this variation might result from greater taxonomic diversity of the producers, which could lead to greater diversity in C and N metabolism.

Consumers from streams with natural riparian vegetation had the narrowest isotopic niches and the lowest niche overlaps. This pattern indicates that the macroinvertebrate functional groups in those sites had more selective feeding habits with a lower overlap of trophic niches and, consequently, less competition for resources. In their natural state, wooded riparian zones are effective in preserving the ecological integrity and trophic dynamics of aquatic ecosystems. Land use changes and the consequent shifts in the input of allochthonous nutrients and autochthonous production can reduce the balance between functional feeding groups [67] and, widen their trophic niches.

The isotopic metrics calculated for the assemblages described in this study were based on the mean $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ values of multiple individuals for each group in a trophic web, and such intraspecific variation was not considered in this analysis (i.e. species within the same FFG) [21]. The highest mean dNR_b and dCR_b values observed in the pasture sites indicate that macroinvertebrates use a wider range of the available food sources in this environment, especially in contrast with the sugar cane sites. This result is consistent with the SEA_c values, which were highest in pasture sites. The highest mean CD_b value was also observed in pasture sites, indicating higher trophic diversity at those sites. The highest mean MNND_b values were observed for pasture sites, indicating low trophic redundancy. However, the highest SDNND_b values were also observed in the pasture sites, suggesting the existence of a less uniform trophic

niche distribution, despite the low trophic redundancy. This is most likely a result of the greater availability of periphyton and algae in this environment, which are resources with wider $\delta^{13}\text{C}$ ranges and which are used by many consumers. According to Layman et al. [21], MNND_b and SDNND_b increase because consumers have more distinct trophic positions (greater distance among consumers in isotopic space).

Another noteworthy result is the occurrence of the crustacean, *Macrobrachium amazonicus*, considered a shrimp-shredder in this study, which is an alien species in the region found in pasture and in natural cover sites. The isotopic niche (SEA_c) of shrimp-shredders was one of the highest compared with the other functional groups in those land uses. However, the niche of shrimp-shredders did not overlap with the others, suggesting that this group is exploiting resources that would otherwise not be fully exploited by the native fauna. In addition, the shrimp-shredders were the group least preyed upon, with virtually no contribution to predators. Recently in a global evaluation of the consequences of non-native species on the isotopic structure of freshwater fish communities, Sagouis et al. [68] found that communities in lotic ecosystems containing non-native species had a larger total isotopic niche than communities without non-native species and those non-native species were mainly located at the edges of the isotopic niche. Thus, we highlight the importance of studies assessing how invasive alien species are directly competing for resources with native species or not (e.g., [56,69,70]), where the comparison of isotopic niches and assimilated items may be important tools.

We conclude that land use changes, such as sugar cane culture and livestock pasturing, may lead to benthic macroinvertebrate assemblages with more generalist feeding behaviors and higher trophic niche overlap. In addition, our results reinforce the idea that stable isotope analysis is a relevant tool for biomonitoring and evaluating the effects of land use changes on the dynamics and functioning of tropical streams.

Supporting Information

S1 Table. Physical characteristics, land use and environmental variables calculated to the nine streams in the three land use categories. The numbers 1, 2 and 3 correspond to each of the three streams sampled in each land use category (See Fig 1). Order = rank of the stream orders according to Strahler; Veg. cover = Vegetation Cover. All environmental variables were calculated according to the proportion in which they occur in each assessed stream. (DOCX)

S2 Table. Mean $\pm$ S.D. isotopic signatures of resources and consumers sampled in the three land use categories. The letters *a* and *b* indicate which signatures are different according to *post hoc* test. The letter “n” indicates the number of replicates used in each group analysis. (DOCX)

S3 Table. Stable isotope analysis in R (SIAR) results of the food source proportions in the diet of the functional trophic groups (FTG) (95% confidence interval). (DOCX)

S4 Table. Stable isotope analysis in R (SIAR) results of the prey proportions in predator diets (95% confidence interval). (DOCX)

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Author Contributions

Conceived and designed the experiments: DMPC DRC PSP MC. Performed the experiments: DMPC DRC MZM. Analyzed the data: DMPC DRC. Contributed reagents/materials/analysis tools: MZM. Wrote the paper: DMPC DRC PSP MZM GBN MC.

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S1 Table: Physical characteristics, land use and environmental variables for nine streams for three categories of land use. The numbers 1, 2 and 3 correspond to each of the three streams sampled in each land use category (See Figure 1). Order = rank of the stream orders according to Strahler; Veg. cover = Vegetation Cover. All environmental variables were computed in terms of their proportion in each assessed stream.

Streams	Characteristics of streams					Land use				Environmental variables					
	Altitude	Order	Mean depth	Mean width	Natural cover	Pasture	Cane	Others	Fine subst.	Veg. cover	Rapid flow	Aquatic plant	Leaf banks	Algae	
	(m)		(m)	(m)	(%)	(%)	(%)	(%)	(%)	(%)	(%)	(%)	(%)	(%)	
Natural cover	1	482	2 nd	0.20	3.42	53.14	0	46.86	0	<0.01	0.94	0.69	<0.01	0.17	<0.01
	2	434	3 th	0.19	7.29	39.13	57.87	0	3.00	<0.01	0.47	0.46	<0.01	0.14	<0.01
	3	509	3 th	0.19	7.35	50.86	49.14	0	0	<0.01	0.90	0.51	<0.01	0.18	<0.01
Sugar cane	1	516	2 nd	0.23	3.98	14.05	36.56	45.81	3.59	0.01	0.73	0.38	<0.01	0.11	<0.01
	2	441	3 th	0.19	1.85	14.63	0	85.37	0	<0.01	0.99	0.17	0.04	0.16	<0.01
	3	463	2 nd	0.27	1.27	0	43.39	56.61	0	0.03	1.0	0.67	0.02	0.07	<0.01
Pasture	1	425	3 th	0.64	3.49	8.57	62.35	0	29.08	0.3	0.33	0.43	0.66	0.02	0.22
	2	461	3 th	0.13	2.00	0	97.69	0	2.31	0.21	0.01	0.45	0.05	<0.01	0.14
	3	479	2 nd	0.17	4.80	16.41	65.35	0	18.24	0.02	0.38	0.15	0.02	0.02	<0.01

Table S2: Mean $\pm$ S.D. isotopic signatures of resources and consumers sampled in the three land use categories. The letters *a* and *b* indicate which signatures are different according to *post hoc* test. The letter “n” indicates the number of replicates used in each group analysis.

Resources	$\delta^{13}\text{C}$										$\delta^{15}\text{N}$									
	Natural cover		n	Pasture		n	Sugar cane		n	p	Natural cover		n	Pasture		n	Sugar cane		n	p
Algae	-29.96	± 5.44	10	-32.76	± 5.81	10	-30.10	± 2.83	5	0.45	6.21	± 2.43	10	6.32	± 1.98	10	4.52	± 1.56	5	0.27
CPOM	-30.15	± 0.55	30	-30.17	± 0.46	17	-30.08	± 0.61	30	0.91	0.68	± 0.56	b 30	2.19	± 1.03	b 17	4.13	± 2.46	a 30	<0.01
Grasses	–	–	–	-16.83	± 3.55	15	–	–	–	–	–	–	–	4.90	± 2.74	15	–	–	–	–
Periphyton	-27.16	± 1.93	15	-25.86	± 4.71	15	-25.84	± 0.97	15	0.39	4.60	± 0.85	b 15	6.15	± 0.77	a 15	6.71	± 1.94	a 15	<0.01
Sugarcane	–	–	–	–	–	–	-13.11	± 0.25	10	–	–	–	–	–	–	–	4.46	± 0.75	10	–
FPOM	-27.18	± 1.28	b 17	-24.01	± 2.98	a 18	-24.88	± 2.39	a 25	<0.01	3.38	± 0.98	b 17	4.01	± 1.07	b 18	6.31	± 1.87	a 25	<0.01
Consumers																				
Collector	-27.12	± 0.93	15	-26.94	± 4.58	12	-25.97	± 1.57	15	0.10	4.65	± 1.20	b 15	6.15	± 0.79	a 12	7.22	± 2.05	a 15	<0.01
Filter Shrimp-shredder	-26.94	± 1.32	a 15	-28.64	± 4.44	a 15	-25.02	± 0.90	b 15	<0.01	5.90	± 1.01	b 15	7.37	± 0.62	a 15	7.76	± 1.60	a 15	<0.01
Insect-shredder	-26.20	± 1.89	13	-29.68	± 4.44	7	–	–	–	0.12	8.20	± 0.94	b 13	9.64	± 0.80	a 7	–	–	–	<0.01
Predator	–	–	–	-21.14	± 5.12	6	-27.10	± 2.07	3	0.10	–	–	–	5.64	± 1.02	b 6	8.75	± 1.44	a 3	<0.05
Scraper	-27.30	± 1.52	b 15	-28.08	± 4.48	ab 15	-24.93	± 1.93	a 15	<0.01	6.61	± 0.92	b 15	8.09	± 0.60	a 15	9.40	± 2.45	a 15	<0.01
Scraper	-28.53	± 1.58	b 15	-27.25	± 2.79	a 12	-26.39	± 0.87	a 14	<0.01	4.32	± 1.03	c 15	5.45	± 1.25	b 12	7.41	± 2.22	a 14	<0.01

Table S3. Stable isotope analysis (SIAR) results of the food source proportions in the diet of the functional trophic groups (FTG) (95% confidence interval).

Category	Resources	Consumers				
		Collectors	Filter-feeders	Shrimp-shredders	Insect-shredders	Scrapers
Natural Cover	Algae	0.04 (0.00-0.10)	0.09 (0.00-0.22)	0.40 (0.14-0.60)	-	0.08 (0.00-0.19)
	CPOM	0.26 (0.11-0.43)	0.13 (0.00-0.26)	0.03 (0.00-0.09)	-	0.57 (0.40-0.72)
	Periphyton	0.21 (0.00-0.43)	0.34 (0.02-0.61)	0.43 (0.11-0.74)	-	0.13 (0.00-0.31)
	FPOM	0.49 (0.19-0.78)	0.44 (0.11-0.81)	0.14 (0.00-0.36)	-	0.22 (0.00-0.44)
	Algae	0.14 (0.00-0.29)	0.29 (0.13-0.45)	0.44 (0.16-0.76)	0.09 (0.00-0.25)	0.11 (0.00-0.27)
Pasture	CPOM	0.38 (0.21-0.54)	0.19 (0.05-0.32)	0.10 (0.00-0.28)	0.28 (0.02-0.49)	0.49 (0.26-0.72)
	Grasses	0.12 (0.00-0.26)	0.07 (0.00-0.18)	0.10 (0.00-0.26)	0.27 (0.01-0.48)	0.10 (0.00-0.22)
	Periphyton	0.13 (0.00-0.30)	0.29 (0.08-0.50)	0.25 (0.00-0.48)	0.12 (0.00-0.30)	0.10 (0.00-0.27)
	FPOM	0.23 (0.00-0.44)	0.16 (0.00-0.34)	0.11 (0.00-0.30)	0.24 (0.00-0.45)	0.20 (0.00-0.41)
	Algae	0.26 (0.01-0.47)	0.18 (0.00-0.33)	-	0.23 (0.00-0.43)	0.21 (0.01-0.37)
Sugar cane	CPOM	0.24 (0.01-0.44)	0.22 (0.02-0.39)	-	0.22 (0.00-0.42)	0.3 (0.09-0.50)
	Periphyton	0.19 (0.00-0.38)	0.24 (0.01-0.44)	-	0.23 (0.00-0.44)	0.23 (0.01-0.43)
	Sugarcane	0.10 (0.02-0.19)	0.15 (0.07-0.21)	-	0.10 (0.00-0.27)	0.07 (0.00-0.14)
	FPOM	0.21 (0.00-0.41)	0.21 (0.01-0.38)	-	0.22 (0.00-0.42)	0.19 (0.00-0.37)

Table S4: Stable isotope analysis in R (SIAR) results of the prey proportions in predator diets (95% confidence interval).

Resources	Category		
	Natural Cover	Pasture	Sugar cane
Collectors	0.33 (0.00-0.61)	0.28 (0.01-0.54)	0.28 (0.00-0.54)
Filter-feeders	0.10 (0.00-0.29)	0.11 (0.00-0.26)	0.31 (0.01-0.57)
Shrimp-shredders	0.04 (0.00-0.11)	0.04 (0.00-0.10)	-
Insect-shredders	-	0.17 (0.00-0.37)	0.17 (0.00-0.38)
Scrapers	0.53 (0.24-0.85)	0.40 (0.17-0.64)	0.24 (0.00-0.48)



Chapter II

Landscape variables influence taxonomic and trait composition of insect assemblages in neotropical savanna streams

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Landscape variables influence taxonomic and trait composition of insect assemblages in neotropical savanna streams

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Abstract

1. Stream invertebrate assemblages are structured by environmental factors acting at multiple spatial scales. Identifying the spatial scale that most influences the species-environment relationships is a major goal of community ecology.
2. We evaluated the importance of catchment and site scales and associated environmental variables in shaping Ephemeroptera, Plecoptera and Trichoptera (EPT) assemblages in neotropical savanna headwater streams.
3. Sampling sites were associated with 20 catchment-scale variables that depicted land cover and land use as well as natural geophysical variables such as altitude and climate. Site-scale habitat was characterized by 55 variables that described habitat hydromorphology, substrate, flow, canopy, in-stream cover, and water quality. EPT traits were assessed using 28 categories of 7 biological traits, which represented the best available current knowledge for EPT in neotropical savanna streams.
4. We analyzed the relationships between the catchment- and site-scale habitat variables and the taxonomic and trait composition of insect assemblages using 1760 samples collected in 160 stream sites.
5. Catchment- and site-scale variables both explained significant variation of EPT taxon and trait composition. Substrate, habitat hydromorphology, and land use most influenced variation in taxonomic composition whereas trait composition was mainly affected by land use. Catchment geographic position explained less assemblage variation.

6. To our knowledge, our study is the first assessment of the impact of catchment- and site-scale variables on the trait and taxon composition of stream insect assemblages in neotropical savanna streams. It highlights the need for better regional biological knowledge of invertebrates in order to generate more general trait-based approaches in freshwater ecosystem conservation.

Key-words: spatial scale, physical and chemical habitat, aquatic insects, EPT, land use

Introduction

Streams are organized hierarchically in the landscape, within which environmental factors operate at a range of spatial scales (Frissell et al., 1986; Mykrä, Heino & Muotka, 2007; Leps et al., 2015), directly or indirectly affecting the structure and composition of biological assemblages (Townsend et al., 2003; Sandin & Johnson, 2004; Macedo et al., 2014). Therefore, assessing spatial patterns is essential for a comprehensive understanding of the drivers that determine the structural and functional diversity of stream assemblages (Heino, Muotka & Paavola, 2003; Sandin & Johnson, 2004; Hoeinghaus, Winemiller & Birnbaum, 2007; Macedo et al., 2014; Liu et al., 2016).

Site-scale physical and chemical habitat is determined by larger-scale processes (Leal et al., 2016), which hinders disentangling the roles of different environmental drivers in aquatic communities (Frissell et al., 1986; Allan, 2004). For example, catchment characteristics affect riparian zones, substrates and hydrological regimes, which in turn affect habitat availability and thereby influence the structure and composition of aquatic assemblages (Vannote et al., 1980; Allan, 2004; Greenwood & Booker, 2016). Furthermore, geographical position may influence environmental factors that determine spatial patterns in assemblage structure and composition (Townsend et al., 2003).

Understanding the role of catchment- and site-scale environmental variables in determining stream invertebrate biodiversity is especially relevant in tropical freshwater ecosystems (e.g., Al-Shami et al., 2013; Tonkin, Arimoro & Haase, 2016). Although these systems are among the most diverse on earth, they are highly threatened by a broad suite of

stressors (Dudgeon et al., 2006; Strayer & Dudgeon, 2010; Taniwaki et al., 2016). The effects of human activities on tropical streams are poorly understood and the pace of stream deterioration exceeds the pace of scientific research to understand ecosystem responses (Ramírez, Pringle & Wantzen, 2008). For example, the neotropical savanna (Cerrado) is the second largest biome in South America, a biodiversity hotspot (Myers et al., 2000), and one of the most threatened biomes in the world. However, little attention has been paid to the conservation of its freshwater ecosystems and biota (Klink & Machado, 2005; Strassburg et al., 2017). Habitat fragmentation and agriculture are the main threats to biodiversity conservation in this region (Carvalho, De Marco & Ferreira, 2009; Overbeck et al., 2015; Hunke et al., 2015). Although studied worldwide (e.g., Townsend et al., 2003; Beauchard, Gagneur & Brosse, 2003; Heino et al., 2007; Bonada, Dolédec & Statzner, 2012; Al-Shami et al., 2013), spatial patterns of aquatic assemblages are poorly considered in tropical savanna streams (Macedo et al., 2014).

In the neotropics, there have been a few studies addressing the influence of environmental drivers at different scales on functional composition of phytoplankton (e.g., Machado et al., 2016) and fishes (e.g., Terra, Hughes & Araújo, 2016; Leitão et al., 2017), but not invertebrates. Understanding how environmental pressures interact to affect functional composition of aquatic invertebrates at different scales and in different regions is therefore a major challenge for freshwater management in tropical regions and globally.

Most previous studies addressing species traits have been generally restricted to trophic guilds (e.g. Brasil et al., 2014; Castro et al., 2016; Ferreira et al., 2017). However, the Multiple-Trait Based (MTB) approach (Dolédec & Statzner, 2010; Menezes, Baird & Soares, 2010) offers more mechanistic understanding than traditional taxonomy-based approaches for assessing relationships between stream assemblage composition and environmental variables. This is because multiple traits reflect multiple functional relationships between biota and environmental characteristics (Townsend, Dolédec & Scarsbrook, 1997; Feld & Hering, 2007; Dolédec, Phillips & Townsend, 2011). For example, Townsend, Dolédec & Scarsbrook (1997) found that disturbance strengthened the pattern of preponderance of resilience/resistance traits in benthic insect communities. Feld & Hering (2007) observed that, in contrast to taxonomic structure, functional measures were more strongly related to hydromorphological gradients at various spatial scales. Dolédec, Phillips & Townsend (1997), assessing aquatic invertebrate trait

and taxonomic response to land-use, found that trait responses were consistent at the broad and catchment scales, with similar traits responding to land-use at both scales. Functional trait information for neotropical aquatic invertebrates has increased (Tomanova & Usseglio-Polatera, 2007; Tomanova, Moya & Oberdorff, 2008; Reynaga & Santos, 2013; Dedieu et al., 2015; Milesi, Dolédec & Melo, 2016) and provides opportunity for MTB analyses to be used in determining their interactions with multi-scale pressures. Nonetheless, this approach has not been attempted previously in the neotropical savanna.

Ephemeroptera, Plecoptera and Trichoptera (EPT) comprise diverse aquatic assemblages in headwater streams (Vinson & Hawkins, 1998; Bispo et al., 2006), and they have important roles in nutrient cycling and energy transfer (Graça, 2001; Ferreira et al., 2014). In addition, the EPT are commonly used for assessing the biological condition of stream ecosystems in North America (e.g., Lenat, 1988; Stoddard et al., 2008), South America (e.g., Pereira et al., 2016; Chen et al., 2017), Europe (e.g., Hering et al., 2006), Asia (e.g., Chen et al., 2014), and Australia (e.g., Chessman et al., 2006). In this study, we investigated the response of taxonomic and trait composition of EPT assemblages to several physical and chemical variables at catchment and site scales and geographic position in neotropical savanna headwater streams. We sought to answer three questions: (i) Which of those two scales most accounts for the relationships between landscape variables and EPT assemblages in terms of taxonomy and traits? (ii) Are these relationships the same for both natural and human-modified environmental variables? (iii) To what degree does geographic position (longitude/latitude) explain EPT assemblage distribution?

Methods

Study area

The study area was located in the neotropical savanna of south-eastern Brazil (the Cerrado), which has two well-defined seasons: a wet season from October to April (rainfall 100-330 mm/mo), and a dry season from May to September (rainfall 10-55 mm/mo), with 1600 mm mean annual rainfall (Ferreira et al., 2017). We sampled wadeable 1st-3rd order streams (average width = 3.4 ± 1.9 m, average depth = 0.25 ± 0.12 m) belonging to four different

hydrological units (HU): São Francisco, Rio Grande, Paranaíba, and Araguari (Fig. 1). In each HU, we sampled a drainage area within 35 km upstream of each hydropower dam: Três Marias, Volta Grande, São Simão, and Nova Ponte, respectively in each of these HUs. We collected samples in a given HU in a given year over the period between 2010 and 2013 at the end of the dry season (September).

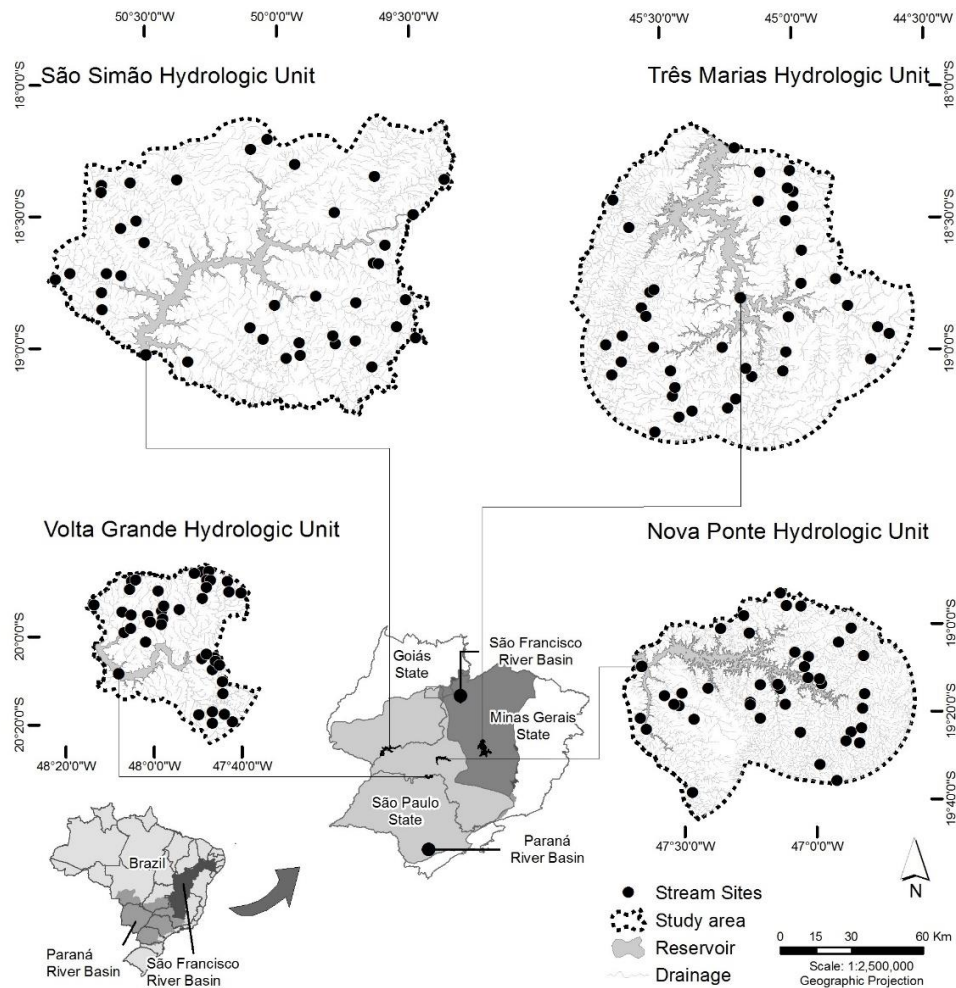


Figure 1. Locations of wadeable stream sites ($n=160$) in four hydrological units in the neotropical savanna.

Site selection

In each HU, we randomly selected 40 perennial stream sites, totaling 160 sites for the 4 HUs. Site selection followed the generalized random tessellation stratified sampling design developed for the U.S. EPA's national Wadeable Stream Assessment (Stevens & Olsen, 2004; Olsen & Peck, 2008). In this approach, a master sample frame is first established using a digital

hydrographical map (1:100,000 scale) and then the sample sites are selected via a hierarchical, spatially weighted criterion (Stevens & Olsen, 2004). This procedure ensures a balanced selection of sites across the range of stream orders and geographic location, besides enabling the selection of sites along different disturbance levels (Macedo et al., 2014).

Environmental variables

Environmental variables acting at varying spatial scales within HUs were classified into three groups: catchment-scale, site-scale, and geographic position (Fig. 2, Table S1). A total of ~250 catchment- and site-scale variables were initially measured. We eliminated those variables that had more than 90% zero values, low variability, and high correlation with each other ($r > |0.8|$). For those variables that correlated with each other, we retained the most ecologically meaningful ones. Because we initially produced many environmental variables (~250), we defined criteria to select the most important variables, based on the literature. Those steps yielded a final set of 75 variables (Macedo et al., 2014).

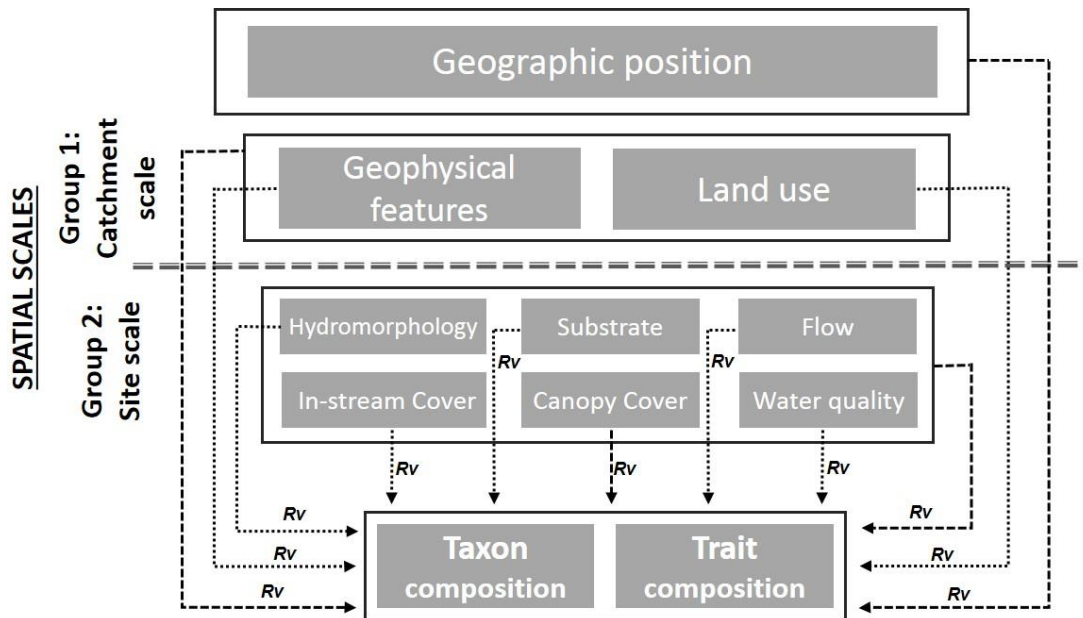


Figure 2: Hierarchical organization used in this study to quantify the relationship between geographic position, environmental variables, and the taxonomic and trait composition of EPT assemblages. Environmental variables (see Table S1) were classified into catchment-scale variables, which comprise geophysical features and land use, and site-scale variables, which depicted habitat hydromorphology, substrate, flow, in-stream cover, riparian canopy cover, and water quality. R_v -coefficients were computed for each set of environmental variables to assess

their respective contribution to the variability of the aquatic invertebrate taxonomic or trait composition.

Catchment-scale variables included land use and land cover variables as well as natural geophysical variables: rainfall, altitude, drainage area, elevation and slope (range, average and standard deviation). Catchment total annual rainfall time series were obtained from the Brazilian National Water Agency (ANA, 2014). Using GIS software, we extracted geophysical variables from 160 catchments, which were manually delineated to the entire catchment area (km²) for each site. Basin elevation data (range, mean and standard deviation) was extracted from Shuttle Radar Topographic Mission - SRTM imagery (USGS 2005) and catchment slope was calculated from the maximum rate of change in elevation in every grid cell, based on SRTM elevation raster.

We assessed catchment land use and land cover for each site by interpreting high-resolution satellite images (0.6-5 m spatial resolution, Google Earth data; Google 2014) in conjunction with Landsat multispectral satellite images (R4G3B2 false color band combination). The high-resolution images provided information about the shape and texture of the elements, and the multispectral images allowed distinguishing vegetation leaf structure. We identified four natural savanna cover types (woodland savanna, grassy-woody savanna, parkland savanna, and wetland palm swamp) (IBGE, 2012) and four human-induced land uses (pasture, agriculture, eucalyptus forest, and urban areas) in the 160 catchments. We also calculated the total percentage of natural land cover by summing the preceding four natural land covers. Additionally, to further characterize potential anthropogenic influences on the sites, we measured Euclidian distance to cities and to paved highways (km) and we calculated the density of households (houses/km²) in each catchment.

Physical habitat at the site scale was characterized using the U.S. EPA field methods (Peck et al., 2006; Hughes & Peck, 2008) adapted to neotropical savanna headwater streams by Callisto et al. (2014). The length of each sampled site was 40 times its mean wetted width, with a minimum length of 150 m. Each reach was divided into 11 equally spaced transects. At each site, we characterized the physical habitat by 10 channel hydromorphological variables (e.g., thalweg depth, bank angle, channel sinuosity; see Table S1), 12 substrate variables (e.g.,

% of boulders, % of sand, % of total organic matter, % of large wood); 6 flow variables (e.g., velocity, % of glides, % of pools), 11 riparian canopy cover variables (e.g., herbaceous cover, exposed soil, ground cover) and 8 in-stream habitat variables (e.g., aquatic macrophytes, large woody debris). All site variables were calculated according to Kaufmann et al. (1999), who described concepts and analytical procedures for calculating metrics based on data generated from the physical habitat field protocols. We also measured temperature, electrical conductivity, pH, turbidity, and total dissolved solids (TDS) in situ using a multi-parameter probe (YSI, 650 MDS, model 6920). In the laboratory, we determined total alkalinity, total nitrogen, and dissolved oxygen concentrations from preserved water following Standard Methods (APHA, 2005). Water samples and parameters were always obtained at each site at the same time of day (around 10 AM).

Benthic macroinvertebrate sampling

We sampled benthic macroinvertebrates at all 160 sites with a D-frame kick net (30 cm aperture, 500 μm mesh). Eleven sub-sample units (0.09 m^2 quadrat) were taken per site, one per transect (see above), generating one composite sample for each site and totaling an area of $\sim 1 \text{ m}^2$ per site. Thus, stream sites were our replicates. The sample units were obtained by following a systematic zigzag trajectory along the reach to avoid bias in habitat selection (Peck et al., 2006; Hughes & Peck, 2008). Immediately after collection, samples were placed in individual plastic buckets and preserved with 4% formalin. In the laboratory, macroinvertebrates were sorted, and EPT individuals were identified to genus by means of taxonomic keys (Pes, Hamada & Nessimian, 2005; Dominguez et al., 2006; Mugnai, Nessimian & Baptista, 2010) and counted under a 80x magnification stereomicroscope.

Biological traits

We used trait information that was available exclusively for neotropical macroinvertebrates (Baptista et al., 2006; Tomanova & Usseglio-Polatera, 2007; Reynaga & Santos, 2012; Dedieu et al., 2015). Biological trait categories described EPT genus profiles in

terms of resilience or resistance ability (including morphology and life cycle) and feeding habits. Feeding habits and body size potentially reflect stream functional aspects (e.g., nutrient cycling, biomass accumulation), and other morphological and behavioral traits were potentially linked to physical habitat constraints (Tomanova & Usseglio-Polatera, 2007). We produced a trait database comprising 7 biological traits and 28 trait categories (Table 1). The affinity of each taxon for each category within a trait was described using a fuzzy coding approach (Chevenet, Dolédec & Chessel, 1994). The score for each taxon belonging to each trait category ranged from 0 to 3, with 0 indicating no affinity with the category, 1 indicating weak affinity, 2 indicating moderately strong affinity, and 3 indicating strong affinity. This coding methodology helps to compensate for different types and levels of information available, and the inclusion of within-species trait variation associated to the natural variation of populations (Chevenet et al., 1994; Menezes et al., 2010). To determine the body size of each EPT genus, we measured the body lengths (from head to the end of the abdomen) of ~10% of all EPT organisms sampled in the 160 sites. These measurements were then classified into 6 categories according to the distribution of sizes in a histogram, where the breaks were defined so that the categories had a normal distribution (Table 1).

Affinity scores were standardized so that their sum for a given taxon and a given trait equaled 1. As recommended by Gayraud et al. (2003), we described the trait composition of assemblages by multiplying the frequency of each category per trait by the $\ln$ -transformed abundances of taxa in a site. The resulting trait-by-sites table, which contained the abundance of each category per trait in each site, was further analyzed.

Table 1. Traits and their categories and codes used for 73 EPT genera collected in neotropical savanna streams.

Traits	Code	Categories
Body Size	SIZE_<1.5	<1.5
	SIZE_1.5_2.5	1.5 - 2.5
	SIZE_2.5_3.5	2.5 - 3.5
	SIZE_3.5_5	3.5 - 5.0
	SIZE_5_10	5.0 - 10.0
	SIZE_large	>10
Potential number of cycles per year	CY_<1y	< or = 1
	CY_>1y	> 1
Feeding Habits	FG_collector	Collector-Gatherer
	FG_shredder	Shredder
	FG_scraper	Scraper
	FG_filterer	Collector-Filterer
	FG_predator	Predator
Locomotion	LO_burrower	Burrow
	LO_climber	Climber
	LO_sprawler	Sprawl
	LO_clinger	Clinger
	LO_swimmer	Swimmer
Body flexibility	FL_low	<10
	FL_inter	>10-45
	FL_high	>45
Body form	FO_streamlined	Streamlined
	FO_flattened	Flattened
	FO_cylindrical	Cylindrical
	FO_spherical	Spherical
Relation to substrate	RS_free	Free Living
	RS_silknet	Silk net builders
	RS_case	Case builder

Data analysis

To obtain scores for sites based on taxon composition, we performed principal components analysis (PCA) on the $\ln(x+1)$ -transformed abundance of taxa, and to obtain scores for sites based on trait composition, we used a fuzzy principal components analysis (FPCA) on the table that contained the $\ln(x+1)$ -transformed trait-category abundances in each site

(Chevenet et al. 1994). To test for homogeneity among HUs, which would allow using all 160 sites together, we compared the observed variance across the sites in each HU and the distribution of simulated variances obtained after 999 permutations of the rows (sites) of the taxon (or trait) composition table. For taxon and trait composition, the tests indicated a very weak separation of sites grouped by HU (explained variance=0.094 and 0.078, simulated- p =0.001, for taxa and traits respectively). We thus considered the totality of sites in further analyses.

Continuous environmental variables were log-transformed and proportional variables were arcsine-squared root transformed to meet normality of distributions. To identify and produce smaller sets of the most representative variables, we performed PCA on catchment- and site-scale variables as a whole, and for separate sets (i.e. geophysical features, land use, habitat hydromorphology, substrate, flow, riparian canopy cover, in-stream cover, water physical and chemical, Table S1). We further investigated the relationships between geographical locations and the above environmental variables and taxon (or trait) composition of EPT assemblages by using co-inertia analyses (Dolédéc & Chessel, 1994; Dray, Chessel & Thioulouse, 2003). This analysis is an eigenvector technique that matches two data sets (in this case, environmental variables and invertebrate data) in a symmetric way. The correlation between each set of environmental variables and EPT taxon or trait composition was measured with the R_v -coefficient (Fig. 2), which is a multidimensional equivalent of the ordinary correlation coefficient between two variables (Robert & Escoufier, 1976). We performed Monte-Carlo tests to evaluate the statistical significance of R_v -coefficients by comparing the observed R_v -coefficient to the distribution of 999 replicated matches of the two tables (after the random permutations of their rows, i.e., sites). In addition, to assess the importance of the site and catchment scales in comparison to geographical position in determining EPT taxon (or trait) composition, we used a procedure proposed in Townsend et al. (2003). In this approach, we let $E1$ and $E2$ denote the two environment tables at the site- and/or the catchment-scales, and considered F the EPT taxon (or trait) composition table. We tested the null hypothesis $R_v(E1,F) = R_v(E2,F)$ against the alternative $R_v(E1,F) > R_v(E2,F)$ and we performed bootstraps on the statistics $t = R_v(E1,F) - R_v(E2,F)$ using 999 replicates. We assessed the statistical significance of the observed R_v -coefficient difference by comparing it to the distribution of the simulated

values. Percent changes between Rv-coefficients were obtained by $[(Rv(E1,F) - Rv(E2,F)) / (Rv(E1,F)) \times 100]$.

Finally, given that the variability within a table is related to the number of variables, which differed between taxonomic and trait composition (73 genera vs. 28 trait categories), we simulated taxonomic-composition tables by randomly selecting 28 genera (i.e. the same number as trait categories) and recalculated the RV-coefficient for each set of environments with this reduced taxon composition. The distribution of 999 simulated variances was then compared with the observed variance obtained from the analysis of the entire taxonomic and trait composition tables (see e.g. Bonada et al. 2007). All analyses were conducted in R (R Core Development Team, 2015) with the ade4 package (Chessel, Dufour & Thioulouse, 2004).

Results

Taxonomy

We collected 53,698 EPT individuals distributed in 20 families and 73 genera. Four sites had no EPT and were excluded from further analysis (hereafter n=156 sites). Co-inertia analysis showed a significant relationship between EPT taxon composition and catchment-scale variables ($R_v = 0.247$, $P = 0.001$; Table 2). The first two axes incorporated 95.5% of the environmental variability and 55% of the EPT variability (Table 2). The most significant variables along the first co-inertia axis included the percentage of parkland and natural cover as opposed to percentage of agricultural lands (Fig. 3a). Along the second axis, prominent variables included altitude, catchment elevation range, and rainfall as opposed to percentage of palm swamp, drainage area, and elevation standard deviation (Fig. 3b). EPT taxonomic richness was significantly related to the first co-inertia axis ($R^2 = 0.068$, $P < 0.001$). Taxa most responding to the environmental patterns described by the first co-inertia axis included Ephemeroptera, such as *Callibaetis*, *Cloeodes*, *Caenis*, and *Traverhyphes* (Fig. 3c). Taxa less sensitive to land use included Trichoptera (*Smicridea*) and Ephemeroptera (*Leptohyphes* and *Zelus*). Along the second co-inertia axis, taxa colonizing higher elevation streams included Plecoptera (*Tupiperla*) and Ephemeroptera (*Tricorythopsis*). In contrast, lower elevation streams

supported Ephemeroptera such as *Hydrosmilodon* and *Farrodes* and Trichoptera such as *Helicopsyche* (Fig. 3c).

Table 2: Results of co-inertia analyses performed between geographic position, catchment- and site-scale variables and (a) taxonomic and (b) trait composition of EPT assemblages. *Rv*: correlation coefficient between tables, *P*: simulated probability equal to the frequency of random values higher than the observed *Rv*-coefficient, %: percentage of variance in EPT taxonomic (a) or trait (b) composition explained by the first-two axes of a co-inertia analysis.

	<i>Rv</i>	<i>P</i>	%
(a)			
Geographic position	0.140	0.001	43.7
Catchment	0.247	0.001	55.1
Site	0.320	0.001	84.9
(b)			
Geographic position	0.067	0.001	69.1
Catchment	0.133	0.001	80.7
Site	0.118	0.001	92.7

At the site scale, the relation between EPT taxon composition and environmental variables was slightly stronger than for catchment-scale variables ($Rv = 0.320$, $P = 0.001$; Table 2). The first two co-inertia axes represented up to 85.9% of the environmental variability and 84.9% of the EPT variability (Table 2). The most important site-scale variables along the first co-inertia axis included mean bankfull and wetted width, substrate diameter, and mean width/depth ratio as opposed to embeddedness, percentage of fines, percentage of areal cover in live trees, and turbidity (Fig. 3d). The most significant variables along the second co-inertia axis included mean water velocity, and percentage of pools, rapids and glides (Fig. 3e). The first co-inertia axis separated sites with high EPT diversity from those having lower diversity ($R^2 = 0.268$, $P < 0.001$) with *Traverhyphes*, *Thraulodes*, *Cloeodes* as opposed to *Waltzoyphius*. Taxa most related to slow waters were the Ephemeroptera *Callibaetis*, *Caenis* and *Cloeodes*, as opposed to *Tricorythopsis*, *Tupiperla*, *Smicridea* and *Itaura* at higher flow velocities (Fig. 3f).

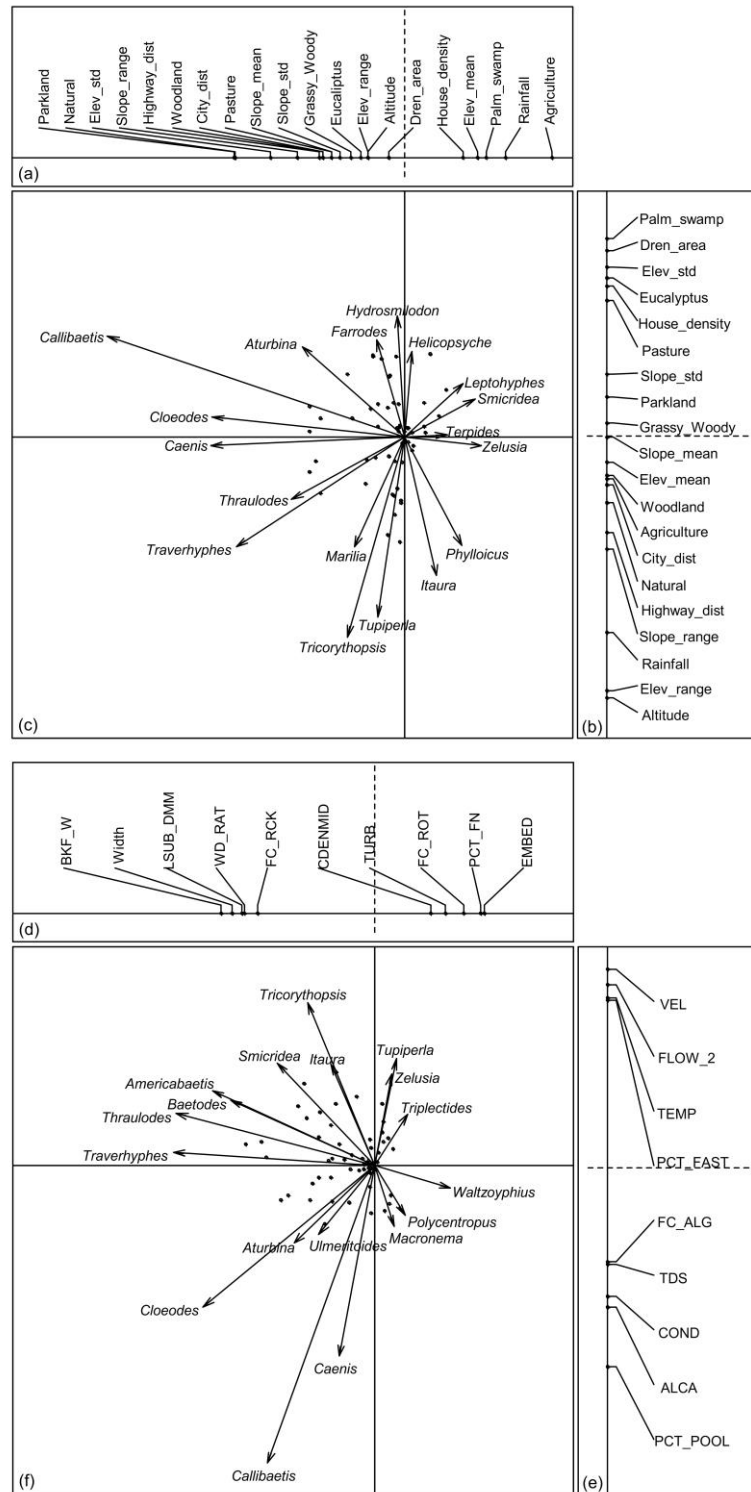


Figure 3: First two axes of a co-inertia analysis depicting the relationship between the taxonomic composition of EPT assemblages and (a-c) catchment-scale variables and (d-f) site-scale variables. (a) and (b) show the prominent catchment-scale variables along the first and second co-inertia axis respectively. (d) and (e) show the prominent site-scale variables along the first and second co-inertia axis respectively. (c) and (f) show the taxa loadings associated with the response of taxa to catchment-scale and site-scale variables respectively. Dots represent taxa with low loadings whose names are not shown for clarity (see Table S1 for variable acronyms).

The patterns observed above were significantly related ($R_v = 0.140$, $P < 0.001$; Table 2) to geographic position: an East-West gradient along the first co-inertia axis and a North-South gradient along the second co-inertia axis. However, the extracted variance was substantially lower than that obtained from catchment- and site-scale variables (Table 2).

Biological traits

Co-inertia analysis showed a significant relationship between EPT trait composition and catchment-scale variables ($R_v = 0.133$, $P = 0.001$). The first-two axes accounted for 90.3% of environmental variability and 80.7% of the trait variability (Table 2). Like EPT taxon composition, environmental variables were not equally important in accounting for trait composition. Along the first co-inertia axis, the percentage of natural cover, highway distance, and percentage of woodland and parkland were opposed to house density, percentage of agriculture, and palm-swamp (Fig. 4a). The most important variables along the second co-inertia axis included rainfall, elevation range, altitude, and percentage of agriculture as opposed to percentage of palm-swamp, percentage of eucalyptus, and standard deviation of elevation (Fig. 4b). The fauna responding to this gradient along the first co-inertia axis were free-living univoltine organisms with streamlined body form and/or intermediate body flexibility as opposed to silk net-builder organisms, having cylindrical body form and/or being multi-voltine. Along the second co-inertia axis, sprawlers, shredders, case-builders, and organisms with low body flexibility ($<10^\circ$) and/or cylindrical body forms were opposed to scrapers and organisms with high body flexibility ($>45^\circ$) (Fig. 4c).

The correlation between the trait composition of EPT assemblages and site-scale variables was slightly weaker than at the catchment scale ($R_v = 0.118$, $P = 0.001$). The first two axes accounted for 62.8% of the environmental variability and 92.7% of the trait variability (Table 2). The most important site-scale variables along the first co-inertia axis included relative bed stability, percentage of coarse gravel, mean substrate diameter, and percentage of fine gravel as opposed to water turbidity, percentage of fines, conductivity, embeddedness, and total dissolved solids (Fig. 4d). Along the second co-inertia axis, the most important variables were mean water velocity, discharge, temperature, and percentage of riffles opposed to percentage

of pools, mean exposed soil, mean riparian canopy cover, mean thalweg depth, and reach length (Fig. 4e). Along this first co-inertia axis, sprawlers and univoltine organisms, with low body flexibility ($<10^\circ$) and/or small body size were opposed to swimmers and multi-voltine organisms with high body flexibility ($>45^\circ$). Along the second co-inertia axis, silk-net builders and organisms with cylindrical body form were opposed to scrapers and free-living organisms with streamlined body shape and intermediate body flexibility (Fig. 4f).

Like taxonomic composition, the patterns observed above were significantly related ($R_v = 0.067$, $P < 0.001$; Table 2) to geographic position: an East-West gradient along the first co-inertia axis and a North-South gradient along the second co-inertia axis (not shown). However the extracted variance was markedly lower than that obtained from catchment- and site-scale variables (Table 2).

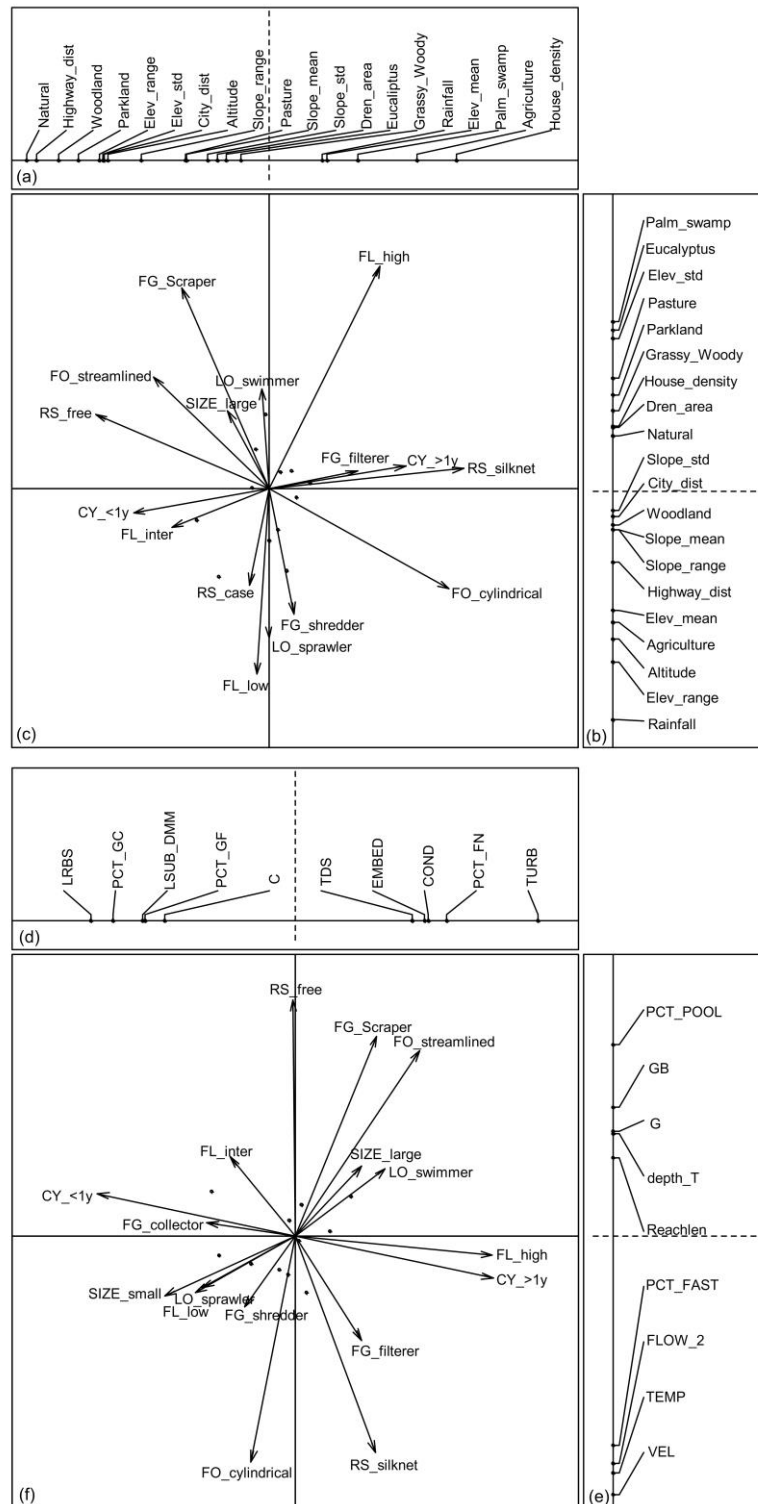


Figure 4: First two axes of a co-inertia analysis depicting the relationships between the *trait* composition of EPT assemblages and (a-c) catchment-scale variables and (d-f) site-scale variables. (a) and (b) show the prominent catchment-scale variables along the first and second co-inertia axis respectively. (d) and (e) show the prominent site-scale variables along the first and second co-inertia axis respectively. (c) and (f) show the taxa loadings associated to the variation in trait composition in response to catchment-scale and site-scale variables respectively. Dots represent taxa with low loadings whose names are not shown for clarity (see Table S1 for variable acronyms).

Catchment- vs site-scale: taxa and traits

Different environmental variables most influenced different taxa and trait variables. The taxa that were most influenced by catchment-scale variables, those most correlated with the first co-inertia axis, were *Aturbina*, *Tricorythopsis*, *Smicridea*, *Callibaetis*, whereas taxa most influenced by site-scale variables were *Traverhypes*, *Itaura* and *Cloeodes* (Fig. 5a). Traits most influenced by catchment-scale variables were shredders and organisms with cylindrical or streamlined body form, and small body size, whereas traits most influenced by site-scale variables were silk-net builders, filterers, and organisms with more than one reproductive cycle per year and large body size (Fig. 5b).

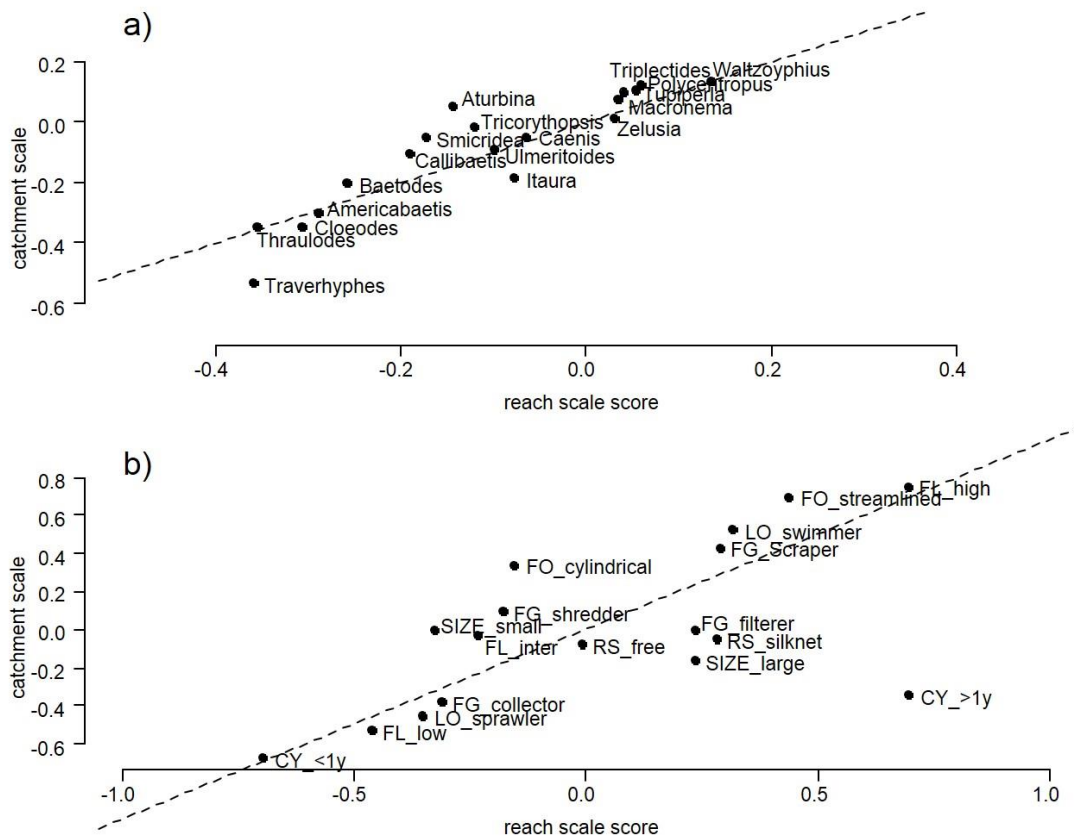


Figure 5: Influence of catchment and site scales on both a) taxa and b) traits most correlated with the first co-inertia axis. Each axis has the same variance. Taxa or traits above the dotted line are more influenced by catchment-scale variables and those below the line are more related to site-scale variables.

Subsets of variables: taxa vs. traits

We performed co-inertia analyses between each subset of environmental variables and taxon (or trait) composition. Substrate, hydromorphology, and land use were most correlated with EPT taxon composition (Fig. 6a, Table S2), whereas land use, flow, and water quality were most correlated with EPT trait composition (Fig. 6b, Table S2). Overall, the taxonomic structure of EPT assemblages exhibited stronger relationships with all groups of environmental variables than the functional trait composition ($R_v = 0.181 \pm 0.05$ and $R_v = 0.076 \pm 0.03$ for taxonomic and trait composition, respectively). Simulating the variance explained by each group of environmental variables for taxon composition by randomly selecting 28 genera (corresponding to the number of trait categories) confirmed that the higher variability in taxonomic data was not responsible for the difference in overall R_v -coefficients observed for taxon in comparison to trait composition (Fig. S1).

Table 3: Results from the bootstraps performed on the differences between R_v -coefficients resulting from the comparison between EPT *taxonomic* composition and geographic position, and catchment- and site-scale variables. P: probability that the observed difference [$R_v(E_1, F) - R_v(E_2, F)$] is significantly positive. (n.s. = non significant).

	Observed	P
Site – Geographic position	0.180	0.001
Catchment – Geographic position	0.107	0.001
Site – Catchment	0.073	n.s.
Land use – Canopy cover	0.144	0.001
Geophysical features – Canopy cover	0.117	0.001
Geophysical features – In-stream cover	0.044	0.002
Land use – Water Quality	0.043	0.003
Land use – In-stream cover	0.070	0.001
Land use – Flow	0.040	0.012
Geophysical features – Water Quality	0.016	0.026
Geophysical features – Land use	0.027	n.s.
Geophysical features – Flow	0.013	n.s.
Land Use – Hydromorphology	0.010	n.s.
Geophysical features – Hydromorphology	-0.017	n.s.
Land Use – Substrate	-0.017	n.s.
Geophysical features – Substrate	-0.043	n.s.

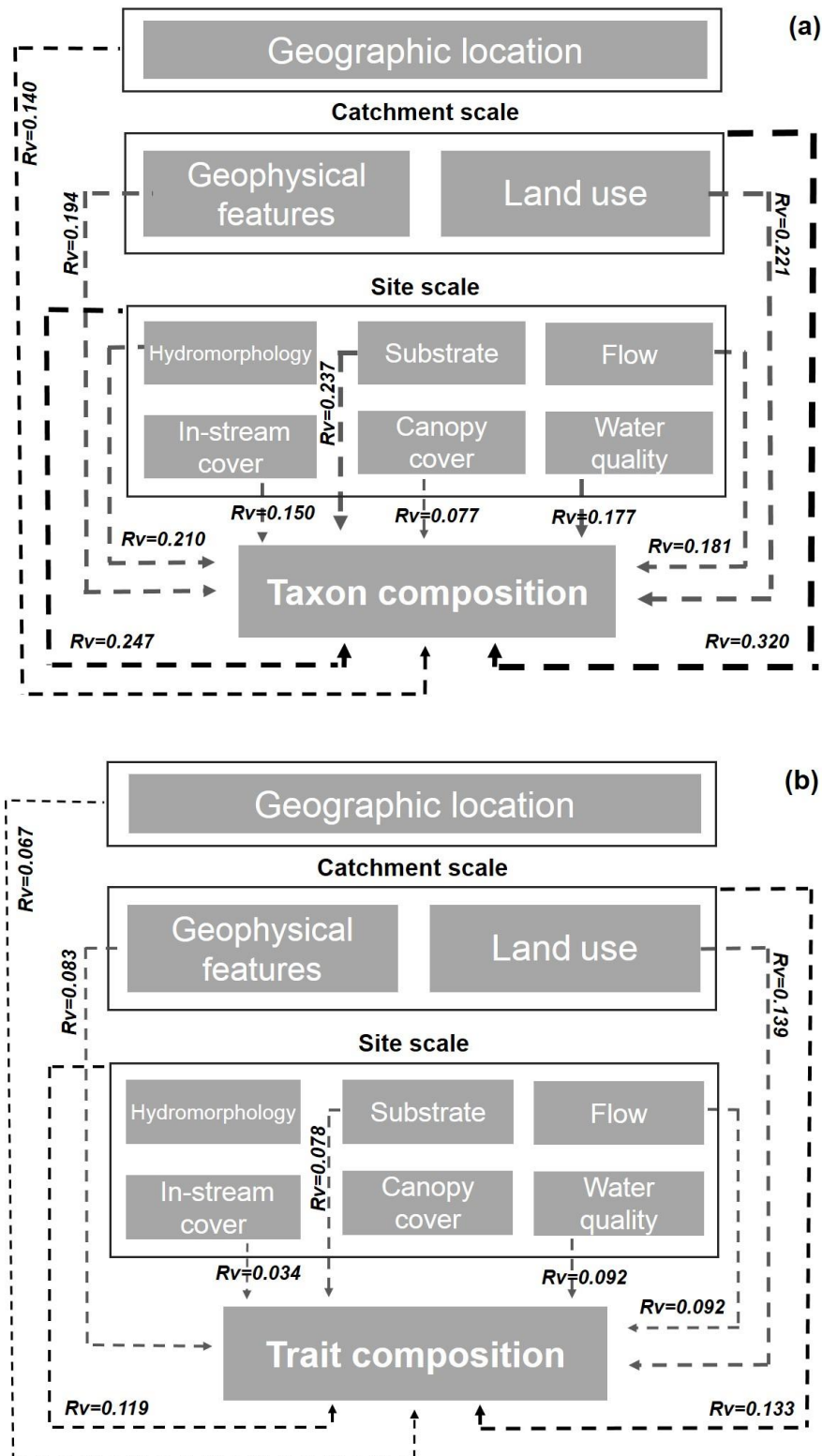


Figure 6: Relationships between the environmental variables and (a) taxon and (b) trait composition of EPT assemblages. Arrow width is proportional to the Rv -coefficient. Arrows not shown means that the correlation is not significant.

Comparative importance of geographic position and catchment- and site-scale variables

Considering EPT taxonomic composition, the differences in R_v -coefficients between the catchment- and site-scale variables as a whole were not significantly different from zero, suggesting that both groups equally influenced EPT taxon composition (Table 3). In this analysis, geographic position was less influential than catchment- and site-scale variables. Significant positive R_v -coefficient differences occurred between the geophysical features and site-scale variables describing riparian canopy cover (60.3% higher), in-stream cover (22.6%), and water quality (8.2%) (Table 3). In addition, significant positive R_v -coefficients differences occurred between land use and site-scale variables describing riparian canopy cover (65.1%), in-stream habitat cover (31.6%), water quality (19.4%), and flow (18.1%), suggesting that land use had a greater influence on taxon composition than site-scale variables (Table 3).

Considering the trait composition of EPT assemblages, the significant positive differences in R_v -coefficients between catchment and site-scale variables as a whole indicated that catchment-scale variables were slightly more influential than site-scale variables (11.2% higher; Table 4). Similar to taxonomic composition, geographic position was less influential than catchment and site-scale variables for traits. Significant positive R_v -coefficients differences occurred between geophysical variables and site-scale variables describing in-stream cover (59% higher), hydromorphology (50%), and riparian canopy cover (39.7%) (Table 4). Significant positive R_v -coefficients differences occurred between land use and all site-scale variables suggesting a greater influence of land use (between 33.8% and 75.5%) on EPT trait composition.

Table 4: Results from the bootstraps performed on the differences between Rv -coefficients resulting from the comparison between EPT *trait* composition and geographic position, and catchment- and site-scale variables. P : probability that the observed difference [$Rv(E_1, F) - Rv(E_2, F)$] is significantly positive. (n.s. = non significant).

	Observed	P
Catchment – Geographic position	0.066	0.001
Site – Geographic position	0.051	0.020
Catchment – Site	0.015	0.005
Land use – In-stream cover	0.105	0.001
Land use – Morphology	0.098	0.001
Land use – Canopy cover	0.089	0.001
Land use – Substrate	0.061	0.002
Geophysical features – In-stream cover	0.049	0.001
Land use – Flow	0.047	0.004
Land use – Water Quality	0.047	0.011
Geophysical features – Hydromorphology	0.042	0.002
Geophysical features – Riparian canopy cover	0.033	0.010
Geophysical features – Substrate	0.006	n.s.
Geophysical features – Flow	-0.008	n.s.
Geophysical features – Water quality	-0.009	n.s.
Geophysical features – Land use	-0.056	n.s.

Discussion

Our aim was to assess the influence of environmental variables at varying spatial scales on taxonomic and trait composition of EPT assemblages found in neotropical savanna headwater streams. Both catchment- and site-scale variable groups equally influenced EPT taxon composition, and geographic position was less influential than both. Considering EPT trait composition, catchment-scale variables were more influential than site-scale variables, and geographic location was also less influential than the two groups. Substrate, hydromorphology, and land use were prominent in explaining the variation in EPT taxonomic composition whereas land use mainly explained the variation in EPT trait composition.

Traits such as relation to substrate and potential number of reproductive cycles per year best discriminated EPT assemblages. Substrate conditions are known to constrain invertebrate distribution and abundance in streams (Wood & Armitage, 1997; Rabení, Doisy & Zweig, 2005). Fine sediments have direct effects on benthic habitats and are key stressors for benthic invertebrates (Bryce et al., 2010), being a result of increased agricultural runoff, elimination of riparian vegetation, and channelization of streams (Wood & Armitage, 1997; Jones et al., 2012). Corroborating Rabení et al. (2005), we also observed that sprawlers were particularly intolerant to increased fine sediment and embeddedness. Assemblages with more multi-voltine organisms generally have a higher resilience to frequent disturbance. Our results corroborate the findings of Dolédec et al. (2006) who observed that the number of cycles per year of New Zealand stream invertebrates increased with the intensity of land use.

Environmental variables at both catchment- and site-scales explained significant amounts of variation in EPT taxon and trait composition. Although the relationship between catchment-scale variables and EPT taxon composition was generally higher than that observed between site-scale variables and EPT taxon composition (Fig. 6a), the overall difference between them was not significant. Hydromorphology, substrate, and land use accounted for most of the variation in EPT taxonomic composition. Hydromorphology characteristics such as stream size and mean wetted and bankfull width and depth particularly influenced the taxonomic composition of EPT assemblages. Stream size is the primary determinant of the amount of lotic habitat in a locality and modifications in channel dimensions change the quantity and quality of aquatic habitat (Kaufmann et al., 1999; Ligeiro et al., 2013). Furthermore, hydromorphological alterations are considered major stressors of lotic ecosystems and their biology (Vaughan et al., 2009), although the links between river ecology and hydromorphology are still incomplete (Feld, de Bello & Dolédec, 2014). In addition, percentage of fines, substrate diameter, and relative bed stability were important variables to the taxonomic composition of EPT assemblages. Bottom characteristics are often cited as major parameters that control macroinvertebrate composition (Rabéní et al., 2005; Jones et al., 2012). Substrate size influences the hydraulic roughness and consequently the range of water velocities in a stream channel. It also influences the size range of interstices that provide living space and cover for aquatic assemblages (Kaufmann et al., 1999). Decreases in the mean substrate size and

increases in the percentage of fine sediments may destabilize channels and indicate changes in the rates of upland erosion and sediment supply (Dietrich et al., 1989; Bryce et al., 2010). Additionally, substrate heterogeneity (i.e., proportion of different sediment types, sizes, or textures) allows more species to coexist and positively affects macroinvertebrate assemblage structure, acting as an abiotic filter that selects for a set of functionally different organisms (Milesi et al., 2016). In an earlier study conducted in the Nova Ponte and Três Marias HUs, Ferreira et al. (2014) pointed out the importance of site-scale physical habitat in the distribution of EPT richness and concluded that channel morphology (width and depth), riparian structure, substrate composition, and water quality were important for structuring macroinvertebrate richness in headwater streams. The percentage of natural cover influenced both the taxonomic and trait composition of EPT assemblages, the relation for traits being weaker than for taxa. Modifications of natural vegetation land cover can cause multiple influencing factors, including increased nutrients in the water, fine sediments in the streambed, chemical contamination, loss of habitat heterogeneity, and increased light availability and aquatic macrophyte growth through the clearing of riparian vegetation (Allan, 2004); Leitão et al., 2017).

Catchment-scale variables, mainly land use, were more influential on the trait composition of EPT assemblages in comparison with site-scale variables. In general, taxonomic structure should be more strongly affected by regional processes, whereas functional structure should be mostly shaped by site-scale characteristics (Hoeinghaus et al., 2007) because of their greater proximity and interaction with the organisms. However, a mismatch between patterns of taxonomic and functional structure may also be related to spatial scales. Large-scale processes shape the pool of species in a local assemblage. Sites may be located within a single regional species pool, then all species and functional trait combinations may colonize each site, and taxonomic and functional structure should exhibit similar patterns along major environmental gradients (Heino et al., 2007). The multiple spatial scales regulating assemblage structure are related to multiple environmental filters, where each spatial scale acts as an environmental filter and only species possessing a specific set of traits pass the filter at each scale and become established in a community (Tonn, 1990; Poff, 1997). In fact, land use influenced assemblages in our study through its effects on canopy cover, water quality, in-stream cover, flow, and hydromorphology. Such a high influence of land use induced stressors on the functional trait

composition of stream macroinvertebrate assemblages supports the findings of previous studies (Richards et al. 1997; Dolédec et al. 2011).

We also observed that the correlations with environmental variables were generally lower for trait than for taxon composition of EPT assemblages at both spatial scales. In contrast, in New Zealand streams subjected to intensive land use, both taxonomy and trait approaches were able to discriminate land use practices, but the trait approach accounted for more variance between different land uses (Dolédec et al., 2006). However, this study may not be comparable to ours because the intensity of land use and the taxa differ. Nonetheless taxa that naturally fluctuate with environmental conditions and geography may have similar traits, thus smoothing the response of traits to environmental variation at larger scales. This higher spatial stability of traits is potentially linked to the physical harshness of the stream conditions, which act as a strong abiotic filter on biological traits and involves trait convergence in stream biota (e.g. Poff, 1997; Statzner et al., 2004).

Similar to the findings of Townsend et al. (2003), geographic position accounted for less assemblage variation than catchment- and site-scale variables for both taxa and traits. This suggests three alternative hypotheses. (i) Different species have evolved in an ecologically divergent way in the different locations not ignoring that geography and environmental variables may be correlated. (ii) EPT evolutionary history may have constrained the colonization of various locations. (iii) Weak dispersal capabilities of neotropical savanna EPT have prevented them from overcoming geographic barriers (see Townsend et al. 2003). However, our current lack of biological knowledge of Cerrado EPT taxa prevents us from confirming one or more of those hypotheses. Townsend et al. (2003) also observed a lower relationship between geographical location and invertebrate assemblage composition in comparison to catchment- and site-scale variables, possibly due to a correlation between geography and those environmental conditions.

To our knowledge, our study is the first that considers environmental variables at catchment and site scales to explain both invertebrate taxonomic and functional composition in tropical savanna streams. Our results demonstrate four key issues regarding those streams: i) Aquatic invertebrate taxonomic composition is mainly structured by land use, substrate, and

hydromorphology. ii) Land use filters specific traits in EPT assemblages. iii) It is essential to increase our biological knowledge of invertebrates if we want to include the multiple-trait based approach in water resource conservation. iv) Identification of variables driving the taxonomic and functional structure of macroinvertebrate assemblages determines the scale at which efforts for protection and/or rehabilitation would best be directed to improve and/or maintain environmental and ecological condition.

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Table S1: Environmental variables and their codes and definitions. Average values and standard deviation (in parentheses) are given for each HU.

Variables	Variable code	Hydrologic unit			
		TM	VG	SS	NP
Catchment scale					
Geophysical features					
Drainage area (km²)	Dren_area	46.26 (47.3)	17.14 (16.33)	30.42 (26.66)	10.74 (10.71)
Site altitude (m)	Altitude	659.94 (63.46)	623.74 (66.93)	485.43 (54.77)	885.28 (41.97)
Range basin elevation (m)	Elev_range	731.66 (78.42)	723.74 (66.72)	563.33 (51.5)	968.08 (43.59)
Average basin elevation (m)	Elev_mean	35.8 (20.72)	171.18 (54.97)	195.2 (73.61)	149.18 (68.8)
Std. Dev. Basin elevation	Elev_std	167.51 (89.04)	37.11 (12.69)	42.65 (21.09)	34.23 (15.96)
Range basin slope (%)	Slope_range	7.43 (3.23)	6.03 (1.84)	5.67 (1.87)	8.24 (3.03)
Average basin slope (%)	Slope_mean	4.98 (4.24)	3.54 (1.45)	4.55 (2.81)	4.48 (1.58)
Std. Dev. Basin slope	Slope_std	48.54 (92.72)	22.91 (10.13)	31.92 (17.78)	23.78 (9.5)
Total annual rainfall (mm/m²)	Rainfall	1299.23 (79.17)	1536.08 (37.8)	1464.11 (77.75)	1564.09 (40.36)
Land Use					
% Woodland savanna	Woodland	16.08 (13.14)	12.23 (5.46)	13.42 (6.41)	15.09 (7.18)
% Parkland savanna	Parkland	18.15 (18.92)	0 (0)	0.84 (2.29)	9.56 (23.57)
% Grassy-woody savanna	Grassy_Woody	10.56 (8.96)	1.43 (1.47)	1.51 (2.86)	10.1 (14.3)
% Palm swamp	Palm_swamp	1.39 (3.23)	0.42 (1.16)	2.48 (2.59)	0.58 (1.29)
% Pasture use	Pasture	41.24 (18.1)	12.22 (10.68)	10.4 (14.62)	13.65 (17.29)
% Agricultural use	Agriculture	3.07 (4.12)	71.34 (14.24)	68.2 (20.41)	50.13 (29.9)
% Eucaliptus forest	Eucaliptus	9.14 (11.17)	0.21 (1.32)	0.85 (1.64)	0 (0)
% Natural land use	Natural	46.17 (19.21)	14.08 (5.35)	18.25 (7.35)	35.33 (25.15)
Distance to cities (km)	City_dist	17.17 (10.38)	11.81 (5.64)	17.09 (7.69)	15.68 (8.6)
Distance to paved highways (km)	Highway_dist	5.31 (4.79)	1.39 (0.8)	2.93 (2.52)	6.89 (4.77)
Density of homes in the basin (houses/km²)	House_density	0.96 (2.62)	12.53 (26.54)	20.6 (115.83)	8.42 (44.22)
Site scale					
Hydromorphology					
Site length (m)	Reachlen	181.28 (62.88)	165.53 (30.91)	172.65 (47.65)	151.5 (8.02)
Mean thalweg depth (cm)	depth_T	42.21 (17.28)	39.15 (16.9)	36.19 (14.23)	28.68 (16.48)
Mean wetted width (m)	width	3.77 (2.34)	3.7 (1.62)	3.92 (2.08)	2.54 (1.06)
Mean bankfull width (m)	BKF_W	6.59 (3.61)	6.11 (2.72)	6.91 (3.18)	4.72 (1.99)
Mean bankfull height (m)	BKF_H	0.95 (0.34)	0.96 (0.34)	1.14 (0.37)	0.89 (0.24)
Mean width x mean depth (m²)	WXD	1.69 (1.49)	1.56 (1.12)	1.48 (1.02)	0.78 (0.75)
Mean width/depth ratio (m/m)	WD_RAT	9.88 (6.97)	10.35 (4.66)	11.85 (6.48)	10.57 (5.23)
Mean bank angle (degrees)	BKA	50.31 (21.78)	44.34 (13.15)	42.18 (12.54)	37.71 (11.99)
Water surface gradient over site (%)	SLOPE	0.01 (0.01)	0.01 (0.01)	0.01 (0.01)	0.01 (0.01)
Channel sinuosity	SINU	1.24 (0.07)	1.22 (0.07)	1.24 (0.08)	1.19 (0.09)
Substrate					
Mean embeddedness (%)	EMBED	57.87 (24.92)	64.3 (14.61)	59.16 (20.25)	61.01 (19.98)
% bedrock (>4000 mm)	PCT_BDRK	13.18 (21.18)	8.33 (17.87)	6.28 (14.29)	2.81 (6.42)
% boulders (250 to 4000 mm)	PCT_BL	11.89 (16.29)	6.39 (8.08)	3.98 (6.14)	2.41 (3.84)
% cobble (64 to 250mm)	PCT_CB	9.07 (12.95)	10.07 (12.41)	8.11 (9.91)	6.82 (8.5)
% coarse gravel (16 to 64 mm)	PCT_GC	2.88 (4.93)	4.87 (8.81)	6.32 (7.2)	12.52 (13.26)
% fine gravel (2 to 16mm)	PCT_GF	5.9 (12.67)	12.69 (11.95)	10.95 (10.71)	16.53 (11.91)

	Variables	Variable code	Hydrologic unit			
			TM	VG	SS	NP
Flow	% sand (0.6 to 2 mm)	PCT_SA	7.84 (11.32)	14.01 (12.72)	23.74 (25.61)	19.05 (15.04)
	% fines (<0.6 mm)	PCT_FN	32.36 (33.57)	27.58 (22.64)	17.05 (19.18)	16.55 (18.79)
	% Organic matter	PCT_ORG	14.53 (18.18)	13.01 (13.32)	19.21 (16.35)	18.36 (11.86)
	% Large Wood	PCT_WD	1.49 (3.33)	1.38 (3.18)	1.31 (2.24)	0.33 (0.85)
	Log10 estimated geometric mean substrate diameter (mm)	LSUB_DMM	0.28 (1.87)	0.23 (1.25)	0.24 (1.03)	0.18 (1)
	Log10 - Relative Bed Stability (dimensionless: m/m))	LRBS	-1.12 (1.64)	-1.34 (1.13)	-1.48 (1)	0.08 (0.57)
	Flow - instantaneous discharge(m ³ /s)	FLOW_2	0.05 (0.08)	0.29 (0.23)	0.54 (1.27)	0.12 (0.12)
	Velocity mean (m/s)	VEL	0.05 (0.07)	0.29 (0.15)	0.93 (3.5)	0.38 (0.31)
	% Glides	PCT_GL	36.74 (30.58)	59.75 (28.11)	67.72 (21.97)	65.13 (24.93)
	% rapids and riffles	PCT_FAST	10.92 (12.34)	35.25 (28.22)	27.88 (20.7)	26.38 (24.86)
	% pools	PCT_POOL	52.33 (37.44)	5 (12.71)	4.4 (12.88)	8.49 (14.83)
	Sequence fasts, glides and pools (1= maximum Heterogeneity, 0= maximum homogeneity)	SEQ_FLO_1	0.07 (0.06)	0.06 (0.04)	0.06 (0.04)	0.07 (0.04)
	Canopy cover					
	Mean mid-channel canopy density (%)	CDENMID	72.61 (25.01)	78.27 (15.86)	76.01 (24.44)	84.85 (19.61)
In-stream cover	Mean canopy cover > 0.3m DBH	CL	6.24 (8.56)	9.96 (8.79)	8.11 (7.13)	13.64 (11.65)
	Mean canopy cover <= 0.3m DBH	CS	12.57 (9.45)	16.36 (11.4)	19.53 (19.76)	29.18 (19.11)
	Mean woody mid-layer cover	MW	20.87 (12.08)	25.44 (16)	23.95 (16.01)	29.08 (15.22)
	Mean herbaceous mid-layer cover	MH	15.31 (11.95)	15.21 (16.74)	10.5 (10.36)	16.93 (14.7)
	Mean woody ground-layer cover	GW	12.66 (8.73)	15.09 (11.12)	12.83 (10.06)	18.47 (13.25)
	Mean herbaceous ground-layer cover	GH	27.03 (21.44)	17.91 (14.36)	21.05 (18)	19.19 (15.33)
	Mean exposed soil	GB	26.05 (16.8)	18.06 (14.44)	23.74 (16.42)	14.63 (9.86)
	Mean riparian veg canopy cover	C	18.81 (16.94)	26.32 (17.29)	27.64 (24.87)	42.82 (28.24)
	Mean riparian veg mid-layer cover	M	36.19 (20.1)	40.65 (26.64)	34.46 (21.46)	46.01 (24.2)
	Mean riparian veg ground cover	G	39.69 (22.22)	33 (18.6)	33.88 (21.56)	37.66 (23.88)
	Prop. Areal cover filamentous algae	FC_ALG	5.11 (9.72)	0.15 (0.92)	3.16 (8.05)	0.52 (1.98)
	Prop. Areal cover aquatic macrophytes	FC_AQM	1.43 (4.3)	0.5 (1.56)	2.85 (10.47)	2.86 (7.94)
	Prop. Areal cover large wood	FC_LWD	3.81 (7.05)	5.69 (8.59)	3.13 (5.27)	1.84 (2.82)
	Prop. Areal cover brush	FC_BRS	7.07 (9.61)	10.64 (10.21)	11.56 (10.6)	8.56 (6.4)
	Prop. Areal cover live trees	FC_ROT	8.19 (10.31)	12.75 (7.68)	13.69 (15.56)	20.07 (13.34)

Variables	Variable code	Hydrologic unit			
		TM	VG	SS	NP
Prop. Areal cover leaf pack	FC_LEB	20.49 (19.23)	20.85 (19.85)	17.06 (15.32)	22.84 (17.43)
Prop. Areal cover undercut banks	FC_UCB	3.63 (5.35)	5.72 (5.7)	5.84 (6.95)	6.64 (6.88)
Prop. Areal cover boulders	FC_RCK	18.05 (24.9)	10.53 (16.5)	10.97 (15.98)	5.72 (8.13)
Water quality					
DO (mg/L)	OXY	7.84 (2.67)	8.74 (2.91)	7.8 (1.15)	7.86 (0.89)
pH	pH	7.67 (0.5)	7.5 (0.83)	6.9 (0.53)	6.82 (0.74)
Turbidity (UNT)	TURB	6.36 (8.67)	5.93 (4.53)	6.88 (4.19)	4.88 (5.8)
Conductivity(μS/cm)	COND	63.67 (49.45)	39.34 (17.35)	68.71 (51.17)	22.36 (15.11)
TDS (mg/L)	TDS	42.1 (33.33)	23.54 (15.65)	38.59 (31.54)	11.71 (7.63)
Water temp (°C)	TEMP	17.23 (1.82)	20.45 (1.26)	20.25 (1.7)	19.33 (1.66)
Total Nitrogen (mg/L)	NO3	0.08 (0.02)	0.11 (0.03)	0.1 (0.03)	0.09 (0.02)
Alkalinity	ALCA	0.02 (0.01)	0.02 (0.02)	0.01 (0.05)	0.02 (0.03)

Table S2: Results of co-inertia analyses performed between each set of environmental variables and EPT taxa (and trait) composition. *Rv*: correlation coefficient between tables, *P*: simulated probability equal to the frequency of random values higher than the observed *Rv*-coefficient.

	% variance		% environment	% EPT	<i>Rv</i>	<i>P</i>
Taxa composition	Axis 1	Axis 2				
Geophysical features	43.8	30.1	87.7	52.6	0.194	0.001
Land use	71.1	15.6	92.7	59.7	0.221	0.001
Hydromorphology	80.2	11.8	91.0	83.7	0.210	0.001
Substrate	80.4	9.2	98.2	83.1	0.237	0.001
Flow	79.6	11.3	98.9	40.4	0.181	0.001
Riparian canopy cover	55.9	26.3	92.5	24.8	0.077	0.002
In-stream habitat cover	63.5	15.6	79.6	72.8	0.150	0.001
Water quality	59.6	18.1	92.9	47.6	0.177	0.001
Trait composition						
Geophysical features	60.5	29.7	81.0	85.5	0.083	0.001
Land use	82.2	13.8	86.8	93.8	0.139	0.001
Hydromorphology	50.9	34.5	77.1	42.3	0.041	0.057
Substrate	80.8	7.5	91.8	54.6	0.078	0.001
Flow	80.8	11.8	96.2	67.7	0.092	0.001
Riparian canopy cover	64.5	25.2	98.6	46.8	0.050	0.015
In-stream habitat cover	45.6	25.8	59.2	45.0	0.034	0.140
Water quality	69.9	23.6	65.6	80.5	0.092	0.001

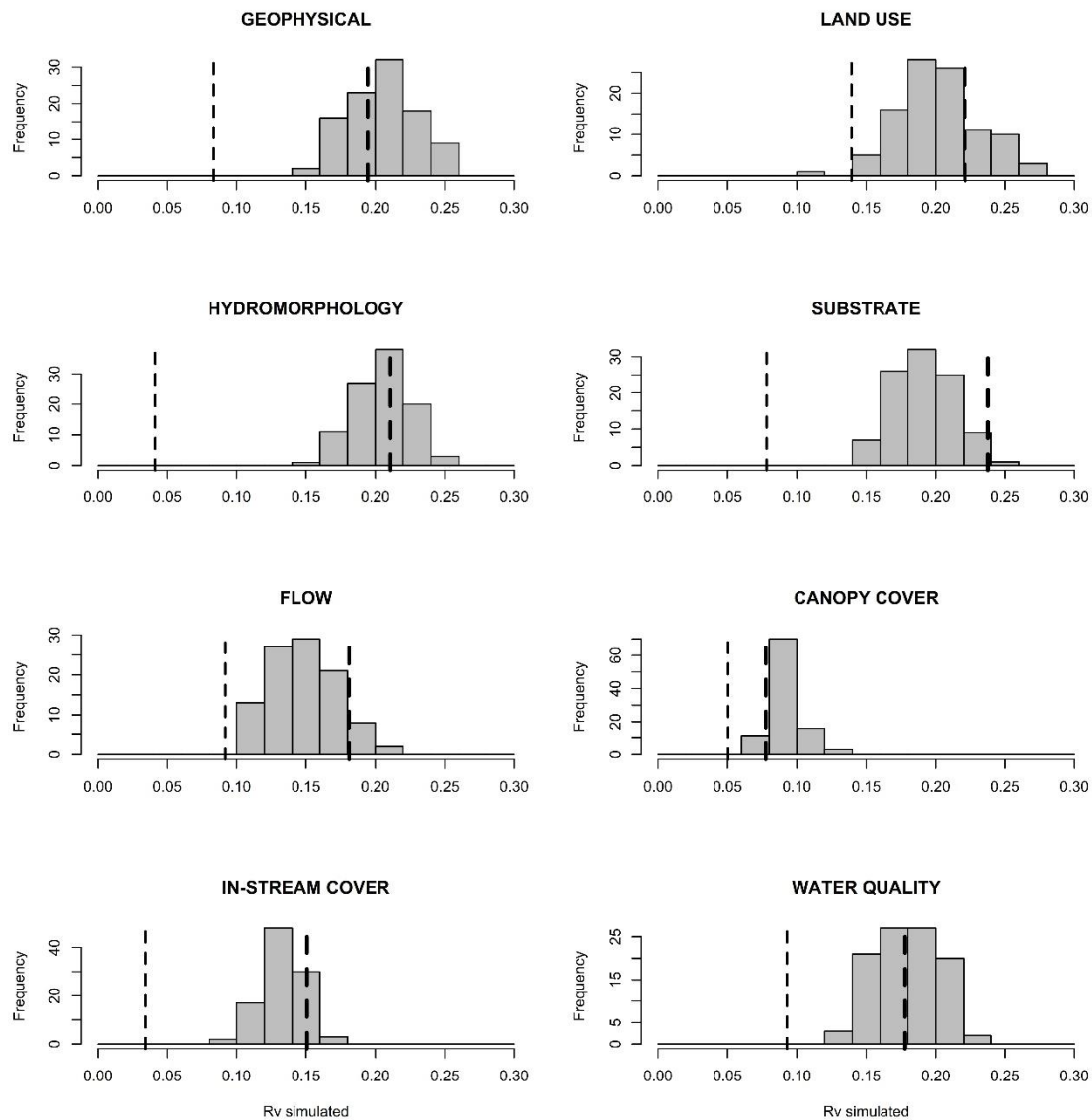


Figure S1: Observed (broken lines) and frequency of 100 simulated values (for 28 randomly selected genera, corresponding to the number of the 28 trait categories) of the variance explained by each group of environmental variables. First broken and thinner line: traits; second dotted and thicker line: taxonomy.

Table S3: Trait profiles (proportion) of 74 neotropical genera of Ephemeroptera, Plecoptera and Trichoptera for 28 categories in 7 biological traits.

Genus	Body size						Potential number of cycles per year		Feeding habits					Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder
Ephemeroptera																												
Americabaetis	0.03	0.48	0.35	0.1	0.05	0	0	1	0.4	0	0.6	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0.25	0	0.75	0	1	0	0
Apobaetis	0.07	0.48	0.38	0.07	0	0	0	1	0.17	0.33	0.5	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Askola	0	0.21	0.42	0.21	0.17	0	0	1	1	0	0	0	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Asthenopus	0	0	0.04	0.27	0.58	0.11	1	0	0.4	0	0.2	0.4	0	0.75	0	0.25	0	0	0	0.25	0.75	1	0	0	0	1	0	0
Aturbina	0.01	0.35	0.34	0.28	0.03	0	0	1	0	0	1	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0	0	1	0	1	0	0
Baetodes	0.37	0.56	0.08	0	0	0	0	1	0.5	0	0.5	0	0	0	0	0.29	0.29	0.43	0	0	1	0.25	0	0.75	0	1	0	0
Caenis	0.07	0.39	0.38	0.14	0.03	0	0	1	0.6	0	0.4	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0	1	0	0	1	0	0
Callibaetis	0	0.11	0.23	0.25	0.41	0	0	1	0	0	1	0	0	0	0	0	0.4	0.6	0	0.25	0.75	1	0	0	0	1	0	0
Camelobaetidius	0.06	0.13	0.31	0.18	0.32	0	0	1	0.5	0	0.5	0	0	0.13	0	0.25	0.25	0.38	0	0.33	0.67	0.4	0	0.6	0	1	0	0
Campsurus	0.02	0.08	0.12	0.15	0.54	0.09	1	0	0.67	0	0	0.33	0	0.75	0	0.25	0	0	0	0.25	0.75	1	0	0	0	1	0	0
Campylocia	0	0	0	0.1	0.35	0.55	0.22	0.78	0.17	0.33	0	0.5	0	0.43	0	0.29	0.29	0	0	0.5	0.5	0.6	0	0.4	0	1	0	0
Cloeodes	0.02	0.47	0.33	0.16	0.02	0	0	1	0.4	0	0.6	0	0	0	0	0.43	0.29	0.29	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Cryptonympha	0	0.31	0.38	0.31	0	0	0	1	0	0	1	0	0	0.14	0	0.29	0.29	0.29	0	0.25	0.75	0	0	1	0	1	0	0
Farrodes	0.06	0.44	0.3	0.16	0.03	0	0	1	0.5	0	0.5	0	0	0	0	0.29	0.29	0.43	0	0	1	0.25	0.75	0	0	0	1	0
Guajirolus	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0.4	0	0.6	0	0.25	0.75	0	0	1	0	1	0	0
Hagenulopsis	0.15	0.35	0.26	0.2	0.04	0	0.4	0.6	0.5	0	0.5	0	0	0.67	0	0.33	0	0	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Hermanella	0	0.27	0.18	0.36	0.18	0	0.4	0.6	0	0	1	0	0	0	0	0.4	0	0.6	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Hexagenia	0	0.17	0	0.5	0.33	0	1	0	0.75	0	0	0.25	0	1	0	0	0	0	0	0.5	0.5	1	0	0	0	1	0	0
Hydrosmilodon	0.02	0.21	0.29	0.36	0.12	0	1	0	0.4	0	0.6	0	0	0.75	0	0.25	0	0	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Latineosus	0.12	0.45	0.14	0.19	0.1	0	0	1	0.6	0	0.4	0	0	0.4	0	0.6	0	0	0	0.5	0.5	0	0.5	0.5	0	1	0	0
Leptohyphes	0.22	0.42	0.24	0.09	0.03	0	1	0	0.5	0.17	0.33	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.17	0.5	0.33	0	1	0	0
Leptohyphodes	0	0	0.07	0.14	0.79	0	0	1	0.5	0.17	0.33	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0
Massartella	0	0.09	0.06	0.21	0.42	0.23	0.4	0.6	0.41	0.04	0.54	0.01	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Miroculis	0.02	0.27	0.26	0.32	0.14	0	0	1	0.5	0	0.5	0	0	0	0	0.5	0	0.5	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Paracloeodes	0.02	0.38	0.35	0.24	0.01	0	0	1	0	0	1	0	0	0	0	0.5	0.17	0.33	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Paramaka	0	1	0	0	0	0	0.4	0.6	0	0	1	0	0	0	0	0.6	0	0.4	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Rivudiva	0	0.13	0.39	0.48	0	0	0	1	0.5	0	0.5	0	0	0	0	0.5	0.17	0.33	0	0.25	0.75	0	0	1	0	1	0	0
Simothraulopsis	0	0	0.11	0.33	0.56	0	0.4	0.6	0.4	0	0.6	0	0	0	0	0.5	0	0.5	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Spiritiops	0	0	0	0	0	0	0	1	0.2	0.2	0.6	0	0	0	0	0	0.4	0.6	0	0.25	0.75	0.5	0	0.5	0	1	0	0
Terpides	0	0.09	0.16	0.28	0.47	0	0.4	0.6	0.38	0.38	0.25	0	0	0.43	0	0.29	0.14	0.14	0	0.67	0.33	0.25	0.75	0	0	1	0	0
Thraulodes	0.05	0.33	0.31	0.18	0.12	0	1	0	0.43	0	0.43	0.14	0	0.33	0	0.22	0.33	0.11	0	0.75	0.25	0.25	0.75	0	0	1	0	0

Genus	Body size						Potential number of cycles per year		Feeding habits						Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder	
<i>Traverhypes</i>	0.08	0.36	0.32	0.22	0.01	0	0	1	1	0	0	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0	
<i>Tricorythodes</i>	0.11	0.28	0.39	0.2	0.03	0	0	1	0.75	0	0.25	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0	
<i>Tricorythopsis</i>	0.19	0.77	0.04	0	0	0	0	1	0.75	0	0.25	0	0	0	0	1	0	0	0	0.5	0.5	0.25	0.75	0	0	1	0	0	
<i>Ulmeritoides</i>	0.03	0.25	0.18	0.21	0.33	0.01	1	0	0.41	0.04	0.54	0.01	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0	
<i>Varipes</i>	0	0	0	0	0	0	0	1	0.5	0.17	0.33	0	0	0	0	0.17	0.33	0.5	0	0	1	0.25	0	0.75	0	1	0	0	
<i>Waltzoyphius</i>	0.02	0.17	0.31	0.4	0.11	0	0	1	0	0	1	0	0	0	0	0.43	0.29	0.29	0	0.25	0.75	1	0	0	0	1	0	0	
<i>Zelus</i>	0.09	0.43	0.3	0.16	0.02	0	0	1	0	0	1	0	0	0	0	0.38	0.25	0.38	0	0.25	0.75	1	0	0	0	1	0	0	
Plecoptera																													
<i>Anacroneuria</i>	0.04	0.15	0.23	0.2	0.28	0.09	0	1	0.2	0.2	0	0	0.6	0	0	0.5	0.33	0.17	0.5	0.5	0	0.33	0.67	0	0	1	0	0	
<i>Grypopteryx</i>	0.12	0.47	0.06	0.18	0.18	0	1	0	0	1	0	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
<i>Kempnya</i>	0	0	0	0.2	0.6	0.2	1	0	0	0	0	0	1	0	0	0	1	0	0.5	0.5	0	1	0	0	0	1	0	0	
<i>Paragrypopteryx</i>	0.12	0.74	0.14	0	0	0	1	0	0.33	0.33	0.33	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
<i>Tupiperla</i>	0.01	0.2	0.35	0.27	0.17	0	1	0	0.33	0.33	0.33	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
Trichoptera																													
<i>Alisotrichia</i>	0.58	0.33	0	0	0.08	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	1	0	0	0	0	0	1	
<i>Anchitrichia</i>	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	0.51	0.14	0.35	0	0	0	1	
<i>Atanatolia</i>	0.14	0	0.14	0.43	0.29	0	1	0	0.07	0.36	0.32	0	0.25	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Atopsyche</i>	0	0.17	0.24	0.28	0.29	0.03	1	0	0	0.25	0	0	0.75	0	0	0.43	0.43	0.14	0	0	1	0	0	1	0	1	0	0	
<i>Austrotinodes</i>	0	0.09	0.28	0.37	0.26	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0.5	0.5	
<i>Barypenthus</i>	0	0	0	0.19	0.25	0.56	1	0	0.43	0.29	0.29	0	0	0	0	0.6	0.4	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Chimarra</i>	0	0.11	0.19	0.23	0.37	0.1	1	0	0	0.25	0	0.75	0	0	0	0.5	0.5	0	0	0	1	0	0	1	0	0	1	0	
<i>Cyrnelus</i>	0	0.11	0.11	0.33	0.44	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Grumichella</i>	0	0	0	1	3	0	0	0	2	1	2	0	0	0	0	0	3	0	3	1	0	0	0	3	0	0	1	3	
<i>Helicopsyche</i>	0	0.18	0.43	0.33	0.08	0	0	1	0.6	0	0.4	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0	0	0	1	0	0.25	0.75	
<i>Hydroptila</i>	0.17	0.76	0.06	0.01	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0.67	0.33	0	0	0	0	1	
<i>Itaura</i>	0.1	0.62	0.26	0.01	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0.25	0.75	0	0	0.4	0.6	
<i>Leptonema</i>	0	0	0.12	0.05	0.13	0.7	0	1	0	0.2	0	0.6	0.2	0	0	0.33	0.5	0.17	0	0	1	0	0	1	0	0	1	0	
<i>Macronema</i>	0	0.12	0.05	0.16	0.26	0.41	0	1	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Macrostemun</i>	0	0.08	0.08	0.15	0.23	0.46	1	0	0	0.13	0	0.73	0.13	0	0	0	1	0	0	0	1	0	0	1	0	0	0.5	0.5	
<i>Marilia</i>	0.01	0.09	0.23	0.27	0.39	0.01	1	0	0.38	0.13	0.38	0	0.13	0	0.5	0.5	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Metrichia</i>	0.4	0.53	0.07	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	0	0.5	0.5	0	0	0	1	
<i>Mortoniella</i>	0.1	0.7	0.2	0	0	0	1	0	0.5	0	0.5	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0	0.17	0.5	0.33	0	0.4	0.6	
<i>Nectopsyche</i>	0.02	0.28	0.21	0.28	0.21	0	1	0	0.29	0.43	0.29	0	0	0	0.17	0.5	0.33	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Neotrichia</i>	0.71	0.29	0	0	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0.4	0	0.6	0	0	0	1	

Genus	Body size						Potential number of cycles per year		Feeding habits						Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder	
<i>Notalina</i>	0.22	0.11	0.11	0.22	0.33	0	1	0	0	0	1	0	0	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Nyctiophylax</i>	0.11	0.67	0.11	0	0	0.11	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Oecetis</i>	0.1	0.31	0.34	0.2	0.05	0	0	1	0	0	0	0	1	0	0	0.5	0.5	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Oxyetira</i>	0.05	0.66	0.24	0.06	0	0	1	0	0	0	1	0	0	0	0.5	0.5	0	0	0.75	0.25	0	0.5	0	0.5	0	0	0	1	
<i>Phylloicus</i>	0.05	0.21	0.19	0.13	0.3	0.11	0	1	0.25	0.75	0	0	0	0	0	0.75	0.25	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Polycentropus</i>	0	0.12	0.19	0.27	0.41	0.02	1	0	0	0.2	0	0.2	0.6	0	0	0.5	0.5	0	0	0	1	0	0	1	0	0	1	0	
<i>Polyplectropus</i>	0	0.01	0.09	0.24	0.66	0	1	0	0	0.07	0	0.4	0.53	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Protoptila</i>	0.05	0.47	0.34	0.14	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	1	0	0	0	0	1	0	0	0.4	0.6	
<i>Smicridea</i>	0	0.25	0.25	0.24	0.24	0	0	1	0	0.2	0	0.6	0.2	0	0	0.33	0.5	0.17	0	0	1	0	0	1	0	0	1	0	
<i>Triplectides</i>	0	0.07	0.07	0.1	0.5	0.27	1	0	0	1	0	0	0	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Wormaldia</i>	0	0.91	0	0.03	0.06	0	1	0	0	0	0.4	0.6	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	



Chapter III

Land cover disturbance homogenizes aquatic insect trait composition in savanna streams

Chapter 3 is a version of a manuscript in coauthoring with Sylvain Dolédec and Marcos Callisto.

Land cover disturbance homogenizes aquatic insect trait composition in savanna streams

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Highlights

- We assessed the influence of human-induced disturbances on the taxonomic and trait composition of Neotropical aquatic invertebrates.
- Aquatic assemblages in least disturbed streams were highly specialized, whereas assemblages in disturbed streams demonstrated functional homogenization.
- Riparian canopy cover was the main driver of the functional trait composition of least disturbed streams.

Abstract

By modifying local habitat conditions, the alteration of land cover results in potentially severe faunal impairment, which subsequently affects ecosystem function. We analyzed changes in the composition of Ephemeroptera, Plecoptera and Trichoptera (EPT) assemblages along a gradient of human disturbance intensity in 186 Neotropical savanna headwater streams. Whereas EPT genus richness did not differ among the levels of disturbance, functional richness and diversity significantly decreased from least to highly disturbed streams. Using a combination of RLQ and fourth-corner analyses, we found that 12 of 28 trait categories were significantly associated with changes in land use and cover intensity across the catchment, local physical habitat and water quality. The proportion of individuals with large body size and low body flexibility with <1 reproductive cycle per year, building case, and climbing characterized EPT assemblages of least disturbed streams. In addition, least disturbed streams demonstrated

high community specialization compared with disturbed streams. To our knowledge, this study is the first that examines the response of invertebrate functional trait composition and diversity along a gradient of human disturbance at a large spatial scale in the Neotropics, thus demonstrating the applicability of multiple trait-based approaches.

Key-words: functional diversity, multiple traits, aquatic invertebrates, biotic homogenization.

Introduction

Human pressures related to agriculture and land cover modifications are the main drivers of ecological worsening of stream and river ecosystems, primarily due to increases in nutrients and sedimentation and hydromorphological alterations (Carpenter et al., 2011; Dudgeon et al., 2006; Vörösmarty et al., 2010). These changes have led to the simplification of habitats and reduced the diversity of aquatic communities, imperiling the ecological integrity and the sustainability of ecological processes and associated ecosystem services (Cardinale et al., 2012; Hooper et al., 2005). Furthermore, multiple human pressures yield taxonomic and functional losses in assemblages through the reduction of the number of specialized species (Mondy and Usseglio-Polatera, 2014). Ecological specialization refers to the limitation in ecological niche space used by a species due to its specific traits (Futuyma and Moreno, 1988). As a result, homogenization at the community level limits the functions provided by the community and their ability to respond to human pressures, which may lead to the alteration of ecosystem functioning and services (Clavel et al., 2011; Petsch, 2016).

Functional traits are morphological, physiological, or behavioral characteristics that are expressed in the phenotypes of individuals and considered relevant to their ecological requirement and/or their effects on ecosystem properties (Violle et al., 2007). Trait-based approaches have been successfully used to assess the effects of human pressures on aquatic invertebrate communities (e.g., Dolédec et al., 1999; Culp et al. 2011; Gutiérrez-Cánovas et al., 2015; Piló et al., 2016) with the following advantages: (i) biological trait responses are spatially stable in least-disturbed situations (e.g., Statzner et al. 2004; Bonada et al., 2007), which potentially offer a more reliable assessment of ecological integrity compared with the use taxonomic composition that naturally varies across large spatial scales; (ii) biological traits allow

a more mechanistic understanding to identify the causes of changes in communities (e.g., Dolédec et al., 2011; Verberk et al., 2013); and (iii) biological traits respond to a broad range of stressors in a predictable manner (e.g., Dolédec et al., 1999; Usseglio & Beisel 2002; Culp et al., 2011; Mondy & Usseglio, 2014; Mouillot et al., 2013).

In the Neotropics, the main human disturbances include habitat fragmentation and land cover conversion for agricultural purposes (Overbeck et al., 2015; Hunke et al., 2015), leading to several consequences for stream environments, such as reduced water quality, excess bottom siltation, altered flow regimes, and changes in stream channel structure (Allan et al., 1997; Leal et al., 2016). In other regions, authors have demonstrated that not only the composition and richness but also the trait composition of benthic invertebrate assemblages is affected by human disturbances (e.g., Archaimbault et al., 2010; Mondy *et al.*, 2016; Ding et al., 2017). Neotropical savanna (Cerrado biome), the second largest biome in Brazil and a biodiversity hotspot (Myers et al., 2000), encompasses three of the largest watersheds in South America. Despite its enormous importance for freshwater species conservation and the provision of ecosystem services (Strassburg et al., 2017), the effects of human disturbances in the functional structure of aquatic invertebrate assemblages have been largely overlooked given that research and conservation efforts are very limited. Therefore, assessing changes in trait composition may facilitate disentangling the effects of disturbance on species assemblages (Leitão et al., 2017) and understanding how human disturbances affect the functional structure of aquatic assemblages.

As a result, we made *a priori* predictions on the potential response of the trait composition of benthic invertebrate assemblages to land cover alteration (e.g., deforestation) and the associated impairment of the hydromorphology (e.g., sedimentation and flow regime) and stream water quality (e.g., increase in nutrient inputs). Direct effects of riparian vegetation cover removal include the reduction of litter input, which should subsequently limit the proportion of shredders. Indirect effects of riparian vegetation cover removal include more frequent flow disturbances, which should involve a selection of organisms with traits conferring resilience, such as small size and several reproduction cycles per year (multivoltinism), and resistance capabilities (streamlined/flattened shape and crawling locomotion). In addition, changing land cover for agricultural purposes may directly involve an increase in sediment

deposition, which should favor burrowers and potentially lead to flow reduction (i.e., due to water abstraction), which should favor swimmers. Finally, changes in water quality associated with organic contamination should favor filter feeders and collector gatherers, and the associated expansion of biofilms should favor scrapers (Table 1). Although we make individual predictions, we are aware that traits correlate in organisms (Verberck et al., 2013).

Table 1. Predictions for trait category responses to human impacts. Impacts may decrease (↓) or increase (↑) the relative abundance of a single trait category (after Statzner and Bêche 2010 and Feio and Dolédec 2012).

Impact type	Effect	Trait response	Rationale
Riparian canopy cover changes	Removal of riparian vegetation cover	↓ Shredders ↑ Scrapers	Decreased leaf litter input and increased autochthonous primary production
Hydromorphological changes	More frequent flow disturbance	↑ Small size ↑ Multivoltinism ↑ Streamlined/flattened ↑ Crawling	Better resilience capacity of smaller sizes and more reproductive cycles
	Increased bottom siltation	↑ Burrowers ↑ High body flexibility ↑ Collectors-gatherers	Use of substrate as refuge Increased deposition of dissolved organic matter in pools
Flow constraints	Flow reduction	↑ Swimmers	Release from flow action in remnant pools
Organic contamination	Organic matter input	↑ Filter-feeders ↑ Collector-gatherers ↑ Scrapers	Food web changes due to increase in organic matter in suspension and more-abundant periphyton algae and biofilms

We designed our study using Ephemeroptera, Plecoptera and Trichoptera (EPT) assemblages to assess the following: (1) potential differences in reliability between taxonomic and trait composition of aquatic insect assemblages to depict human disturbance in the Neotropics similar to those observed elsewhere (e.g., Dolédec et al. 1999); and (2) whether human disturbances also altered community specialization. We hypothesized that (1) because

taxa possess traits that confer different sensitivities to land cover alteration intensity and associated hydromorphological degradation, one would expect a selection of specific co-adapted traits within benthic assemblages, and (2) the more diversified habitat conditions in least-disturbed streams should result in higher taxonomic richness, functional diversity and community specialization compared with streams affected by anthropogenic stressors.

Methods

Study area

We conducted our study in wadeable streams located in the Neotropical savanna (Cerrado biome) of southeastern Brazil. A total of 160 sites (1st- to 3rd-order streams sensu Strahler (1957), defined at a 1:100,000 scale) were sampled in four hydrological units (defined as the contributing drainage areas within 35 km upstream of each of four major hydropower reservoirs) of Nova Ponte, Três Marias, Volta Grande and São Simão (Fig. 1), comprising a total geographic area of 45,180 km². Site details are available in Ferreira et al. (2017) and Firmiano et al. (2017). A set of 26 sites representing least disturbed conditions was additionally sampled in the Nova Ponte hydrological unit (Martins et al. 2017). As recommended by other authors (Hughes et al., 1986; Stoddard et al., 2006), we assessed the good ecological condition at sites based on the minimal human disturbance in the catchment, the absence of direct local influence of human alterations, and the presence of native riparian vegetation at sampling sites.

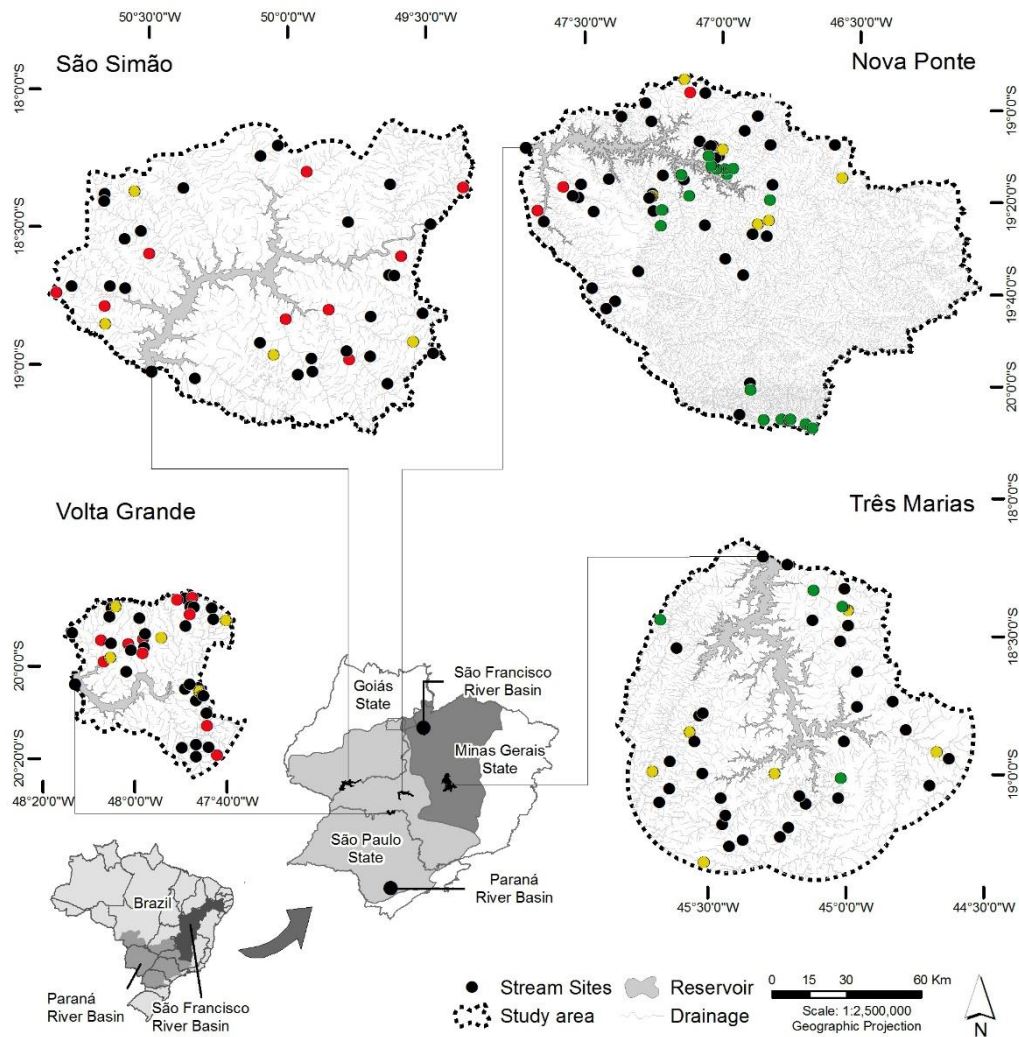


Fig. 1. Locations of wadeable stream sites ($n=186$) in four hydrological units in the Neotropical savanna, Minas Gerais state, southeastern Brazil. Green circles represent least disturbed streams, yellow circles represent intermediately disturbed streams, and red circles represent disturbed sites.

Site selection

We ranked sites from least to most disturbed based on the Integrated Disturbance Index (IDI) developed by Ligeiro et al. (2013). At each site, we measured human activities at local (LDI – Local Disturbance Index) and catchment (CDI – Catchment Disturbance Index) scales and analyzed both scales together through IDI. Briefly, CDI measures land uses in the catchment using a weighted average procedure. Urban areas receive a higher weight than agricultural areas, which receive a higher weight than pasture. LDI is based on the presence of local human pressures (garbage, sewages, buildings, domestic animals, row crops, pasture, erosion and dams) at each site (see Kaufmann et al., 1999). IDI scores were ranked (Table A1), and we

calculated the mean and standard deviation (SD) of the IDI distribution to define the limits of least and most disturbed sites. Least and most disturbed sites were assessed as those deviating from the mean by $-1SD$ and $+1SD$, respectively. The intermediately disturbed sites were those that occurred between these values.

After eliminating five sites with a genus richness <4 , we retained 37 sites classified as least disturbed ($IDI < 0.21$), 22 as disturbed ($IDI > 0.63$) and 122 classified as intermediately disturbed (>0.21 and <0.63). To respect an equal number of sites across human disturbance levels, we randomly selected 22 sites among the least disturbed sites and 22 among the intermediately disturbed sites (Fig. 2). Following this random selection, we eliminated those sites with IDI values close to boundaries. Therefore, we analyzed a total of 66 sites with 22 sites in each level of human disturbance (least, intermediate, and most).

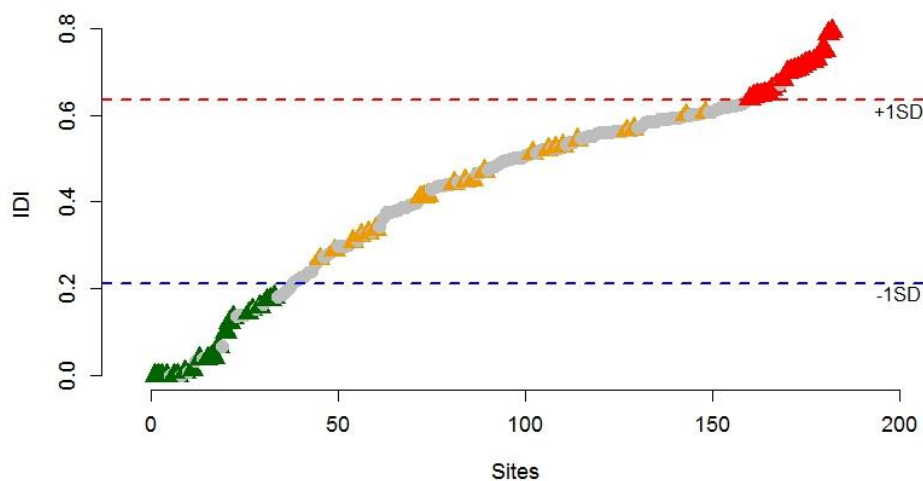


Fig. 2. Cumulative ranking of 181 stream sites from low to high values of human pressure based on the Integrated Disturbance Index (IDI). The mean and standard deviation of the IDI distribution was calculated and defined the least-disturbed and disturbed sites, respectively, as those deviating from the mean by $-1SD$ (blue dotted line) and $+1SD$ (red dotted lined). Green triangles represent the least disturbed streams, yellow triangles represent intermediately disturbed streams, and red triangles represent disturbed sites.

Environmental variables

Environmental variables at each site were described in terms of land use and cover, riparian canopy cover, physical habitat (habitat hydromorphology, substrate size, flow regime, in-stream habitat cover), and water quality (Table A2). Sites were described by a set of 61 environmental metrics (see Castro et al. in revision for further details) (Table A2).

Sampling and biological traits

Benthic macroinvertebrates were sampled with a D-frame kick net (30 cm aperture, 500 μ m mesh). Eleven sub-sample units were taken at each stream following a systematic zig-zag trajectory along the site, generating one composite sample for each site (see Firmiano et al. (2017) for further details). Identification keys at genus or species levels remain limited for Neotropical macroinvertebrates (Moya et al., 2011), and the use of family level identification can lead to the loss of potentially important ecological information (Tomanova et al., 2008). Therefore, we restricted our study to Ephemeroptera, Plecoptera and Trichoptera (EPT) assemblages, given that they are the most studied groups of aquatic invertebrates in the Neotropics. In the laboratory, EPT individuals were identified at the genus level using various taxonomic keys (e.g., Dominguez et al., 2006; Mugnai et al., 2010; Pes et al., 2005). EPT abundances were log-transformed [$\ln(x+1)$] to reduce the effect of dominant species and approximate a normal distribution.

In the Neotropics, the use of multiple trait-based (MTB) approaches is still in the beginning. One important limitation of the use of MTB approaches involves the difficulty to identify information on biological traits, which are lacking for a majority of Neotropical aquatic invertebrate species. We used a trait database recently developed for Neotropical macroinvertebrates fully described in Castro et al. in revision (Table A3). This database contains biological traits and their respective trait categories describing EPT genus profiles in terms of morphology, life cycle, resilience or resistance ability to natural disturbance or human disturbance, and feeding behavior (Table 2).

Table 2. Traits and their categories and codes used for 73 EPT genera collected in Neotropical savanna streams.

Trait	Code	Category
Body size (mm)	less_1.5	<1.5
	bet_1.5_2.5	>1.5 - 2.5
	bet_2.5_3.5	>2.5 - 3.5
	bet_3.5_5	>3.5 - 5.0
	bet_5_10	>5.0 - 10.0
	more_10	>10
Potential number of reproductive cycles per year	less_1y	≤ 1
	more_1y	> 1
Feeding habits	collector_gat	Collector-Gatherer
	shredder	Shredder
	scraper	Scraper
	filter_feeder	Collector-Filterer
	predator	Predator
Locomotion	burrow	Burrower
	climber	Climber
	sprawler	Sprawler
	clinger	Clinger
	swimmer	Swimmer
Body flexibility (°)	flex_less_10	<10
	flex_10_45	>10-45
	flex_more_45	>45
Body form	streamlined	Streamlined
	flattened	Flattened
	cylindrical	Cylindrical
	spherical	Spherical
Relation to substrate	free_living	Free living
	silk_net_builder	Silk net builders
	case_builder	Case builder

Taxonomic richness, functional diversity and community specialization

We assessed traditional metrics, such as taxonomic richness (rarefied) and Shannon index. In addition, we computed functional richness (FRic), which represents the volume in trait space occupied by a community as the smallest convex volume in the n -dimensional trait space, including all organisms in the community (Villéger et al., 2008). We also calculated functional diversity using the functional dispersion index (FDis) proposed by Laliberté and

Legendre (2010). FDis is the mean distance in multidimensional trait space of individual species to the centroid of all species weighted by their relative abundances (Laliberté and Legendre, 2010).

Finally, we assessed community specialization using the indices proposed by Mondy and Usseglio-Polatera (2014). For each taxon and each trait, we calculated a taxon specialization index (TSI). A community specialization index (CSI) was deduced for each trait and each site by averaging the scaled TSIs of taxa weighted by the respective log-transformed abundances (see Mondy and Usseglio-Polatera, 2014 for further details). We further computed a global specialization index by averaging each trait CSI.

After testing for normality of residuals and homoscedasticity, we used ANOVA to evaluate whether the above biological metrics were affected by disturbance. We used the *post hoc* Tukey test to identify differences among the categories when tests were significant ($P < 0.05$).

Trait response of EPT assemblages to human disturbance

To assess the significance of associations between a combination of trait categories and environmental variables, we combined RLQ and fourth-corner analyses as recommended by Dray et al. (2014). This method involves performing correspondence analysis (COA) on the log-transformed abundance of EPT genera (66 sites and 73 EPT genera) to derive scores for sites and genera that have the maximal correlation (Dolédec et al., 1996). To reduce the number of variables (61 initial variables) involved in RLQ, principal components analysis (PCA) was conducted on each group of variables (i.e., land use and cover, habitat morphology, substrate, flow, riparian canopy cover, in-stream cover, and water quality), and we extracted the first four axes of each PCA. Axes significantly related to the IDI index (i.e., human disturbance) were then used as new environmental variables in the RLQ analysis. We tested the global significance of the relationship between EPT biological traits and these environmental variables using a Monte Carlo test (9,999 permutations). As suggested by Dray et al. (2014), we considered model 6, which combines two permutation tests to determine the overall significance of the relationship between trait categories and environmental variables. The first model tests

the null hypothesis that “species assemblages are randomly attributed to sites, irrespective of the site characteristics” (rows of the abundance table; model 2). The second model tests the null hypothesis that “species are distributed irrespective of their traits” (columns of the abundance table; model 4). Finally, for a more detailed and specific interpretation of trait-environment associations, fourth-corner analysis aided the quantifying and testing of all possible bivariate correlations between each trait category or their combination and each environmental variable. In all tests, we applied a false discovery rate adjustment of probabilities to correct for multiple comparisons. Fourth-corner tests were then directly applied onto the RLQ axes.

All analyses were performed in the R environment (R Core Development Team, 2016) with the *vegan* (Oksanen, 2017), *FD* (Laliberté et al., 2014), and *ade4* (Chessel et al., 2004) packages. A schematic diagram with all methodological steps is presented in Fig. 3.

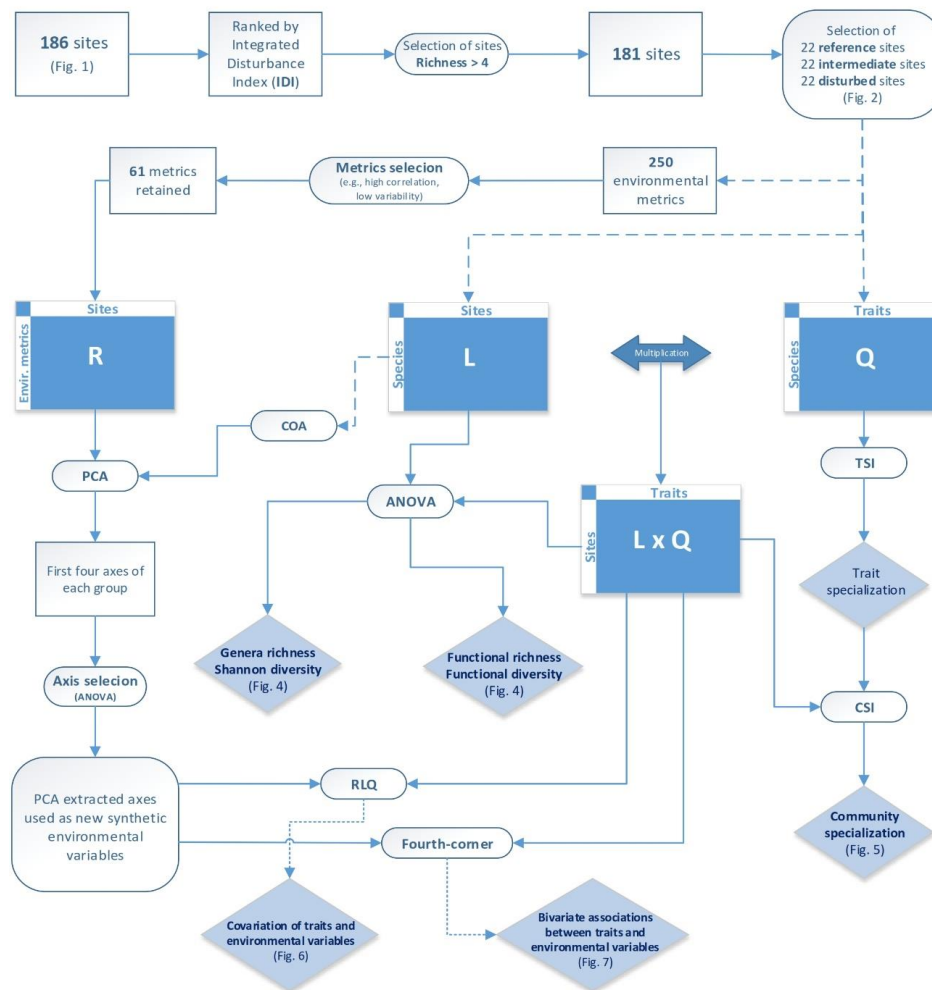


Fig. 3. Schematic diagram presenting the methodological design of site selection and statistical analyses used in this paper.

Results

Taxonomic richness, functional diversity and community specialization

EPT genus rarefied richness did not significantly differ among the levels of human disturbance ($F_{2,63} = 1.39$, $P = 0.255$, Fig. 4a). In contrast, functional richness was increased in the least-disturbed streams ($F_{2,63} = 9.13$, $P < 0.001$, Fig. 4b), which also supported EPT assemblages with higher Shannon ($F_{2,63} = 4.04$, $P = 0.023$, Fig. 4c) and functional diversities ($F_{2,63} = 10.6$, $P < 0.001$, Fig. 4d). In addition, EPT assemblages were overall more specialized in least disturbed compared with most disturbed streams (Fig. 5).

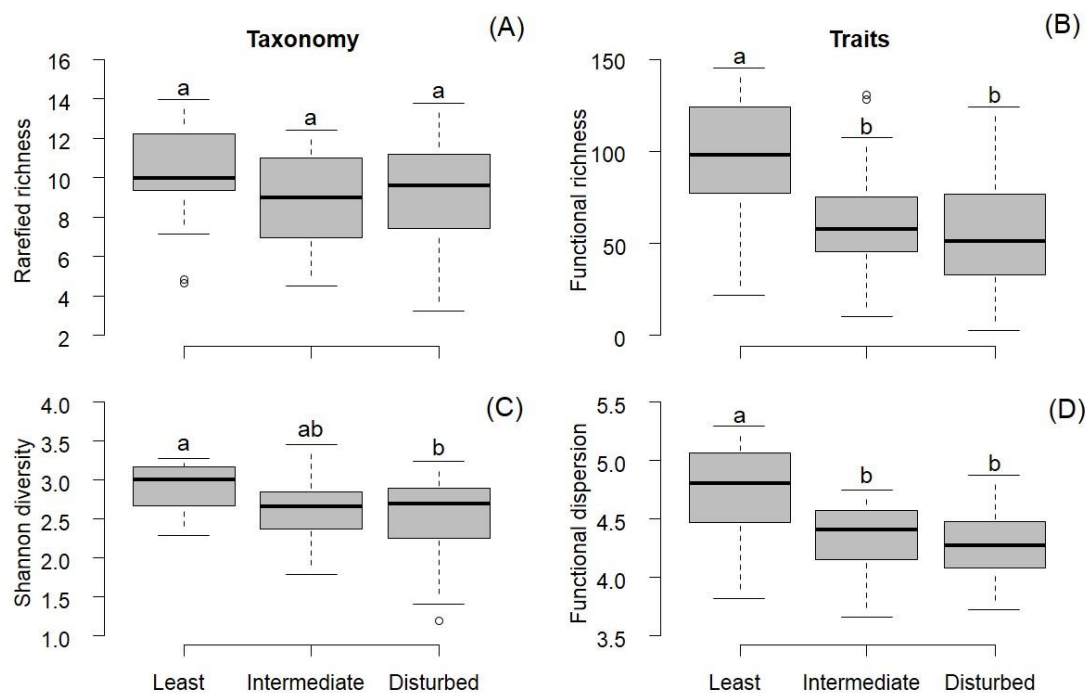


Fig. 4. Difference in (A) genus rarefied richness, (B) functional richness, (C) Shannon diversity, and (D) functional diversity (Functional dispersion) among the three categories of human pressure. Lines in boxes are medians, and box end are quantiles. Whiskers indicate maximum and minimum values, and circles represent outliers. Tukey *post hoc* tests were used for pairwise comparisons. Different letters indicate significant differences among the categories of disturbance.

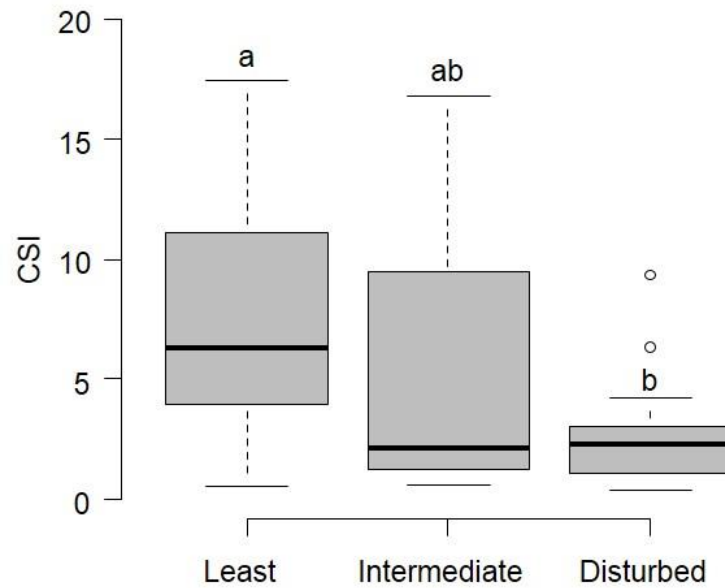


Fig. 5. Overall community specialization index (CSI) for EPT assemblages in each disturbance category. Lines in boxes are medians, and box end are quantiles. Whiskers indicate maximum and minimum values, and circles represent outliers. Tukey HSD *post hoc* tests were used for pairwise comparisons. Different letters indicate significant differences among the categories of human pressure.

Trait response of EPT assemblages to human disturbance

The global RLQ test revealed a significant relationship between genus abundance and environmental variables (model 2, $P=0.001$) as well as genus abundance and biological traits (model 4, $P=0.045$). We focused on the first RLQ axis, given that it explained most of the variability (i.e., 79.3% vs. 8.9% for the second axis; Fig. 6; Table 3) and strongly differentiated least from intermediately disturbed and disturbed streams (Fig. 6b). Environmental variables associated with least disturbed streams included increased mean herbaceous and woody ground-layer cover, higher mean herbaceous and woody mid-layer cover, reduced mean exposed soil (Cano_1 in Fig. 6a), higher percentage of grassy-wood and woodland, lower percentage of agriculture (LandUse_2), and higher sequence of flow types and mean velocity (Flow_4; see supplementary material Fig A1). Intermediate and disturbed streams on the positive side of the first RLQ axis exhibited increased conductivity, total dissolved solids, total nitrogen, total phosphorus (Quality_1 in Fig. 6a), percentage of boulders and cobbles, mean substrate diameter, and percentage of agriculture as well as reduced relative bed stability

(Subs_3), house density, and percentage of natural and parkland cover and highway distance (LandUse_1; see supplementary material Fig A1).

Table 3. Statistics obtained from multivariate analysis with (A) separate analyses demonstrating eigenvalues and percentages of variance that represented the first axis of each analysis, and (B) RLQ analysis demonstrating eigenvalues and percentage of total variance that accounted for the first RLQ axis, covariance and correlation, projected variance of the environment, abundance, trait tables onto the first RLQ axis, and associated percentage of variance compared with separate analyses along the same axis.

	Axis 1	
	eigenvalue	% of variance
(A) Separate analysis		
Environment (PCA)	4.07	40.7
Abundance (COA)	0.27	10.1
Trait (FCA)	0.35	23.9
(B) RLQ analysis		
Eigenvalue	0.03	78.9
Covariance	0.18	
Correlation	0.16	
R/RLQ	3.92	96.2
L/RLQ	0.16	30.9
Q/RLQ	0.30	88.1

Trichoptera, such as *Barypenthus*, *Marilia*, *Triplectides*, and *Oxyetira*, *Nectopsyche*, were associated with least disturbed streams, whereas Ephemeroptera genera mainly occurred in intermediate and disturbed streams (e.g., *Zelus*, *Callibaetis*, *Waltzophius*, *Farrodes*, *Miroculis*) (Fig. 6c). Least disturbed sites had higher proportions of individuals with large body size (>10 mm) and low flexibility (<10°), with <1 reproductive cycle per year, building cases and climbing (Fig. 6d). Intermediate and disturbed sites had increased proportions of free-living and highly flexible (>45°) individuals with small body size (<3.5 mm) and streamlined bodies, reproducing more than once a year, and swimming (Fig. 6d).

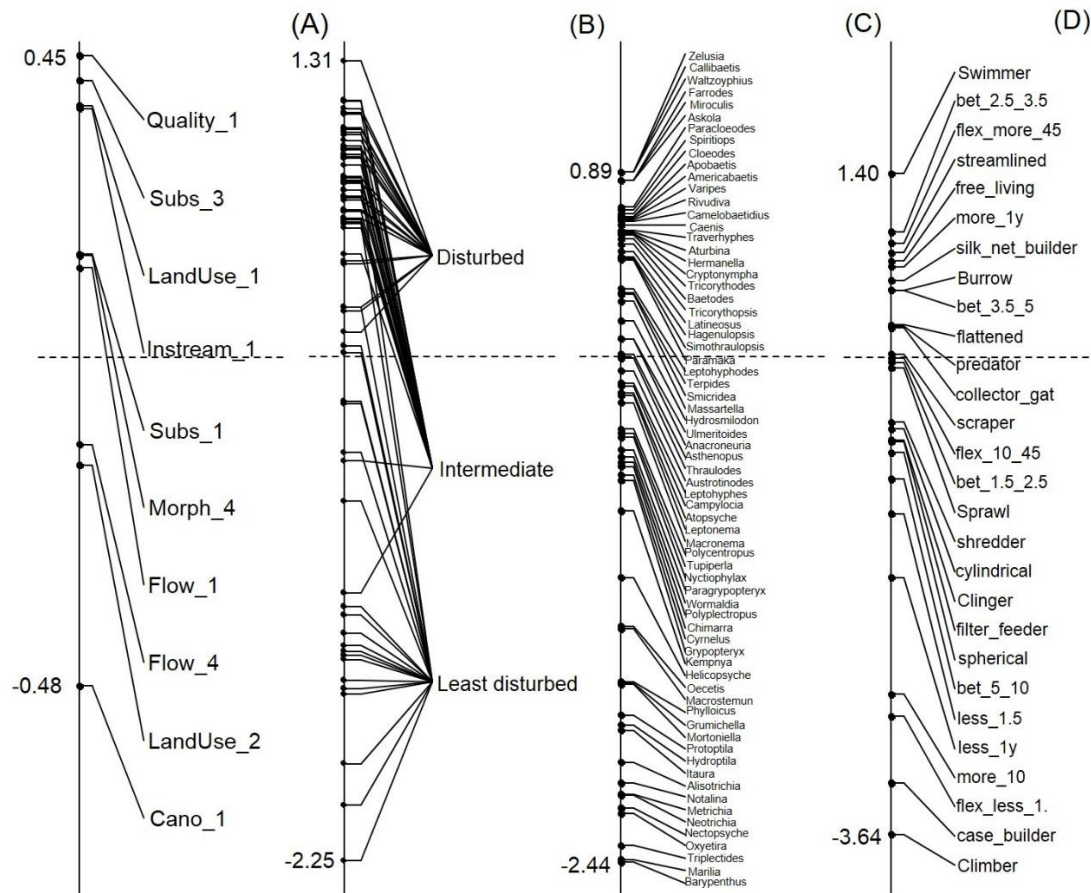


Fig. 6. RLQ analysis first axis scores demonstrating (A) environmental variable loadings (acronyms stand for the type of variable and the axis of the separate PCA), (B) distribution of site scores grouped by disturbance category, (C) EPT genus scores at the weighted average of sites where they are present, and (D) trait scores at the weighted average of their species. Dotted line is the axis center. Acronyms for traits and environmental variables are provided in Tables 1 and S1, respectively.

Fourth-corner analysis revealed significant correlations between several trait categories and environmental variables (Fig. 7). Higher riparian vegetation cover was positively associated with individuals with <1 reproductive cycle per year with a low flexibility of the body (<10°) and building case and negatively associated with swimming individuals with high flexibility of the body (>45°) and smaller body size (<3.5 mm). Lower water quality and bed stability and higher mean substrate diameter were positively associated with organisms with small body size (<3.5 mm), swimming and high body flexibility (Fig. 7). The first trait axis (AxcQ1) is significantly negatively correlated with canopy cover (Cano_1) and positively correlated with land use and cover (LandUse_1), substrate (Subst_3), in-stream cover (Instream_1) and water quality (Quality_1) (Table 4).

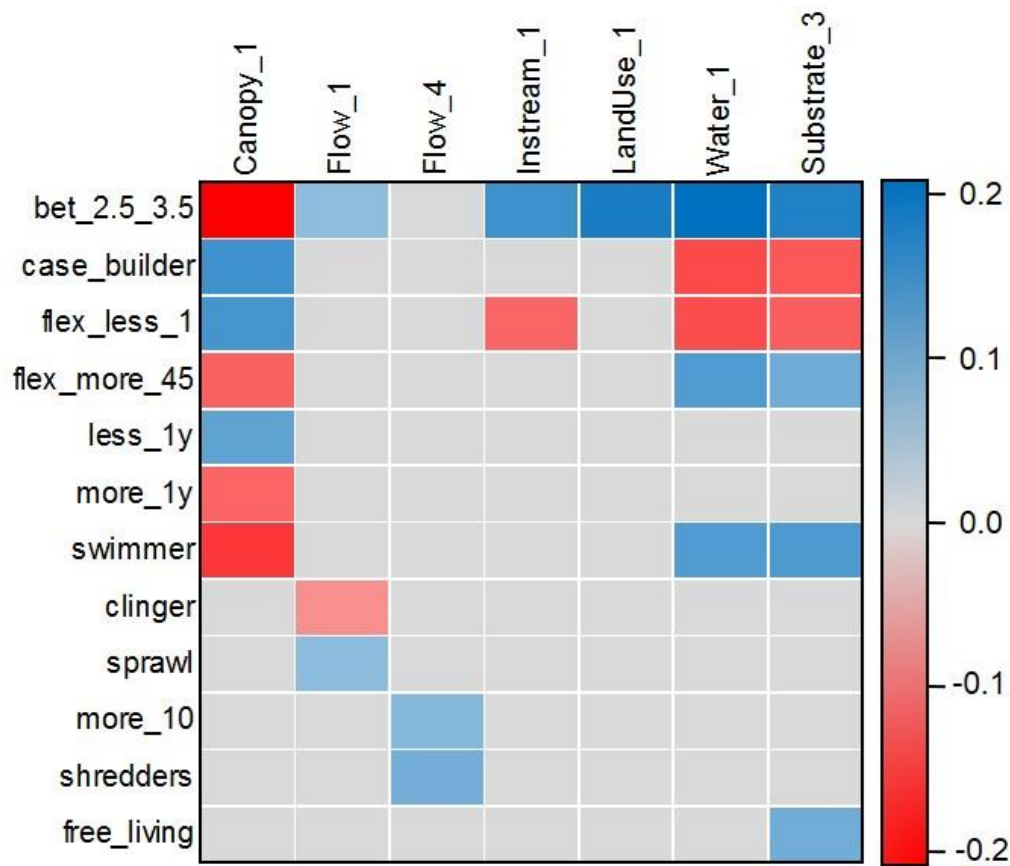


Fig. 7. Trait environment relationship resulting from fourth-corner analysis. Significant positive associations ($P < 0.05$) between the environmental variables and EPT trait categories are represented by blue cells, whereas significant negative associations are represented by red cells. The relative color tone indicates the strength of association. Non-significant associations are gray. The PCA axes of each group of environmental variables are noted along the x-axis. The trait categories are noted along the y-axis. Environmental variables and traits without any association are not presented for clarity. Codes for traits and environmental variables are provided in Table 1 and Table S1, respectively.

Table 4. Correlations between environmental variables (PCA loadings) and trait axis (AxcQ1). *P*-values in bold are significant relationships.

Test	Std.Obs	<i>P</i> value
LandUse_1 / AxcQ1	0.1200	0.0188
LandUse_2 / AxcQ1	-0.0510	0.1329
Morph_4 / AxcQ1	0.0488	0.1512
Subs_1 / AxcQ1	0.0495	0.2697
Subs_3 / AxcQ1	0.1319	0.0005
Flow_1 / AxcQ1	0.0428	0.1511
Flow_4 / AxcQ1	-0.0411	0.1794
Cano_1 / AxcQ1	-0.1557	0.0003
Instream_1 / AxcQ1	0.1188	0.0096
Quality_1 / AxcQ1	0.1436	0.0035

Discussion

Our aim was to examine the reliability of the taxonomic and trait responses of EPT assemblages to overall human disturbance and to assess the effects of human disturbances on community specialization. Trait composition was more reliable than taxonomic composition in the assessment of the effects of human disturbances on the stream environment. In addition, the consequences of human disturbance included reducing the functional richness and diversity of EPT assemblages and increasing their homogenization.

Taxonomic richness, functional diversity and community specialization

In aquatic systems, land cover modification is a major driving force of biodiversity loss (Allan, 2004). The reduced functional richness and diversity observed in our study in the disturbed streams somewhat corroborate the habitat-filter hypothesis (Poff, 1997). This hypothesis postulates that only those taxa possessing a specific set of traits can pass the habitat filter and establish population in a given environment. Environmental filtering occurs when environmental pressures exceed the physiological limits of tolerance of individuals in local populations (Somero, 2010). In this context, human disturbances are additional environmental filters that can change the expected trait composition of assemblages observed in natural conditions (Floury et al., 2017). An increased functional richness implies that more niches are filled by taxa, whereas an increased functional dispersion indicates a more even distribution of a dissimilar trait. In our study, both functional richness and functional dispersion were increased in the least disturbed streams, suggesting that most of the functional trait space was occupied and that the species were well distributed in the functional space in least disturbed streams despite a lack of significant differences in taxonomic richness among the three categories of human disturbance.

In freshwater ecosystems, the replacement of habitat specialists by habitat generalists occurs as a response of assemblages to habitat degradation and land cover alteration (Petsch, 2016). In our study, EPT assemblages of disturbed streams were more functionally homogenous compared with least disturbed streams, suggesting a non-random effect of stress on homogenization (e.g., Mondy and Usseglio-Polatera, 2014; Smart et al., 2006). Specifically,

we observed an increasing homogenization of traits providing resilience (e.g., body size, number of reproductive cycles per year) and resistance (e.g., relation to substrate, body form) capabilities to individuals in impacted sites. Given that homogenization causes a reduction in ecosystem resilience and resistance to environmental changes (Olden et al., 2004), we infer that most disturbed streams have lost the ability to resist future changes in a global human change scenario.

Trait response of EPT assemblages to human disturbance

Predictions of response to human disturbance made for 28 trait categories were fulfilled in 12 cases. Organisms with large body size and low body flexibility with <1 reproductive cycle per year, building case, and climbing characterized EPT assemblages of least-disturbed streams, whereas disturbed sites had increased proportions of organisms with small body size, streamlined, highly flexible, free-living, swimming, and reproducing more than once a year.

The first RLQ ordination axis accounted for a large fraction of the total variance explained, indicating the existence of a strong environmental gradient structuring the trait composition of EPT assemblages, which partially matched our *a priori* classification based on IDI (Fig. 2). Least disturbed streams were clearly separated from disturbed streams, whereas intermediate disturbed streams were generally superimposed with disturbed streams (Fig. 6). Riparian canopy cover and water quality were the main environmental drivers of the trait composition of EPT assemblages. In their natural state, wooded riparian zones are effective in preserving the ecological integrity and trophic dynamics of aquatic ecosystems (Ferreira et al., 2017). The replacement, reduction or removal of riparian vegetation cover generally leads to changes in physical habitat and hydromorphological and water quality characteristics (Ferreira et al., 2012; Pusey and Arthington, 2003), directly influencing the trophic dynamics and ecological integrity of aquatic ecosystems (e.g., Castro et al., 2016).

Body size and the number of reproductive cycles per year respond as expected *a priori* with the proportion of large body size individuals having <1 reproductive cycle per year occurring in the least disturbed streams, and small body size organisms with >1 reproductive cycles per year occurring in the disturbed streams. These latter trait categories confer resilience

and/or resistance to disturbance, allowing for faster recolonization of disturbed environments as observed by other authors [Díaz et al., 2008; Dolédec et al., 2006; but see Ding et al., (2017) who recently observed the opposite effects in China headwater streams].

Organisms with small body size and low body flexibility increased in sites with reduced bed stability, heterogeneity and higher proportion of fine sediments. Heterogeneous substrates allow for more diverse benthic communities and provide refuge, whereas homogeneous substrates imply more exposition to physical disturbances, such as current velocity and shear stress (Beisel et al., 2000; Milesi et al., 2016). In addition, high flexibility provides advantages to taxa in sites with a high percentage of fine sediments, enabling the use of small interstices within the bed sediments (Gayraud and Philippe, 2001; Lamouroux et al., 2004, Descoux et al., 2014).

Small body size, high body flexibility and swimmers were also positively associated with low water quality related to wastewater (Stalter et al., 2013) and agricultural activities (Johnson et al., 1997). In our study, water quality correlated with land use intensity, especially with an increased percentage of agriculture and pasture areas and house density. We believe that the association of these traits is associated with the fact that water quality covaries with the substrate, which directly affects the trait composition of assemblages. However, conductivity, total dissolved solids and other water parameters may also causally affect invertebrate composition, acting as one of the environmental filters determining assemblage composition (Olson and Hawkins, 2017). For example, salinity and total dissolved solids can induce physiological stress in freshwater organisms adapted to low concentrations and could affect their fitness (Berger et al., 2017; Cañedo-Argüelles et al., 2013; Olson and Hawkins, 2017), eliminating some species and indirectly changing the trait composition of assemblages.

Functional feeding groups exhibited weak relationships with environmental variables. We did not identify the expected relationship between shredders and riparian cover or filter feeders and water quality. These results are associated with the great trophic plasticity and opportunistic feeding habits of Neotropical aquatic insects (Castro et al., 2016; Ceneviva-Bastos et al., 2017; Ferreira et al., 2015).

Identifying how human pressures modify the trait composition of assemblages can improve our predictive capability about patterns and processes in freshwater ecosystem and help the development of tools that complement traditional assessment for management actions and conservation initiatives (Jonsson et al., 2016; Pallottini et al., 2016). Our MTB approach has proven to improve our ability to evaluate the functional response of assemblages to human disturbance gradients. The RLQ and fourth-corner integrated analysis significantly discriminated streams with different levels of human disturbance. However, the lack of information about Neotropical invertebrate traits is one of the main limitations in using the trait approach. Nevertheless, few studies have established the foundation for building a database for Neotropical aquatic invertebrate species (Dedieu et al., 2015; Milesi et al., 2016; Reynaga and Santos, 2013; Tomanova and Usseglio-Polatera, 2007, Castro et al., in review). Gathering the maximum information possible and including more biological traits known to respond to specific human pressures is crucial to improve our understanding of the functioning of lotic ecosystems, providing tools for biomonitoring and conservation of Neotropical streams.

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Table A.1. Local, Catchment and Integrated Disturbance indexes to each sample site.

Site	Categorie	IDI	LDI	CDI
Distur_01	Disturbed	0.7048	2.2735	161.5385
Distur_02	Disturbed	0.7284	2.3565	166.6287
Distur_03	Disturbed	0.7870	2.5466	180.0000
Distur_04	Disturbed	0.7216	2.2579	168.8525
Distur_05	Disturbed	0.6822	1.8940	170.1961
Distur_06	Disturbed	0.6481	1.3340	177.1845
Distur_07	Disturbed	0.7223	2.1064	176.0000
Distur_08	Disturbed	0.7115	1.8335	182.9268
Distur_09	Disturbed	0.6430	1.6445	165.7511
Distur_10	Disturbed	0.6487	0.2045	194.2149
Distur_11	Disturbed	0.6583	1.0005	188.1549
Distur_12	Disturbed	0.6991	2.1970	163.1274
Distur_13	Disturbed	0.7169	1.9244	181.4531
Distur_14	Disturbed	0.7463	2.0761	186.0285
Distur_15	Disturbed	0.6370	1.3340	173.5434
Distur_16	Disturbed	0.7007	2.0383	170.9561
Distur_17	Disturbed	0.6685	1.6667	173.8549
Distur_18	Disturbed	0.7076	2.6445	141.0109
Distur_19	Disturbed	0.6447	0.9928	184.0084
Distur_20	Disturbed	0.6453	2.1289	145.4732
Distur_21	Disturbed	0.7920	2.5761	180.4462
Distur_22	Disturbed	0.7474	2.0909	185.8335
Interm_01	Intermediate	0.2877	1.3409	31.2085
Interm_02	Intermediate	0.3364	1.6521	18.9990
Interm_03	Intermediate	0.4479	1.9705	63.8457
Interm_04	Intermediate	0.2682	0.5608	73.0925
Interm_05	Intermediate	0.4115	1.4621	86.8439
Interm_06	Intermediate	0.3092	1.2123	57.5777
Interm_07	Intermediate	0.6052	0.3032	180.6452
Interm_08	Intermediate	0.5676	0.8565	162.3529
Interm_09	Intermediate	0.5634	1.0380	157.1429
Interm_10	Intermediate	0.5996	0.8337	172.7880
Interm_11	Intermediate	0.5291	0.1364	158.5185
Interm_12	Intermediate	0.5114	0.6670	148.1030
Interm_13	Intermediate	0.4511	0.9547	122.6042
Interm_14	Intermediate	0.5207	1.1290	140.7660
Interm_15	Intermediate	0.5413	0.7880	155.3528
Interm_16	Intermediate	0.4710	0.6670	135.5098
Interm_17	Intermediate	0.4413	1.7274	82.3565
Interm_18	Intermediate	0.5245	0.8488	148.8730
Interm_19	Intermediate	0.4145	0.0000	124.3464
Interm_20	Intermediate	0.4102	0.0000	123.0575
Interm_21	Intermediate	0.3224	1.3896	49.0330
Interm_22	Intermediate	0.3283	0.9449	80.5397
Ref_01	Least disturbed	0.1739	0.1213	51.6676
Ref_02	Least disturbed	0.0130	0.0000	3.8880
Ref_03	Least disturbed	0.1331	0.0000	39.9275
Ref_04	Least disturbed	0.1428	0.0000	42.8442
Ref_05	Least disturbed	0.0423	0.0910	11.4647
Ref_06	Least disturbed	0.1588	0.2727	44.7354
Ref_07	Least disturbed	0.0404	0.1136	10.0203
Ref_08	Least disturbed	0.0000	0.0000	0.0000
Ref_09	Least disturbed	0.0997	0.0000	29.9221
Ref_10	Least disturbed	0.0000	0.0000	0.0000

Site	Categorie	IDI	LDI	CDI
Ref_11	Least disturbed	0.0000	0.0000	0.0000
Ref_12	Least disturbed	0.1512	0.1250	44.7354
Ref_13	Least disturbed	0.1797	0.6670	36.1362
Ref_14	Least disturbed	0.0382	0.0000	11.4647
Ref_15	Least disturbed	0.0000	0.0000	0.0000
Ref_16	Least disturbed	0.0000	0.0000	0.0000
Ref_17	Least disturbed	0.0000	0.0000	0.0000
Ref_18	Least disturbed	0.0667	0.3335	0.0000
Ref_19	Least disturbed	0.1217	0.3891	28.0517
Ref_20	Least disturbed	0.0077	0.0000	2.3121
Ref_21	Least disturbed	0.0397	0.0000	11.9122
Ref_22	Least disturbed	0.1751	0.0000	52.5151

Table A.2. Environmental variables and their codes and definitions. Average values and standard deviation (in parentheses) are provided for each group of environment disturbance. Each disturbance category includes 22 streams.

Variable groups and names	Variable code	Human pressure			
		Disturbed	Intermediate	Least disturbed	
Land use and cover					
% of Woodland savanna	Woodland	3.076 (0.498)	3.947 (1.327)	3.044 (1.774)	
% of Parkland savanna	Parkland	0 (0)	0.761 (1.019)	2.535 (0.852)	
% of Grassy-woody savanna	Grassy_Woody	0.689 (0.736)	1.089 (0.962)	0.743 (1.144)	
% of Palm swamp	Palm_swamp	0.878 (1.095)	0.842 (1.177)	0.185 (0.601)	
% of Pasture use	Pasture	0.938 (0.995)	1.982 (0.815)	1.001 (1.067)	
% of Agricultural use	Agriculture	80.999 (11.925)	43.356 (33.025)	5.094 (7.784)	
% of Eucalyptus forest	Eucaliptus	0.068 (0.317)	0.579 (0.899)	0.2 (0.649)	
% of Natural land use	Natural	1.055 (0.157)	1.399 (0.302)	1.926 (0.086)	
Distance to cities (km)	City_dist	12.381 (5.224)	16.732 (7.683)	21.811 (6.841)	
Distance to paved highways (km)	Highway_dist	1.17 (0.421)	1.438 (0.432)	1.804 (0.659)	
Density of homes in the basin (houses/km²)	House_density	2.093 (0.985)	1.251 (0.754)	0.631 (0.77)	
Hydromorphology					
Mean thalweg depth (cm)	depth_T	1.533 (0.184)	1.496 (0.246)	1.519 (0.233)	
Mean wetted width (m)	width	1.43 (0.214)	1.553 (0.189)	1.512 (0.243)	
Mean bankfull width (m)	BKF_W	1.658 (0.233)	1.78 (0.163)	1.761 (0.195)	
Mean bankfull height (m)	BKF_H	-0.039 (0.191)	0.036 (0.151)	0.052 (0.21)	
Mean width x mean depth (m²)	WXD	1.962 (0.351)	2.049 (0.378)	2.031 (0.431)	
Mean width/depth ratio (m/m)	WD_RAT	0.897 (0.189)	1.058 (0.224)	0.994 (0.2)	
Mean bank angle (degrees)	BA	1.648 (0.125)	1.619 (0.152)	1.606 (0.157)	
Water surface gradient over reach (%)	SLOPE	0.859 (0.418)	0.493 (0.472)	1.211 (0.528)	
Substrate					
Mean embeddedness (%)	EMBED	0.638 (0.237)	0.676 (0.285)	0.412 (0.266)	
% of bedrock (>4000 mm)	PCT_BDRK	0.683 (1.07)	0.935 (1.095)	2.143 (0.806)	
% of boulders (250 to 4000 mm)	PCT_BL	1.175 (0.973)	1.06 (0.956)	1.313 (1.067)	
% of cobble (64 to 250mm)	PCT_CB	1.397 (0.897)	1.341 (0.919)	1.572 (0.83)	
% of coarse gravel (16 to 64 mm)	PCT_GC	1.129 (0.933)	1.19 (0.974)	1.424 (1.036)	
% of fine gravel (2 to 16mm)	PCT_GF	1.589 (0.953)	1.648 (0.894)	1.297 (1.025)	
% of sand (0.6 to 2 mm)	PCT_SA	1.515 (0.935)	2.082 (0.739)	1.596 (0.958)	
% of fines (<0.6 mm)	PCT_FN	1.951 (0.933)	1.803 (0.886)	1.041 (1.087)	
Total Organic matter (%)	PCT_ORG	2.151 (0.379)	1.754 (0.834)	1.405 (0.924)	
% of Wood	PCT_WD	0.415 (0.589)	0.49 (0.766)	0.136 (0.443)	
Log10 estimated geometric mean substrate diameter (mm)	LSUB_DMM	0.302 (1.242)	0.214 (1.183)	0.14 (1.496)	
Log10 - Relative Bed Stability (dimensionless: m/m))	LRBS	-1.186 (1.321)	-0.641 (1.055)	1.692 (1.15)	
Flow					
Flow - instantaneous discharge(m³/s)	FLOW_2	0.66 (0.173)	0.565 (0.209)	0.434 (0.243)	
Velocity mean (m/s)	VEL	0.749 (0.111)	0.632 (0.213)	0.503 (0.245)	
Glides (%)	PCT_GL	0.715 (0.357)	0.801 (0.435)	0.691 (0.474)	
Percentage of rapids and riffles (%)	PCT_FAST	0.497 (0.24)	0.447 (0.306)	0.54 (0.324)	
Percentage of pools	PCT_POOL	0.857 (1.124)	0.736 (1.037)	0.621 (1.067)	
Sequence fasts, glides and pools (1= maximum Heterogeneity, 0= maximum homogeneity)	SEQ_FLO_1	0.852 (0.309)	0.587 (0.258)	1.152 (0.395)	
Canopy cover					
Mean mid-channel canopy density (%)	CDENMID	1.036 (0.25)	0.933 (0.313)	0.471 (0.331)	
Mean canopy cover > 0.3m DBH	CL	0.72 (0.552)	0.882 (0.467)	0.272 (0.461)	
Mean canopy cover ≤ 0.3m DBH	CS	3.816 (2.196)	4.22 (1.647)	2.884 (2.047)	
Mean woody mid-layer cover	MW	4.416 (2.058)	5.325 (1.096)	6.063 (2.106)	

Variable groups and names	Variable code	Human pressure		
		Disturbed	Intermediate	Least disturbed
Mean herbaceous mid-layer cover	MH	2.801 (2.024)	4.435 (1.492)	5.209 (2.736)
Mean woody ground-layer cover	GW	1.023 (0.371)	1.221 (0.353)	1.569 (0.437)
Mean herbaceous ground-layer cover	GH	3.632 (2.074)	5 (1.767)	7.609 (2.304)
Mean exposed soil	GB	0.406 (0.178)	0.384 (0.175)	0.166 (0.234)
Mean riparian veg canopy cover	C	4.785 (2.577)	5.29 (2.125)	3.172 (2.297)
In-stream cover				
% of Areal cover filamentous algae	FC_ALG	0.06 (0.193)	0.33 (0.694)	0.751 (0.88)
% of Areal cover aquatic macrophytes	FC_AQM	0.411 (0.597)	0.373 (0.587)	1.098 (0.866)
% of Areal cover large woody debris	FC_LWD	1.155 (0.829)	1.208 (0.736)	1.271 (0.912)
% of Areal cover brush	FC_BRS	1.997 (0.438)	1.651 (0.764)	0.294 (0.67)
% of Areal cover live trees	FC_ROT	4.122 (1.598)	3.519 (1.415)	3.909 (1.725)
% of Areal cover leaves bank	FC_LEB	4.456 (2.435)	4.62 (1.743)	2.852 (2.454)
% of Areal cover undercut banks	FC_UCB	2.161 (1.592)	2.342 (1.345)	2.69 (1.718)
% of Areal cover boulders	FC_RCK	1.241 (1.052)	1.298 (1.003)	1.96 (0.683)
Water quality				
pH	pH	7.214 (0.673)	7.431 (0.874)	6.671 (1.042)
Turbidity (UNT)	TURB	0.659 (0.279)	0.71 (0.273)	0.224 (0.602)
Conductivity(μS/cm)	COND	1.456 (0.311)	1.456 (0.576)	0.735 (0.652)
TDS (mg/L)	TDS	1.999 (0.745)	2.218 (0.572)	1.015 (0.987)
Water temperature (°C)	TEMP	20.245 (1.813)	19.05 (1.986)	19.014 (1.321)
Total Nitrogen (mg/L)	NO3	3.233 (0.431)	3.069 (0.547)	2.485 (0.543)
Total Phosphorus (mg/L)	PHOS	0.846 (0.575)	0.901 (0.481)	0.418 (0.422)

Table A.3. Trait profiles (proportion) of 74 Neotropical genus of Ephemeroptera, Plecoptera and Trichoptera for 28 categories in 7 biological traits.

Genus	Body size						Potential number of cycles per year		Feeding habits					Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	>1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder
Ephemeroptera																												
Americabaetis	0.03	0.48	0.35	0.1	0.05	0	0	1	0.4	0	0.6	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0.25	0	0.75	0	1	0	0
Apobaetis	0.07	0.48	0.38	0.07	0	0	0	1	0.17	0.33	0.5	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Askola	0	0.21	0.42	0.21	0.17	0	0	1	1	0	0	0	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Asthenopus	0	0	0.04	0.27	0.58	0.11	1	0	0.4	0	0.2	0.4	0	0.75	0	0.25	0	0	0	0.25	0.75	1	0	0	0	1	0	0
Aturbina	0.01	0.35	0.34	0.28	0.03	0	0	1	0	0	1	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0	0	1	0	1	0	0
Baetodes	0.37	0.56	0.08	0	0	0	0	1	0.5	0	0.5	0	0	0	0	0.29	0.29	0.43	0	0	1	0.25	0	0.75	0	1	0	0
Caenis	0.07	0.39	0.38	0.14	0.03	0	0	1	0.6	0	0.4	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0	1	0	0	1	0	0
Callibaetis	0	0.11	0.23	0.25	0.41	0	0	1	0	0	1	0	0	0	0	0	0.4	0.6	0	0.25	0.75	1	0	0	0	1	0	0
Camelobaetidius	0.06	0.13	0.31	0.18	0.32	0	0	1	0.5	0	0.5	0	0	0.13	0	0.25	0.25	0.38	0	0.33	0.67	0.4	0	0.6	0	1	0	0
Campsurus	0.02	0.08	0.12	0.15	0.54	0.09	1	0	0.67	0	0	0.33	0	0.75	0	0.25	0	0	0	0.25	0.75	1	0	0	0	1	0	0
Campylocia	0	0	0	0.1	0.35	0.55	0.22	0.78	0.17	0.33	0	0.5	0	0.43	0	0.29	0.29	0	0	0.5	0.5	0.6	0	0.4	0	1	0	0
Cloeodes	0.02	0.47	0.33	0.16	0.02	0	0	1	0.4	0	0.6	0	0	0	0	0.43	0.29	0.29	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Cryptonympha	0	0.31	0.38	0.31	0	0	0	1	0	0	1	0	0	0.14	0	0.29	0.29	0.29	0	0.25	0.75	0	0	1	0	1	0	0
Farrodes	0.06	0.44	0.3	0.16	0.03	0	0	1	0.5	0	0.5	0	0	0	0	0.29	0.29	0.43	0	0	1	0.25	0.75	0	0	0	1	0
Guajirolus	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0.4	0	0.6	0	0.25	0.75	0	0	1	0	1	0	0
Hagenulopsis	0.15	0.35	0.26	0.2	0.04	0	0.4	0.6	0.5	0	0.5	0	0	0.67	0	0.33	0	0	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Hermanella	0	0.27	0.18	0.36	0.18	0	0.4	0.6	0	0	1	0	0	0	0	0.4	0	0.6	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Hexagenia	0	0.17	0	0.5	0.33	0	1	0	0.75	0	0	0.25	0	1	0	0	0	0	0	0.5	0.5	1	0	0	0	1	0	0
Hydrosmilodon	0.02	0.21	0.29	0.36	0.12	0	1	0	0.4	0	0.6	0	0	0.75	0	0.25	0	0	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Latineosus	0.12	0.45	0.14	0.19	0.1	0	0	1	0.6	0	0.4	0	0	0.4	0	0.6	0	0	0	0.5	0.5	0	0.5	0.5	0	1	0	0
Leptohyphes	0.22	0.42	0.24	0.09	0.03	0	1	0	0.5	0.17	0.33	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.17	0.5	0.33	0	1	0	0
Leptohyphodes	0	0	0.07	0.14	0.79	0	0	1	0.5	0.17	0.33	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0
Massartella	0	0.09	0.06	0.21	0.42	0.23	0.4	0.6	0.41	0.04	0.54	0.01	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Miroculis	0.02	0.27	0.26	0.32	0.14	0	0	1	0.5	0	0.5	0	0	0	0	0.5	0	0.5	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Paracloeodes	0.02	0.38	0.35	0.24	0.01	0	0	1	0	0	1	0	0	0	0	0.5	0.17	0.33	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Paramaka	0	1	0	0	0	0	0.4	0.6	0	0	1	0	0	0	0	0.6	0	0.4	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Rivudiva	0	0.13	0.39	0.48	0	0	0	1	0.5	0	0.5	0	0	0	0	0.5	0.17	0.33	0	0.25	0.75	0	0	1	0	1	0	0
Simothraulopsis	0	0	0.11	0.33	0.56	0	0.4	0.6	0.4	0	0.6	0	0	0	0	0.5	0	0.5	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Spiritiops	0	0	0	0	0	0	0	1	0.2	0.2	0.6	0	0	0	0	0	0.4	0.6	0	0.25	0.75	0.5	0	0.5	0	1	0	0
Terpides	0	0.09	0.16	0.28	0.47	0	0.4	0.6	0.38	0.38	0.25	0	0	0.43	0	0.29	0.14	0.14	0	0.67	0.33	0.25	0.75	0	0	1	0	0
Thraulodes	0.05	0.33	0.31	0.18	0.12	0	1	0	0.43	0	0.43	0.14	0	0.33	0	0.22	0.33	0.11	0	0.75	0.25	0.25	0.75	0	0	1	0	0
Traverhyphes	0.08	0.36	0.32	0.22	0.01	0	0	1	1	0	0	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0
Tricorythodes	0.11	0.28	0.39	0.2	0.03	0	0	1	0.75	0	0.25	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0

Genus	Body size						Potential number of cycles per year		Feeding habits						Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder	
<i>Tricorythopsis</i>	0.19	0.77	0.04	0	0	0	0	1	0.75	0	0.25	0	0	0	0	1	0	0	0	0.5	0.5	0	0.25	0.75	0	0	1	0	0
<i>Ulmeritoides</i>	0.03	0.25	0.18	0.21	0.33	0.01	1	0	0.41	0.04	0.54	0.01	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0	
<i>Varipes</i>	0	0	0	0	0	0	0	1	0.5	0.17	0.33	0	0	0	0	0.17	0.33	0.5	0	0	1	0.25	0	0.75	0	1	0	0	
<i>Waltzoyphius</i>	0.02	0.17	0.31	0.4	0.11	0	0	1	0	0	1	0	0	0	0	0.43	0.29	0.29	0	0.25	0.75	1	0	0	0	1	0	0	
<i>Zelus</i>	0.09	0.43	0.3	0.16	0.02	0	0	1	0	0	1	0	0	0	0	0.38	0.25	0.38	0	0.25	0.75	1	0	0	0	1	0	0	
Plecoptera																													
<i>Anacroneuria</i>	0.04	0.15	0.23	0.2	0.28	0.09	0	1	0.2	0.2	0	0	0.6	0	0	0.5	0.33	0.17	0.5	0.5	0	0.33	0.67	0	0	1	0	0	
<i>Grypopteryx</i>	0.12	0.47	0.06	0.18	0.18	0	1	0	0	1	0	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
<i>Kempnya</i>	0	0	0	0.2	0.6	0.2	1	0	0	0	0	0	1	0	0	0	1	0	0.5	0.5	0	1	0	0	0	1	0	0	
<i>Paragrypopteryx</i>	0.12	0.74	0.14	0	0	0	1	0	0.33	0.33	0.33	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
<i>Tupiperla</i>	0.01	0.2	0.35	0.27	0.17	0	1	0	0.33	0.33	0.33	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
Trichoptera																													
<i>Alisotrichia</i>	0.58	0.33	0	0	0.08	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	1	0	0	0	0	0	0	1
<i>Anchitrichia</i>	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	0.51	0.14	0.35	0	0	0	0	1
<i>Atanatolia</i>	0.14	0	0.14	0.43	0.29	0	1	0	0.07	0.36	0.32	0	0.25	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	0	1
<i>Atopsyche</i>	0	0.17	0.24	0.28	0.29	0.03	1	0	0	0.25	0	0	0.75	0	0	0.43	0.43	0.14	0	0	1	0	0	1	0	1	0	0	
<i>Austrotinodes</i>	0	0.09	0.28	0.37	0.26	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0.5	0.5	
<i>Barypenthus</i>	0	0	0	0.19	0.25	0.56	1	0	0.43	0.29	0.29	0	0	0	0	0.6	0.4	0	0.75	0.25	0	0	0	1	0	0	0	0	1
<i>Chimarra</i>	0	0.11	0.19	0.23	0.37	0.1	1	0	0	0.25	0	0.75	0	0	0	0.5	0.5	0	0	0	1	0	0	1	0	0	1	0	0
<i>Cyrnelus</i>	0	0.11	0.11	0.33	0.44	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	0
<i>Grumichella</i>	0	0	0	1	3	0	0	0	2	1	2	0	0	0	0	0	3	0	3	1	0	0	0	3	0	0	1	3	0
<i>Helicopsyche</i>	0	0.18	0.43	0.33	0.08	0	0	1	0.6	0	0.4	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0	0	0	1	0	0.25	0.75	
<i>Hydroptila</i>	0.17	0.76	0.06	0.01	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0.67	0.33	0	0	0	0	0	1
<i>Itaura</i>	0.1	0.62	0.26	0.01	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0.25	0.75	0	0	0	0.4	0.6
<i>Leptonema</i>	0	0	0.12	0.05	0.13	0.7	0	1	0	0.2	0	0.6	0.2	0	0	0.33	0.5	0.17	0	0	1	0	0	1	0	0	1	0	0
<i>Macronema</i>	0	0.12	0.05	0.16	0.26	0.41	0	1	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	0
<i>Macrostemum</i>	0	0.08	0.08	0.15	0.23	0.46	1	0	0	0.13	0	0.73	0.13	0	0	0	1	0	0	0	1	0	0	1	0	0	0.5	0.5	
<i>Marilia</i>	0.01	0.09	0.23	0.27	0.39	0.01	1	0	0.38	0.13	0.38	0	0.13	0	0.5	0.5	0	0	0.75	0.25	0	0	0	1	0	0	0	0	1
<i>Metrichia</i>	0.4	0.53	0.07	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	0	0.5	0.5	0	0	0	0	1
<i>Mortoniella</i>	0.1	0.7	0.2	0	0	0	1	0	0.5	0	0.5	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0	0.17	0.5	0.33	0	0.4	0.6	
<i>Nectopsyche</i>	0.02	0.28	0.21	0.28	0.21	0	1	0	0.29	0.43	0.29	0	0	0	0.17	0.5	0.33	0	0.75	0.25	0	0	0	1	0	0	0	0	1
<i>Neotrichia</i>	0.71	0.29	0	0	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0.4	0	0.6	0	0	0	0	1
<i>Notalina</i>	0.22	0.11	0.11	0.22	0.33	0	1	0	0	0	1	0	0	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	0	1
<i>Nyctiophylax</i>	0.11	0.67	0.11	0	0	0.11	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	0
<i>Oecetis</i>	0.1	0.31	0.34	0.2	0.05	0	0	1	0	0	0	0	1	0	0	0.5	0.5	0	0.75	0.25	0	0	0	1	0	0	0	0	1
<i>Oxyetira</i>	0.05	0.66	0.24	0.06	0	0	1	0	0	0	1	0	0	0	0.5	0.5	0	0	0.75	0.25	0	0.5	0	0.5	0	0	0	0	1

Genus	Body size						Potential number of cycles per year		Feeding habits						Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	>1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder	
<i>Phylloicus</i>	0.05	0.21	0.19	0.13	0.3	0.11	0	1	0.25	0.75	0	0	0	0	0	0	0.75	0.25	0	0	0	0	0	1	0	0	0	1	
<i>Polycentropus</i>	0	0.12	0.19	0.27	0.41	0.02	1	0	0	0.2	0	0.2	0.6	0	0	0.5	0.5	0	0	0	1	0	0	1	0	0	1	0	
<i>Polyplectropus</i>	0	0.01	0.09	0.24	0.66	0	1	0	0	0.07	0	0.4	0.53	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Protoptila</i>	0.05	0.47	0.34	0.14	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	1	0	0	0	0	1	0	0	0.4	0.6	
<i>Smicridea</i>	0	0.25	0.25	0.24	0.24	0	0	1	0	0.2	0	0.6	0.2	0	0	0.33	0.5	0.17	0	0	1	0	0	1	0	0	1	0	
<i>Triplectides</i>	0	0.07	0.07	0.1	0.5	0.27	1	0	0	1	0	0	0	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Wormaldia</i>	0	0.91	0	0.03	0.06	0	1	0	0	0	0.4	0.6	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	

Table A.4. Output of the significant values of the fourth-corner analysis. Codes for traits and environmental variables are provided in Tables 1 and S1, respectively.

Test	Obs	Std.Obs	Pvalue	Pvalue.adj
Cano_1 / bet_2.5_3.5	-0.178	-4.180	0.001	0.070
Cano_1 / case_builder	0.126	2.970	0.003	0.105
Cano_1 / flex_less_1.	0.123	2.988	0.005	0.127
Cano_1 / flex_more_45	-0.107	-2.661	0.008	0.147
Cano_1 / less_1y	0.103	2.519	0.006	0.129
Cano_1 / more_1y	-0.103	-2.519	0.006	0.129
Cano_1 / Swimmer	-0.137	-3.363	0.001	0.070
Flow_1 / bet_2.5_3.5	0.070	2.391	0.015	0.183
Flow_1 / Clinger	-0.072	-2.324	0.020	0.215
Flow_1 / Sprawl	0.071	2.423	0.015	0.183
Flow_4 / more_10	0.077	2.881	0.010	0.147
Flow_4 / shredder	0.088	3.249	0.002	0.093
Instream_1 / bet_2.5_3.5	0.128	2.772	0.008	0.147
Instream_1 / flex_less_1.	-0.102	-2.316	0.021	0.218
LandUse_1 / bet_2.5_3.5	0.154	3.173	0.004	0.112
LandUse_2 / free_living	-0.074	-2.192	0.019	0.213
Quality_1 / bet_2.5_3.5	0.171	3.728	0.001	0.070
Quality_1 / case_builder	-0.123	-2.553	0.009	0.147
Quality_1 / flex_less_1.	-0.121	-2.589	0.009	0.147
Quality_1 / flex_more_45	0.115	2.499	0.010	0.147
Quality_1 / Swimmer	0.115	2.492	0.018	0.210
Subs_3 / bet_2.5_3.5	0.149	4.177	0.001	0.070
Subs_3 / case_builder	-0.113	-2.906	0.003	0.105
Subs_3 / flex_less_1.	-0.108	-2.859	0.004	0.112
Subs_3 / flex_more_45	0.092	2.494	0.011	0.147
Subs_3 / free_living	0.091	2.475	0.011	0.147
Subs_3 / Swimmer	0.117	3.314	0.002	0.093

Figure A.1. PCAs of each group of environmental variables demonstrating the main variables discriminating each disturbance group (see acronyms in Table A1). We used those axes significantly related to the IDI index in the RLQ and fourth-corner analyses. In each graph, the black bars identify the selected axes.

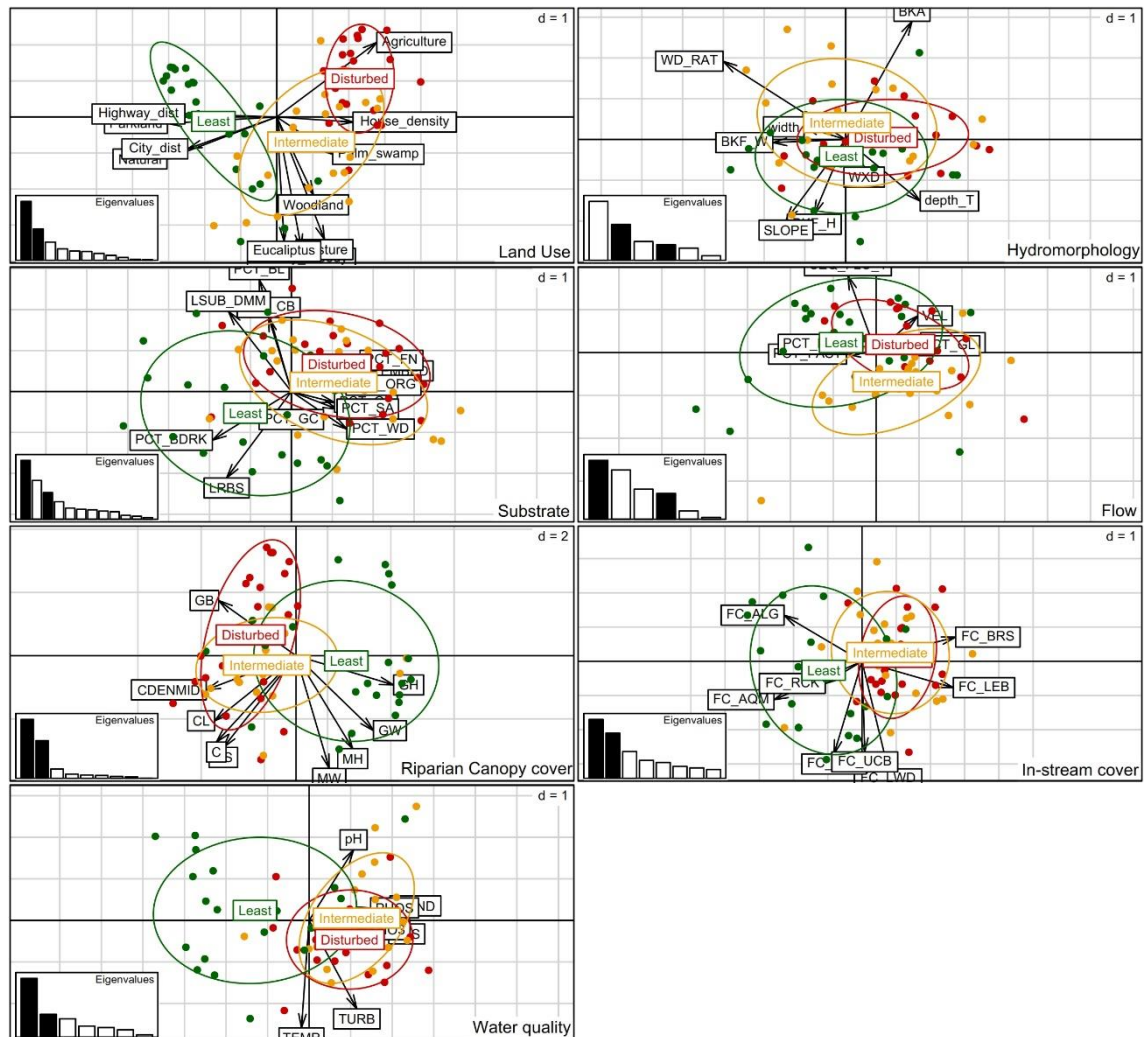
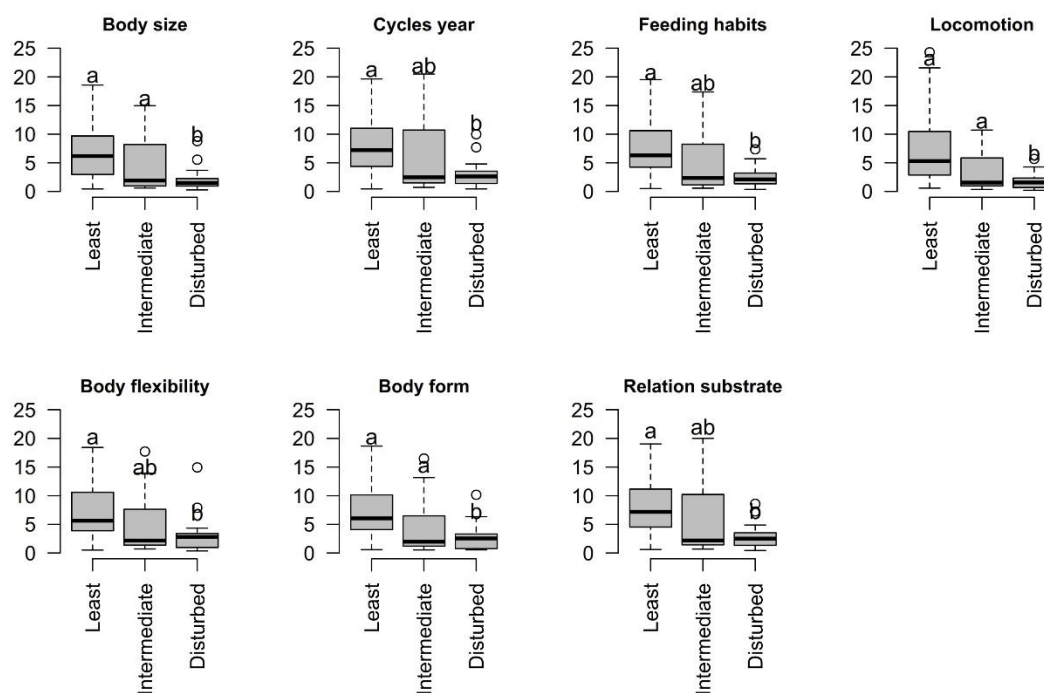


Figure A.2. Box-and-whisker plots demonstrating the values of the community specialization index (CSI) for each trait in each disturbance category. Lines in boxes are medians, and box end are quartiles. Whiskers indicate maximum and minimum values. Tukey *post hoc* tests were used for pairwise comparisons. Different letters indicate significant differences among the categories of disturbance.



THESIS CONCLUSIONS

This thesis represents the first quantitative and multi-scale assessment of the impacts of human disturbances on the taxonomic and trait compositions of EPT assemblages and on their trophic relationships in neotropical savanna headwater streams. First, a specific EPT trait database was developed after a robust and extensive survey of exclusively neotropical literature and in which six traits were selected (among ~15 possible) that had sufficient and reliable information and were relevant to natural and human-type disturbances. Second, we identified which spatial scale and human disturbance variables drove the taxonomic and trait composition of the EPT assemblages in headwater streams. Finally, we observed that changes in land use led to homogenized communities in terms of their functional composition.

The main objective of this thesis was to investigate how the intensity of land use, through several pathways and spatial scales, influenced the functional structure of macroinvertebrate assemblages in neotropical savanna headwaters. The findings presented here demonstrate that an increase in land use intensity led to macroinvertebrate assemblages with more generalist feeding behaviors and a greater overlap of trophic niches (Chapter 1); that environmental variables at both the catchment and reach scales explain a significant amount of the variation in EPT taxa and trait composition, but that land use variables explain the greatest proportion of the trait composition differences between sites (Chapter 2); and that assemblages at the least-disturbed sites show a higher community specialization compared to disturbed sites (Chapter 3).

Losing biodiversity means losing ecosystem services (Cadotte et al. 2011, Cardinale et al. 2012). Therefore, assessing multiple components of the functional structure of assemblages using a trait-based approach is an appropriate alternative strategy because the diversity of ecological processes is likely closely related to the diversity of species' functional traits (Diaz and Cabido 2001, Hooper et al. 2005, Reiss et al. 2009).

Overall, my thesis findings clearly corroborate that biodiversity should be assessed in a multifaceted framework that considers the functional elements of biotic assemblages. In addition, this study contributes to a better understanding of the structure and functioning of

neotropical savanna headwater streams. This is especially important in the context of designing assessment tools to define priority conservation areas in the future and is important to the development of biological and functional integrity indices. Such approaches will aid the development of suitable management and conservation actions that will allow for evaluation of the impacts on biota of further degradation of ecological conditions, providing tools for the biomonitoring and conservation of tropical streams.

FUTURE PERSPECTIVES

In a biodiversity hotspot and poorly studied region such as the neotropical Savanna, it is challenging to design research priorities with a scarcity of basic information on the distribution and natural history of macroinvertebrates. Further studies that expand our understanding of the effects of anthropogenic disturbances on neotropical savanna freshwater system integrity are greatly needed. Such studies would contribute to the improvement of knowledge about the natural history and traits of the other groups of macroinvertebrates that were not used in this thesis, as well as those in other aquatic systems, such as lagoons, reservoirs and large rivers. I particularly emphasize the development of the following approaches:

- i. **Key functional traits:** some single functional traits (e.g., size or diet) may contribute to the provision of several ecosystem services while responding to specific drivers of change (e.g., land-use intensity). Specific functional traits that influence the provision of diverse ecosystem services and respond to drivers of change across a variety of systems and organisms might be considered “key functional traits” (Hevia et al. 2017). In fact, these are traits that, if affected by a given driver of change, will have major consequences on ecosystem functioning. Identifying those “key functional traits” and establishing relationships with the direct drivers of change and ecosystem services could lead to major advances in ecological research. For example, the ‘shredder’ feeding group acts as a response trait under the removal of riparian vegetation but also acts as an effect trait that contributes to the processing of leaf litter.
- ii. **Linking functional traits to ecosystem process:** determining which functional traits have a significant impact on ecosystem processes remains an open empirical question in aquatic ecology. Controlled experiments asking specific questions should help to disentangle the key roles played by trait identity and diversity in mediating the effects of human disturbance on ecosystem functioning (Loreau et al. 2001, Hooper et al. 2005). The findings of this thesis may support this future approach by providing information about the main human impacts affecting trait compositions.

- iii. **Functional Beta Diversity:** examining functional diversity at a variety of different scales—between species within a community (alpha diversity), between communities (i.e., beta diversity) and on a regional scale (i.e., gamma diversity)— may help to reveal changes in assembly processes along ecological gradients and how species' traits influence the ecological network structure.

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THESIS APPENDICES

Appendix 1: Trait profiles (proportion) of 74 Neotropical genus of Ephemeroptera, Plecoptera and Trichoptera for 28 categories in 7 biological traits

Appendix 2: Tables with all raw environmental variables and their codes and definitions sampled in each site used in the thesis.

Table 2.1. Geophysical variables

Table 2.2. Land use variables

Table 2.3. Hydromorphological variables

Table 2.4. Substrate variables.

Table 2.5. Flow variables.

Table 2.6. Vegetation canopy cover variables.

Table 2.7. In-stream cover variables.

Table 2.8. Water quality variables.

Table 2.9. Index of Disturbance Integrated (Ligeiro et al. 2013) to each sampled site.

Appendix 3: Table with the abundance of Ephemeroptera, Plecoptera and Trichoptera in each sample site.

Appendix 4: Table with the abundance, count and average body size of each taxon measured in each sample site.

Appendix 5: Geographic coordinates of each sampled site.

Note: Appendices are available in the PDF version.

Appendix 1: Trait profiles (proportion) of 74 Neotropical genus of Ephemeroptera, Plecoptera and Trichoptera for 28 categories in 7 biological traits.

Genus	Body size						Potential number of cycles per year		Feeding habits					Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder
Ephemeroptera																												
Americabaetis	0.03	0.48	0.35	0.1	0.05	0	0	1	0.4	0	0.6	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0.25	0	0.75	0	1	0	0
Apobaetis	0.07	0.48	0.38	0.07	0	0	0	1	0.17	0.33	0.5	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Askola	0	0.21	0.42	0.21	0.17	0	0	1	1	0	0	0	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Asthenopus	0	0	0.04	0.27	0.58	0.11	1	0	0.4	0	0.2	0.4	0	0.75	0	0.25	0	0	0	0.25	0.75	1	0	0	0	1	0	0
Aturbina	0.01	0.35	0.34	0.28	0.03	0	0	1	0	0	1	0	0	0	0	0.29	0.29	0.43	0	0.25	0.75	0	0	1	0	1	0	0
Baetodes	0.37	0.56	0.08	0	0	0	0	1	0.5	0	0.5	0	0	0	0	0.29	0.29	0.43	0	0	1	0.25	0	0.75	0	1	0	0
Caenis	0.07	0.39	0.38	0.14	0.03	0	0	1	0.6	0	0.4	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0	1	0	0	1	0	0
Callibaetis	0	0.11	0.23	0.25	0.41	0	0	1	0	0	1	0	0	0	0	0	0.4	0.6	0	0.25	0.75	1	0	0	0	1	0	0
Camelobaetidius	0.06	0.13	0.31	0.18	0.32	0	0	1	0.5	0	0.5	0	0	0.13	0	0.25	0.25	0.38	0	0.33	0.67	0.4	0	0.6	0	1	0	0
Campsurus	0.02	0.08	0.12	0.15	0.54	0.09	1	0	0.67	0	0	0.33	0	0.75	0	0.25	0	0	0	0.25	0.75	1	0	0	0	1	0	0
Campylocia	0	0	0	0.1	0.35	0.55	0.22	0.78	0.17	0.33	0	0.5	0	0.43	0	0.29	0.29	0	0	0.5	0.5	0.6	0	0.4	0	1	0	0
Cloeodes	0.02	0.47	0.33	0.16	0.02	0	0	1	0.4	0	0.6	0	0	0	0	0.43	0.29	0.29	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Cryptonympha	0	0.31	0.38	0.31	0	0	0	1	0	0	1	0	0	0.14	0	0.29	0.29	0.29	0	0.25	0.75	0	0	1	0	1	0	0
Farrodes	0.06	0.44	0.3	0.16	0.03	0	0	1	0.5	0	0.5	0	0	0	0	0.29	0.29	0.43	0	0	1	0.25	0.75	0	0	0	1	0
Guajirulus	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0.4	0	0.6	0	0.25	0.75	0	0	1	0	1	0	0
Hagenulopsis	0.15	0.35	0.26	0.2	0.04	0	0.4	0.6	0.5	0	0.5	0	0	0.67	0	0.33	0	0	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Hermanella	0	0.27	0.18	0.36	0.18	0	0.4	0.6	0	0	1	0	0	0	0	0.4	0	0.6	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Hexagenia	0	0.17	0	0.5	0.33	0	1	0	0.75	0	0	0.25	0	1	0	0	0	0	0	0.5	0.5	1	0	0	0	1	0	0
Hydrosmilodon	0.02	0.21	0.29	0.36	0.12	0	1	0	0.4	0	0.6	0	0	0.75	0	0.25	0	0	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Latineosus	0.12	0.45	0.14	0.19	0.1	0	0	1	0.6	0	0.4	0	0	0.4	0	0.6	0	0	0	0.5	0.5	0	0.5	0.5	0	1	0	0
Leptohyphes	0.22	0.42	0.24	0.09	0.03	0	1	0	0.5	0.17	0.33	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.17	0.5	0.33	0	1	0	0
Leptohyphodes	0	0	0.07	0.14	0.79	0	0	1	0.5	0.17	0.33	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0
Massartella	0	0.09	0.06	0.21	0.42	0.23	0.4	0.6	0.41	0.04	0.54	0.01	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Miroculis	0.02	0.27	0.26	0.32	0.14	0	0	1	0.5	0	0.5	0	0	0	0	0.5	0	0.5	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Paracloeodes	0.02	0.38	0.35	0.24	0.01	0	0	1	0	0	1	0	0	0	0	0.5	0.17	0.33	0	0.25	0.75	0.4	0	0.6	0	1	0	0
Paramaka	0	1	0	0	0	0	0.4	0.6	0	0	1	0	0	0	0	0.6	0	0.4	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Rivudiva	0	0.13	0.39	0.48	0	0	0	1	0.5	0	0.5	0	0	0	0	0.5	0.17	0.33	0	0.25	0.75	0	0	1	0	1	0	0
Simothraulopsis	0	0	0.11	0.33	0.56	0	0.4	0.6	0.4	0	0.6	0	0	0	0	0.5	0	0.5	0	0.47	0.53	0.25	0.75	0	0	1	0	0
Spiritiops	0	0	0	0	0	0	0	1	0.2	0.2	0.6	0	0	0	0	0	0.4	0.6	0	0.25	0.75	0.5	0	0.5	0	1	0	0
Terpides	0	0.09	0.16	0.28	0.47	0	0.4	0.6	0.38	0.38	0.25	0	0	0.43	0	0.29	0.14	0.14	0	0.67	0.33	0.25	0.75	0	0	1	0	0
Thraulodes	0.05	0.33	0.31	0.18	0.12	0	1	0	0.43	0	0.43	0.14	0	0.33	0	0.22	0.33	0.11	0	0.75	0.25	0.25	0.75	0	0	1	0	0

Genus	Body size						Potential number of cycles per year		Feeding habits						Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder	
<i>Traverhyphes</i>	0.08	0.36	0.32	0.22	0.01	0	0	1	1	0	0	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0	
<i>Tricorythodes</i>	0.11	0.28	0.39	0.2	0.03	0	0	1	0.75	0	0.25	0	0	0.29	0	0.43	0.29	0	0	0.5	0.5	0.2	0.4	0.4	0	1	0	0	
<i>Tricorythopsis</i>	0.19	0.77	0.04	0	0	0	0	1	0.75	0	0.25	0	0	0	0	1	0	0	0	0.5	0.5	0.25	0.75	0	0	1	0	0	
<i>Ulmeritoides</i>	0.03	0.25	0.18	0.21	0.33	0.01	1	0	0.41	0.04	0.54	0.01	0	0.24	0	0.38	0.08	0.3	0	0.47	0.53	0.25	0.75	0	0	1	0	0	
<i>Varipes</i>	0	0	0	0	0	0	0	1	0.5	0.17	0.33	0	0	0	0	0.17	0.33	0.5	0	0	1	0.25	0	0.75	0	1	0	0	
<i>Waltzoyphius</i>	0.02	0.17	0.31	0.4	0.11	0	0	1	0	0	1	0	0	0	0	0.43	0.29	0.29	0	0.25	0.75	1	0	0	0	1	0	0	
<i>Zelus</i>	0.09	0.43	0.3	0.16	0.02	0	0	1	0	0	1	0	0	0	0	0.38	0.25	0.38	0	0.25	0.75	1	0	0	0	1	0	0	
Plecoptera																													
<i>Anacroneuria</i>	0.04	0.15	0.23	0.2	0.28	0.09	0	1	0.2	0.2	0	0	0.6	0	0	0.5	0.33	0.17	0.5	0.5	0	0.33	0.67	0	0	1	0	0	
<i>Grypopteryx</i>	0.12	0.47	0.06	0.18	0.18	0	1	0	0	1	0	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
<i>Kempnya</i>	0	0	0	0.2	0.6	0.2	1	0	0	0	0	0	1	0	0	0	1	0	0.5	0.5	0	1	0	0	0	1	0	0	
<i>Paragrypopteryx</i>	0.12	0.74	0.14	0	0	0	1	0	0.33	0.33	0.33	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
<i>Tupiperla</i>	0.01	0.2	0.35	0.27	0.17	0	1	0	0.33	0.33	0.33	0	0	0	0	0.25	0.5	0.25	0.5	0.5	0	0.78	0.22	0	0	1	0	0	
Trichoptera																													
<i>Alisotrichia</i>	0.58	0.33	0	0	0.08	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	1	0	0	0	0	0	1	
<i>Anchitrichia</i>	0	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	0.51	0.14	0.35	0	0	0	1	
<i>Atanatolia</i>	0.14	0	0.14	0.43	0.29	0	1	0	0.07	0.36	0.32	0	0.25	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Atopsyche</i>	0	0.17	0.24	0.28	0.29	0.03	1	0	0	0.25	0	0	0.75	0	0	0.43	0.43	0.14	0	0	1	0	0	1	0	1	0	0	
<i>Austrotinodes</i>	0	0.09	0.28	0.37	0.26	0	0	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0	1	0	0	0.5	0.5	
<i>Barypenthus</i>	0	0	0	0.19	0.25	0.56	1	0	0.43	0.29	0.29	0	0	0	0	0.6	0.4	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Chimarra</i>	0	0.11	0.19	0.23	0.37	0.1	1	0	0	0.25	0	0.75	0	0	0	0.5	0.5	0	0	0	1	0	0	1	0	0	1	0	
<i>Cyrnelus</i>	0	0.11	0.11	0.33	0.44	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Grumichella</i>	0	0	0	1	3	0	0	0	2	1	2	0	0	0	0	0	3	0	3	1	0	0	0	3	0	0	1	3	
<i>Helicopsyche</i>	0	0.18	0.43	0.33	0.08	0	0	1	0.6	0	0.4	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0	0	0	1	0	0.25	0.75	
<i>Hydroptila</i>	0.17	0.76	0.06	0.01	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0.67	0.33	0	0	0	0	1	
<i>Itaura</i>	0.1	0.62	0.26	0.01	0	0	1	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0.25	0.75	0	0	0.4	0.6	
<i>Leptonema</i>	0	0	0.12	0.05	0.13	0.7	0	1	0	0.2	0	0.6	0.2	0	0	0.33	0.5	0.17	0	0	1	0	0	1	0	0	1	0	
<i>Macronema</i>	0	0.12	0.05	0.16	0.26	0.41	0	1	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
<i>Macrostemun</i>	0	0.08	0.08	0.15	0.23	0.46	1	0	0	0.13	0	0.73	0.13	0	0	0	1	0	0	0	1	0	0	1	0	0	0.5	0.5	
<i>Marilia</i>	0.01	0.09	0.23	0.27	0.39	0.01	1	0	0.38	0.13	0.38	0	0.13	0	0.5	0.5	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Metrichia</i>	0.4	0.53	0.07	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0.75	0.25	0	0	0.5	0.5	0	0	0	1	
<i>Mortoniella</i>	0.1	0.7	0.2	0	0	0	1	0	0.5	0	0.5	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0	0.17	0.5	0.33	0	0.4	0.6	
<i>Nectopsyche</i>	0.02	0.28	0.21	0.28	0.21	0	1	0	0.29	0.43	0.29	0	0	0	0.17	0.5	0.33	0	0.75	0.25	0	0	0	1	0	0	0	1	
<i>Neotrichia</i>	0.71	0.29	0	0	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	0.75	0.25	0	0.4	0	0.6	0	0	0	1	

Genus	Body size						Potencial number of cycles per year		Feeding habits						Locomotion					Body flexibility			Body form				Relation to substrate		
	<1.5	1.5 - 2.5	2.5 - 3.5	3.5 - 5.0	5.0 - 10.0	>10	< ou = 1	> 1	Collector-Gatherer	Shredder	Scraper	Collector-Filterer	Predator	Burrower	Climber	Sprawler	Clinger	Swimmer	<10°	>10-45°	>45°	Streamlined	Flattened	Cylindrical	Spherical	Free living	Silk-net builder	Case builder	
Notalina	0.22	0.11	0.11	0.22	0.33	0	1	0	0	0	1	0	0	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
Nyctiophylax	0.11	0.67	0.11	0	0	0.11	1	0	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
Oecetis	0.1	0.31	0.34	0.2	0.05	0	0	1	0	0	0	0	1	0	0	0.5	0.5	0	0.75	0.25	0	0	0	1	0	0	0	1	
Oxyetira	0.05	0.66	0.24	0.06	0	0	1	0	0	0	1	0	0	0	0.5	0.5	0	0	0.75	0.25	0	0.5	0	0.5	0	0	0	1	
Phylloicus	0.05	0.21	0.19	0.13	0.3	0.11	0	1	0.25	0.75	0	0	0	0	0	0.75	0.25	0	0.75	0.25	0	0	0	1	0	0	0	1	
Polycentropus	0	0.12	0.19	0.27	0.41	0.02	1	0	0	0.2	0	0.2	0.6	0	0	0.5	0.5	0	0	0	1	0	0	1	0	0	1	0	
Polyplectropus	0	0.01	0.09	0.24	0.66	0	1	0	0	0.07	0	0.4	0.53	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	
Protoptila	0.05	0.47	0.34	0.14	0	0	1	0	0	0	1	0	0	0	0	0.5	0.5	0	1	0	0	0	0	1	0	0	0.4	0.6	
Smicridea	0	0.25	0.25	0.24	0.24	0	0	1	0	0.2	0	0.6	0.2	0	0	0.33	0.5	0.17	0	0	1	0	0	1	0	0	1	0	
Triplectides	0	0.07	0.07	0.1	0.5	0.27	1	0	0	1	0	0	0	0	0	1	0	0	0.75	0.25	0	0	0	1	0	0	0	1	
Wormaldia	0	0.91	0	0.03	0.06	0	1	0	0	0	0.4	0.6	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	

Appendix 2: Tables with all raw environmental variables and their codes and definitions sampled in each site used in the thesis.

Table 2.1. Geophysical variables

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
TMMS0003	87.83	590	672.02	78.70	317.00	5.46	7.29	50.52	1184.673
TMMS0007	104.98	623	698.52	45.39	199.00	6.30	3.07	27.36	1198.299
TMMS0009	17.26	647	759.90	52.36	209.00	11.56	6.75	37.78	1355.000
TMMS0027	7.49	765	838.55	13.86	67.00	4.47	2.60	13.92	1261.700
TMMS0028	7.48	666	761.12	41.29	221.00	16.72	8.25	48.96	1412.444
TMMS0033	1.57	659	704.72	9.32	45.00	8.46	3.44	16.47	1364.000
TMMS0040	0.45	815	930.02	39.89	151.00	10.39	4.38	19.53	1449.000
TMMS0043	7.36	784	815.50	18.21	79.00	4.15	2.64	12.36	1264.625
TMMS0058	5.54	639	622.89	15.69	93.00	7.20	2.80	18.51	1267.571
TMMS0072	9.09	734	783.35	17.21	76.00	8.80	26.78	475.30	1386.167
TMMS0082	44.78	584	611.60	19.66	105.00	5.51	2.53	18.45	1363.558
TMMS0088	3.16	770	791.92	15.23	82.00	8.53	5.99	35.31	1376.250
TMMS0090	5.13	648	721.60	27.22	121.00	6.77	3.77	16.93	1303.250
TMMS0091	103.51	709	839.01	47.71	229.00	7.98	3.87	30.23	1253.375
TMMS0106	1.87	645	692.29	18.82	70.00	7.53	3.97	18.85	1262.000
TMMS0119	72.48	600	680.64	64.05	337.00	4.59	5.06	47.34	1184.565
TMMS0126	37.96	591	636.90	25.74	143.00	4.84	2.28	13.34	1204.156
TMMS0133	11.92	614	646.54	16.35	81.00	6.09	2.51	16.92	1319.133
TMMS0134	1.1	669	675.79	15.12	57.00	6.10	2.20	8.76	1222.000
TMMS0137	62.01	611	712.72	69.30	269.00	10.50	7.07	44.34	1338.819
TMMS0159	164.84	729	827.53	34.38	181.00	6.00	3.49	20.70	1257.568
TMMS0171	162.09	675	794.44	43.18	213.00	5.80	3.36	25.31	1258.631
TMMS0178	30.14	586	614.73	22.98	134.00	4.84	2.15	16.02	1277.027
TMMS0183	53.79	616	678.79	43.86	246.00	3.40	2.55	37.45	1186.000
TMMS0187	24.96	742	796.71	19.35	98.00	4.22	1.92	13.25	1265.563

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
TMMS0193	109.1	621	673.05	23.19	133.00	6.24	7.88	396.25	1402.259
TMMS0209	53.25	637	642.13	18.35	89.00	5.74	2.74	18.46	1386.615
TMMS0214	44.44	636	680.00	29.64	167.00	4.77	2.30	15.33	1229.574
TMMS0220	10.91	671	813.19	36.92	181.00	14.24	8.76	52.18	1415.250
TMMS0279	157.1	642	754.23	39.61	255.00	5.95	3.56	25.03	1201.771
TMMS0283	55.27	753	834.13	23.95	132.00	4.44	2.52	14.14	1262.059
TMMS0290	22.96	606	630.16	16.84	68.00	5.04	2.21	16.41	1381.172
TMMS0296	24.57	682	871.57	68.93	380.00	14.81	8.28	47.73	1435.467
TMMS0381	106.73	587	688.66	79.65	291.00	10.44	8.02	55.99	1364.258
TMMS0391	71.31	652	717.39	41.53	186.00	6.29	3.09	27.36	1200.047
TMMS0437	30.14	594	703.82	50.45	234.00	9.78	6.59	36.89	1349.973
TMMS1865	65.84	608	707.65	70.36	272.00	10.15	7.02	44.34	1336.038
TMMS3195	3.39	739	775.07	11.59	53.00	3.67	2.16	9.73	1284.000
TMMS3962	20.45	599	735.84	70.20	269.00	11.85	8.39	49.20	1205.958
VGMS00002	2.64	769	808.52	74.00	20.92	4.63	1.94	10.59	1587.750
VGMS00004	16.38	593	707.67	231.00	55.61	7.96	4.56	30.92	1529.524
VGMS00016	7.78	602	725.14	200.00	38.56	4.72	3.12	21.71	1541.773
VGMS00018	3.28	737	812.81	120.00	27.44	4.66	2.25	10.62	1586.400
VGMS00022	3.07	701	795.55	158.00	39.22	8.70	5.01	22.22	1585.000
VGMS00034	5.07	736	802.63	108.00	26.20	6.16	2.67	15.73	1586.125
VGMS00037	11.22	585	658.07	123.00	27.37	4.27	2.69	16.18	1496.500
VGMS00044	6.87	709	755.38	91.00	17.19	4.05	2.88	16.40	1550.500
VGMS00048	12.06	581	637.60	97.00	20.66	3.84	2.55	15.78	1472.467
VGMS00080	25.5	593	686.30	174.00	32.58	4.17	3.11	28.30	1510.806
VGMS00109	20.96	625	706.57	161.00	30.42	5.29	2.66	18.52	1557.192
VGMS00112	52.83	576	692.60	229.00	49.49	4.62	2.82	18.44	1511.284
VGMS00121	8.53	598	676.51	121.00	28.49	5.51	2.69	13.88	1530.000
VGMS00124	25.62	683	749.48	115.00	22.22	3.85	2.53	15.54	1543.034
VGMS00126	6.68	674	780.85	177.00	35.28	6.43	3.95	29.99	1535.143
VGMS00128	4.87	584	639.33	100.00	21.88	6.23	3.03	18.32	1457.833

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
VGMS00162	20.71	651	748.26	171.00	32.57	5.09	3.36	24.22	1571.962
VGMS00177	7.58	511	575.99	138.00	32.96	6.59	3.30	19.84	1432.909
VGMS00191	21.73	536	645.11	203.00	44.21	6.17	3.44	25.84	1518.702
VGMS00206	5.28	631	757.40	246.00	78.46	12.74	10.37	53.18	1542.875
VGMS00210	24.77	713	815.69	203.00	36.05	7.15	4.22	28.13	1591.250
VGMS00247	8.25	685	787.33	173.00	39.19	6.85	2.74	17.76	1535.500
VGMS00252	23.13	560	712.00	195.00	40.22	5.17	3.43	21.96	1535.374
VGMS00255	5.83	573	660.04	152.00	41.58	8.85	4.02	24.89	1532.000
VGMS00277	5.49	536	706.44	193.00	39.84	5.29	3.39	21.67	1532.366
VGMS00306	20.78	669	802.23	243.00	43.11	7.31	4.62	29.78	1586.200
VGMS00320	4.11	700	747.03	108.00	21.18	3.85	2.45	14.51	1524.000
VGMS00380	18.05	627	722.80	91.00	20.51	4.23	2.41	11.63	1530.475
VGMS00387	22.38	545	629.39	176.00	40.91	5.00	2.37	16.45	1493.333
VGMS00418	8.43	688	786.64	174.00	41.89	6.90	3.30	18.77	1581.333
VGMS00433	60.04	531	618.27	197.00	45.11	5.17	3.12	24.06	1477.148
VGMS00444	73.34	599	731.25	205.00	38.73	4.43	2.95	21.44	1544.347
VGMS00447	16.12	536	633.50	187.00	48.68	7.97	4.24	22.87	1527.279
VGMS00450	46.46	669	813.28	316.00	61.72	6.93	4.66	29.94	1587.877
VGMS00511	5.05	603	700.57	167.00	41.09	7.48	3.37	23.08	1533.125
VGMS00515	19.92	555	705.70	239.00	54.15	8.62	5.30	34.33	1518.182
VGMS00558	12.16	612	845.24	267.00	31.74	5.36	5.89	61.32	1556.125
VGMS00575	8.51	626	722.79	182.00	42.92	6.71	3.16	21.61	1537.300
SSMS0001	3.32	705	736.22	69.00	16.37	3.68	1.17	7.11	1589.250
SSMS0002	32.68	484	577.85	222.00	29.71	4.14	2.47	33.33	1386.390
SSMS0008	6.05	601	687.70	135.00	35.24	6.13	3.42	18.75	1299.429
SSMS0010	38.24	434	484.31	114.00	22.23	3.25	1.34	10.59	1453.915
SSMS0014	8.96	478	534.15	91.00	16.73	3.10	1.30	10.51	1526.091
SSMS0028	17.52	471	557.27	203.00	54.27	4.65	2.05	17.04	1437.429
SSMS0029	70.14	409	522.01	226.00	50.18	3.79	1.95	13.64	1444.483
SSMS0031	2.13	541	579.59	186.00	41.39	8.53	8.25	43.40	1548.000

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
SSMS0033	18.05	462	516.10	178.00	32.18	5.98	6.24	45.52	1458.636
SSMS0035	108.36	479	587.74	293.00	83.36	6.75	7.65	47.03	1533.582
SSMS0037	31.59	491	567.25	251.00	33.95	4.70	3.85	48.72	1442.237
SSMS0038	27.95	489	555.94	190.00	36.44	6.72	5.41	36.57	1492.361
SSMS0044	68.3	458	559.52	229.00	56.51	4.35	2.39	19.22	1369.679
SSMS0051	12.84	502	571.24	136.00	37.58	3.73	1.78	15.62	1459.933
SSMS0053	4.02	512	558.78	83.00	22.37	4.04	1.72	8.44	1438.750
SSMS0057	3.44	496	528.31	174.00	31.25	7.18	7.32	46.10	1466.250
SSMS0059	4.77	521	565.81	191.00	24.90	6.33	6.53	47.90	1548.000
SSMS0073	67.92	453	572.75	225.00	47.53	4.34	2.69	25.60	1418.557
SSMS0078	18.28	491	659.95	273.00	86.26	9.65	10.42	52.40	1567.773
SSMS0094	9.99	490	533.44	107.00	19.29	3.55	1.43	16.29	1518.500
SSMS0105	19.34	410	491.73	130.00	25.54	4.13	1.81	11.50	1468.348
SSMS0126	23.48	424	578.70	325.00	94.08	6.35	6.49	41.11	1540.103
SSMS0129	70.68	468	551.42	246.00	57.55	9.09	9.32	52.19	1476.600
SSMS0133	43.31	475	544.55	247.00	32.79	5.62	5.45	57.13	1390.019
SSMS0144	17.52	446	532.37	200.00	53.01	4.04	2.26	15.44	1430.850
SSMS0149	43.23	485	548.38	182.00	29.99	4.67	2.76	43.16	1451.259
SSMS0150	25.29	478	550.41	209.00	39.78	6.64	6.25	49.99	1492.290
SSMS0157	2.44	579	617.21	59.00	14.02	3.81	1.45	7.23	1394.000
SSMS0175	7.74	506	563.45	204.00	32.33	5.67	5.04	35.42	1535.111
SSMS0191	18.27	531	632.44	313.00	80.74	9.09	9.36	48.94	1584.391
SSMS0193	70.68	468	551.42	246.00	57.55	9.09	9.32	52.19	1476.600
SSMS0199	40.75	411	477.87	220.00	45.03	3.35	2.52	25.44	1435.860
SSMS0213	46.14	457	535.06	144.00	24.48	3.97	1.59	11.10	1453.276
SSMS0351	42.43	450	558.38	291.00	64.09	7.15	7.20	48.89	1539.182
SSMS0408	18.2	438	514.02	151.00	37.06	6.52	4.64	29.41	1357.273
SSMS0411	93.46	499	626.72	336.00	79.83	7.25	8.85	74.85	1559.345
SSMS0447	30.76	521	597.19	272.00	51.85	6.89	6.53	49.56	1567.339
SSMS1000	11.96	460	560.99	178.00	38.26	4.75	2.68	15.57	1419.857

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
SSMS4173	0.37	513	530.62	43.00	11.00	8.10	3.54	14.86	1333.000
SSMS4330	36.23	431	514.30	236.00	59.14	6.19	5.42	28.93	1260.591
RENP0008	7.72	920	1012.28	106.00	26.63	5.63	5.00	21.79	1558.500
RENP0012	4.19	871	1011.62	226.00	62.88	14.01	5.66	29.64	1619.714
RENP0016	32.73	835	997.77	345.00	81.76	14.44	8.98	56.74	1566.462
RENP0028	15.05	846	934.74	208.00	31.24	8.32	3.98	25.50	1568.368
RENP0047	1.73	900	960.54	84.00	20.23	7.71	3.56	15.24	1611.000
RENP0052	6.02	856	954.11	131.00	34.08	6.62	4.21	19.53	1552.429
RENP0054	50.75	845	989.04	355.00	67.58	10.95	7.27	45.71	1557.092
RENP0055	10.41	947	1024.34	123.00	24.88	6.26	2.65	15.52	1529.250
RENP0075	5.31	855	944.61	176.00	47.32	11.11	5.38	30.83	1544.667
RENP0092	1.69	940	1030.61	190.00	47.24	17.16	8.19	40.83	1608.333
RENP0095	3.22	897	924.71	84.00	19.58	5.90	2.36	12.60	1547.200
RENP0096	17.33	817	895.96	108.00	21.13	6.20	3.46	24.13	1519.300
RENP0097	7.34	865	1014.02	203.00	51.74	8.50	5.78	26.88	1516.500
RENP0100	8.65	823	972.03	307.00	62.20	8.92	5.61	30.22	1564.700
RENP0108	3.40	860	924.23	79.00	18.13	6.10	2.40	14.49	1590.000
RENP0110	6.80	893	1007.63	147.00	34.97	7.66	4.17	17.95	1621.571
RENP0112	7.28	877	943.79	104.00	22.16	6.03	2.89	15.14	1494.222
RENP0128	2.82	841	949.57	206.00	67.38	11.72	7.01	35.53	1504.000
RENP0132	1.38	854	905.49	140.00	27.47	7.74	4.18	20.87	1556.500
RENP0139	15.41	863	942.17	117.00	22.89	5.34	2.78	18.44	1497.316
RENP0144	3.65	826	910.63	204.00	45.06	11.36	4.73	25.45	1503.000
RENP0187	6.37	891	933.67	98.00	22.10	7.12	3.89	19.06	1585.286
RENP0192	23.60	910	1007.22	110.00	26.44	3.44	3.05	15.53	1555.000
RENP0203	15.48	888	1004.53	201.00	47.07	11.56	5.97	37.33	1531.211
RENP0228	4.58	870	961.00	116.00	29.05	6.84	3.31	17.29	1537.400
RENP0240	1.54	960	1029.03	84.00	23.92	7.30	6.02	19.64	1570.500
RENP0251	3.15	909	971.97	94.00	24.41	8.64	4.52	19.37	1602.000
RENP0287	16.96	833	899.57	132.00	29.30	7.55	3.79	21.02	1561.850

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
RENPO368	7.37	967	940.11	117.00	24.22	5.22	2.74	16.07	1496.111
RENPO375	2.32	948	1004.08	104.00	24.70	10.99	5.54	31.61	1537.333
RENPO443	13.40	887	951.22	111.00	25.89	7.75	4.16	21.87	1601.111
RENPO511	28.74	868	919.92	142.00	29.20	7.50	4.18	26.27	1631.771
RENPI524	7.93	914	1019.94	94.00	18.35	3.16	3.07	15.78	1550.667
RENPI2991	5.90	895	947.69	116.00	25.40	8.18	3.72	20.78	1657.429
RENPI5612	29.63	954	1035.86	119.00	25.14	4.27	3.49	18.17	1594.676
RENPI7308	1.39	839	906.89	85.00	21.51	9.00	4.67	21.11	1567.500
RENPI9611	2.92	860	912.57	93.00	21.83	6.99	2.81	13.41	1565.750
RENPI9757	10.81	952	1036.58	171.00	35.46	8.95	4.37	21.31	1618.308
RENPI2892	6.90	904	980.29	209.00	45.78	12.34	6.18	34.44	1599.667
RENPI5048	27.83	931	1011.11	128.00	32.92	5.13	3.65	17.95	1569.811
RCA02	0.14	1203	1067.6	58	16.10	11.06	2.90	9.22	1542.000
RCA08	5.07	917	1054.87	243	46.47	12.65	5.51	35.00	1634.333
RCA22	3.85	1218	1321.28	134	34.14	6.41	3.13	16.49	1600.333
RCA23	3.29	1240	1309.66	173	44.00	8.02	3.70	19.40	1603.250
RCA30	0.13	1243	1243.79	41	12.81	12.35	6.56	22.28	1579.000
RCA31	3.07	1033	1081.63	99	26.72	8.74	4.02	18.32	1632.667
RCA44	0.32	995	1031.63	64	17.28	9.06	3.43	13.51	1634.000
RCA48	9.2	828	973.11	318	66.27	8.74	5.69	33.76	1563.231
RCA49	0.77	836	886.32	125	38.68	13.55	9.11	35.15	1533.000
RCA50	4.73	1217	959.19	280	72.35	15.82	7.86	38.63	1562.000
RCA52	21.76	900	1017.83	282	52.26	9.10	6.74	46.43	1559.233
RCA53	5.46	876	1012.16	271	78.98	15.02	9.35	43.94	1573.000
RCA57	5.53	1245	1332.56	178	41.18	7.69	4.14	24.51	1611.833
RCA58	3.74	1210	1312.39	143	34.31	7.15	3.68	18.65	1601.250
RCA59	11.02	1220	1320.87	193	44.98	6.86	3.95	20.64	1615.818
RCA60	6.67	1215	1279.83	145	33.05	7.97	4.49	21.24	1611.857
RCA62	14.69	1199	939.27	190	44.80	9.56	4.52	28.36	1536.750
RCA64	16.26	1039	1002.58	212	47.80	11.26	5.71	31.66	1531.500

	Drainage area (km ²)	Site altitude (m)	Range basin elevation (m)	Average basin elevation (m)	Std. Dev. Basin elevation	Range basin slope (%)	Average basin slope (%)	Std. Dev. Basin slope	Total annual rainfall (mm/m ²)
	Dren_area	Altitude	Elev_range	Elev_mean	Elev_std	Slope_range	Slope_mean	Slope_std	Rainfall
RCA65	12.41	1048	1312.41	162	34.70	6.73	3.11	18.35	1600.688
RCA66	0.72	997	1071.25	123	38.31	12.72	7.22	27.06	1623.000
RCA67	0.78	903	975.70	155	41.75	13.26	4.11	17.98	1603.000
RCA68	6.52	927	1025.44	285	87.02	12.26	7.72	43.78	1565.500
RCA69	6.52	851	1025.59	285	87.03	12.32	7.70	43.78	1565.500
RCA70	2.49	840	904.38	190	48.02	13.14	7.90	33.45	1547.000
RCA71	1.56	852	905.54	91	21.50	8.86	3.87	18.38	1567.500
RCA72	4.15	898	919.33	204	47.34	9.61	5.00	34.12	1532.250
RCA73	50.77	863	949.64	342	59.59	12.09	6.97	44.43	1555.894
RCA74	2.29	858	979.33	114	25.50	10.50	5.25	26.54	1562.000
RCA90	2.29	916	979.81	114	25.25	10.57	5.22	26.54	1562.000

Table 2.2. Land use variables.

	% of Woodland savanna	% of Parkland savanna	% of Grassy-woody savanna	% of Palm swamp	% of Pasture	% of Agriculture
	%_Woodland	%_Parkland	%_Grassy_Woody	%_Palm_swamp	%_Pasture	%_Agriculture
TMMS0003	9.20	4.92	6.56	1.70	61.10	3.83
TMMS0007	8.93	27.59	7.10	0.00	34.85	1.21
TMMS0009	48.87	9.86	10.07	0.00	31.21	0.00
TMMS0027	8.16	0.74	19.01	1.72	35.21	0.34
TMMS0028	56.19	24.81	0.00	0.00	19.00	0.00
TMMS0033	11.23	20.69	18.63	0.00	41.12	0.00
TMMS0040	16.18	4.71	11.00	0.00	68.11	0.00
TMMS0043	5.68	9.80	29.57	0.00	28.40	8.91
TMMS0058	7.31	24.24	6.69	0.00	59.94	0.00
TMMS0072	24.13	23.77	3.55	0.00	45.42	3.12
TMMS0082	12.30	3.39	5.81	2.97	72.23	1.70
TMMS0088	4.72	74.71	0.00	0.00	20.57	0.00
TMMS0090	21.33	21.48	6.70	0.00	44.63	1.60
TMMS0091	16.32	20.07	11.97	0.00	49.71	0.94
TMMS0106	9.32	30.73	11.24	0.00	38.43	0.00
TMMS0119	10.98	6.64	7.94	0.74	60.05	1.53
TMMS0126	8.34	17.43	24.69	0.00	7.64	4.74
TMMS0133	10.06	4.24	10.30	0.71	63.49	2.72
TMMS0134	2.36	93.76	0.00	0.00	3.89	0.00
TMMS0137	37.37	18.54	5.50	0.15	37.54	0.65
TMMS0159	8.37	31.50	8.47	0.89	16.32	1.74
TMMS0171	7.82	34.23	18.82	0.79	24.24	1.59
TMMS0178	15.26	2.18	11.57	0.00	64.33	2.11
TMMS0183	4.92	3.60	12.32	2.41	48.42	5.42
TMMS0187	8.63	10.43	27.25	0.00	46.24	7.44
TMMS0193	7.66	0.64	1.33	4.59	69.90	1.06
TMMS0209	17.70	1.05	1.39	4.32	38.45	14.50
TMMS0214	7.07	7.78	8.52	0.54	48.85	16.69
TMMS0220	43.55	20.33	5.48	0.00	30.64	0.00
TMMS0279	8.88	13.60	8.68	1.65	38.70	13.45

	% of Woodland savanna	% of Parkland savanna	% of Grassy-woody savanna	% of Palm swamp	% of Pasture	% of Agriculture
	%_Woodland	%_Parkland	%_Grassy_Woody	%_Palm_swamp	%_Pasture	%_Agriculture
TMMS0283	6.70	19.98	31.49	1.50	17.38	2.51
TMMS0290	10.34	0.00	6.66	6.16	72.08	4.75
TMMS0296	29.60	29.64	11.94	0.00	28.83	0.00
TMMS0381	28.04	8.10	10.23	1.55	50.87	0.96
TMMS0391	9.91	24.05	3.35	0.00	32.92	0.68
TMMS0437	21.50	6.96	2.47	1.85	63.74	3.49
TMMS1865	35.73	18.49	5.43	0.89	37.99	1.24
TMMS3195	1.55	0.00	36.11	18.96	23.99	5.04
TMMS3962	24.87	32.97	4.13	0.00	32.06	5.97
VGMS00002	19.23	0.00	0.00	0.00	0.00	80.77
VGMS00004	12.88	0.00	1.84	0.00	17.79	67.48
VGMS00016	10.02	0.00	1.94	0.11	28.36	50.00
VGMS00018	9.09	0.00	0.00	0.00	0.00	90.91
VGMS00022	9.68	0.00	0.00	0.00	0.00	90.32
VGMS00034	10.00	0.00	0.00	0.00	0.00	90.00
VGMS00037	6.31	0.00	2.70	0.00	11.71	79.28
VGMS00044	10.14	0.00	0.00	0.00	47.83	37.68
VGMS00048	8.20	0.00	1.64	0.00	11.48	78.69
VGMS00080	9.02	0.00	1.57	0.78	7.06	81.57
VGMS00109	11.00	0.00	1.91	0.00	3.35	83.73
VGMS00112	10.82	0.00	1.33	0.57	12.90	70.78
VGMS00121	4.71	0.00	0.00	0.00	28.24	67.06
VGMS00124	10.55	0.00	4.69	0.00	26.95	44.53
VGMS00126	18.18	0.00	0.00	0.00	12.12	69.70
VGMS00128	18.37	0.00	0.00	0.00	6.12	67.35
VGMS00162	12.14	0.00	0.00	0.00	2.43	83.50
VGMS00177	6.67	0.00	0.00	2.67	5.33	85.33
VGMS00191	9.16	0.00	1.57	0.26	10.47	73.82
VGMS00206	22.64	0.00	3.77	0.00	13.21	60.38
VGMS00210	29.44	0.00	0.40	0.00	18.15	52.02
VGMS00247	8.54	0.00	0.00	0.00	0.00	91.46
VGMS00252	9.73	0.00	2.88	0.09	24.32	55.41

	% of Woodland savanna	% of Parkland savanna	% of Grassy-woody savanna	% of Palm swamp	% of Pasture	% of Agriculture
	%_Woodland	%_Parkland	%_Grassy_Woody	%_Palm_swamp	%_Pasture	%_Agriculture
VGMS00255	11.98	0.00	3.65	0.00	10.42	73.96
VGMS00277	9.79	0.00	2.83	0.09	23.26	56.82
VGMS00306	24.31	0.00	0.40	0.00	12.25	63.04
VGMS00320	9.52	0.00	0.00	4.76	14.29	71.43
VGMS00380	13.66	0.00	3.78	0.42	25.21	49.79
VGMS00387	3.14	0.00	0.00	4.93	1.35	90.58
VGMS00418	14.29	0.00	0.00	0.00	0.00	85.71
VGMS00433	9.35	0.00	2.34	0.17	3.51	84.64
VGMS00444	9.50	0.00	1.63	0.13	27.63	50.63
VGMS00447	11.30	0.00	2.26	0.00	6.78	78.53
VGMS00450	19.35	0.00	0.81	0.00	9.07	70.56
VGMS00511	13.33	0.00	2.96	0.00	8.89	74.81
VGMS00515	17.42	0.00	3.79	0.00	16.29	62.50
VGMS00558	8.26	0.00	0.00	0.83	9.09	71.07
VGMS00575	13.10	0.00	3.57	0.00	8.33	75.00
SSMS0001	5.92	0.00	0.00	0.00	0.00	94.08
SSMS0002	15.27	0.00	2.45	0.00	13.29	65.82
SSMS0008	14.09	0.00	3.38	0.00	1.93	80.60
SSMS0010	5.39	0.00	0.00	5.85	12.39	76.36
SSMS0014	2.18	0.00	0.00	3.78	24.75	69.29
SSMS0028	7.29	0.00	0.00	3.21	0.00	88.14
SSMS0029	6.62	0.00	0.00	2.66	0.00	90.73
SSMS0031	17.56	5.38	0.00	11.33	3.71	62.03
SSMS0033	11.85	13.00	0.92	0.31	49.87	21.21
SSMS0035	24.34	0.00	1.11	2.20	20.74	50.25
SSMS0037	10.98	0.00	2.59	3.05	7.48	75.89
SSMS0038	21.44	0.00	1.60	2.47	2.93	66.27
SSMS0044	9.05	0.00	0.31	3.16	2.11	85.38
SSMS0051	12.32	0.00	1.86	1.16	1.89	82.77
SSMS0053	10.52	0.00	0.00	0.00	0.00	89.48
SSMS0057	18.18	0.11	0.00	0.00	61.35	20.36
SSMS0059	13.81	2.27	8.70	5.22	2.35	67.66

	% of Woodland savanna	% of Parkland savanna	% of Grassy-woody savanna	% of Palm swamp	% of Pasture	% of Agriculture
	%_Woodland	%_Parkland	%_Grassy_Woody	%_Palm_swamp	%_Pasture	%_Agriculture
SSMS0073	10.95	0.00	0.53	0.08	0.00	83.87
SSMS0078	24.89	0.00	0.00	1.48	10.66	61.74
SSMS0094	8.78	0.00	0.00	0.00	8.90	82.32
SSMS0105	8.19	0.00	3.64	2.69	0.00	85.48
SSMS0126	19.48	0.00	0.00	0.20	13.77	66.54
SSMS0129	12.14	0.00	0.65	2.08	7.20	72.12
SSMS0133	13.68	3.27	4.49	0.00	16.31	60.63
SSMS0144	6.45	0.00	4.03	2.60	0.00	86.93
SSMS0149	13.55	0.58	0.00	3.97	26.76	55.14
SSMS0150	10.56	0.00	2.33	8.49	13.17	62.39
SSMS0157	8.00	0.00	0.00	0.00	0.00	92.00
SSMS0175	22.72	2.55	0.00	4.18	2.78	67.78
SSMS0191	25.08	2.75	0.00	4.56	11.25	56.36
SSMS0193	12.14	0.00	0.65	2.08	7.20	72.12
SSMS0199	14.54	0.00	0.54	6.72	1.06	77.15
SSMS0213	7.00	0.00	1.72	5.17	52.10	32.58
SSMS0351	16.11	1.65	1.61	2.29	16.33	62.01
SSMS0408	20.12	0.00	1.24	1.35	0.76	76.53
SSMS0411	25.82	1.00	0.00	1.21	8.44	63.54
SSMS0447	16.23	1.03	0.00	4.87	9.69	67.00
SSMS1000	14.00	0.00	0.69	0.29	0.00	85.02
SSMS4173	0.00	0.00	15.48	0.00	0.00	0.00
SSMS4330	19.53	0.00	0.00	0.67	4.90	72.44
RENP0008	8.89	0.00	4.99	2.15	3.99	79.99
RENP0012	30.06	0.00	57.52	0.00	11.40	1.02
RENP0016	11.89	81.18	0.00	0.00	2.39	4.54
RENP0028	17.72	0.00	13.11	0.00	15.32	53.84
RENP0047	27.72	0.00	8.24	0.00	38.60	25.44
RENP0052	8.26	0.00	21.51	0.00	15.55	54.68
RENP0054	10.56	56.83	0.00	0.00	12.69	19.91
RENP0055	9.38	0.00	0.00	0.00	0.00	90.62
RENP0075	5.84	88.31	0.00	0.00	0.00	5.85

	% of Woodland savanna	% of Parkland savanna	% of Grassy-woody savanna	% of Palm swamp	% of Pasture	% of Agriculture
	%_Woodland	%_Parkland	%_Grassy_Woody	%_Palm_swamp	%_Pasture	%_Agriculture
REN0092	21.33	0.00	0.00	2.10	70.80	5.78
REN0095	12.69	0.00	0.00	0.00	2.48	84.83
REN0096	12.68	0.00	0.85	0.00	5.08	81.39
REN0097	19.31	0.00	2.50	0.00	31.98	46.21
REN0100	9.03	68.61	0.00	0.00	0.00	22.37
REN0108	24.34	0.00	0.00	0.00	0.00	75.66
REN0110	23.35	0.00	3.66	0.00	14.75	58.24
REN0112	14.19	0.00	0.00	0.00	22.74	63.07
REN0128	25.23	0.00	21.77	1.10	30.19	21.71
REN0132	18.65	25.10	0.00	0.00	0.00	56.26
REN0139	14.51	0.00	0.00	0.42	0.00	85.07
REN0144	14.24	0.00	34.99	0.00	6.35	44.42
REN0187	9.35	0.00	27.80	0.00	1.36	61.49
REN0192	4.54	0.00	13.03	1.34	1.46	79.64
REN0203	20.20	16.59	24.59	0.00	28.23	10.40
REN0228	16.97	0.00	8.79	0.00	3.00	71.24
REN0240	11.27	0.00	0.00	0.00	34.72	54.01
REN0251	19.13	0.00	10.34	0.00	8.83	61.70
REN0287	13.28	0.00	14.15	0.00	15.80	56.78
REN0368	7.92	0.00	1.86	0.00	0.00	90.22
REN0375	17.37	45.61	2.08	0.00	32.77	2.16
REN0443	13.87	0.00	24.60	0.00	0.00	61.53
REN0511	11.33	0.00	8.01	0.00	3.13	77.53
REN1524	7.08	0.00	0.00	0.00	0.00	92.92
REN2991	14.49	0.00	11.86	0.00	0.00	70.12
REN5612	5.32	0.00	9.72	4.40	4.29	76.27
REN7308	33.21	0.00	57.56	0.00	8.46	0.78
REN9611	14.77	0.00	5.19	0.00	18.31	61.73
REN9757	10.01	0.00	6.41	3.31	19.60	30.91
REN12892	27.09	0.00	0.00	3.22	68.27	1.42
REN15048	6.63	0.00	9.00	5.01	13.51	63.26
RCA02	0.57	99.43	0.00	0.00	0.00	0.00

	% of Woodland savanna	% of Parkland savanna	% of Grassy-woody savanna	% of Palm swamp	% of Pasture	% of Agriculture
	%_Woodland	%_Parkland	%_Grassy_Woody	%_Palm_swamp	%_Pasture	%_Agriculture
RCA08	50.39	20.84	5.68	0.00	16.26	6.83
RCA22	1.89	98.11	0.00	0.00	0.00	0.00
RCA23	3.50	96.50	0.00	0.00	0.00	0.00
RCA30	2.33	23.34	0.00	0.00	23.69	50.64
RCA31	28.04	37.79	0.00	0.00	2.89	31.27
RCA44	23.63	0.00	0.00	0.00	76.37	0.00
RCA48	9.03	68.61	0.00	0.00	0.00	22.37
RCA49	6.39	75.54	0.00	0.00	0.00	18.07
RCA50	11.89	81.18	0.00	0.00	2.39	4.54
RCA52	5.43	93.01	0.00	0.00	0.00	1.56
RCA53	15.14	77.39	0.00	0.00	4.50	2.97
RCA57	1.05	98.95	0.00	0.00	0.00	0.00
RCA58	2.89	97.11	0.00	0.00	0.00	0.00
RCA59	0.66	99.34	0.00	0.00	0.00	0.00
RCA60	0.59	99.41	0.00	0.00	0.00	0.00
RCA62	4.71	95.29	0.00	0.00	0.00	0.00
RCA64	8.40	38.71	52.90	0.00	0.00	0.00
RCA65	0.00	100.00	0.00	0.00	0.00	0.00
RCA66	13.78	0.00	5.93	0.00	66.63	13.66
RCA67	28.53	44.51	0.00	0.00	25.88	1.08
RCA68	9.81	89.04	0.00	0.00	0.00	1.16
RCA69	6.84	58.29	0.00	0.00	13.84	21.03
RCA70	13.58	52.65	32.32	0.00	0.00	1.44
RCA71	31.61	0.00	59.68	0.00	5.50	3.21
RCA72	20.20	16.59	24.59	0.00	28.23	10.40
RCA73	5.84	88.31	0.00	0.00	0.00	5.85
RCA74	10.56	56.83	0.00	0.00	12.69	19.91
RCA90	10.29	36.16	0.00	0.00	26.55	27.00

Table 2.2. Land use variables. Continuation.

	% of Eucalyptus forest	% of Natural land	Distance to cities (km)	Distance to paved highways (km)	Density of homes in the basin (houses/km ²)
	%_Eucalyptus	%_Natural	City_dist	Highway_dist	House_density
TMMS0003	12.69	22.38	6.41	3.88	0.78
TMMS0007	20.32	43.63	30.04	1.60	0.18
TMMS0009	0.00	68.79	6.98	0.82	0.87
TMMS0027	34.82	29.64	34.37	7.21	0.27
TMMS0028	0.00	81.00	17.85	15.01	0.13
TMMS0033	8.33	50.55	11.61	3.05	0.00
TMMS0040	0.00	31.89	6.44	3.05	2.22
TMMS0043	17.63	45.06	34.68	9.25	0.00
TMMS0058	1.82	38.24	23.37	8.44	0.00
TMMS0072	0.00	51.45	20.42	20.80	0.11
TMMS0082	1.44	24.47	8.24	5.69	2.59
TMMS0088	0.00	79.43	27.70	20.53	0.00
TMMS0090	4.27	49.51	15.73	3.22	0.58
TMMS0091	0.98	48.37	29.61	3.39	0.28
TMMS0106	10.28	51.29	19.46	5.60	0.53
TMMS0119	12.13	26.29	7.78	2.00	0.80
TMMS0126	37.17	50.46	17.75	3.00	0.11
TMMS0133	8.50	25.29	11.60	6.89	0.75
TMMS0134	0.00	96.11	22.84	3.22	0.00
TMMS0137	0.26	61.56	3.03	3.61	0.82
TMMS0159	32.70	49.24	28.90	4.57	0.04
TMMS0171	12.51	61.66	19.25	0.80	0.39
TMMS0178	4.55	29.01	26.89	2.33	0.46
TMMS0183	22.91	23.25	15.04	0.85	0.69
TMMS0187	0.00	46.32	28.56	3.40	0.56
TMMS0193	14.83	14.21	6.65	2.15	0.72
TMMS0209	22.59	24.46	11.50	7.54	0.66
TMMS0214	10.55	23.91	15.03	7.38	0.31
TMMS0220	0.00	69.36	12.07	9.40	0.00
TMMS0279	15.04	32.81	37.83	4.24	1.16

	% of Eucalyptus forest	% of Natural land	Distance to cities (km)	Distance to paved highways (km)	Density of homes in the basin (houses/km²)
	% <u>Eucalyptus</u>	% <u>Natural</u>	<u>City_dist</u>	<u>Highway_dist</u>	<u>House_density</u>
TMMS0283	20.44	59.67	31.96	8.00	0.16
TMMS0290	0.00	23.17	2.20	0.85	1.35
TMMS0296	0.00	71.17	13.21	9.23	0.20
TMMS0381	0.25	47.92	10.36	2.97	0.85
TMMS0391	29.09	37.31	28.99	5.77	0.11
TMMS0437	0.00	32.78	2.95	0.57	0.93
TMMS1865	0.24	60.53	1.79	2.00	0.88
TMMS3195	0.00	56.62	4.94	0.20	16.52
TMMS3962	0.00	61.97	15.68	4.67	0.59
VGMS00002	0.00	19.23	9.12	1.08	0.38
VGMS00004	0.00	14.72	6.23	1.53	0.61
VGMS00016	0.00	12.07	10.74	1.68	78.73
VGMS00018	0.00	9.09	23.57	0.84	0.30
VGMS00022	0.00	9.68	16.50	1.38	0.00
VGMS00034	0.00	10.00	11.04	1.48	0.20
VGMS00037	0.00	9.01	19.03	0.98	0.27
VGMS00044	0.00	10.14	9.45	1.27	1.75
VGMS00048	0.00	9.84	19.77	1.15	0.17
VGMS00080	0.00	11.37	17.70	0.80	1.37
VGMS00109	0.00	12.92	14.36	4.38	0.33
VGMS00112	0.00	12.71	15.67	0.97	3.07
VGMS00121	0.00	4.71	15.99	1.15	0.82
VGMS00124	0.00	15.23	11.08	1.28	14.31
VGMS00126	0.00	18.18	8.81	1.22	0.45
VGMS00128	8.16	18.37	18.53	0.52	0.41
VGMS00162	0.00	12.14	13.42	3.80	1.60
VGMS00177	0.00	9.33	6.80	1.27	0.53
VGMS00191	0.00	10.99	4.15	1.13	38.57
VGMS00206	0.00	26.42	3.57	1.05	1.14
VGMS00210	0.00	29.84	15.25	2.77	0.89
VGMS00247	0.00	8.54	9.83	0.87	0.49
VGMS00252	0.00	12.70	12.16	1.73	62.55

	% of Eucalyptus forest	% of Natural land	Distance to cities (km)	Distance to paved highways (km)	Density of homes in the basin (houses/km²)
	<u>%_Eucalyptus</u>	<u>%_Natural</u>	<u>City_dist</u>	<u>Highway_dist</u>	<u>House_density</u>
VGMS00255	0.00	15.63	3.38	0.84	1.19
VGMS00277	0.00	12.70	12.53	1.77	59.66
VGMS00306	0.00	24.70	15.81	2.10	0.77
VGMS00320	0.00	14.29	12.02	1.29	3.66
VGMS00380	0.00	17.86	17.47	1.94	8.37
VGMS00387	0.00	8.07	6.62	0.92	0.54
VGMS00418	0.00	14.29	17.49	1.24	0.71
VGMS00433	0.00	11.85	14.75	1.07	0.64
VGMS00444	0.00	11.25	10.08	1.67	86.28
VGMS00447	0.00	13.56	2.91	1.15	5.86
VGMS00450	0.00	20.16	21.66	1.58	0.85
VGMS00511	0.00	16.30	5.29	0.54	1.25
VGMS00515	0.00	21.21	7.88	1.50	0.56
VGMS00558	0.00	9.09	1.77	0.55	95.23
VGMS00575	0.00	16.67	6.32	0.45	1.65
SSMS0001	0.00	5.92	11.17	0.99	0.90
SSMS0002	3.17	17.72	13.43	0.95	0.31
SSMS0008	0.00	17.47	16.11	0.93	0.50
SSMS0010	0.00	11.24	27.63	1.59	0.29
SSMS0014	0.00	5.96	24.09	1.00	0.11
SSMS0028	1.36	10.49	18.48	3.64	0.51
SSMS0029	0.00	9.27	20.02	2.37	0.91
SSMS0031	0.00	34.26	19.93	0.75	0.00
SSMS0033	2.86	26.07	26.88	9.83	0.44
SSMS0035	1.37	27.65	12.65	3.66	0.17
SSMS0037	0.00	16.63	18.19	1.67	0.41
SSMS0038	5.29	25.50	19.34	9.81	0.79
SSMS0044	0.00	12.51	15.80	1.13	0.60
SSMS0051	0.00	15.34	25.73	0.61	0.62
SSMS0053	0.00	10.52	24.93	0.63	0.50
SSMS0057	0.00	18.29	29.55	8.27	0.58
SSMS0059	0.00	30.00	15.52	6.22	0.00

	% of Eucalyptus forest	% of Natural land	Distance to cities (km)	Distance to paved highways (km)	Density of homes in the basin (houses/km²)
	%_Eucalyptus	%_Natural	City_dist	Highway_dist	House_density
SSMS0073	0.00	11.56	4.02	1.22	58.97
SSMS0078	1.23	26.37	14.96	3.02	0.00
SSMS0094	0.00	8.78	12.81	5.38	0.00
SSMS0105	0.00	14.52	9.41	2.06	0.31
SSMS0126	0.00	19.69	27.69	2.86	0.26
SSMS0129	5.81	14.87	23.89	5.79	0.20
SSMS0133	1.62	21.44	16.52	2.06	0.42
SSMS0144	0.00	13.07	22.63	3.32	0.29
SSMS0149	0.00	18.10	19.95	2.45	0.39
SSMS0150	3.07	21.38	14.19	7.80	0.63
SSMS0157	0.00	8.00	16.14	0.55	1.64
SSMS0175	0.00	29.44	20.62	4.27	0.90
SSMS0191	0.00	32.40	24.60	3.10	0.93
SSMS0193	5.81	14.87	0.00	0.00	0.20
SSMS0199	0.00	21.80	21.99	1.18	0.07
SSMS0213	1.42	13.89	25.01	3.71	0.52
SSMS0351	0.00	21.66	17.03	1.47	0.43
SSMS0408	0.00	22.70	5.39	2.88	0.71
SSMS0411	0.00	28.03	13.29	1.90	0.03
SSMS0447	1.18	22.13	23.33	3.52	0.63
SSMS1000	0.00	14.98	5.01	2.40	0.33
SSMS4173	0.00	15.48	1.12	0.18	732.43
SSMS4330	0.00	20.20	4.40	1.96	16.25
RENP0008	0.00	16.02	1.48	4.53	1.69
RENP0012	0.00	87.58	7.44	6.80	0.00
RENP0016	0.00	93.07	28.16	13.78	0.06
RENP0028	0.00	30.84	15.00	6.61	2.66
RENP0047	0.00	35.96	14.30	2.27	0.00
RENP0052	0.00	29.77	15.85	8.63	0.00
RENP0054	0.00	67.40	23.39	15.86	0.34
RENP0055	0.00	9.38	14.15	0.00	1.92
RENP0075	0.00	94.15	18.75	14.33	0.00

	% of Eucalyptus forest	% of Natural land	Distance to cities (km)	Distance to paved highways (km)	Density of homes in the basin (houses/km²)
	<u>%_Eucalyptus</u>	<u>%_Natural</u>	<u>City_dist</u>	<u>Highway_dist</u>	<u>House_density</u>
REN0092	0.00	23.42	5.78	7.17	0.00
REN0095	0.00	12.69	22.22	4.53	0.31
REN0096	0.00	13.53	18.88	8.01	1.10
REN0097	0.00	21.80	28.30	8.01	1.23
REN0100	0.00	77.63	27.56	16.50	0.12
REN0108	0.00	24.34	18.52	16.50	0.00
REN0110	0.00	27.01	24.62	4.53	0.59
REN0112	0.00	14.19	14.05	4.81	0.14
REN0128	0.00	48.10	25.51	12.82	0.71
REN0132	0.00	43.74	29.66	11.55	0.72
REN0139	0.00	14.93	5.18	0.00	0.58
REN0144	0.00	49.23	27.92	9.06	0.00
REN0187	0.00	37.15	22.23	8.01	0.47
REN0192	0.00	18.90	4.68	0.00	0.25
REN0203	0.00	61.37	14.15	1.60	0.90
REN0228	0.00	25.76	15.69	8.01	4.15
REN0240	0.00	11.27	6.33	4.53	0.00
REN0251	0.00	29.47	16.31	8.17	0.32
REN0287	0.00	27.42	27.95	5.78	0.29
REN0368	0.00	9.78	11.11	1.60	0.95
REN0375	0.00	65.06	15.00	5.07	2.16
REN0443	0.00	38.47	19.26	3.20	0.15
REN0511	0.00	19.34	20.75	8.63	0.00
REN1524	0.00	7.08	6.37	0.00	0.38
REN2991	0.00	26.35	5.24	0.00	1.69
REN5612	0.00	19.44	8.44	8.01	0.24
REN7308	0.00	90.76	19.93	10.75	0.00
REN9611	0.00	19.96	19.55	12.92	0.00
REN9757	0.00	19.74	0.00	1.60	279.19
REN12892	0.00	30.31	6.83	6.61	0.29
REN15048	0.00	20.63	0.74	4.81	33.24
RCA02	0.00	100.00	19.44	17.12	0.00

	% of Eucalyptus forest	% of Natural land	Distance to cities (km)	Distance to paved highways (km)	Density of homes in the basin (houses/km²)
	<u>%_Eucalyptus</u>	<u>%_Natural</u>	<u>City_dist</u>	<u>Highway_dist</u>	<u>House_density</u>
RCA08	0.00	76.91	10.79	0.00	0.79
RCA22	0.00	100.00	25.58	11.48	0.00
RCA23	0.00	100.00	27.50	13.80	0.00
RCA30	0.00	25.67	24.42	11.48	0.00
RCA31	0.00	65.84	3.81	3.83	0.65
RCA44	0.00	23.63	26.96	3.83	0.00
RCA48	0.00	77.63	30.74	13.80	0.11
RCA49	0.00	81.93	30.74	16.24	1.30
RCA50	0.00	93.07	11.44	0.00	0.00
RCA52	0.00	98.44	26.96	12.11	0.51
RCA53	0.00	92.53	30.51	13.80	0.00
RCA57	0.00	100.00	19.44	12.11	0.00
RCA58	0.00	100.00	20.53	12.11	0.00
RCA59	0.00	100.00	19.44	13.80	0.00
RCA60	0.00	100.00	19.44	13.80	0.15
RCA62	0.00	100.00	13.75	8.56	0.54
RCA64	0.00	100.00	13.75	10.83	0.92
RCA65	0.00	100.00	21.57	8.56	0.00
RCA66	0.00	19.71	5.39	0.00	0.00
RCA67	0.00	73.03	7.63	5.41	0.00
RCA68	0.00	98.84	26.96	12.11	0.00
RCA69	0.00	65.13	24.12	7.66	0.00
RCA70	0.00	98.56	30.74	10.83	0.00
RCA71	0.00	91.29	19.07	5.41	0.00
RCA72	0.00	61.37	15.25	3.83	0.24
RCA73	0.00	94.15	24.12	7.66	0.37
RCA74	0.00	67.40	27.76	8.56	0.00
RCA90	0.00	46.46	23.19	15.78	0.00

Table 2.3. Hydromorphology.

	Mean thalweg depth (cm)	Mean wetted width (m)	Mean bankfull width (m)	Mean bankfull height (m)	Mean width x mean depth (m ²)	Mean width/depth ratio (m/m)	Mean bank angle (degrees)	Water surface gradient over reach (%)	Channel sinuosity
	Xdepth_T	Xwidth	XBKF_W	XBKF_H	XWXD	XWD_RAT	XBKA	XSLOPE_%	SINU
TMMS0003	25.673	1.945	3.855	0.973	0.499	7.576	51.864	0.003	1.253
TMMS0007	87.253	4.082	5.754	0.877	3.561	4.678	50.545	0.000	1.224
TMMS0009	29.067	2.535	9.600	1.109	0.737	8.721	26.455	0.003	1.219
TMMS0027	22.213	2.629	4.850	0.609	0.584	11.835	25.000	0.016	1.192
TMMS0028	28.020	4.964	9.285	1.215	1.391	17.714	90.000	0.003	1.293
TMMS0033	25.607	1.955	3.976	1.243	0.500	7.633	73.182	0.009	1.211
TMMS0040	14.866	1.470	4.064	0.936	0.219	9.888	33.500	0.024	1.263
TMMS0043	37.980	3.565	7.034	1.064	1.354	9.387	44.091	0.002	1.202
TMMS0058	25.667	4.110	8.955	1.223	1.055	16.013	24.727	0.003	1.339
TMMS0072	47.750	4.039	8.376	0.918	1.928	8.458	120.455	0.002	1.244
TMMS0082	41.802	2.993	4.360	0.580	1.251	7.159	46.650	0.001	1.140
TMMS0088	33.936	3.573	7.488	1.156	1.212	10.527	44.091	0.009	1.279
TMMS0090	39.527	2.300	2.864	0.682	0.909	5.819	36.364	0.008	1.243
TMMS0091	48.647	6.665	12.682	1.073	3.242	13.701	39.318	0.002	1.236
TMMS0106	40.847	2.425	6.036	1.950	0.991	5.937	76.591	0.003	1.145
TMMS0119	31.121	1.929	5.095	0.859	0.600	6.198	43.182	0.001	1.203
TMMS0126	25.007	1.455	2.389	0.653	0.364	5.817	37.045	0.003	1.238
TMMS0133	64.823	2.565	4.318	1.318	1.663	3.957	90.909	0.003	1.135
TMMS0134	35.593	2.328	3.623	1.116	0.828	6.539	55.682	0.019	1.178
TMMS0137	63.779	2.602	4.668	0.899	1.659	4.079	83.409	0.000	1.316
TMMS0159	61.133	10.035	13.300	0.798	6.135	16.415	51.000	0.001	1.390
TMMS0171	61.723	9.400	13.991	0.581	5.802	15.229	39.545	0.017	1.340
TMMS0178	33.173	4.343	7.291	1.468	1.441	13.092	44.318	0.002	1.345
TMMS0183	39.420	2.988	4.332	0.465	1.178	7.579	50.773	0.007	1.146
TMMS0187	51.073	4.780	5.800	0.391	2.441	9.359	33.636	0.008	1.195
TMMS0193	55.792	2.492	2.819	1.033	1.390	4.466	51.591	0.001	1.207
TMMS0209	73.086	2.553	3.104	1.224	1.866	3.493	41.111	0.004	1.169
TMMS0214	51.133	2.069	3.350	0.971	1.058	4.046	61.455	0.001	1.236
TMMS0220	30.327	4.180	9.605	1.063	1.268	13.783	70.455	0.016	1.313
TMMS0279	63.027	9.163	11.164	1.043	5.775	14.537	57.818	0.007	1.237
TMMS0283	28.020	5.329	12.795	0.735	1.493	19.018	23.864	0.012	1.236
TMMS0290	73.813	1.674	2.381	0.407	1.235	2.267	82.955	0.002	1.153

	Mean thalweg depth (cm)	Mean wetted width (m)	Mean bankfull width (m)	Mean bankfull height (m)	Mean width x mean depth (m ²)	Mean width/depth ratio (m/m)	Mean bank angle (degrees)	Water surface gradient over reach (%)	Channel sinuosity
	Xdepth_T	Xwidth	XBKF_W	XBKF_H	XWXD	XWD_RAT	XBKA	XSLOPE_%	SINU
TMMS0296	41.250	7.724	12.627	1.359	3.186	18.725	30.455	0.005	1.353
TMMS0381	18.960	0.919	1.481	0.546	0.174	4.844	42.273	0.012	1.182
TMMS0391	17.248	7.133	12.604	0.738	1.230	41.355	23.636	0.007	1.256
TMMS0437	42.587	1.464	2.677	0.584	0.623	3.438	48.409	0.005	1.145
TMMS1865	46.401	2.686	6.073	1.682	1.246	5.788	51.909	0.002	1.288
TMMS3195	32.827	1.900	4.091	0.755	0.624	5.788	35.909	0.014	1.266
TMMS3962	56.207	5.984	8.145	0.801	3.364	10.647	27.727	0.002	1.205
VGMS00002	24.980	1.000	0.936	0.286	0.250	4.003	25.227	0.008	1.249
VGMS00004	43.260	4.725	5.960	0.568	2.044	10.922	44.409	0.006	1.239
VGMS00016	68.245	5.505	6.609	0.955	3.757	8.066	53.864	0.001	1.281
VGMS00018	15.607	2.815	6.073	0.939	0.439	18.037	27.273	0.007	1.237
VGMS00022	18.153	1.961	4.315	0.668	0.356	10.803	30.364	0.015	1.227
VGMS00034	28.440	3.200	4.036	0.345	0.910	11.252	40.682	0.005	1.186
VGMS00037	37.286	1.842	2.538	0.681	0.687	4.941	44.688	0.004	0.921
VGMS00044	33.620	2.899	4.582	0.959	0.975	8.623	44.909	0.005	1.198
VGMS00048	58.859	1.825	3.520	0.550	1.074	3.101	57.750	0.008	1.226
VGMS00080	44.507	4.971	6.875	0.836	2.212	11.168	38.136	0.006	1.298
VGMS00109	53.173	2.851	3.956	0.745	1.516	5.362	49.909	0.002	1.293
VGMS00112	78.367	3.932	5.253	0.823	3.081	5.017	53.864	0.001	1.243
VGMS00121	32.213	2.957	5.291	1.478	0.953	9.179	88.455	0.004	1.189
VGMS00124	30.113	5.300	10.336	1.345	1.596	17.600	37.045	0.007	1.246
VGMS00126	22.527	3.425	3.857	0.680	0.771	15.203	41.591	0.003	1.172
VGMS00128	25.707	1.569	6.368	1.427	0.403	6.102	42.818	0.007	1.241
VGMS00162	45.420	2.533	3.864	1.191	1.150	5.576	65.364	0.005	1.315
VGMS00177	24.033	1.453	2.782	1.064	0.349	6.044	50.909	0.010	1.157
VGMS00191	48.420	4.160	7.155	1.266	2.014	8.591	55.318	0.004	1.209
VGMS00206	11.060	1.563	11.509	1.973	0.173	14.127	20.591	0.004	1.103
VGMS00210	26.913	4.085	8.005	0.999	1.099	15.178	35.864	0.004	1.268
VGMS00247	29.827	1.558	2.092	0.717	0.465	5.222	59.545	0.009	1.194
VGMS00252	68.973	5.304	6.659	1.083	3.658	7.689	44.591	0.001	1.143
VGMS00255	32.133	3.958	5.223	0.895	1.272	12.318	45.682	0.004	1.189
VGMS00277	69.660	6.845	7.512	1.070	4.768	9.826	43.325	0.001	1.279
VGMS00306	29.873	5.487	10.645	1.169	1.639	18.366	37.136	0.004	1.178

	Mean thalweg depth (cm)	Mean wetted width (m)	Mean bankfull width (m)	Mean bankfull height (m)	Mean width x mean depth (m ²)	Mean width/depth ratio (m/m)	Mean bank angle (degrees)	Water surface gradient over reach (%)	Channel sinuosity
	Xdepth_T	Xwidth	XBKF_W	XBKF_H	XWXD	XWD_RAT	XBKA	XSLOPE_%	SINU
VGMS00320	35.967	6.540	6.636	1.153	2.352	18.184	35.952	0.046	1.177
VGMS00380	42.367	4.431	7.009	0.905	1.877	10.459	42.500	0.003	1.252
VGMS00387	50.133	2.953	3.782	0.568	1.480	5.890	44.773	0.008	1.117
VGMS00418	31.093	2.265	5.045	1.136	0.704	7.285	46.364	0.013	1.140
VGMS00433	77.080	4.699	8.155	1.055	3.622	6.096	49.682	0.002	1.274
VGMS00444	43.633	7.310	11.873	0.856	3.190	16.753	41.409	0.010	1.205
VGMS00447	52.827	4.120	6.373	1.435	2.176	7.799	74.318	0.003	1.308
VGMS00450	33.013	6.129	11.438	1.027	2.023	18.565	32.591	0.003	1.277
VGMS00511	34.267	3.075	4.448	0.659	1.054	8.973	37.864	0.002	1.206
VGMS00515	24.393	4.158	5.889	1.050	1.014	17.044	30.682	0.069	1.245
VGMS00558	27.800	3.775	10.555	1.277	1.049	13.579	35.000	0.016	1.262
VGMS00575	33.607	3.479	5.039	0.642	1.169	10.352	34.636	0.007	1.314
SSMS0001	37.560	1.563	2.691	0.775	0.587	4.162	39.773	0.014	1.288
SSMS0002	41.080	5.010	8.368	2.300	2.058	12.196	23.409	0.006	1.374
SSMS0008	20.747	2.208	8.673	1.414	0.458	10.641	26.136	0.026	1.171
SSMS0010	82.480	3.401	6.084	0.605	2.805	4.123	40.909	0.002	1.176
SSMS0014	40.727	1.991	5.159	0.901	0.811	4.889	46.364	0.016	1.164
SSMS0028	36.100	2.940	6.255	0.895	1.061	8.144	32.773	0.013	1.179
SSMS0029	49.767	4.782	4.810	0.655	2.380	9.609	54.727	0.002	1.022
SSMS0031	25.307	2.179	5.773	0.595	0.551	8.610	27.318	0.011	1.279
SSMS0033	17.067	2.105	3.614	1.455	0.359	12.334	43.409	0.003	1.285
SSMS0035	57.167	6.823	9.809	1.501	3.901	11.936	44.545	0.004	1.182
SSMS0037	28.500	5.430	8.818	1.859	1.548	19.053	35.455	0.001	1.330
SSMS0038	45.693	2.490	5.955	1.277	1.138	5.449	45.182	0.003	1.227
SSMS0044	39.833	3.426	4.573	0.991	1.365	8.602	51.136	0.005	1.107
SSMS0051	38.040	1.536	3.273	0.627	0.584	4.037	31.773	0.006	1.320
SSMS0053	11.527	2.360	7.627	1.118	0.272	20.474	55.818	0.015	1.236
SSMS0057	54.047	2.953	4.955	0.936	1.596	5.463	67.500	0.008	1.210
SSMS0059	15.200	1.500	4.178	1.909	0.228	9.868	37.727	0.014	1.245
SSMS0073	52.867	4.530	6.473	1.215	2.395	8.569	50.727	0.002	1.218
SSMS0078	24.527	5.050	7.923	1.241	1.239	20.590	37.045	0.006	1.222
SSMS0094	27.220	3.333	5.523	1.341	0.907	12.243	41.136	0.013	1.245
SSMS0105	40.527	3.245	6.091	1.782	1.315	8.007	75.455	0.008	1.222

	Mean thalweg depth (cm)	Mean wetted width (m)	Mean bankfull width (m)	Mean bankfull height (m)	Mean width x mean depth (m ²)	Mean width/depth ratio (m/m)	Mean bank angle (degrees)	Water surface gradient over reach (%)	Channel sinuosity
	Xdepth_T	Xwidth	XBKF_W	XBKF_H	XWXD	XWD_RAT	XBKA	XSLOPE_%	SINU
SSMS0126	30.685	4.687	9.518	1.377	1.438	15.274	38.182	0.003	1.186
SSMS0129	33.867	3.465	5.699	0.968	1.173	10.231	39.091	0.004	1.128
SSMS0133	38.787	9.637	18.714	1.119	3.738	24.846	35.909	0.011	1.129
SSMS0144	17.073	2.414	5.791	0.929	0.412	14.138	39.227	0.006	1.324
SSMS0149	46.340	4.780	6.695	0.814	2.215	10.315	33.864	0.006	1.214
SSMS0150	49.247	3.195	7.091	1.264	1.573	6.488	69.545	0.011	1.208
SSMS0157	36.215	1.806	4.091	1.007	0.654	4.987	40.000	0.013	1.206
SSMS0175	25.393	4.590	8.677	0.955	1.166	18.076	28.273	0.019	1.360
SSMS0191	28.580	3.708	6.177	1.105	1.060	12.974	36.818	0.006	1.249
SSMS0193	28.707	3.435	6.764	1.036	0.986	11.966	60.000	0.002	1.291
SSMS0199	31.773	3.433	5.427	1.191	1.091	10.806	28.864	0.006	1.315
SSMS0213	68.560	5.240	9.173	0.988	3.593	7.643	47.864	0.011	1.296
SSMS0351	26.727	7.033	12.036	1.155	1.880	26.313	24.318	0.004	1.288
SSMS0408	28.613	1.893	3.045	1.114	0.542	6.614	51.136	0.004	1.261
SSMS0411	33.593	8.603	11.591	1.268	2.890	25.608	42.136	0.003	1.281
SSMS0447	27.460	6.974	9.759	1.182	1.915	25.396	34.091	0.004	1.240
SSMS1000	34.740	1.196	1.873	0.900	0.415	3.443	63.318	0.009	1.108
SSMS4173	44.507	8.287	12.827	1.250	3.688	18.619	35.227	0.014	1.270
SSMS4330	30.580	3.400	4.918	0.757	1.040	11.118	31.136	0.009	1.348
RENP0008	63.800	2.283	3.896	1.464	1.457	3.579	42.045	0.007	1.048
RENP0012	17.752	3.977	6.127	0.586	0.706	22.405	39.227	0.009	1.316
RENP0016	96.393	4.198	5.255	0.705	4.046	4.355	52.273	0.009	1.206
RENP0028	27.980	3.305	4.914	1.205	0.925	11.812	25.409	0.019	1.280
RENP0047	13.800	1.812	3.509	0.764	0.250	13.127	30.000	0.014	1.190
RENP0052	20.660	2.484	5.359	0.795	0.513	12.023	18.273	0.008	1.299
RENP0054	14.247	0.815	1.950	0.691	0.116	5.721	27.273	0.048	1.184
RENP0055	28.653	1.925	3.264	1.109	0.552	6.718	50.000	0.009	1.243
RENP0075	46.287	4.323	12.227	0.805	2.001	9.339	35.227	0.005	1.148
RENP0092	7.013	1.533	3.791	0.477	0.107	21.851	37.500	0.006	1.153
RENP0095	41.087	1.282	2.132	0.632	0.527	3.119	38.409	0.023	1.174
RENP0096	27.407	2.500	4.445	1.100	0.685	9.122	33.636	0.006	1.189
RENP0097	21.727	3.135	5.591	0.968	0.681	14.430	57.955	0.014	1.227
RENP100	34.727	2.890	4.359	0.845	1.004	8.322	33.182	0.005	1.212

	Mean thalweg depth (cm)	Mean wetted width (m)	Mean bankfull width (m)	Mean bankfull height (m)	Mean width x mean depth (m ²)	Mean width/depth ratio (m/m)	Mean bank angle (degrees)	Water surface gradient over reach (%)	Channel sinuosity
	Xdepth_T	Xwidth	XBKF_W	XBKF_H	XWXD	XWD_RAT	XBKA	XSLOPE_%	SINU
REN0108	14.460	2.111	4.691	1.055	0.305	14.599	28.864	0.020	1.263
REN0110	25.687	2.188	2.645	0.845	0.562	8.516	67.273	0.018	1.195
REN0112	17.820	2.759	3.718	0.886	0.492	15.480	45.909	0.006	1.072
REN0128	41.787	1.525	3.391	0.927	0.637	3.649	29.455	0.004	1.147
REN0132	21.580	1.824	4.691	0.950	0.394	8.451	32.455	0.013	1.040
REN0139	22.480	2.425	4.500	0.964	0.545	10.787	29.955	0.004	1.162
REN0144	41.747	3.398	6.368	0.927	1.418	8.138	30.318	0.005	1.258
REN0187	17.053	2.223	4.659	0.886	0.379	13.033	21.545	0.003	1.285
REN0192	30.667	1.915	2.909	1.173	0.587	6.245	48.182	0.005	1.006
REN0203	31.487	3.685	7.355	1.136	1.160	11.703	20.682	0.005	1.189
REN0228	23.027	2.164	3.205	0.836	0.498	9.396	39.762	0.020	1.160
REN0240	16.567	1.715	7.682	0.735	0.284	10.352	24.318	0.007	1.078
REN0251	19.500	3.180	4.316	0.700	0.620	16.308	41.818	0.017	1.233
REN0287	20.027	1.327	4.164	0.641	0.266	6.626	25.682	0.014	1.059
REN0368	18.567	2.640	4.818	1.214	0.490	14.219	39.545	0.013	1.134
REN0375	48.587	5.780	9.511	1.732	2.808	11.896	45.909	0.005	1.230
REN0443	24.107	2.616	3.614	0.800	0.631	10.850	48.636	0.003	1.280
REN0511	35.513	4.570	7.518	0.655	1.623	12.868	35.227	0.005	1.307
REN1524	22.153	1.883	4.491	1.018	0.417	8.498	32.857	0.023	1.253
REN2991	22.207	2.515	5.064	0.864	0.558	11.325	22.273	0.010	1.248
REN5612	37.820	2.040	2.982	0.891	0.772	5.394	62.143	0.003	1.154
REN7308	18.307	1.855	5.491	0.723	0.340	10.133	38.409	0.013	1.222
REN9611	15.693	3.882	4.036	0.745	0.609	24.735	39.773	0.017	0.904
REN9757	13.327	2.277	3.741	0.842	0.303	17.088	51.818	0.008	1.295
REN12892	31.527	1.440	4.250	0.805	0.454	4.568	26.455	0.013	1.212
REN15048	54.040	1.116	2.336	0.618	0.603	2.065	58.864	0.010	1.292
RCA02	48.000	4.089	9.833	0.633	1.963	8.518	24.250	0.062	0.655
RCA08	16.100	1.735	3.417	1.400	0.279	10.776	32.500	0.045	0.613
RCA22	52.160	6.800	8.500	0.700	3.547	13.037	31.917	0.014	0.679
RCA23	24.000	2.045	6.333	0.800	0.491	8.521	36.667	0.063	0.625
RCA30	77.400	65.878	8.000	1.500	50.990	85.114	50.333	0.033	0.630
RCA31	18.400	2.880	7.500	1.250	0.530	15.652	56.667	0.016	0.659
RCA44	12.133	0.835	3.217	1.417	0.101	6.882	54.167	0.018	0.700

	Mean thalweg depth (cm)	Mean wetted width (m)	Mean bankfull width (m)	Mean bankfull height (m)	Mean width x mean depth (m ²)	Mean width/depth ratio (m/m)	Mean bank angle (degrees)	Water surface gradient over reach (%)	Channel sinuosity
	Xdepth_T	Xwidth	XBKF_W	XBKF_H	XWXD	XWD_RAT	XBKA	XSLOPE_%	SINU
RCA48	19.100	3.135	4.250	0.867	0.599	16.414	35.000	0.012	0.578
RCA49	39.167	3.060	4.333	0.900	1.199	7.813	32.500	0.008	0.622
RCA50	67.867	6.310	5.567	2.250	4.282	9.298	24.583	0.001	0.688
RCA52	14.167	7.520	7.933	1.117	1.065	53.082	54.583	0.004	0.629
RCA53	23.100	3.290	7.167	2.250	0.760	14.242	34.583	0.022	0.589
RCA57	76.920	3.260	4.500	1.517	2.508	4.238	62.083	0.004	0.611
RCA58	27.960	1.690	7.167	1.000	0.473	6.044	60.167	0.046	0.628
RCA59	23.960	4.660	6.917	1.300	1.117	19.449	49.333	0.072	0.675
RCA60	20.040	4.255	7.833	2.383	0.853	21.233	44.000	0.178	0.660
RCA62	23.800	0.661	4.833	1.000	0.157	2.777	20.417	0.173	0.657
RCA64	19.760	1.054	2.417	3.750	0.208	5.334	36.667	0.112	0.590
RCA65	7.733	1.160	5.000	1.800	0.090	15.000	54.167	0.014	0.666
RCA66	15.433	1.610	6.667	2.000	0.248	10.432	55.417	0.013	0.650
RCA67	17.933	2.055	6.167	1.283	0.369	11.459	50.000	0.014	0.619
RCA68	25.500	1.730	3.667	1.500	0.441	6.784	52.500	0.020	0.657
RCA69	22.533	2.765	4.733	1.100	0.623	12.271	47.500	0.019	0.592
RCA70	42.067	1.825	3.583	0.733	0.768	4.338	47.917	0.027	0.623
RCA71	19.367	1.778	3.833	1.450	0.344	9.180	35.833	0.018	0.630
RCA72	14.533	4.664	7.385	1.692	0.678	32.089	44.583	0.003	0.664
RCA73	13.667	5.475	8.167	1.917	0.748	40.061	39.583	0.007	0.548
RCA74	44.833	6.790	8.667	1.683	3.044	15.145	42.917	0.008	0.613
RCA90	33.633	4.805	6.500	1.233	1.616	14.286	41.250	0.001	0.697

Table 2.4. Substrate.

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m))
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
TMMS0003	44.182	0.000	0.000	0.000	0.000	26.667	20.952	9.524	40.000	9.524	-0.161	-1.440
TMMS0007	72.549	0.000	0.000	0.000	0.000	0.000	10.476	56.190	33.333	13.333	-1.852	-1.787
TMMS0009	61.273	0.000	11.429	0.000	7.619	64.762	5.714	10.476	0.000	0.000	0.697	-0.674
TMMS0027	49.455	0.000	22.857	43.810	5.714	0.000	0.000	19.048	5.714	0.000	1.369	-0.495
TMMS0028	34.000	10.476	2.857	17.143	7.619	37.143	8.571	8.571	7.619	0.000	1.097	-0.277
TMMS0033	19.455	28.571	20.000	8.571	4.762	21.905	12.381	1.905	1.905	0.000	2.030	0.151
TMMS0040	50.364	0.000	28.571	40.000	2.857	12.381	15.238	0.952	0.000	0.000	1.744	-0.467
TMMS0043	61.091	0.000	50.476	4.762	0.000	2.857	40.000	0.000	1.905	0.952	1.480	0.387
TMMS0058	30.909	56.190	0.000	0.000	0.952	0.000	18.095	3.810	20.952	0.000	2.479	1.024
TMMS0072	30.962	18.095	10.476	11.429	5.714	5.714	29.524	6.667	12.381	0.000	1.239	0.077
TMMS0082	79.800	0.000	0.000	0.000	0.000	0.000	0.000	6.000	94.000	0.000	-2.111	-2.778
TMMS0088	21.633	47.619	20.000	1.905	0.000	10.476	8.571	8.571	2.857	0.000	2.353	0.432
TMMS0090	26.111	0.000	59.048	40.952	0.000	0.000	0.000	0.000	0.000	0.000	2.632	1.004
TMMS0091	71.782	7.619	20.952	19.048	2.857	7.619	31.429	7.619	1.905	0.000	1.131	-0.166
TMMS0106	81.818	0.000	0.000	0.000	0.000	0.000	0.000	81.905	14.286	0.952	-2.017	-3.533
TMMS0119	62.545	0.000	0.000	1.000	0.000	0.000	0.000	59.000	40.000	2.000	-2.041	-2.806
TMMS0126	57.818	0.952	0.000	4.762	4.762	0.000	16.190	20.952	31.429	0.952	-0.451	-1.426
TMMS0133	90.909	0.000	0.000	0.000	0.000	0.000	0.000	92.381	7.619	1.905	-2.111	-3.561
TMMS0134	40.182	4.762	13.333	28.571	0.000	0.000	5.714	12.381	13.333	0.000	1.029	-1.162
TMMS0137	83.091	0.000	0.000	0.000	0.000	0.000	0.000	83.810	16.190	10.476	-2.111	-2.557
TMMS0159	70.577	1.923	31.731	6.731	5.769	0.962	41.346	1.923	9.615	0.000	1.138	0.156
TMMS0171	54.727	21.905	60.000	2.857	0.000	0.000	0.000	15.238	0.000	0.000	2.360	0.328
TMMS0178	47.455	9.524	5.714	19.048	19.048	5.714	13.333	16.190	10.476	1.905	0.956	-0.378
TMMS0183	64.727	5.714	11.429	25.714	0.000	0.000	0.000	40.952	13.333	0.000	0.269	-1.192
TMMS0187	45.091	43.810	6.667	0.000	0.000	0.000	1.905	38.095	9.524	0.000	1.140	-0.342
TMMS0193	96.364	0.000	0.000	0.000	0.000	0.000	0.000	85.714	14.286	9.524	-2.111	-3.121
TMMS0209	97.600	0.000	0.000	0.000	0.000	0.000	0.000	58.824	41.176	0.000	-2.111	-3.505
TMMS0214	91.636	0.000	0.000	1.905	0.000	0.000	7.619	67.619	21.905	0.000	-1.821	-2.765
TMMS0220	26.545	37.143	11.429	4.762	7.619	13.333	4.762	8.571	12.381	0.000	2.110	0.019
TMMS0279	18.455	60.952	13.333	6.667	0.000	0.000	0.000	15.238	2.857	0.000	2.579	0.805

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m))
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
TMMS0283	22.909	50.000	32.692	9.615	0.000	0.000	7.692	0.000	0.000	0.000	3.024	1.163
TMMS0290	100.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	-2.111	-2.995
TMMS0296	34.818	15.238	13.333	34.286	9.524	5.714	0.000	14.286	7.619	0.000	1.707	-0.019
TMMS0381	61.818	0.000	0.000	0.000	0.000	0.000	0.000	59.048	40.952	4.762	-2.111	-3.801
TMMS0391	51.818	80.952	13.333	5.714	0.000	0.000	0.000	0.000	0.000	0.000	3.558	1.985
TMMS0437	94.182	0.000	0.000	0.000	2.857	7.619	0.000	82.857	6.667	0.000	-1.766	-3.145
TMMS1865	81.818	0.000	0.000	0.000	4.000	2.000	0.000	78.000	16.000	2.000	-1.871	-3.302
TMMS3195	87.273	12.381	1.905	0.000	0.000	0.000	0.000	85.714	0.000	0.000	-1.288	-3.187
TMMS3962	39.245	0.000	2.083	14.583	20.833	5.208	6.250	4.167	14.583	0.000	0.708	-0.463
VGMS00002	94.545	0.000	0.000	0.000	0.000	0.000	0.000	42.857	57.143	0.000	-2.111	-3.302
VGMS00004	44.909	2.857	0.000	3.810	27.619	4.762	12.381	20.952	26.667	1.905	0.190	-1.288
VGMS00016	81.455	0.000	1.905	0.952	1.905	21.905	22.857	41.905	8.571	0.952	-0.787	-1.593
VGMS00018	63.455	24.762	10.476	10.476	0.952	0.000	0.000	34.286	19.048	0.000	0.932	-0.728
VGMS00022	40.727	23.810	4.762	12.381	1.905	6.667	14.286	6.667	26.667	0.000	1.594	-0.243
VGMS00034	64.909	0.000	35.238	17.143	0.000	0.000	0.000	32.381	15.238	0.000	0.866	-0.304
VGMS00037	96.250	0.000	0.000	0.000	0.000	5.333	18.667	74.667	1.333	0.000	-1.644	-2.738
VGMS00044	65.455	0.000	0.000	0.000	0.952	28.571	6.667	15.238	47.619	7.619	-0.235	-1.846
VGMS00048	68.400	0.000	0.000	20.000	0.000	5.263	4.211	50.526	20.000	0.000	-0.782	-2.447
VGMS00080	37.273	15.238	18.095	15.238	8.571	9.524	3.810	17.143	6.667	0.000	1.346	-0.290
VGMS00109	56.364	0.000	0.000	0.000	0.000	36.190	4.762	15.238	41.905	16.190	-0.123	-1.218
VGMS00112	66.364	0.000	0.000	10.476	1.905	16.190	23.810	33.333	11.429	2.857	-0.500	-1.560
VGMS00121	74.727	0.000	8.571	0.952	16.190	14.286	48.571	7.619	0.000	0.000	0.244	-1.408
VGMS00124	54.364	36.190	16.190	10.476	0.000	0.000	19.048	8.571	9.524	0.000	1.984	0.154
VGMS00126	63.273	0.952	6.667	5.714	5.714	7.619	19.048	36.190	15.238	0.000	-0.416	-1.682
VGMS00128	69.455	0.000	3.810	0.000	0.000	24.762	4.762	60.000	0.952	0.000	-0.997	-2.855
VGMS00162	68.182	0.000	9.524	1.905	0.000	30.476	4.762	31.429	11.429	3.810	-0.147	-1.850
VGMS00177		0.000	0.000	0.000	0.000	0.000	0.000	89.524	0.952	0.952	-1.908	-3.803
VGMS00191	67.636	0.000	0.952	3.810	8.571	22.857	4.762	41.905	16.190	5.714	-0.593	-2.222
VGMS00206	76.111	0.000	1.905	20.000	0.000	15.238	58.095	4.762	0.000	0.000	0.224	-1.508
VGMS00210	57.636	0.000	4.762	19.048	40.000	16.190	10.476	0.000	6.667	0.000	1.306	-0.172
VGMS00247	58.182	0.000	0.000	0.000	3.810	20.000	14.286	34.286	27.619	0.952	-0.804	-2.539

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m))
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
VGMS00252	59.909	0.000	1.905	2.857	0.952	40.952	18.095	0.000	15.238	0.952	0.420	-0.599
VGMS00255	63.091	0.000	23.000	2.000	2.000	13.000	14.000	39.000	7.000	0.000	-0.030	-1.559
VGMS00277	66.007	0.952	18.095	1.905	3.810	4.762	17.143	40.952	12.381	0.000	-0.264	-1.327
VGMS00306	66.818	0.000	15.238	40.000	22.857	5.714	11.429	0.000	4.762	0.000	1.714	0.147
VGMS00320	48.800	35.106	3.191	23.404	8.511	6.383	20.213	3.191	0.000	0.000	1.921	-0.681
VGMS00380	63.636	0.000	0.000	0.000	0.000	40.000	23.810	28.571	7.619	0.000	-0.446	-1.840
VGMS00387	67.045	28.571	0.000	0.000	0.000	0.000	0.952	53.333	17.143	7.619	-0.070	-1.748
VGMS00418	54.364	0.000	1.905	29.524	3.810	12.381	8.571	25.714	18.095	0.952	0.300	-1.733
VGMS00433	63.636	0.000	8.081	2.020	0.000	0.000	4.040	50.505	2.020	0.000	-0.816	-2.140
VGMS00444	42.909	0.000	3.810	30.476	17.143	22.857	14.286	4.762	6.667	1.905	1.091	-0.784
VGMS00447	96.667	0.000	3.774	0.000	0.000	3.774	34.906	57.547	0.000	0.000	-1.234	-2.729
VGMS00450	94.364	86.667	0.000	0.000	0.000	4.762	5.714	0.000	1.905	0.000	3.325	2.021
VGMS00511	62.000	0.000	1.887	5.660	0.943	26.415	16.981	31.132	9.434	0.000	-0.383	-1.473
VGMS00515	47.451	42.453	8.491	18.868	1.887	2.830	25.472	0.000	0.000	0.000	2.177	-0.558
VGMS00558	59.636	18.868	16.981	48.113	1.887	0.943	4.717	0.000	8.491	0.000	2.451	0.323
VGMS00575	53.273	0.000	13.684	25.263	3.158	11.579	16.842	13.684	12.632	0.000	0.812	-0.772
SSMS0001	67.818	0.000	2.857	8.571	7.619	2.857	49.524	0.952	26.667	4.762	0.210	-1.554
SSMS0002	13.091	51.429	0.000	5.714	9.524	13.333	19.048	0.000	0.952	0.000	2.227	0.228
SSMS0008	40.545	36.190	0.000	11.429	0.000	0.000	5.714	19.048	27.619	0.000	1.616	-0.824
SSMS0010	77.909	0.000	0.000	0.000	0.000	0.000	52.703	41.892	5.405	0.000	-1.191	-2.408
SSMS0014	20.000	0.000	1.923	16.346	14.423	11.538	0.000	16.346	33.654	0.962	0.543	-1.535
SSMS0028	51.273	0.000	0.000	14.423	12.500	16.346	1.923	21.154	32.692	0.000	0.236	-1.748
SSMS0029	48.000	0.000	16.190	2.857	1.905	37.143	3.810	31.429	6.667	0.000	0.185	-0.816
SSMS0031	67.273	0.000	0.000	0.000	0.000	1.000	6.000	41.000	52.000	0.000	-1.845	-3.586
SSMS0033	84.455	0.000	0.952	0.000	18.095	18.095	41.905	20.952	0.000	0.000	-0.198	-1.676
SSMS0035	55.545	0.000	27.619	19.048	3.810	0.952	33.333	0.000	12.381	0.000	1.301	-0.369
SSMS0037	63.091	0.000	0.000	0.000	2.000	16.000	38.000	9.000	23.000	0.000	-0.278	-1.122
SSMS0038	67.455	4.762	0.000	1.905	0.000	6.667	45.714	11.429	27.619	4.762	-0.253	-1.721
SSMS0044	52.909	5.769	6.731	3.846	6.731	22.115	0.962	18.269	26.923	0.962	0.516	-1.068
SSMS0051	45.818	0.000	0.000	0.000	2.885	17.308	0.000	13.462	66.346	9.615	-0.328	-1.791
SSMS0053	82.545	11.000	1.000	1.000	0.000	0.000	0.000	65.000	22.000	1.000	-1.164	-3.224

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m))
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
SSMS0057	74.727	0.000	0.952	0.952	0.952	1.905	1.905	58.095	35.238	1.905	-1.788	-3.571
SSMS0059	84.182	0.000	0.000	0.000	0.952	3.810	67.619	0.952	24.762	3.810	-0.383	-2.632
SSMS0073	44.545	8.571	1.905	3.810	1.905	29.524	14.286	16.190	12.381	0.952	0.345	-0.921
SSMS0078	76.727	1.905	5.714	4.762	2.857	14.286	65.714	1.905	1.905	0.000	0.154	-1.616
SSMS0094	58.636	0.000	1.905	14.286	18.095	20.952	34.286	0.000	9.524	0.000	0.696	-1.416
SSMS0105	78.000	0.000	12.500	8.654	6.731	6.731	1.923	33.654	6.731	0.962	-0.011	-2.073
SSMS0126	95.091	0.000	0.000	0.000	0.000	0.000	76.190	0.952	20.000	5.714	-0.464	-1.945
SSMS0129	97.818	0.000	0.000	0.000	0.000	0.000	90.476	3.810	5.714	0.000	-0.527	-1.998
SSMS0133	70.636	7.619	18.095	1.905	9.524	0.952	60.000	0.000	0.952	0.000	0.750	-1.245
SSMS0144	22.364	60.952	0.000	0.000	0.000	0.000	0.000	10.476	28.571	0.000	2.893	1.369
SSMS0149	68.909	0.000	12.381	3.810	12.381	1.905	0.952	68.571	0.000	0.000	-0.800	-2.379
SSMS0150	61.636	0.000	2.857	16.190	24.762	14.286	0.000	24.762	11.429	0.000	0.433	-1.631
SSMS0157	30.000	0.000	0.000	0.000	0.000	17.308	2.885	14.423	42.308	0.962	-0.325	-2.355
SSMS0175	40.000	2.857	10.476	34.286	0.952	11.429	5.714	10.476	23.810	0.000	1.306	-0.841
SSMS0191	72.182	0.952	0.000	18.095	9.524	14.286	49.524	0.952	6.667	0.000	0.449	-1.239
SSMS0193	89.636	0.000	0.000	0.000	0.000	0.952	0.000	54.286	39.048	3.810	-1.868	-3.064
SSMS0199	49.636	0.000	2.857	12.381	0.000	11.429	0.000	8.571	58.095	2.857	0.599	-1.144
SSMS0213	50.909	10.476	6.667	26.667	21.905	2.857	14.286	5.714	8.571	0.000	1.442	-0.535
SSMS0351	62.727	0.952	0.000	10.476	14.286	28.571	38.095	0.000	7.619	0.000	0.553	-0.953
SSMS0408	36.727	0.000	0.000	2.857	0.000	37.143	29.524	0.000	7.619	5.714	0.220	-1.317
SSMS0411	51.455	11.538	4.808	17.308	10.577	2.885	25.962	14.423	12.500	0.000	0.798	-0.701
SSMS0447	55.636	36.190	5.714	0.000	0.000	3.810	46.667	0.000	6.667	0.000	1.439	-0.068
SSMS1000	34.818	0.000	0.000	0.000	13.333	28.571	15.238	2.857	10.476	3.810	0.319	-1.425
SSMS4173	56.818	0.000	7.619	32.381	5.714	4.762	7.619	35.238	6.667	0.000	0.270	-1.882
SSMS4330	64.727	0.000	7.619	30.476	19.048	16.190	1.905	5.714	17.143	0.000	1.386	-0.346
RENP0008	78.364	0.000	0.000	2.000	10.000	11.000	2.000	24.000	45.000	0.000	-0.436	-0.230
RENP0012	25.545	0.000	7.619	11.429	11.429	36.190	18.095	0.000	15.238	0.000	0.952	0.586
RENP0016	13.818	28.571	7.619	2.857	45.714	10.476	0.952	0.000	3.810	0.000	2.207	1.206
RENP0028	72.909	0.000	16.190	17.143	0.000	11.429	32.381	6.667	16.190	0.000	0.708	0.318
RENP0047	74.909	0.000	0.952	12.381	4.762	1.905	21.905	32.381	25.714	0.000	-0.554	-0.290
RENP0052	66.000	0.000	0.000	0.952	31.429	15.238	23.810	21.905	6.667	0.000	0.039	0.023

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m))
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
REN0054	74.182	0.000	0.000	0.000	0.000	0.952	25.714	39.048	34.286	0.000	-1.422	-0.590
REN0055	54.727	0.000	0.000	0.000	17.925	11.321	4.717	8.491	19.811	0.000	0.192	0.102
REN0075	39.636	14.286	0.000	9.524	24.762	18.095	15.238	0.952	17.143	0.000	1.394	0.922
REN0092	97.273	1.000	3.000	0.000	0.000	0.000	71.000	1.000	24.000	0.000	-0.302	-0.241
REN0095	79.818	0.000	0.000	0.000	0.000	0.943	2.830	62.264	21.698	0.000	-1.684	-0.794
REN0096	59.091	0.000	2.857	2.857	15.238	24.762	24.762	10.476	11.429	0.000	0.246	0.146
REN0097	55.818	14.286	0.000	22.857	3.810	4.762	26.667	9.524	18.095	0.000	0.960	0.483
REN0100	51.636	0.000	0.000	15.238	18.095	23.810	16.190	11.429	9.524	0.000	0.504	0.323
REN0108	81.636	0.000	0.000	8.571	11.429	21.905	15.238	19.048	21.905	0.000	0.058	0.026
REN0110	37.091	0.000	0.952	41.905	19.048	4.762	20.000	0.000	13.333	0.952	1.312	0.628
REN0112	76.545	0.000	0.000	0.000	0.000	5.714	23.810	40.000	30.476	1.905	-1.309	-0.827
REN0128	100.000	0.000	0.000	0.000	0.000	0.000	0.962	53.846	45.192	0.962	-2.079	-1.444
REN0132	40.564	0.000	6.667	6.667	30.476	21.905	1.905	1.905	29.524	0.000	1.270	0.647
REN0139	58.727	0.000	0.000	0.000	0.000	36.792	39.623	0.000	23.585	0.943	0.123	0.086
REN0144	55.818	6.667	6.667	0.952	2.857	43.810	23.810	3.810	11.429	0.952	0.727	0.480
REN0187	41.091	0.000	0.000	1.905	13.333	30.476	21.905	0.952	17.143	0.000	0.421	0.316
REN0192	51.636	0.000	0.000	6.667	39.048	16.190	17.143	20.952	0.000	0.000	0.329	0.196
REN0203	56.000	0.000	11.429	15.238	48.571	14.286	0.952	1.905	5.714	0.000	1.521	0.913
REN0228	28.182	20.952	8.571	1.905	12.381	14.286	25.714	1.905	14.286	0.000	1.392	0.659
REN0240	72.075	0.000	0.000	0.000	0.000	6.667	5.714	45.714	41.905	4.762	-1.618	-1.062
REN0251	36.000	7.619	2.857	17.143	14.286	29.524	26.667	0.000	1.905	0.000	1.058	0.558
REN0287	87.273	0.000	0.000	0.000	0.962	13.462	38.462	25.000	22.115	0.000	-0.756	-0.412
REN0368	73.000	0.000	0.000	0.952	5.714	15.238	50.476	0.000	24.762	0.000	-0.016	-0.008
REN0375	41.073	10.476	0.000	3.810	24.762	26.667	15.238	4.762	13.333	0.000	1.011	0.564
REN0443	86.364	0.000	0.000	5.714	4.762	14.286	38.095	31.429	5.714	0.000	-0.571	-0.441
REN0511	60.909	0.000	3.000	3.000	27.000	19.000	27.000	10.000	11.000	1.000	0.402	0.272
REN1524	58.545	0.000	3.810	16.190	26.667	12.381	2.857	1.905	35.238	0.000	1.366	0.607
REN2991	75.818	0.000	0.000	10.476	3.810	43.810	16.190	3.810	21.905	0.000	0.579	0.316
REN5612	72.182	0.000	1.905	0.952	2.857	36.190	5.714	46.667	4.762	0.952	-0.654	-0.482
REN7308	62.909	6.731	8.654	10.577	2.885	11.538	14.423	17.308	27.885	0.000	0.565	0.304
REN9611	59.216	1.905	2.857	7.619	15.238	19.048	19.048	6.667	27.619	0.952	0.626	0.314

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m))
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
REN9757	33.333	0.000	0.000	0.000	0.000	0.000	0.000	1.905	4.762	0.000	-0.042	-0.025
REN12892	72.182	0.000	0.952	13.333	6.667	16.190	22.857	29.524	3.810	0.000	-0.207	-0.108
REN15048	78.364	0.000	0.000	1.905	4.762	16.190	1.905	64.762	6.667	0.000	-1.222	-0.687
RCA02	1.667	73.810	19.048	0.000	0.000	0.000	0.000	0.000	7.143	0.000	-0.570	2.250
RCA08	77.222	9.091	9.091	0.000	0.000	3.030	33.333	45.455	0.000	0.000	-3.082	2.606
RCA22	27.667	9.091	38.636	11.364	15.909	9.091	6.818	0.000	9.091	0.000	0.194	2.023
RCA23	57.667	4.444	0.000	8.889	22.222	22.222	13.333	15.556	13.333	0.000	-2.017	2.555
RCA30	13.667	46.667	28.889	2.222	20.000	0.000	0.000	0.000	2.222	0.000	0.354	2.679
RCA31	75.000	0.000	0.000	18.182	12.121	18.182	51.515	0.000	0.000	0.000	-1.602	2.067
RCA44	83.889	3.030	0.000	15.152	6.061	15.152	15.152	24.242	9.091	3.030	-2.203	2.265
RCA48	44.000	6.667	0.000	33.333	20.000	6.667	11.111	0.000	20.000	4.444	-0.333	1.896
RCA49	52.667	22.222	0.000	0.000	13.333	17.778	15.556	6.667	24.444	2.222	-0.569	1.835
RCA50	42.000	42.222	0.000	8.889	17.778	11.111	15.556	0.000	4.444	0.000	0.726	1.420
RCA52	62.833	0.000	0.000	20.000	28.889	15.556	6.667	0.000	22.222	0.000	-0.271	1.482
RCA53	30.500	26.667	0.000	40.000	22.222	4.444	6.667	0.000	0.000	0.000	-0.390	2.568
RCA57	5.000	63.636	20.455	4.545	4.545	0.000	0.000	0.000	6.818	0.000	1.571	1.826
RCA58	5.000	64.444	31.111	4.444	0.000	0.000	0.000	0.000	0.000	0.000	0.905	2.540
RCA59	0.667	95.556	2.222	2.222	0.000	0.000	0.000	0.000	0.000	0.000	0.859	2.841
RCA60	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.269	3.484
RCA62	7.667	13.636	0.000	0.000	9.091	9.091	2.273	0.000	65.909	0.000	-1.045	3.118
RCA64	26.167	53.333	6.667	2.222	26.667	6.667	2.222	0.000	2.222	0.000	-0.711	3.462
RCA65	87.778	0.000	3.030	0.000	0.000	12.121	81.818	0.000	3.030	0.000	-2.404	2.203
RCA66	80.556	0.000	24.242	9.091	12.121	15.152	30.303	0.000	9.091	0.000	-1.088	2.271
RCA67	71.111	0.000	9.091	18.182	12.121	18.182	30.303	3.030	6.061	0.000	-1.313	2.133
RCA68	42.222	42.424	0.000	3.030	18.182	9.091	15.152	0.000	12.121	0.000	-0.149	2.343
RCA69	53.500	4.444	0.000	42.222	13.333	6.667	17.778	0.000	8.889	0.000	-0.816	2.159
RCA70	22.778	46.875	0.000	3.125	0.000	0.000	18.750	0.000	15.625	3.125	-0.234	2.294
RCA71	67.778	18.182	0.000	15.152	3.030	0.000	39.394	24.242	0.000	0.000	-1.885	2.239
RCA72	54.250	9.091	0.000	13.636	34.091	20.455	11.364	6.818	4.545	0.000	-0.344	1.495
RCA73	47.333	2.222	0.000	35.556	44.444	0.000	17.778	0.000	0.000	0.000	-0.553	1.971
RCA74	59.333	18.605	2.326	16.279	11.628	23.256	13.953	9.302	2.326	0.000	-0.843	2.072

	Mean embeddedness (%)	% of bedrock (>4000 mm)	% of boulders (250 to 4000 mm)	% of cobble (64 to 250mm)	% of coarse gravel (16 to 64 mm)	% of fine gravel (2 to 16mm)	% of sand (0.6 to 2 mm)	% of fines (<0.6 mm)	Total Organic matter (%)	% of Wood	Log10 estimated geometric mean substrate diameter (mm)	Log10 - Relative Bed Stability (dimensionless: m/m)
	XEMBED	PCT_BDRK	PCT_BL	PCT_CB	PCT_GC	PCT_GF	PCT_SA	PCT_FN	PCT_ORG	PCT_WD	LSUB_DMM	LRBS
RCA90	64.000	17.778	0.000	0.000	6.667	20.000	20.000	22.222	13.333	0.000	-0.680	1.091

Table 2.5. Flow variables.

	Flow - instantaneous discharge (m3/s)	Velocity mean (m/s)	Glides (%)	Percentage of rapids and riffles (%)	Percentage of pools	Sequence fasts, glides and pools (1= maximum Heterogeneity, 0= maximum homogeneity)
	FLOW_2	XVEL	PCT_GL	PCT_FAST	PCT_POOL	SEQ_FLO_1
TMMS0003	0.0291	0.0932	76.0000	24.0000	0.0000	0.0940
TMMS0007	0.0675	0.0484	50.0000	20.0000	30.0000	0.0268
TMMS0009	0.0000	0.0000	0.0000	0.0000	100.0000	0.0000
TMMS0027	0.0000	0.0000	17.3333	0.0000	82.6667	0.0940
TMMS0028	0.0597	0.1104	73.0000	17.0000	10.0000	0.1111
TMMS0033	0.0002	0.0044	48.6667	6.0000	45.3333	0.0671
TMMS0040	0.0001	0.0036	16.1074	4.6980	79.1946	0.2365
TMMS0043	0.0020	0.0074	80.0000	16.6667	3.3333	0.0604
TMMS0058	0.0000	0.0000	0.0000	0.0000	100.0000	0.0000
TMMS0072	0.0121	0.0288	18.0000	21.0000	61.0000	0.1313
TMMS0082	0.0359	0.0497	0.0000	0.0000	100.0000	0.0000
TMMS0088	0.0000	0.0000	0.0000	0.0000	100.0000	0.0000
TMMS0090	0.0013	0.0049	10.6667	6.6667	82.6667	0.0671
TMMS0091	0.0949	0.0703	59.3333	40.6667	0.0000	0.0537
TMMS0106	0.0002	0.0007	4.0000	0.0000	96.0000	0.0134
TMMS0119	0.0171	0.0465	71.4286	7.1429	21.4286	0.1357
TMMS0126	0.0000	0.0000	0.0000	0.0000	100.0000	0.0000
TMMS0133	0.0568	0.1420	40.0000	2.6667	57.3333	0.0822
TMMS0134	0.0003	0.0029	1.3333	7.3333	91.3333	0.1074
TMMS0137	0.0003	0.0003	0.0000	0.0000	100.0000	0.0000
TMMS0159	0.3901	0.0813	90.6667	9.3333	0.0000	0.0403
TMMS0171	0.1584	0.0495	38.6667	45.3333	16.0000	0.1088
TMMS0178	0.0652	0.1195	86.0000	14.0000	0.0000	0.0336
TMMS0183	0.0199	0.0354	15.9722	13.1944	70.8333	0.1141
TMMS0187	0.1932	0.2609	26.6667	32.0000	41.3333	0.1007
TMMS0193	0.1372	0.1579	88.0000	6.6667	5.3333	0.0405
TMMS0209	0.0197	0.0172	2.7972	0.0000	97.2028	0.0250
TMMS0214	0.0110	0.0183	68.6667	0.0000	31.3333	0.0268
TMMS0220	0.0002	0.0038	38.0000	34.6667	27.3333	0.1208
TMMS0279	0.1146	0.0537	78.0000	22.0000	0.0000	0.0872
TMMS0283	0.0648	0.0956	65.3333	22.6667	12.0000	0.2081

	Flow - instantaneous discharge (m3/s)	Velocity mean (m/s)	Glides (%)	Percentage of rapids and riffles (%)	Percentage of pools	Sequence fasts, glides and pools (1= maximum Heterogenity, 0= maximum homogenity)
	FLOW_2	XVEL	PCT_GL	PCT_FAST	PCT_POOL	SEQ_FLO_1
TMMS0290	0.0002	0.0011	40.6667	2.0000	57.3333	0.0336
TMMS0296	0.1425	0.1043	49.0000	21.0000	30.0000	0.1818
TMMS0381	0.0076	0.0773	62.0000	4.6667	33.3333	0.1342
TMMS0391	0.0170	0.0874	38.6667	1.3333	60.0000	0.0946
TMMS0437	0.0570	0.2983	50.0000	17.3333	32.6667	0.1141
TMMS1865	0.0018	0.0060	2.6667	0.0000	97.3333	0.0137
TMMS3195	0.0003	0.0042	14.6667	6.0000	79.3333	0.0805
TMMS3962	0.0033	0.0047	10.6667	0.0000	89.3333	0.0403
VGMS00002	0.0151	0.1415	67.3333	4.6667	28.0000	0.1074
VGMS00004	0.1499	0.1363	70.0000	26.0000	4.0000	0.0671
VGMS00016	0.9078	0.3875	84.5455	15.4545	0.0000	0.0642
VGMS00018	0.0407	0.5286	62.6667	37.3333	0.0000	0.1007
VGMS00022	0.0530	0.1867	32.6667	67.3333	0.0000	0.1141
VGMS00034	0.0840	0.0909	23.3333	9.3333	67.3333	0.1208
VGMS00037	0.1299	0.3335	6.6667	93.3333	0.0000	0.0096
VGMS00044	0.0520	0.0796	93.1034	6.8966	0.0000	0.0537
VGMS00048	0.3971	0.4971	46.6667	53.3333	0.0000	0.0672
VGMS00080	0.5496	0.4129	16.0000	84.0000	0.0000	0.0268
VGMS00109	0.3092	0.2691	96.6667	3.3333	0.0000	0.0134
VGMS00112	0.7043	0.3340	46.6667	53.3333	0.0000	0.0470
VGMS00121	0.0354	0.0817	72.6667	27.3333	0.0000	0.0403
VGMS00124	0.4258	0.3047	47.0588	46.2185	6.7227	0.0470
VGMS00126	0.0873	0.3355	48.0000	52.0000	0.0000	0.0604
VGMS00128	0.0602	0.2688	96.0000	2.0000	2.0000	0.0336
VGMS00162	0.2480	0.3301	94.6667	4.0000	1.3333	0.0268
VGMS00177	0.1036	0.4403	81.6176	16.9118	1.4706	0.0940
VGMS00191	0.3891	0.3180	69.3333	30.6667	0.0000	0.0805
VGMS00206	0.0184	0.1591	70.3704	0.0000	29.6296	0.1208
VGMS00210	0.3277	0.5722	100.0000	0.0000	0.0000	0.0000
VGMS00247	0.0568	0.1491	74.0000	26.0000	0.0000	0.0940
VGMS00252	0.5816	0.2761	78.0000	22.0000	0.0000	0.0671
VGMS00255	0.5092	0.4935	86.0000	14.0000	0.0000	0.0134

	Flow - instantaneous discharge (m3/s)	Velocity mean (m/s)	Glides (%)	Percentage of rapids and riffles (%)	Percentage of pools	Sequence fasts, glides and pools (1= maximum Heterogeneity, 0= maximum homogeneity)
	FLOW_2	XVEL	PCT_GL	PCT_FAST	PCT_POOL	SEQ_FLO_1
VGMS00277	0.5601	0.1877	82.0000	18.0000	0.0000	0.0671
VGMS00306	0.1891	0.1751	26.0000	74.0000	0.0000	0.0738
VGMS00320	0.2405	0.1121	0.0000	88.0000	12.0000	0.0268
VGMS00380	0.2816	0.2283	74.6667	25.3333	0.0000	0.0201
VGMS00387	0.2427	0.2549	80.0000	19.3333	0.6667	0.0403
VGMS00418	0.0472	0.1341	55.3333	26.0000	18.6667	0.1208
VGMS00433	0.3676	0.1324	96.0000	4.0000	0.0000	0.0201
VGMS00444	0.6650	0.3421	40.0000	60.0000	0.0000	0.1007
VGMS00447	0.4492	0.3289	76.0000	24.0000	0.0000	0.0537
VGMS00450	0.7561	0.6293	57.0370	35.5556	7.4074	0.0738
VGMS00511	0.2233	0.3191	11.3333	88.6667	0.0000	0.0403
VGMS00515	0.1105	0.1869	36.9231	52.3077	10.7692	0.0940
VGMS00558	0.3000	0.5949	50.6667	49.3333	0.0000	0.1409
VGMS00575	0.3267	0.3721	20.6667	79.3333	0.0000	0.0671
SSMS0001	0.2007	0.4589	36.0000	64.0000	0.0000	0.0671
SSMS0002	0.2408	0.1599	58.6667	41.3333	0.0000	0.0336
SSMS0008	0.0302	0.1748	46.6667	33.3333	20.0000	0.1611
SSMS0010	0.5715	0.2525	56.6667	43.3333	0.0000	0.0671
SSMS0014	0.1076	0.1817	36.6667	63.3333	0.0000	0.0940
SSMS0028	0.0813	0.1741	70.6667	29.3333	0.0000	0.0671
SSMS0029	0.5194	0.2731	100.0000	0.0000	0.0000	0.0000
SSMS0031	0.0029	0.0150	98.6667	1.3333	0.0000	0.0134
SSMS0033	6.1153	22.3056	56.6667	43.3333	0.0000	0.0604
SSMS0035	0.7591	0.2823	42.6667	57.3333	0.0000	0.0470
SSMS0037	0.1039	0.1276	90.0000	10.0000	0.0000	0.0268
SSMS0038	0.0907	0.1341	95.3333	0.0000	4.6667	0.0268
SSMS0044	0.1495	0.1999	85.3333	14.6667	0.0000	0.0134
SSMS0051	0.0594	0.1573	77.3333	20.6667	2.0000	0.1074
SSMS0053	0.1649	0.7061	89.3333	8.6667	2.0000	0.0403
SSMS0057	0.2127	0.4248	44.0000	6.0000	50.0000	0.1275
SSMS0059	0.0313	0.2177	86.6667	13.3333	0.0000	0.1007
SSMS0073	0.3291	0.2159	80.6667	19.3333	0.0000	0.0537

	Flow - instantaneous discharge (m3/s)	Velocity mean (m/s)	Glides (%)	Percentage of rapids and riffles (%)	Percentage of pools	Sequence fasts, glides and pools (1= maximum Heterogenity, 0= maximum homogenity)
	FLOW_2	XVEL	PCT_GL	PCT_FAST	PCT_POOL	SEQ_FLO_1
SSMS0078	0.2808	0.3466	85.3333	14.6667	0.0000	0.0537
SSMS0094	0.2233	0.2824	22.6667	77.3333	0.0000	0.0268
SSMS0105	0.4215	0.4995	77.3333	22.6667	0.0000	0.1275
SSMS0126	0.3048	0.3761	96.6667	3.3333	0.0000	0.0135
SSMS0129	0.2592	0.3381	100.0000	0.0000	0.0000	0.0000
SSMS0133	0.2934	0.1289	86.6667	11.3333	2.0000	0.0738
SSMS0144	0.0267	0.2040	54.0000	14.6667	31.3333	0.2081
SSMS0149	0.4450	0.3222	80.0000	20.0000	0.0000	0.0268
SSMS0150	0.4061	0.3880	65.3333	28.0000	6.6667	0.1342
SSMS0157	0.1957	1.2776	24.6667	18.0000	57.3333	0.0946
SSMS0175	0.1113	0.2013	59.3333	40.6667	0.0000	0.0671
SSMS0191	0.1790	0.1898	58.6667	41.3333	0.0000	0.0671
SSMS0193	0.2062	0.2543	98.0000	2.0000	0.0000	0.0134
SSMS0199	0.1552	0.1590	78.5235	21.4765	0.0000	0.0537
SSMS0213	5.7423	3.2617	67.3333	32.6667	0.0000	0.0872
SSMS0351	0.7221	0.4760	54.0000	46.0000	0.0000	0.0336
SSMS0408	0.1012	0.2662	82.6667	17.3333	0.0000	0.0470
SSMS0411	0.3034	0.1894	64.6667	35.3333	0.0000	0.0470
SSMS0447	0.7193	0.4445	47.6510	52.3490	0.0000	0.0470
SSMS1000	0.1738	0.5327	32.6667	67.3333	0.0000	0.0671
SSMS4173	0.5314	0.2638	62.6667	37.3333	0.0000	0.0336
SSMS4330	0.1910	0.2365	58.0000	42.0000	0.0000	0.0671
RENP0008	0.0999	0.1580	47.3684	27.8195	24.8120	0.0746
RENP0012	0.0734	0.1739	50.0000	40.0000	10.0000	0.1892
RENP0016	0.2859	0.0568	76.6667	13.3333	10.0000	0.0671
RENP0028	0.1208	0.2016	64.6667	31.3333	4.0000	0.1611
RENP0047	0.0565	0.7683	87.3333	2.6667	10.0000	0.0336
RENP0052	0.0659	0.2340	50.0000	50.0000	0.0000	0.0604
RENP0054	0.0019	1.3738	88.6667	3.3333	8.0000	0.1208
RENP0055	0.0780	0.2456	96.0000	1.3333	2.6667	0.0268
RENP0075	0.1676	0.1790	62.0000	16.0000	22.0000	0.0604
RENP0092	0.0067	1.0079	96.0000	4.0000	0.0000	0.0268

	Flow - instantaneous discharge (m3/s)	Velocity mean (m/s)	Glides (%)	Percentage of rapids and riffles (%)	Percentage of pools	Sequence fasts, glides and pools (1= maximum Heterogeneity, 0= maximum homogeneity)
	FLOW_2	XVEL	PCT_GL	PCT_FAST	PCT_POOL	SEQ_FLO_1
REN0095	0.0219	0.2623	83.3333	16.6667	0.0000	0.0671
REN0096	0.0877	0.2438	80.0000	20.0000	0.0000	0.0805
REN0097	0.1081	0.2818	37.3333	45.3333	17.3333	0.1141
REN100	0.1099	0.2790	74.0000	26.0000	0.0000	0.0604
REN0108	0.0402	0.4055	43.3333	56.6667	0.0000	0.0872
REN0110	0.1924	0.1784	38.0000	62.0000	0.0000	0.1141
REN0112	0.2303	1.2099	90.6667	4.0000	5.3333	0.0671
REN0128	0.0717	0.2317	92.0000	2.0000	6.0000	0.0671
REN0132	0.0258	0.4516	78.0000	17.3333	4.6667	0.1007
REN0139	0.0813	0.2149	100.0000	0.0000	0.0000	0.0000
REN0144	0.0253	0.1572	18.0000	9.3333	72.6667	0.1074
REN0187	0.0623	0.3585	90.0000	10.0000	0.0000	0.0134
REN0192	0.3894	0.2228	31.3333	68.6667	0.0000	0.0268
REN0203	0.0943	0.1899	88.0000	3.3333	8.6667	0.0537
REN0228	0.1228	0.3144	65.3333	34.6667	0.0000	0.0872
REN0240	0.0142	0.5865	71.3333	2.0000	26.6667	0.0537
REN0251	0.0284	0.4233	36.6667	54.6667	8.6667	0.1409
REN0287	0.0036	0.8560	72.0000	0.0000	28.0000	0.0537
REN0368	0.0759	0.2086	80.6667	19.3333	0.0000	0.0537
REN0375	0.1719	0.0726	72.0000	15.3333	12.6667	0.0872
REN0443	0.1006	0.2209	55.3333	44.6667	0.0000	0.0537
REN0511	0.2879	0.1332	42.0000	58.0000	0.0000	0.0671
REN1524	0.0460	0.3196	80.0000	12.0000	8.0000	0.0671
REN2991	0.0624	0.2043	90.0000	10.0000	0.0000	0.0671
REN5612	0.3644	0.1625	32.0000	68.0000	0.0000	0.0067
REN7308	0.0297	0.6503	82.6667	17.3333	0.0000	0.1879
REN9611	0.0257	0.5661	92.6667	7.3333	0.0000	0.0805
REN9757	0.1994	0.3649	39.3333	11.3333	49.3333	0.0134
REN12892	0.1274	0.8781	20.6667	79.3333	0.0000	0.1007
REN15048	0.5958	0.1926	10.0000	90.0000	0.0000	0.0537
RCA02	0.0514	0.0573	35.0000	65.0000	0.0000	0.2917
RCA08	0.0013	0.0060	100.0000	0.0000	0.0000	0.2414

	Flow - instantaneous discharge (m3/s)	Velocity mean (m/s)	Glides (%)	Percentage of rapids and riffles (%)	Percentage of pools	Sequence fasts, glides and pools (1= maximum Heterogenity, 0= maximum homogenity)
	FLOW_2	XVEL	PCT_GL	PCT_FAST	PCT_POOL	SEQ_FLO_1
RCA22	0.0431	0.0201	60.8696	30.4348	4.3478	0.3750
RCA23	0.0204	0.0499	100.0000	0.0000	0.0000	0.2500
RCA30	0.2476	0.0753	66.6667	33.3333	0.0000	0.0833
RCA31	0.0713	0.1852	52.6316	47.3684	0.0000	0.3793
RCA44	0.0151	0.3262	58.3333	41.6667	0.0000	0.5862
RCA48	0.2086	0.5424	0.0000	100.0000	0.0000	0.0345
RCA49	0.1257	0.2602	86.9565	13.0435	0.0000	0.2069
RCA50	1.2634	0.5041	83.3333	16.6667	0.0000	0.1034
RCA52	0.4571	0.4594	88.4615	11.5385	0.0000	0.0690
RCA53	0.2878	0.6923	23.3333	76.6667	0.0000	0.1379
RCA57	0.0633	0.0336	100.0000	0.0000	0.0000	0.0000
RCA58	0.0097	0.0749	40.0000	60.0000	0.0000	0.2500
RCA59	0.0386	0.0465	63.6364	36.3636	0.0000	0.2083
RCA60	0.0000	0.0000	8.0000	92.0000	0.0000	0.1250
RCA62	0.0007	0.0587	100.0000	0.0000	0.0000	0.4167
RCA64	0.0035	0.0544	56.2500	43.7500	0.0000	0.4583
RCA65	0.0077	0.1763	72.4138	27.5862	0.0000	0.3448
RCA66	0.0086	0.0517	65.2174	34.7826	0.0000	0.3448
RCA67	0.0086	0.0513	61.9048	38.0952	0.0000	0.3448
RCA68	0.0705	0.4447	31.8182	68.1818	0.0000	0.1379
RCA69	0.2382	0.5061	34.6154	65.3846	0.0000	0.1034
RCA70	0.1505	0.4132	50.0000	50.0000	0.0000	0.2069
RCA71	0.0212	0.1122	68.1818	31.8182	0.0000	0.4828
RCA72	0.1355	0.1598	86.6667	13.3333	0.0000	0.0690
RCA73	0.4721	0.6092	30.0000	70.0000	0.0000	0.1034
RCA74	0.0000	0.0000	33.3333	66.6667	0.0000	0.0690
RCA90	0.4612	0.4363	100.0000	0.0000	0.0000	0.0345

Table 2.6. Vegetation canopy cover variables.

	Mean mid-channel canopy density (%)	Mean canopy cover > 0.3m DBH	Mean canopy cover <= 0.3m DBH	Mean woody mid-layer cover	Mean herbaceous mid-layer cover	Mean woody ground-layer cover	Mean herbaceous ground-layer cover	Mean exposed soil	Mean riparian veg canopy cover	Mean riparian veg mid-layer cover	Mean riparian veg ground cover
	XCDENMID	XCL	XCS	XMW	XMH	XGW	XGH	XGB	XC	XM	XG
TMMS0003	93.984	2.273	8.182	13.636	14.659	12.273	18.864	15.000	10.455	28.295	31.136
TMMS0007	75.802	39.545	45.227	48.864	53.523	41.705	50.455	8.636	84.773	102.386	92.159
TMMS0009	65.909	3.636	6.818	17.955	12.841	8.636	25.455	42.614	10.455	30.795	34.091
TMMS0027	88.235	4.318	12.955	24.886	7.727	9.545	12.273	27.841	17.273	32.614	21.818
TMMS0028	84.893	6.591	13.182	19.091	16.477	19.886	22.045	22.159	19.773	35.568	41.932
TMMS0033	94.519	2.045	18.636	21.136	20.227	21.250	17.955	29.886	20.682	41.364	39.205
TMMS0040	84.492	2.045	3.182	15.568	41.705	12.273	41.591	5.000	5.227	57.273	53.864
TMMS0043	79.813	1.591	10.341	12.841	10.227	11.250	15.909	29.091	11.932	23.068	27.159
TMMS0058	75.668	2.500	7.955	26.364	2.955	8.636	17.045	50.000	10.455	29.318	25.682
TMMS0072	71.791	6.591	18.295	17.045	18.295	9.318	22.955	36.023	24.886	35.341	32.273
TMMS0082	83.021	1.591	4.091	12.727	19.091	3.864	13.295	66.818	5.682	31.818	17.159
TMMS0088	68.583	1.364	5.000	19.091	15.568	18.295	22.500	26.023	6.364	34.659	40.795
TMMS0090	97.727	4.545	18.636	21.364	6.818	9.545	14.318	22.159	23.182	28.182	23.864
TMMS0091	53.476	1.364	8.864	13.977	9.773	12.273	10.000	35.227	10.227	23.750	22.273
TMMS0106	99.599	4.318	9.545	40.000	11.023	20.114	11.932	53.068	13.864	51.023	32.045
TMMS0119	95.722	3.182	5.227	22.386	32.386	5.000	29.545	15.909	8.409	54.773	34.545
TMMS0126	94.251	5.455	15.795	30.909	11.023	19.205	15.227	8.182	21.250	41.932	34.432
TMMS0133	83.021	4.091	4.773	13.750	37.045	9.545	31.705	17.159	8.864	50.795	41.250
TMMS0134	94.385	12.727	28.750	25.227	5.909	5.909	13.409	37.159	41.477	31.136	19.318
TMMS0137	87.701	16.364	10.909	7.045	4.091	10.000	9.659	30.227	27.273	11.136	19.659
TMMS0159	43.182	7.727	20.909	27.273	22.614	17.841	33.523	27.045	28.636	49.886	51.364
TMMS0171	16.578	0.227	0.682	19.886	12.273	5.000	45.568	36.023	0.909	32.159	50.568
TMMS0178	82.888	1.591	8.864	36.136	12.386	20.682	20.114	30.227	10.455	48.523	40.795
TMMS0183	96.524	4.545	26.932	40.341	14.318	27.841	5.000	17.727	31.477	54.659	32.841
TMMS0187	92.914	2.727	6.136	33.750	11.932	10.455	14.318	31.705	8.864	45.682	24.773
TMMS0193	76.070	15.455	19.091	17.386	15.568	11.932	63.523	5.682	34.545	32.955	75.455
TMMS0209	89.037	36.250	27.727	42.727	47.159	28.977	20.341	1.591	63.977	89.886	49.318
TMMS0214	75.000	0.227	2.500	4.091	3.636	1.591	3.636	43.409	2.727	7.727	5.227
TMMS0220	65.241	2.500	12.500	15.682	11.136	14.432	21.477	21.591	15.000	26.818	35.909
TMMS0279	53.877	0.909	11.705	38.409	15.227	23.750	36.932	8.636	12.614	53.636	60.682
TMMS0283	35.963	7.273	23.864	26.364	9.205	6.591	21.477	12.386	31.136	35.568	28.068
TMMS0290	26.203	0.909	2.045	3.409	18.068	6.136	84.773	1.136	2.955	21.477	90.909
TMMS0296	72.995	2.955	12.727	5.909	13.750	5.909	27.273	37.273	15.682	19.659	33.182

	Mean mid-channel canopy density (%)	Mean canopy cover > 0.3m DBH	Mean canopy cover <= 0.3m DBH	Mean woody mid-layer cover	Mean herbaceous mid-layer cover	Mean woody ground-layer cover	Mean herbaceous ground-layer cover	Mean exposed soil	Mean riparian veg canopy cover	Mean riparian veg mid-layer cover	Mean riparian veg ground cover
	XCDENMID	XCL	XCS	XMW	XMH	XGW	XGH	XGB	XC	XM	XG
TMMS0381	96.390	3.636	10.909	35.795	14.091	23.750	26.705	8.977	14.545	49.886	50.455
TMMS0391	53.476	12.955	15.682	15.909	6.818	5.909	12.273	38.977	28.636	22.727	18.182
TMMS0437	9.358	1.591	3.636	4.318	4.545	4.091	87.500	4.091	5.227	8.864	91.591
TMMS1865	79.679	3.182	4.773	3.864	6.364	4.545	20.682	43.068	7.955	10.227	25.227
TMMS3195	8.690	0.000	0.000	1.136	1.364	0.455	87.500	5.909	0.000	2.500	87.955
TMMS3962	85.027	12.727	23.182	17.841	5.455	5.455	5.455	62.273	35.909	23.295	10.909
VGMS00002	88.770	2.500	6.364	3.864	5.455	6.136	14.659	12.159	8.864	9.318	20.795
VGMS00004	61.364	17.386	13.864	41.023	4.205	28.636	15.114	19.091	31.250	45.227	43.750
VGMS00016	78.342	0.682	1.364	6.591	5.227	6.818	6.136	45.568	2.045	11.818	12.955
VGMS00018	90.642	5.909	17.955	40.000	2.955	14.318	0.909	6.136	23.864	42.955	15.227
VGMS00022	73.930	14.886	20.114	17.955	18.295	16.477	13.750	8.864	35.000	36.250	30.227
VGMS00034	92.112	28.182	31.364	28.182	4.773	11.818	5.000	13.977	59.545	32.955	16.818
VGMS00037	64.037	6.705	26.477	17.500	18.295	9.886	16.136	15.455	33.182	35.795	26.023
VGMS00044	87.433	3.182	5.455	33.864	1.818	14.545	15.795	32.614	8.636	35.682	30.341
VGMS00048	60.829	1.364	1.364	4.091	4.318	4.773	8.182	5.455	2.727	8.409	12.955
VGMS00080	88.235	6.591	16.136	13.636	15.000	7.727	6.364	19.432	22.727	28.636	14.091
VGMS00109	77.941	16.591	20.568	42.614	0.455	57.273	3.864	15.227	37.159	43.068	61.136
VGMS00112	94.118	3.182	13.409	28.523	31.705	18.068	17.386	10.455	16.591	60.227	35.455
VGMS00121	62.834	26.932	11.364	19.773	16.250	12.045	15.682	8.636	38.295	36.023	27.727
VGMS00124	77.005	5.455	12.273	26.364	4.205	12.273	8.182	33.409	17.727	30.568	20.455
VGMS00126	95.321	10.227	14.773	31.932	22.273	9.091	10.455	10.682	25.000	54.205	19.545
VGMS00128	93.048	4.773	23.977	28.523	51.818	18.409	49.886	7.159	28.750	80.341	68.295
VGMS00162	96.791	6.136	30.795	26.818	11.705	18.523	5.000	28.182	36.932	38.523	23.523
VGMS00177	89.973	27.955	40.455	63.977	68.295	26.136	25.682	2.273	68.409	132.273	51.818
VGMS00191	86.497	28.636	9.432	54.773	1.591	9.318	1.591	45.795	38.068	56.364	10.909
VGMS00206	85.695	14.659	4.091	6.136	10.114	4.205	33.068	2.727	18.750	16.250	37.273
VGMS00210	35.294	1.591	3.636	4.545	6.591	3.182	26.932	19.432	5.227	11.136	30.114
VGMS00247	70.321	2.273	6.250	24.886	0.000	9.886	66.250	12.841	8.523	24.886	76.136
VGMS00252	83.422	7.273	8.182	10.227	0.455	6.136	3.636	27.500	15.455	10.682	9.773
VGMS00255	65.508	11.364	12.614	15.568	15.568	13.750	13.409	5.227	23.977	31.136	27.159
VGMS00277	72.892	0.682	2.273	4.545	3.864	6.364	6.705	33.864	2.955	8.409	13.068
VGMS00306	75.000	9.432	12.955	7.614	26.250	6.932	16.477	1.364	22.386	33.864	23.409
VGMS00320	70.856	19.318	35.227	33.295	7.273	10.682	34.091	20.568	54.545	40.568	44.773
VGMS00380	88.369	25.000	31.477	40.795	0.000	20.909	0.000	44.318	56.477	40.795	20.909

	Mean mid-channel canopy density (%)	Mean canopy cover > 0.3m DBH	Mean canopy cover <= 0.3m DBH	Mean woody mid-layer cover	Mean herbaceous mid-layer cover	Mean woody ground-layer cover	Mean herbaceous ground-layer cover	Mean exposed soil	Mean riparian veg canopy cover	Mean riparian veg mid-layer cover	Mean riparian veg ground cover
	XCDENMID	XCL	XCS	XMW	XMH	XGW	XGH	XGB	XC	XM	XG
VGMS00387	77.807	14.432	48.636	54.432	64.318	29.432	35.227	0.227	63.068	118.750	64.659
VGMS00418	94.118	20.114	12.500	37.955	1.818	21.932	14.432	55.341	32.614	39.773	36.364
VGMS00433	97.460	4.091	20.227	33.295	24.091	30.568	25.227	25.000	24.318	57.386	55.795
VGMS00444	34.759	0.227	14.659	39.432	1.818	24.205	40.568	32.045	14.886	41.250	64.773
VGMS00447	70.989	3.182	9.205	7.159	9.091	1.364	17.955	0.682	12.386	16.250	19.318
VGMS00450	47.193	2.045	10.341	10.227	23.182	4.318	8.523	13.182	12.386	33.409	12.841
VGMS00511	96.390	8.182	22.500	42.841	29.659	21.364	17.500	12.955	30.682	72.500	38.864
VGMS00515	85.963	11.591	11.364	10.000	27.045	4.886	22.841	2.955	22.955	37.045	27.727
VGMS00558	78.877	4.545	31.136	34.432	23.409	35.909	23.068	30.909	35.682	57.841	58.977
VGMS00575	84.091	1.136	7.045	19.432	14.773	15.000	35.000	4.659	8.182	34.205	50.000
SSMS0001	96.658	29.318	70.909	24.545	7.727	2.500	2.841	0.227	100.227	32.273	5.341
SSMS0002	96.791	13.068	17.727	26.364	15.227	12.841	15.909	19.773	30.795	41.591	28.750
SSMS0008	57.219	1.818	11.591	17.614	0.909	3.864	3.864	33.864	13.409	18.523	7.727
SSMS0010	33.021	1.136	4.545	3.409	25.455	3.409	40.341	67.727	5.682	28.864	43.750
SSMS0014	95.187	2.273	61.477	17.614	10.909	6.818	4.432	0.455	63.750	28.523	11.250
SSMS0028	94.786	20.114	27.045	16.818	16.818	16.818	18.636	36.023	47.159	33.636	35.455
SSMS0029	60.829	6.136	2.273	0.909	0.000	11.250	35.909	5.682	8.409	0.909	47.159
SSMS0031	90.775	4.318	11.023	11.932	11.932	11.932	11.932	38.636	15.341	23.864	23.864
SSMS0033	0.802	0.000	0.000	0.000	0.000	0.000	87.500	25.795	0.000	0.000	87.500
SSMS0035	86.364	9.432	32.045	30.341	31.250	21.591	20.000	45.341	41.477	61.591	41.591
SSMS0037	88.503	4.205	9.773	38.750	9.205	11.932	3.636	27.727	13.977	47.955	15.568
SSMS0038	83.155	7.955	4.318	39.432	6.932	11.705	6.932	24.886	12.273	46.364	18.636
SSMS0044	93.850	9.545	32.386	26.705	25.227	30.000	25.568	25.795	41.932	51.932	55.568
SSMS0051	96.524	12.273	74.205	52.045	36.023	1.818	7.273	0.682	86.477	88.068	9.091
SSMS0053	91.578	4.318	4.545	8.182	5.000	11.136	8.636	18.068	8.864	13.182	19.773
SSMS0057	94.251	0.909	3.409	4.545	4.318	2.955	5.227	3.864	4.318	8.864	8.182
SSMS0059	89.706	3.182	15.455	22.500	10.682	2.955	12.955	21.250	18.636	33.182	15.909
SSMS0073	75.401	9.091	0.909	30.455	3.409	13.864	5.000	40.341	10.000	33.864	18.864
SSMS0078	38.102	0.682	4.773	12.614	0.000	14.432	40.341	47.500	5.455	12.614	54.773
SSMS0094	93.583	24.773	43.409	48.750	7.159	36.477	25.000	20.455	68.182	55.909	61.477
SSMS0105	96.123	2.273	2.727	5.455	10.000	4.318	6.364	22.273	5.000	15.455	10.682
SSMS0126	60.963	3.409	8.409	14.432	3.636	2.727	23.750	27.273	11.818	18.068	26.477
SSMS0129	75.668	6.364	21.023	31.364	0.000	30.227	10.114	4.773	27.386	31.364	40.341
SSMS0133	24.198	2.955	28.295	36.477	11.477	14.545	40.568	10.682	31.250	47.955	55.114

	Mean mid-channel canopy density (%)	Mean canopy cover > 0.3m DBH	Mean canopy cover <= 0.3m DBH	Mean woody mid-layer cover	Mean herbaceous mid-layer cover	Mean woody ground-layer cover	Mean herbaceous ground-layer cover	Mean exposed soil	Mean riparian veg canopy cover	Mean riparian veg mid-layer cover	Mean riparian veg ground cover
	XCDENMID	XCL	XCS	XMW	XMH	XGW	XGH	XGB	XC	XM	XG
SSMS0144	73.128	1.818	10.795	14.091	6.364	7.045	32.614	3.864	12.614	20.455	39.659
SSMS0149	58.289	20.227	23.409	23.068	10.455	15.568	54.091	7.045	43.636	33.523	69.659
SSMS0150	83.155	0.909	1.818	2.500	3.636	3.864	15.682	33.182	2.727	6.136	19.545
SSMS0157	93.316	15.568	21.023	58.295	0.000	6.818	0.000	18.182	36.591	58.295	6.818
SSMS0175	91.043	12.841	28.295	30.455	30.455	25.455	25.455	19.432	41.136	60.909	50.909
SSMS0191	72.861	7.273	8.182	24.545	7.386	19.773	41.250	10.114	15.455	31.932	61.023
SSMS0193	95.053	1.591	2.273	12.727	3.864	3.864	3.409	26.705	3.864	16.591	7.273
SSMS0199	79.679	12.614	60.341	40.568	8.636	3.636	2.955	2.500	72.955	49.205	6.591
SSMS0213	65.107	3.750	7.159	30.795	6.364	16.477	8.068	40.341	10.909	37.159	24.545
SSMS0351	46.791	8.409	17.045	30.227	4.545	18.864	24.886	25.000	25.455	34.773	43.750
SSMS0408	98.663	7.614	14.091	17.273	1.364	11.818	16.477	42.727	21.705	18.636	28.295
SSMS0411	77.139	10.000	25.795	20.455	22.841	19.205	23.750	23.636	35.795	43.295	42.955
SSMS0447	90.374	20.909	46.250	64.545	10.795	38.864	32.614	10.341	67.159	75.341	71.477
SSMS1000	99.332	6.364	7.955	16.136	0.455	8.750	19.659	50.682	14.318	16.591	28.409
SSMS4173	21.390	2.727	4.545	5.682	10.114	2.955	51.136	15.568	7.273	15.795	54.091
SSMS4330	81.150	12.045	10.000	45.568	39.545	30.114	27.386	51.136	22.045	85.114	57.500
REN0008	95.588	17.841	35.114	28.864	6.136	28.295	1.818	17.386	52.955	35.000	30.114
REN0012	89.439	4.659	19.432	16.818	3.182	5.568	11.023	14.091	24.091	20.000	16.591
REN0016	57.487	4.318	16.818	18.977	0.455	26.364	2.500	25.455	21.136	19.432	28.864
REN0028	98.128	12.727	33.523	20.455	22.727	16.477	20.682	12.841	46.250	43.182	37.159
REN0047	99.599	16.250	40.341	45.455	42.500	5.909	5.909	5.000	56.591	87.955	11.818
REN0052	90.775	8.182	15.682	27.955	17.614	24.773	26.250	17.159	23.864	45.568	51.023
REN0054	100.000	57.500	87.500	57.500	57.500	5.000	5.000	0.000	145.000	115.000	10.000
REN0055	99.465	21.818	19.091	20.114	18.636	14.432	7.727	30.000	40.909	38.750	22.159
REN0075	72.059	20.341	34.886	31.477	2.500	20.795	21.477	29.091	55.227	33.977	42.273
REN0092	80.882	13.523	23.295	18.295	9.886	2.500	21.477	13.068	36.818	28.182	23.977
REN0095	100.000	11.591	25.227	31.477	30.000	31.364	42.727	20.455	36.818	61.477	74.091
REN0096	68.850	7.614	17.273	27.386	10.000	9.773	18.409	37.727	24.886	37.386	28.182
REN0097	90.909	28.295	35.000	38.864	5.000	12.841	5.909	16.818	63.295	43.864	18.750
REN0100	72.861	1.818	11.136	17.159	18.523	12.386	40.909	19.432	12.955	35.682	53.295
REN0108	98.396	15.568	51.591	42.727	0.682	32.955	2.273	15.568	67.159	43.409	35.227
REN0110	99.465	9.318	77.955	47.841	9.886	2.955	2.955	5.455	87.273	57.727	5.909
REN0112	92.513	40.568	34.091	20.114	7.273	10.455	16.591	5.909	74.659	27.386	27.045
REN0128	29.144	0.000	1.364	3.409	19.545	1.818	32.955	29.545	1.364	22.955	34.773

	Mean mid-channel canopy density (%)	Mean canopy cover > 0.3m DBH	Mean canopy cover <= 0.3m DBH	Mean woody mid-layer cover	Mean herbaceous mid-layer cover	Mean woody ground-layer cover	Mean herbaceous ground-layer cover	Mean exposed soil	Mean riparian veg canopy cover	Mean riparian veg mid-layer cover	Mean riparian veg ground cover
	XCDENMID	XCL	XCS	XMW	XMH	XGW	XGH	XGB	XC	XM	XG
REN0132	99.465	8.409	35.909	29.432	0.455	34.432	0.909	7.500	44.318	29.886	35.341
REN0139	90.909	24.659	43.864	46.136	25.568	5.000	5.000	1.818	68.523	71.705	10.000
REN0144	85.294	5.909	26.364	34.205	14.205	19.886	18.409	15.795	32.273	48.409	38.295
REN0187	97.326	7.955	21.023	33.750	29.432	35.000	27.614	5.000	28.977	63.182	62.614
REN0192	98.128	1.364	5.909	16.818	13.864	18.864	21.250	20.227	7.273	30.682	40.114
REN0203	95.722	20.000	40.909	37.045	34.091	26.705	28.182	17.727	60.909	71.136	54.886
REN0228	95.053	20.000	21.705	48.864	48.864	49.432	49.432	4.318	41.705	97.727	98.864
REN0240	88.503	14.318	34.091	8.864	6.136	3.864	6.477	25.227	48.409	15.000	10.341
REN0251	95.053	20.682	48.182	30.227	18.636	9.318	19.205	3.409	68.864	48.864	28.523
REN0287	99.733	18.977	26.705	23.636	0.000	15.000	0.000	24.886	45.682	23.636	15.000
REN0368	95.588	7.273	34.886	30.000	16.250	35.909	35.568	6.477	42.159	46.250	71.477
REN0375	81.417	24.205	23.068	10.455	6.818	8.068	43.295	22.500	47.273	17.273	51.364
REN0443	94.251	4.773	12.614	21.705	21.932	22.841	24.659	27.045	17.386	43.636	47.500
REN0511	68.717	3.750	28.750	28.636	19.432	2.955	14.091	11.250	32.500	48.068	17.045
REN1524	99.599	21.705	32.045	25.455	12.273	20.114	1.136	28.182	53.750	37.727	21.250
REN2991	86.230	17.159	28.750	51.591	0.000	21.932	0.000	6.364	45.909	51.591	21.932
REN5612	85.027	0.227	7.045	16.250	55.682	8.977	43.977	3.636	7.273	71.932	52.955
REN7308	94.652	9.773	44.545	57.045	22.841	24.659	21.364	3.182	54.318	79.886	46.023
REN9611	94.118	20.568	63.750	68.182	17.955	27.614	26.705	0.682	84.318	86.136	54.318
REN9757	48.529	0.000	0.455	12.045	12.955	19.545	19.545	4.545	0.455	25.000	39.091
REN12892	27.575	0.682	5.341	12.273	16.477	5.227	15.341	19.091	6.023	28.750	20.568
REN15048	37.701	1.136	2.045	5.682	1.364	58.864	58.864	11.364	3.182	7.045	117.727
RCA02	3.209	0.000	0.000	12.917	3.750	28.750	87.500	0.000	0.000	16.667	116.250
RCA08	46.925	1.667	5.000	85.000	85.000	85.000	85.000	0.417	6.667	170.000	170.000
RCA22	6.551	3.750	20.000	42.083	21.458	59.375	77.500	0.000	23.750	63.542	136.875
RCA23	50.802	8.542	29.167	67.292	67.292	77.500	77.500	0.417	37.708	134.583	155.000
RCA30	37.299	0.000	0.000	6.667	2.083	14.375	87.500	0.000	0.000	8.750	101.875
RCA31	51.738	0.000	38.750	87.500	82.500	60.000	51.875	1.667	38.750	170.000	111.875
RCA44	51.070	0.000	13.333	85.000	64.792	62.083	56.667	0.000	13.333	149.792	118.750
RCA48	42.914	0.417	4.167	64.792	59.375	82.500	80.000	0.417	4.583	124.167	162.500
RCA49	42.647	0.000	5.000	62.500	65.000	85.000	87.500	0.000	5.000	127.500	172.500
RCA50	37.166	0.000	0.417	45.000	45.000	82.500	85.000	0.000	0.417	90.000	167.500
RCA52	39.572	0.417	6.667	70.000	70.000	85.000	85.000	0.000	7.083	140.000	170.000
RCA53	37.567	0.000	2.083	75.000	75.000	85.000	85.000	0.000	2.083	150.000	170.000

	Mean mid-channel canopy density (%)	Mean canopy cover > 0.3m DBH	Mean canopy cover <= 0.3m DBH	Mean woody mid-layer cover	Mean herbaceous mid-layer cover	Mean woody ground-layer cover	Mean herbaceous ground-layer cover	Mean exposed soil	Mean riparian veg canopy cover	Mean riparian veg mid-layer cover	Mean riparian veg ground cover
	XCDENMID	XCL	XCS	XMW	XMH	XGW	XGH	XGB	XC	XM	XG
RCA57	39.572	1.667	11.458	47.500	41.875	85.000	87.500	0.000	13.125	89.375	172.500
RCA58	27.807	0.000	0.417	16.042	15.625	40.625	87.500	0.000	0.417	31.667	128.125
RCA59	8.422	0.000	0.000	6.250	0.000	59.583	87.500	0.000	0.000	6.250	147.083
RCA60	0.000	0.000	0.000	2.083	3.750	23.125	87.500	0.000	0.000	5.833	110.625
RCA62	46.257	0.000	2.917	11.667	8.333	35.833	35.833	0.000	2.917	20.000	71.667
RCA64	46.658	2.500	6.667	46.667	33.125	75.000	67.292	0.000	9.167	79.792	142.292
RCA65	51.738	0.833	0.000	67.292	67.292	70.417	70.417	2.083	0.833	134.583	140.833
RCA66	50.401	0.417	21.042	64.583	64.583	80.000	74.792	0.000	21.458	129.167	154.792
RCA67	49.198	0.000	36.250	62.917	57.708	77.500	65.000	0.000	36.250	120.625	142.500
RCA68	40.775	0.000	2.083	45.625	48.333	72.292	72.292	2.083	2.083	93.958	144.583
RCA69	39.171	0.000	2.083	67.500	59.167	79.792	74.792	0.417	2.083	126.667	154.583
RCA70	45.053	0.000	13.333	75.000	72.500	77.500	77.500	0.000	13.333	147.500	155.000
RCA71	47.727	0.000	5.000	72.500	72.500	82.500	82.500	0.000	5.000	145.000	165.000
RCA72	10.561	0.000	0.417	58.958	56.250	64.375	64.375	2.083	0.417	115.208	128.750
RCA73	35.963	0.000	2.083	68.125	65.417	69.792	67.083	1.667	2.083	133.542	136.875
RCA74	32.754	0.000	1.667	57.083	62.500	87.500	87.500	0.000	1.667	119.583	175.000
RCA90	27.941	0.000	4.167	39.583	53.125	85.000	87.500	0.000	4.167	92.708	172.500

Table 2.7. In-stream cover variables.

	Prop. Areal cover filamentous algae	Prop. Areal cover aquatic macrophytes	Prop. Areal cover large woody debris	Prop. Areal cover brush	Prop. Areal cover live trees	Prop. Areal cover leaves bank	Prop. Areal cover undercut banks	Prop. Areal cover boulders
	XFC_ALG	XFC_AQM	XFC_LWD	XFC_BRS	XFC_ROT	XFC_LEB	XFC_UCB	XFC_RCK
TMMS0003	4.091	0.000	3.182	8.636	7.273	26.818	0.909	0.000
TMMS0007	0.000	0.000	30.227	40.682	4.545	71.818	1.818	0.000
TMMS0009	0.000	0.000	0.000	0.000	0.000	19.773	0.000	2.273
TMMS0027	15.909	0.000	0.000	0.000	0.000	5.682	0.000	79.091
TMMS0028	34.773	0.000	0.455	5.909	9.091	23.182	1.364	2.273
TMMS0033	0.000	3.182	1.364	4.091	8.636	11.591	10.000	4.545
TMMS0040	0.000	0.000	0.000	0.000	0.455	0.909	0.000	55.682
TMMS0043	0.000	1.364	3.182	3.636	4.091	15.682	3.636	15.682
TMMS0058	5.000	0.000	0.000	0.000	0.000	17.045	0.000	7.273
TMMS0072	0.000	0.000	0.000	0.909	3.182	44.091	15.227	2.273
TMMS0082	0.000	0.000	1.364	12.955	0.455	79.545	0.455	0.000
TMMS0088	20.682	3.636	0.909	1.818	5.909	22.045	1.818	43.636
TMMS0090	0.000	0.000	0.000	0.000	0.455	3.182	2.727	44.773
TMMS0091	31.364	0.000	1.364	2.727	4.545	5.909	0.455	34.318
TMMS0106	0.909	0.000	8.636	24.318	15.909	43.864	27.273	0.000
TMMS0119	0.000	0.000	1.364	7.727	20.000	42.500	0.000	0.000
TMMS0126	0.000	0.000	2.273	12.045	10.682	23.636	2.727	3.636
TMMS0133	0.909	0.000	22.955	27.955	8.182	22.500	5.000	0.000
TMMS0134	5.000	0.000	0.000	0.000	1.364	10.227	9.773	32.273
TMMS0137	0.000	0.000	18.182	28.636	5.000	6.818	0.455	0.000
TMMS0159	23.182	0.455	2.273	5.909	11.818	24.773	6.818	44.091
TMMS0171	13.636	0.000	0.000	0.000	6.818	0.000	5.909	87.500
TMMS0178	1.818	0.909	6.818	6.818	7.727	39.773	8.182	7.727
TMMS0183	0.000	0.000	7.727	6.818	30.227	36.136	10.000	8.409
TMMS0187	0.000	0.000	0.000	4.091	5.909	20.682	5.000	30.909
TMMS0193	0.000	0.455	7.727	13.182	20.227	1.818	7.045	0.000
TMMS0209	0.000	0.000	0.455	8.182	35.682	32.045	5.000	0.000
TMMS0214	0.000	0.000	0.455	10.455	6.818	10.000	0.909	0.000
TMMS0220	0.000	0.000	0.000	1.818	2.273	20.227	0.000	31.591
TMMS0279	0.000	0.000	0.000	1.364	5.455	5.000	2.727	68.864
TMMS0283	5.227	0.000	0.000	0.000	0.000	0.455	0.455	25.455
TMMS0290	0.000	1.818	0.000	0.000	4.545	3.182	2.273	0.000
TMMS0296	0.000	0.455	1.818	5.455	2.727	7.727	1.364	56.364

	Prop. Areal cover filamentous algae	Prop. Areal cover aquatic macrophytes	Prop. Areal cover large woody debris	Prop. Areal cover brush	Prop. Areal cover live trees	Prop. Areal cover leaves bank	Prop. Areal cover undercut banks	Prop. Areal cover boulders
	XFC_ALG	XFC_AQM	XFC_LWD	XFC_BRS	XFC_ROT	XFC_LEB	XFC_UCB	XFC_RCK
TMMS0381	0.000	6.136	5.909	6.364	47.727	23.636	1.364	0.000
TMMS0391	0.000	0.000	0.000	0.000	0.909	1.364	0.909	13.636
TMMS0437	29.545	15.455	0.909	0.455	12.273	0.000	0.000	0.000
TMMS1865	0.909	0.000	19.091	22.727	8.182	27.955	0.000	0.000
TMMS3195	6.364	21.818	0.000	0.000	0.000	0.000	0.000	0.000
TMMS3962	0.000	0.000	0.000	0.000	0.455	47.500	0.000	1.818
VGMS00002	0.000	0.000	0.000	3.636	17.727	81.818	0.000	0.000
VGMS00004	5.682	0.000	4.545	10.909	21.364	18.409	5.000	2.727
VGMS00016	0.000	0.000	1.364	10.000	18.409	30.227	3.182	0.909
VGMS00018	0.000	0.000	1.364	5.909	7.045	15.455	0.455	48.182
VGMS00022	0.000	0.000	0.455	2.273	17.727	13.409	2.727	20.909
VGMS00034	0.000	0.000	23.864	23.182	20.909	70.682	0.000	9.773
VGMS00037	0.000	0.000	10.682	23.636	13.864	17.727	2.273	0.000
VGMS00044	0.000	0.000	7.500	8.182	9.091	28.182	7.273	0.000
VGMS00048	0.000	2.727	4.545	8.182	18.636	0.909	0.455	0.000
VGMS00080	0.000	0.000	3.182	7.273	8.636	5.000	14.318	37.955
VGMS00109	0.000	0.000	2.273	6.818	14.091	5.000	17.500	0.000
VGMS00112	0.000	0.000	1.364	22.500	8.636	30.227	3.636	2.273
VGMS00121	0.000	0.000	16.136	23.636	14.545	42.727	15.682	2.273
VGMS00124	0.000	0.000	5.000	9.545	15.227	21.818	10.000	20.682
VGMS00126	0.000	8.864	0.909	9.091	20.682	40.682	5.000	8.409
VGMS00128	0.000	0.000	0.000	11.136	23.409	35.000	0.455	0.000
VGMS00162	0.000	0.000	12.955	25.000	24.318	31.364	5.909	0.000
VGMS00177	0.000	0.909	34.318	41.818	15.682	8.636	0.000	0.455
VGMS00191	0.000	0.000	2.727	11.818	7.727	12.955	6.364	1.364
VGMS00206	0.000	2.273	0.000	5.455	3.636	73.409	1.364	0.000
VGMS00210	0.000	0.000	8.864	1.818	7.273	2.273	0.455	2.273
VGMS00247	0.000	0.000	0.000	0.455	26.591	0.000	0.000	0.000
VGMS00252	0.000	0.000	1.364	8.182	19.545	11.364	9.318	0.455
VGMS00255	0.000	0.455	0.000	1.818	7.727	7.045	0.455	22.500
VGMS00277	0.000	0.000	9.773	4.091	2.727	10.455	3.636	5.455
VGMS00306	0.000	0.000	3.182	4.545	0.909	5.455	8.636	1.818
VGMS00320	0.000	0.000	0.455	2.273	4.545	16.591	5.909	0.000
VGMS00380	0.000	0.000	0.000	12.273	7.273	14.091	5.000	0.000

	Prop. Areal cover filamentous algae	Prop. Areal cover aquatic macrophytes	Prop. Areal cover large woody debris	Prop. Areal cover brush	Prop. Areal cover live trees	Prop. Areal cover leaves bank	Prop. Areal cover undercut banks	Prop. Areal cover boulders
	XFC_ALG	XFC_AQM	XFC_LWD	XFC_BRS	XFC_ROT	XFC_LEB	XFC_UCB	XFC_RCK
VGMS00387	0.000	0.000	33.182	40.682	30.909	15.909	14.318	12.500
VGMS00418	0.000	0.000	2.273	5.000	6.818	12.955	16.136	12.500
VGMS00433	0.000	0.000	12.045	20.909	15.227	19.545	13.636	5.227
VGMS00444	0.000	0.000	0.455	4.545	6.364	6.364	3.182	23.864
VGMS00447	0.000	0.000	8.864	1.818	4.545	2.273	19.318	2.727
VGMS00450	0.000	1.364	0.000	0.909	2.727	4.545	0.455	71.591
VGMS00511	0.000	0.000	1.818	14.091	20.682	22.500	1.818	13.182
VGMS00515	0.000	0.000	0.000	2.273	6.364	10.000	9.318	0.455
VGMS00558	0.000	0.000	0.000	5.455	4.091	39.091	3.182	23.182
VGMS00575	0.000	2.273	0.909	3.182	8.636	8.182	0.909	46.591
SSMS0001	0.000	0.000	21.591	52.045	70.909	23.636	12.955	12.955
SSMS0002	1.364	0.000	4.545	4.545	9.091	37.955	2.273	17.727
SSMS0008	0.000	4.091	0.455	3.182	18.864	42.045	9.318	9.091
SSMS0010	21.818	65.682	0.000	15.227	4.545	1.818	1.364	0.000
SSMS0014	0.000	0.000	0.909	7.273	7.273	18.864	15.000	1.818
SSMS0028	0.455	4.545	1.818	6.818	4.091	7.727	0.909	0.000
SSMS0029	0.000	3.182	3.636	7.273	14.545	4.545	21.364	5.909
SSMS0031	0.455	12.955	0.000	3.636	17.727	22.500	0.000	0.000
SSMS0033	13.864	4.545	0.000	0.000	4.545	0.000	0.000	0.000
SSMS0035	0.000	0.000	3.182	3.636	44.318	33.409	20.227	71.818
SSMS0037	0.000	0.909	0.000	2.727	2.727	6.818	1.818	0.000
SSMS0038	0.000	0.000	0.909	29.091	9.545	8.864	19.773	0.000
SSMS0044	0.000	0.000	0.455	12.273	13.636	35.000	2.273	9.773
SSMS0051	0.000	0.455	25.455	37.955	62.727	40.909	6.818	0.000
SSMS0053	0.000	0.000	0.000	1.364	2.727	23.636	0.455	5.227
SSMS0057	0.000	2.727	5.000	6.364	9.545	16.136	0.909	0.455
SSMS0059	0.000	0.000	9.091	21.818	11.364	29.091	10.000	0.000
SSMS0073	0.000	0.000	0.000	15.227	5.455	1.818	3.636	0.000
SSMS0078	0.455	1.818	1.364	2.273	6.364	1.818	0.455	10.455
SSMS0094	0.000	0.000	1.818	12.273	7.727	17.045	0.455	36.591
SSMS0105	0.000	0.000	1.364	16.591	7.273	14.091	1.364	20.227
SSMS0126	0.000	0.909	3.182	11.818	13.636	5.000	3.182	0.000
SSMS0129	3.182	0.000	1.818	11.818	14.091	11.364	9.545	0.000
SSMS0133	29.091	0.000	0.000	0.909	0.909	0.455	2.273	30.227

	Prop. Areal cover filamentous algae	Prop. Areal cover aquatic macrophytes	Prop. Areal cover large woody debris	Prop. Areal cover brush	Prop. Areal cover live trees	Prop. Areal cover leaves bank	Prop. Areal cover undercut banks	Prop. Areal cover boulders
	XFC_ALG	XFC_AQM	XFC_LWD	XFC_BRS	XFC_ROT	XFC_LEB	XFC_UCB	XFC_RCK
SSMS0144	0.455	1.818	0.909	13.864	19.545	22.500	22.045	0.000
SSMS0149	2.273	0.000	7.955	12.955	7.500	1.818	0.455	13.636
SSMS0150	0.000	0.455	4.091	14.318	20.682	5.455	8.636	11.591
SSMS0157	0.000	0.000	0.000	15.227	4.091	55.000	1.364	0.000
SSMS0175	1.364	0.000	0.909	4.545	12.273	8.636	1.364	40.682
SSMS0191	0.000	0.000	6.591	12.955	3.636	11.136	0.909	4.091
SSMS0193	0.000	0.000	4.545	11.364	3.636	15.227	0.909	0.000
SSMS0199	0.000	0.000	2.273	30.455	26.136	63.636	17.727	0.909
SSMS0213	0.000	0.000	0.455	6.818	6.364	1.364	15.909	3.182
SSMS0351	0.455	0.000	2.727	10.455	0.909	14.091	0.000	5.909
SSMS0408	0.000	4.091	1.364	14.091	26.818	15.909	0.455	0.455
SSMS0411	0.455	0.455	0.000	6.364	12.273	15.909	2.273	24.545
SSMS0447	0.000	0.000	4.091	8.636	5.000	17.727	3.182	27.273
SSMS1000	0.000	2.273	2.273	12.273	34.318	6.818	7.273	0.455
SSMS4173	32.500	3.182	0.455	1.364	0.455	0.000	0.000	38.636
SSMS4330	18.409	0.000	0.000	0.455	0.455	22.500	4.545	35.227
RENP0008	0.000	12.500	0.000	3.636	30.909	39.773	20.682	0.455
RENP0012	0.909	0.000	0.000	4.091	10.000	25.455	0.455	18.182
RENP0016	0.000	0.000	2.273	4.545	4.545	4.545	5.909	9.091
RENP0028	1.364	0.000	0.909	7.727	13.636	19.545	1.364	29.773
RENP0047	0.000	0.000	3.636	9.773	37.727	53.636	5.682	0.455
RENP0052	0.000	0.000	1.818	12.500	5.000	28.409	0.000	0.000
RENP0054	0.000	0.000	0.000	25.000	57.500	57.500	1.818	0.000
RENP0055	0.000	0.000	7.273	10.000	19.091	14.091	13.636	2.273
RENP0075	0.000	0.455	0.455	4.091	4.545	10.455	5.000	0.909
RENP0092	0.000	0.455	0.455	3.182	14.091	12.273	0.909	2.727
RENP0095	0.000	0.000	5.909	20.682	21.364	47.727	0.909	0.000
RENP0096	0.000	0.000	3.182	16.591	10.682	18.409	15.000	1.364
RENP0097	0.000	0.000	0.909	5.909	6.364	15.909	6.818	2.273
RENP100	6.818	11.591	0.909	4.091	25.455	14.318	0.455	3.182
RENP0108	0.000	5.909	0.000	9.545	25.000	23.182	10.455	16.591
RENP0110	0.000	0.000	0.455	3.182	24.773	11.364	5.455	20.227
RENP0112	0.000	0.000	2.273	6.818	14.091	27.273	6.818	0.000
RENP0128	0.000	37.727	0.455	3.182	43.636	0.000	0.000	0.000

	Prop. Areal cover filamentous algae	Prop. Areal cover aquatic macrophytes	Prop. Areal cover large woody debris	Prop. Areal cover brush	Prop. Areal cover live trees	Prop. Areal cover leaves bank	Prop. Areal cover undercut banks	Prop. Areal cover boulders
	XFC_ALG	XFC_AQM	XFC_LWD	XFC_BRS	XFC_ROT	XFC_LEB	XFC_UCB	XFC_RCK
REN0132	0.000	3.636	0.000	3.636	25.000	24.318	14.091	3.636
REN0139	0.000	0.000	1.364	11.591	26.818	17.727	5.000	0.000
REN0144	0.455	0.000	2.727	6.364	6.818	60.455	3.182	15.455
REN0187	0.000	0.000	0.000	8.182	13.409	21.364	5.000	0.000
REN0192	0.000	0.000	0.000	5.000	4.545	3.636	26.818	0.000
REN0203	0.000	0.000	0.909	5.000	17.727	13.636	7.273	4.091
REN0228	0.000	0.000	0.909	5.455	44.318	14.773	8.636	13.864
REN0240	0.000	0.000	1.364	18.864	20.000	54.091	0.000	0.000
REN0251	0.000	0.000	11.364	16.591	12.273	8.182	0.455	26.591
REN0287	0.000	5.455	1.364	10.455	27.955	42.727	8.636	0.000
REN0368	0.455	0.455	0.909	15.227	31.364	39.545	15.909	0.000
REN0375	0.000	0.000	0.000	2.727	5.000	20.227	1.364	0.000
REN0443	0.000	0.455	0.455	4.545	5.000	5.000	7.727	0.000
REN0511	0.000	0.000	12.273	13.636	17.273	15.909	4.091	4.091
REN1524	0.000	0.909	0.455	17.045	25.000	42.727	19.545	12.500
REN2991	0.000	3.182	0.455	2.727	27.955	22.500	21.364	10.455
REN5612	0.000	0.455	2.727	2.727	20.682	2.273	8.636	5.227
REN7308	0.000	0.000	2.273	17.727	12.273	49.545	1.364	18.864
REN9611	0.000	0.000	3.182	18.864	22.500	29.091	3.182	5.909
REN9757	0.000	0.000	0.000	0.000	5.000	0.000	0.000	0.000
REN12892	10.682	31.364	0.000	1.364	11.818	1.818	1.364	0.455
REN15048	0.000	0.000	0.000	0.000	51.591	0.000	0.455	0.000
RCA02	6.136	4.091	0.455	0.000	23.409	0.000	5.909	7.273
RCA08	0.000	0.455	17.727	0.000	7.500	39.318	11.818	0.455
RCA22	0.000	16.591	2.273	0.000	4.545	1.364	5.455	42.273
RCA23	0.000	0.455	19.545	0.000	28.182	36.591	1.364	10.000
RCA30	0.000	5.909	7.273	0.000	11.136	0.455	11.136	22.273
RCA31	0.000	2.273	10.682	0.000	19.545	11.136	14.091	14.545
RCA44	0.000	6.364	23.636	0.000	16.591	14.773	4.091	17.727
RCA48	0.909	2.273	20.682	0.000	36.818	4.545	9.318	28.409
RCA49	0.000	0.909	17.045	0.000	29.318	26.591	15.909	3.182
RCA50	0.000	0.455	7.045	0.000	34.091	2.273	45.000	23.636
RCA52	0.000	1.818	15.909	0.000	29.318	6.364	2.727	42.273
RCA53	0.000	0.000	6.818	0.000	20.682	1.818	10.227	39.773

	Prop. Areal cover filamentous algae	Prop. Areal cover aquatic macrophytes	Prop. Areal cover large woody debris	Prop. Areal cover brush	Prop. Areal cover live trees	Prop. Areal cover leaves bank	Prop. Areal cover undercut banks	Prop. Areal cover boulders
	XFC_ALG	XFC_AQM	XFC_LWD	XFC_BRS	XFC_ROT	XFC_LEB	XFC_UCB	XFC_RCK
RCA57	7.045	11.364	5.682	0.000	31.136	2.273	25.455	7.727
RCA58	0.455	5.909	0.000	0.000	17.727	0.000	8.182	2.273
RCA59	5.000	15.909	0.000	0.000	28.182	0.000	0.000	2.273
RCA60	7.727	25.455	0.000	0.000	22.500	0.000	0.000	0.000
RCA62	3.182	17.727	31.364	0.000	30.682	47.727	14.773	0.000
RCA64	0.909	5.909	11.364	0.000	14.773	4.091	31.136	14.773
RCA65	0.455	7.273	4.545	0.000	23.636	7.273	0.455	4.545
RCA66	0.000	4.091	11.818	0.000	20.682	15.909	9.318	31.364
RCA67	0.000	5.455	3.182	0.000	8.182	12.955	5.455	28.409
RCA68	0.000	0.455	18.864	0.000	19.545	12.955	9.545	11.364
RCA69	0.000	0.909	1.364	0.000	20.682	0.000	5.000	47.727
RCA70	0.000	3.182	24.318	0.000	36.818	1.818	7.727	13.182
RCA71	0.000	2.727	17.727	0.000	28.409	39.318	8.409	23.409
RCA72	0.000	2.273	1.364	0.000	14.091	7.273	0.000	23.636
RCA73	0.000	0.000	1.364	0.000	25.455	0.000	8.864	47.727
RCA74	0.000	5.000	3.182	0.000	28.409	0.000	7.273	25.227
RCA90	4.545	13.409	11.818	0.000	34.091	13.636	14.091	9.545

Table 2.8. Water quality variables.

	Dissolved oxygen (mg/L)	pH	Turbidity (UNT)	Conductivity (μ S/cm)	TDS (mg/L)	Water temperature (°C)	Total Nitrogen (mg/L)	Total Phosphorus (mg/L)
TM00003	8.3	7.50	15.31	34.0	22	16.3	0.063	0.008
TM00007	7.1	7.30	9.45	43.0	28	17.1	0.091	0.012
TM00009	6.6	7.40	1.56	108.0	71	15.2	0.063	0.017
TM00027	8.9	8.70	2.31	33.0	20	15.5	0.077	0.001
TM00028	10.6	8.50	2.04	128.0	83	14.9	0.084	0.032
TM00033	7.6	7.80	9.92	53.0	34	15.5	NA	0.014
TM00040	5.7	7.60	3.68	60.0	39	15.6	0.077	0.020
TM00043	10.4	8.50	9.77	34.0	22	16.0	0.098	0.004
TM00058	5.1	7.60	3.04	36.0	27	18.4	0.070	0.024
TM00072	10.1	8.10	1.86	199.0	130	15.3	0.063	0.018
TM00082	6.9	7.50	3.88	135.0	88	16.2	0.070	0.020
TM00088	10.2	7.50	4.76	71.0	52	19.3	0.077	0.033
TM00090	9.9	7.40	4.48	30.0	19	16.8	0.070	0.021
TM00091	10	8.50	4.23	79.0	51	19.4	0.049	0.033
TM00106	2.3	7.20	3.05	39.0	30	16.2	0.056	0.023
TM00119	7.3	7.20	15.36	67.0	44	19.3	0.070	0.031
TM00126	0.8	7.50	6.72	63.0	41	16.6	0.133	0.059
TM00133	7.6	8.00	1.33	15.0	11	17.0	0.084	0.037
TM00134	9	7.60	2.41	44.0	29	18.0	0.098	0.001
TM00137	6.3	7.70	9.58	153.0	99	14.7	0.063	0.001
TM00159	10.1	8.30	1.49	42.0	27	19.0	0.056	0.008
TM00171	10.7	7.70	1.74	41.0	29	21.2	0.077	0.008
TM00178	8.4	7.20	2.45	136.0	101	18.7	0.077	0.028
TM00183	5.8	6.40	3.41	22.0	17	16.2	0.091	0.001
TM00187	9.3	6.80	4.22	22.0	17	17.4	0.056	0.020
TM00193	9.6	7.80	5.90	20.0	13	16.9	0.077	0.029
TM00209	6.9	7.30	4.45	26.0	17	16.3	0.063	0.025
TM00214	5	8.00	54.40	72.0	47	16.3	0.070	0.042
TM00220	9.9	8.30	1.60	219.0	142	16.5	0.140	0.022
TM00279	10.9	7.70	3.22	75.0	57	17.6	0.077	0.020
TM00283	11.7	8.10	3.66	30.0	20	18.7	0.112	0.001
TM00290	6.8	7.50	5.91	28.0	18	15.0	0.084	0.022
TM00296	10.3	7.80	4.07	50.0	37	18.4	0.070	0.020
TM00381	7.4	6.90	1.57	7.0	6	14.2	0.042	0.017
TM00391	9	8.30	10.02	39.0	25	19.6	0.084	0.028

	Dissolved oxygen (mg/L)	pH	Turbidity (UNT)	Conductivity (μ S/cm)	TDS (mg/L)	Water temperature (°C)	Total Nitrogen (mg/L)	Total Phosphorus (mg/L)
TM00437	4.3	7.50	8.54	72.0	46	18.5	0.063	0.020
TM01865	1.8	7.30	7.49	90.0	69	16.9	0.056	0.026
TM03195	11.5	7.70	6.17	21.0	14	22.2	0.070	0.011
TM03962	5.7	7.50	3.04	47.0	0	19.0	0.091	0.015
VG00002	6.1	7.10	3.51	20.0	29	20.3	0.098	0.004
VG00004	NA	7.12	3.98	74.0	18	21.5	0.133	0.015
VG00016	8	6.98	3.43	45.0	50	19.3	0.119	0.009
VG00018	8.3	7.60	5.89	25.0	28	19.4	0.077	0.008
VG00022	16.3	6.49	10.00	44.0	37	18.7	0.126	0.077
VG00034	8.4	7.30	2.08	42.0	30	19.8	0.126	0.010
VG00037	14.7	6.96	3.36	25.0	2	22.6	0.112	0.022
VG00044	7.4	8.10	3.15	35.0	5	21.9	0.133	0.015
VG00048	7.9	NA	21.90	15.0	11	21.4	0.126	0.031
VG00080	4.2	9.30	6.15	16.0	17	22.1	0.105	0.016
VG00109	7.9	7.10	6.85	32.0	4	21.7	0.084	0.009
VG00112	3.8	9.10	4.88	23.0	25	20.4	0.063	0.014
VG00121	8.4	6.15	3.94	30.0	NA	20.5	0.224	0.003
VG00124	6.6	6.41	NA	32.0	NA	20.2	0.112	0.016
VG00126	6.7	9.60	5.42	18.0	20	20.2	0.112	0.015
VG00128	15.6	7.67	3.80	22.0	16	19.9	0.182	0.018
VG00162	15.6	7.44	6.88	23.0	17	19.4	0.091	0.001
VG00177	6.7	7.26	7.92	49.0	35	21.2	0.126	0.011
VG00191	8.1	7.02	5.55	78.0	19	21.3	0.182	0.038
VG00206	6.4	7.60	NA	63.0	NA	21.6	0.070	0.016
VG00210	8.2	8.05	1.29	56.0	NA	19.6	0.063	0.011
VG00247	7.6	6.98	2.35	35.0	5	21.8	0.119	0.015
VG00252	9.2	7.09	3.50	52.0	NA	19.9	0.084	0.007
VG00255	7.9	7.26	10.82	37.0	26	20.7	0.091	0.022
VG00277	10.4	7.50	3.46	44.0	49	19.7	0.126	0.005
VG00306	7.8	7.24	3.19	38.0	NA	19.1	0.126	0.002
VG00320	8.4	NA	4.71	30.0	NA	20.0	0.119	0.008
VG00380	8.6	7.26	3.17	50.0	10	20.5	0.133	0.010
VG00387	7.6	7.06	9.87	38.0	27	21.0	0.154	0.127
VG00418	9.1	7.40	1.63	65.0	15	19.5	0.119	0.008
VG00433	8.5	7.40	4.49	2.0	14	20.4	0.112	0.008
VG00444	8.4	7.31	2.86	58.0	13	19.8	0.112	0.009
VG00447	7.6	7.00	18.50	43.0	NA	20.8	0.126	0.058

	Dissolved oxygen (mg/L)	pH	Turbidity (UNT)	Conductivity (μ S/cm)	TDS (mg/L)	Water temperature (°C)	Total Nitrogen (mg/L)	Total Phosphorus (mg/L)
VG00450	8.6	6.82	3.47	40.0	NA	18.9	0.084	0.004
VG00511	6.4	9.80	9.17	41.0	44	21.7	0.070	0.021
VG00515	8.6	7.50	4.20	55.0	NA	20.7	0.105	NA
VG00558	9.3	7.80	3.58	31.0	24	16.3	0.119	0.031
VG00575	14	8.30	14.39	69.0	69	23.2	0.091	0.014
SSMS0001	7.3	7.80	2.10	8.4	0	21.5	0.084	0.005
SSMS0002	8.3	7.26	3.90	78.9	46.2	20.0	0.084	0.003
SSMS0008	7.2	7.41	6.83	67.4	36.9	19.0	0.098	0.004
SSMS0010	7.6	6.54	4.14	36.0	18.6	19.0	0.084	0.001
SSMS0014	7.8	6.20	1.47	13.5	4.6	20.9	0.098	0.001
SSMS0028	7.3	5.56	4.97	39.8	19.4	21.0	0.091	0.001
SSMS0029	10.1	7.80	11.90	69.9	39.5	22.0	0.077	0.004
SSMS0031	7.2	5.54	9.86	18.7	5.1	21.0	0.119	0.007
SSMS0033	8.2	7.67	15.41	184.9	109.9	25.0	0.091	0.004
SSMS0035	7.3	6.80	6.85	39.6	18.7	21.6	0.112	0.001
SSMS0037	5.5	6.68	6.19	96.5	55.6	21.4	0.098	0.009
SSMS0038	7.7	6.87	12.41	116.2	66.5	19.0	0.105	0.004
SSMS0044	7.3	6.36	4.98	41.6	19.3	19.0	0.091	0.003
SSMS0051	7	7.26	7.73	39.7	18.3	19.0	0.091	0.002
SSMS0053	8.9	6.82	2.96	77.9	13.4	NA	0.077	0.002
SSMS0057	6.7	7.11	3.78	233.0	145	20.0	0.105	0.003
SSMS0059	7.2	6.81	8.70	60.4	32.1	18.0	0.112	0.005
SSMS0073	6.3	6.78	4.46	95.1	56.4	21.5	0.210	0.022
SSMS0078	8.5	6.63	5.33	50.9	26.7	18.0	0.084	0.002
SSMS0094	8.3	6.60	2.45	24.4	9.4	24.5	0.077	0.001
SSMS0105	10.7	6.72	9.30	30.2	13.2	20.0	0.070	0.002
SSMS0126	7.6	6.86	7.73	33.5	15.9	17.0	0.112	0.003
SSMS0129	8	7.59	8.48	172.3	104.2	19.0	0.098	0.004
SSMS0133	10.2	7.66	3.76	94.0	53.8	19.0	0.098	0.003
SSMS0144	8.1	7.31	5.65	40.3	19.9	18.0	0.112	0.002
SSMS0149	8.8	7.60	20.90	58.0	29.5	20.0	0.077	0.006
SSMS0150	6.8	6.85	8.10	9.6	55.2	20.0	0.091	0.003
SSMS0157	7.3	6.57	4.70	76.9	35.3	20.0	0.091	0.345
SSMS0175	7.8	6.12	2.13	44.2	22.3	20.0	0.070	0.002
SSMS0191	7.5	6.77	6.08	45.6	22.6	18.5	0.126	0.003
SSMS0193	7.3	6.89	12.57	189.5	110.8	21.5	0.154	0.006
SSMS0199	NA	6.70	3.71	43.6	22.3	21.4	0.112	0.001

	Dissolved oxygen (mg/L)	pH	Turbidity (UNT)	Conductivity (μ S/cm)	TDS (mg/L)	Water temperature (°C)	Total Nitrogen (mg/L)	Total Phosphorus (mg/L)
SSMS0213	8.3	6.65	7.26	55.3	28.8	21.9	0.105	0.001
SSMS0351	7.3	6.60	3.19	70.1	38.3	22.6	0.112	0.002
SSMS0408	6.8	7.02	14.19	29.5	43.3	20.0	0.091	0.004
SSMS0411	7.2	6.44	4.95	67.8	39.1	18.0	0.098	0.006
SSMS0447	11.1	7.03	3.98	45.8	24	20.0	0.098	0.003
SSMS1000	7	7.54	4.54	75.0	42.2	20.0	0.112	0.004
SSMS4173	7.6	7.30	12.93	131.6	60.3	20.0	0.154	0.004
SSMS4330	7.2	7.10	4.78	42.9	20.8	21.4	0.091	0.001
REN0008	6.6	6.0	4.2	6.3	0.0	19.0	0.084	0.014
REN0012	8.4	6.8	15.0	24.0	10.7	19.1	0.084	0.016
REN0016	8.1	6.3	1.4	9.1	0.0	19.0	0.126	0.007
REN0028	8.5	7.8	2.7	25.0	19.0	19.0	0.105	0.013
REN0047	7.4	6.5	20.4	16.0	10.9	22.7	0.091	0.176
REN0052	7.6	8.2	1.5	22.0	16.0	21.0	0.098	0.005
REN0054	7.2	6.0	2.4	8.5	6.2	19.1	0.084	0.019
REN0055	8.5	6.4	4.2	12.6	0.6	18.0	0.098	0.019
REN0075	8.0	6.5	3.8	18.0	6.5	19.5	0.112	0.016
REN0092	7.9	6.9	3.1	46.0	17.9	20.0	0.077	0.005
REN0095	8.6	8.0	1.6	17.0	13.0	16.4	0.091	0.004
REN0096	8.6	6.9	31.7	27.0	20.0	19.4	0.112	0.011
REN0097	7.5	6, 7	4.3	42.0	25.6	20.7	0.112	0.007
REN0100	9.0	7.9	4.9	21.0	15.0	19.4	0.112	0.009
REN0108	6.7	6.5	6.5	13.5	3.5	19.0	0.126	0.017
REN0110	8.1	6.3	2.7	14.1	10.1	26.2	0.098	0.011
REN0112	6.2	6.3	7.1	6.7	4.9	19.1	0.091	0.015
REN0128	6.7	7.6	4.6	29.0	16.2	20.2	0.084	0.013
REN0132	8.0	6.5	2.4	15.7	2.3	19.0	0.091	0.011
REN0139	7.7	6.5	2.5	13.8	10.1	19.2	0.098	0.030
REN0144	7.5	6.6	1.9	40.0	15.3	16.7	0.070	0.018
REN0187	7.6	8.3	3.2	29.0	21.0	19.0	0.084	0.007
REN0192	8.0	7.6	9.4	28.0	16.0	19.3	0.119	0.045
REN0203	9.4	5.8	1.3	28.0	4.7	17.0	0.084	0.009
REN0228	8.5	5.8	3.8	7.9	5.8	19.4	0.084	0.009
REN0240	8.1	5.9	3.4	16.0	24.8	19.7	0.112	0.022
REN0251	8.1	6.5	4.1	14.0	NA	18.9	0.098	0.020
REN0287	6.1	6.8	2.1	62.5	27.5	19.0	0.077	0.003
REN0368	8.4	7.3	1.8	14.8	10.5	21.2	0.119	0.002

	Dissolved oxygen (mg/L)	pH	Turbidity (UNT)	Conductivity (μ S/cm)	TDS (mg/L)	Water temperature (°C)	Total Nitrogen (mg/L)	Total Phosphorus (mg/L)
REN0375	8.8	7.3	1.5	20.0	14.0	21.2	0.112	0.006
REN0443	7.2	7.9	3.5	23.0	16.0	20.1	0.091	0.017
REN0511	7.4	6.6	2.3	17.0	8.1	17.5	0.015	0.005
REN1524	9.4	6.6	2.3	23.0	0.0	17.0	0.071	0.007
REN2991	9.0	7.7	NA	11.8	10.3	19.3	0.119	0.019
REN5612	9.5	7.7	4.0	11.8	8.6	19.3	0.091	0.000
REN7308	6.4	5.8	1.6	18.0	11.8	19.1	0.098	0.008
REN9611	8.0	6.8	3.0	11.0	NA	19.4	0.070	0.009
REN9757	8.2	6.3	2.8	81.1	5.3	17.8	0.091	0.021
REN12892	6.4	7.3	2.2	37.0	27.0	18.7	0.105	0.004
REN15048	7.0	5.7	9.3	13.4	9.9	18.6	0.091	0.009
RCA02	6.7	6.79	0.27	1.4	0	19.3	0.063	0.002
RCA08	3.3	7.11	10.74	7.3	3.72	19.9	0.056	0.009
RCA22	9.2	6.58	0.71	1.7	0	17.7	0.056	0.005
RCA23	7	5.68	2.78	4.5	0	16.7	0.049	0.001
RCA30	7.6	6.84	0.43	2.6	0	20.3	0.049	0.006
RCA31	9	6.52	3.01	1.5	0.74	21.0	0.063	0.005
RCA44	8.1	7.92	5.56	4.3	2.14	21.3	0.063	0.003
RCA48	7.6	5.38	41.40	3.1	1.95	20.3	0.028	0.004
RCA49	7.6	5.16	2.46	0.7	0.28	20.1	0.056	0.002
RCA50	8.7	5.68	2.85	0.6	0.25	19.1	0.042	0.001
RCA52	8.6	5.22	1.40	2.5	1.24	18.2	0.035	0.001
RCA53	8.2	7.33	3.44	0.6	0.27	17.0	0.028	0.001
RCA57	7.6	8.01	0.26	2.6	0	18.4	0.042	0.001
RCA58	7.6	7.12	0.27	3.5	0	19.2	0.042	0.000
RCA59	7.7	7.43	0.13	1.9	0	19.2	0.077	0.001
RCA60	9.2	6.90	0.10	1.2	0	18.2	0.035	0.001
RCA62	1.8	7.43	0.96	6.3	0	18.7	0.077	0.010
RCA64	8.6	6.47	4.16	12.2	0	19.4	0.070	0.005
RCA65	7.6	8.40	2.72	2.7	1.21	21.3	0.028	0.000
RCA66	7.1	7.39	1.69	4.4	2.28	19.8	0.035	0.004
RCA67	8.2	7.60	1.13	4.4	2.31	20.8	0.042	0.001
RCA68	7.6	5.60	2.42	2.4	1.51	20.1	0.035	0.000
RCA69	7.4	6.60	5.52	0.7	0.35	19.9	0.021	0.001
RCA70	7.8	5.34	2.37	3.3	1.43	19.8	0.070	0.001
RCA71	7.5	6.06	1.09	2.5	1.24	18.8	0.035	0.003
RCA72	7.9	8.03	21.00	1.5	0.72	19.6	0.112	0.004

	Dissolved oxygen (mg/L)	pH	Turbidity (UNT)	Conductivity (μ S/cm)	TDS (mg/L)	Water temperature (°C)	Total Nitrogen (mg/L)	Total Phosphorus (mg/L)
RCA73	8	7.80	9.82	1.0	0.5	21.3	0.021	0.003
RCA74	8.3	4.82	3.85	2.1	0.88	19.6	0.049	0.002
RCA90	9.1	7.94	4.08	1.8	0.94	21.2	0.028	0.004

Table 2.9. Local (LDI), catchment (DI) and integrated disturbances (IDI) indexes for each sampling site.

	IDI	LDI	CDI
TMMS0003	0.376	1.304	81.444
TMMS0007	0.309	1.212	57.578
TMMS0009	0.288	1.341	31.209
TMMS0027	0.285	0.803	70.705
TMMS0028	0.336	1.652	18.999
TMMS0033	0.383	1.728	49.450
TMMS0040	0.362	1.409	68.112
TMMS0043	0.448	1.971	63.846
TMMS0058	0.518	2.379	61.759
TMMS0072	0.174	0.121	51.668
TMMS0082	0.298	0.735	77.718
TMMS0088	0.154	0.690	20.567
TMMS0090	0.205	0.545	52.090
TMMS0091	0.238	0.803	52.567
TMMS0106	0.166	0.174	48.711
TMMS0119	0.331	1.084	75.238
TMMS0126	0.181	0.068	54.278
TMMS0133	0.312	0.879	77.425
TMMS0134	0.013	0.000	3.888
TMMS0137	0.375	1.758	39.087
TMMS0159	0.389	1.735	52.498
TMMS0171	0.133	0.000	39.927
TMMS0178	0.268	0.561	73.093
TMMS0183	0.274	0.000	82.174
TMMS0187	0.239	0.622	61.124
TMMS0193	0.411	1.462	86.844
TMMS0209	0.302	0.152	90.042
TMMS0214	0.487	1.879	92.779
TMMS0220	0.139	0.470	30.643
TMMS0279	0.395	1.448	80.639
TMMS0283	0.143	0.000	42.844
TMMS0290	0.561	2.455	81.583
TMMS0296	0.298	1.409	28.828
TMMS0381	0.195	0.409	53.046
TMMS0391	0.225	0.386	63.371
TMMS0437	0.379	1.485	70.709
TMMS1865	0.559	2.712	40.709
TMMS3195	0.498	1.970	91.496
TMMS3962	0.388	1.795	43.998
VGMS0002	0.705	2.273	161.538
VGMS0004	0.532	0.773	152.761
VGMS0016	0.728	2.357	166.629
VGMS0018	0.621	0.667	181.818
VGMS0022	0.605	0.303	180.645
VGMS0034	0.787	2.547	180.000
VGMS0037	0.592	0.834	170.270
VGMS0044	0.549	1.432	140.580
VGMS0048	0.722	2.258	168.852
VGMS0080	0.682	1.894	170.196
VGMS0109	0.593	0.826	170.813
VGMS0112	0.618	1.281	168.880
VGMS0121	0.568	0.856	162.353
VGMS0124	0.589	0.856	169.141
VGMS0126	0.507	0.227	151.515
VGMS0128	0.595	1.637	148.980
VGMS0162	0.648	1.334	177.184
VGMS0177	0.722	2.106	176.000
VGMS0191	0.626	1.046	176.963
VGMS0206	0.493	1.046	133.962

	IDI	LDI	CDI
VGMS0210	0.510	1.538	122.177
VGMS0247	0.712	1.834	182.927
VGMS0252	0.571	0.743	165.405
VGMS0255	0.537	0.492	158.333
VGMS0277	0.643	1.644	165.751
VGMS0306	0.501	0.977	138.340
VGMS0320	0.563	1.038	157.143
VGMS0380	0.520	0.477	153.361
VGMS0387	0.622	0.637	182.511
VGMS0418	0.593	0.796	171.429
VGMS0433	0.600	0.834	172.788
VGMS0444	0.617	1.190	170.875
VGMS0447	0.584	0.803	168.362
VGMS0450	0.561	1.243	151.008
VGMS0511	0.529	0.136	158.519
VGMS0515	0.502	0.864	141.288
VGMS0558	0.649	0.205	194.215
VGMS0575	0.633	1.750	158.333
SSMS0001	0.658	1.001	188.155
SSMS0002	0.511	0.667	148.103
SSMS0008	0.699	2.197	163.127
SSMS0010	0.605	1.250	165.120
SSMS0014	0.585	1.076	163.324
SSMS0028	0.615	0.834	177.653
SSMS0029	0.717	1.924	181.453
SSMS0031	0.573	1.917	127.763
SSMS0033	0.437	1.500	95.140
SSMS0035	0.451	0.955	122.604
SSMS0037	0.565	0.963	159.269
SSMS0038	0.521	1.129	140.766
SSMS0044	0.600	0.834	172.866
SSMS0051	0.584	0.856	167.434
SSMS0053	0.624	0.917	178.961
SSMS0057	0.441	1.399	102.068
SSMS0059	0.559	1.599	137.658
SSMS0073	0.746	2.076	186.029
SSMS0078	0.512	1.212	135.370
SSMS0094	0.637	1.334	173.543
SSMS0105	0.701	2.038	170.956
SSMS0126	0.671	2.296	146.854
SSMS0129	0.538	0.606	157.243
SSMS0133	0.464	0.000	139.190
SSMS0144	0.669	1.667	173.855
SSMS0149	0.502	1.046	137.045
SSMS0150	0.708	2.645	141.011
SSMS0157	0.645	0.993	184.008
SSMS0175	0.480	0.667	138.333
SSMS0191	0.444	0.818	123.959
SSMS0193	0.590	1.356	157.243
SSMS0199	0.541	0.788	155.353
SSMS0213	0.439	0.955	118.693
SSMS0351	0.468	0.000	140.345
SSMS0408	0.550	1.001	153.832
SSMS0411	0.471	0.667	135.510
SSMS0447	0.483	0.000	144.868
SSMS1000	0.607	1.091	170.033
SSMS4173	1.475	4.758	338.097
SSMS4330	1.141	5.046	159.631
RENPO008	0.561	0.637	163.968
RENPO012	0.342	1.697	13.441

	IDI	LDI	CDI
REN0016	0.042	0.091	11.465
REN0028	0.428	0.614	123.003
REN0047	0.299	0.099	89.473
REN0052	0.435	0.637	124.902
REN0054	0.220	0.667	52.515
REN0055	0.612	0.477	181.242
REN0075	0.139	0.667	11.699
REN0092	0.441	1.727	82.357
REN0095	0.601	0.894	172.138
REN0096	0.561	0.235	167.858
REN0097	0.545	1.766	124.410
REN0100	0.159	0.273	44.735
REN0108	0.525	0.728	151.325
REN0110	0.445	0.402	131.231
REN0112	0.524	0.849	148.873
REN0128	0.593	2.697	73.612
REN0132	0.399	0.682	112.515
REN0139	0.608	1.091	170.141
REN0144	0.393	1.160	95.187
REN0187	0.414	0.000	124.346
REN0192	0.552	0.667	160.742
REN0203	0.216	0.705	49.033
REN0228	0.645	2.129	145.473
REN0240	0.601	1.834	142.746
REN0251	0.449	0.424	132.231
REN0287	0.497	1.235	129.360
REN0368	0.792	2.576	180.446
REN0375	0.279	1.250	37.102
REN0443	0.410	0.000	123.058
REN0511	0.561	0.962	158.198
REN1524	0.747	2.091	185.834
REN2991	0.524	0.500	154.358
REN5612	0.581	1.273	156.831
REN7308	0.040	0.114	10.020
REN9611	0.474	0.197	141.762
REN9757	1.259	5.334	200.435
REN12892	0.556	2.515	71.110
REN15048	1.292	5.955	150.422
RCA02	0.000	0.000	0.000
RCA08	0.100	0.000	29.922
RCA22	0.000	0.000	0.000
RCA23	0.000	0.000	0.000
RCA30	0.437	0.667	124.972
RCA31	0.228	0.334	65.438
RCA44	0.257	0.167	76.370
RCA48	0.151	0.125	44.735
RCA49	0.180	0.667	36.136
RCA50	0.038	0.000	11.465
RCA52	0.068	0.334	3.111
RCA53	0.138	0.667	10.438
RCA57	0.000	0.000	0.000
RCA58	0.000	0.000	0.000
RCA59	0.000	0.000	0.000
RCA60	0.000	0.000	0.000
RCA62	0.000	0.000	0.000
RCA64	0.067	0.334	0.000
RCA65	0.033	0.167	0.000
RCA66	0.326	0.445	93.945
RCA67	0.122	0.389	28.052
RCA68	0.008	0.000	2.312

	IDI	LDI	CDI
RCA69	0.187	0.056	55.901
RCA70	0.010	0.000	2.876
RCA71	0.040	0.000	11.912
RCA72	0.322	1.390	49.033
RCA73	0.039	0.000	11.699
RCA74	0.175	0.000	52.515
RCA90	0.328	0.945	80.540

Appendix 3: Abundance of Ephemeroptera, Plecoptera and Trichoptera in each sampling site.

	<i>Alisotrichia</i>	<i>Americabaetis</i>	<i>Anacroneuria</i>	<i>Anchitrichia</i>	<i>Apobaetis</i>	<i>Askola</i>	<i>Asthenopus</i>	<i>Atanotia</i>	<i>Atopsyche</i>	<i>Aturbina</i>	<i>Austrotinodes</i>	<i>Baetodes</i>	<i>Barypenthus</i>	<i>Caenis</i>	<i>Callibaetis</i>	<i>Camelobaetidium</i>	<i>Campsurus</i>	<i>Campylocia</i>	<i>Chimarra</i>	<i>Cloeodes</i>	<i>Cryptotympha</i>	<i>Cynelus</i>	<i>Farodes</i>	<i>Grumichella</i>	<i>Grypopteryx</i>	<i>Guajirolus</i>
TMMS0003	0	23	1	0	2	0	0	0	0	16	0	0	0	1	0	0	0	0	3	0	0	0	81	0	0	0
TMMS0007	0	1	0	0	0	0	0	0	0	23	0	0	0	5	18	0	0	0	1	0	1	3	2	0	0	0
TMMS0009	0	2	0	0	0	0	0	0	0	0	0	0	0	5	135	0	0	0	0	23	0	0	4	0	0	0
TMMS0027	0	9	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	1	0	0	0	0	0	0	0
TMMS0028	0	43	7	0	0	0	0	0	0	0	0	0	0	112	15	0	0	0	0	16	0	0	35	0	1	0
TMMS0033	0	14	0	0	1	0	0	0	0	24	1	0	0	15	5	0	0	0	0	45	0	0	4	0	0	0
TMMS0040	0	1	0	0	2	8	0	0	0	11	0	0	0	66	57	0	0	4	0	476	1	0	1	0	0	0
TMMS0043	1	1	1	0	2	0	0	0	2	7	0	4	0	19	20	0	0	1	0	22	0	0	2	0	0	0
TMMS0058	0	440	7	0	4	0	0	0	7	1	0	15	0	190	148	0	0	0	26	11	0	0	141	0	0	0
TMMS0072	0	8	11	0	0	0	1	0	0	0	0	0	0	53	8	0	0	0	2	6	0	0	16	0	0	0
TMMS0082	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	9	0	0	0	0	0	1	0	0	0
TMMS0088	1	0	0	0	0	0	0	0	0	0	0	0	0	55	168	0	0	0	0	43	0	0	2	0	0	0
TMMS0090	0	30	22	0	3	4	0	0	0	32	1	0	0	8	85	0	0	17	0	77	0	0	102	0	0	0
TMMS0091	0	18	38	0	0	0	0	0	1	18	0	6	0	13	173	2	0	0	646	19	0	0	14	0	0	0
TMMS0106	0	1	0	0	5	0	0	0	0	0	0	0	0	17	23	0	0	0	0	5	0	0	0	0	0	0
TMMS0119	0	1	5	0	0	0	3	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	5	0	0	0
TMMS0126	0	0	0	0	6	0	0	0	0	51	0	0	0	4	8	0	2	0	0	0	0	0	41	0	0	0
TMMS0133	0	5	0	0	1	0	0	0	0	1	0	0	0	3	2	0	0	0	0	0	0	0	2	0	0	0
TMMS0134	0	1	0	0	0	4	0	0	0	6	0	0	0	7	4	0	0	1	0	5	0	0	2	0	0	0
TMMS0137	0	0	0	0	4	0	22	0	0	2	0	0	0	149	24	0	0	0	0	3	0	5	2	0	0	0
TMMS0159	0	0	0	0	0	0	0	0	0	28	1	0	0	1	60	0	0	2	0	0	0	0	3	0	0	0
TMMS0171	1	32	14	0	0	0	1	0	0	1	0	49	0	1	41	28	0	2	39	56	0	0	2	0	0	0
TMMS0178	0	105	35	0	2	0	0	0	20	3	0	60	0	220	55	0	0	0	8	74	1	0	34	0	0	0
TMMS0183	0	2	0	0	3	0	0	0	3	3	0	0	0	4	3	0	0	0	0	0	0	2	9	0	0	0
TMMS0187	0	38	24	0	2	0	16	0	3	14	2	0	0	18	40	12	0	2	0	44	17	0	61	0	0	0
TMMS0193	0	7	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
TMMS0209	0	0	0	0	1	0	0	0	0	2	0	0	0	5	4	0	30	0	0	0	0	0	0	0	0	0
TMMS0214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	0
TMMS0220	0	51	22	0	0	0	0	0	1	0	0	3	0	66	16	0	0	0	12	129	0	0	124	0	0	0
TMMS0279	0	31	6	0	11	0	0	0	0	1	0	28	0	0	26	2	0	0	0	5	7	0	4	0	0	0
TMMS0283	0	213	2	0	0	0	0	0	11	0	0	5	0	1	1	38	0	0	1	9	6	0	11	0	0	0
TMMS0290	0	0	0	0	0	0	0	0	0	0	0	0	0	1	35	0	0	0	0	0	0	0	0	0	0	0

		<i>Alisotrichia</i>	<i>Americabaetis</i>	<i>Anacronetria</i>	<i>Anchitrichia</i>	<i>Apobaetis</i>	<i>Askola</i>	<i>Asthenopus</i>	<i>Atanetolia</i>	<i>Atopsyche</i>	<i>Aturbina</i>	<i>Austrotinodes</i>	<i>Baetodes</i>	<i>Barypenthus</i>	<i>Caenis</i>	<i>Callibaetis</i>	<i>Camelobaetidiu</i>	<i>Campsurus</i>	<i>Campylocia</i>	<i>Chimarra</i>	<i>Cloeodes</i>	<i>Cryptonympha</i>	<i>Cynelus</i>	<i>Farrodes</i>	<i>Grumichella</i>	<i>Grypopteryx</i>	<i>Guajrolus</i>
TMMS0296	0	56	13	0	3	0	0	0	0	0	8	0	20	0	39	50	2	15	2	10	9	0	0	8	0	0	0
TMMS0381	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
TMMS0391	0	4	0	3	0	0	0	0	0	0	2	0	0	0	1	29	0	0	0	0	10	0	0	0	0	0	0
TMMS0437	0	620	2	0	28	0	6	0	0	0	72	0	0	0	12	39	0	32	0	0	0	0	12	31	0	0	0
TMMS1865	0	3	0	0	2	0	6	0	0	0	34	0	0	0	23	67	0	0	0	0	12	0	5	10	0	0	0
TMMS3195	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	4	0	0	0	0	1	0	0	0	0	0	0
TMMS3962	0	0	0	0	1	0	1	0	0	0	3	0	0	0	38	60	0	0	0	0	16	0	0	3	0	0	0
VGMS00002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00004	0	347	65	0	10	0	0	0	0	0	61	8	10	0	9	0	47	0	0	0	8	0	0	606	0	0	0
VGMS00016	0	30	0	0	1	0	0	0	0	0	10	0	1	0	1	0	0	0	0	0	0	1	0	50	0	0	0
VGMS00018	0	1	2	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00022	6	37	1	0	0	0	0	0	0	0	1	0	387	0	0	0	0	0	0	0	1	0	0	25	0	0	0
VGMS00034	0	7	2	0	1	0	0	0	0	0	0	0	0	0	73	2	0	0	0	0	34	0	0	10	0	0	0
VGMS00037	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
VGMS00044	0	19	8	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	0
VGMS00048	0	3	36	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	1	0	0	0	0
VGMS00080	0	14	4	0	2	0	0	0	0	0	0	0	12	0	1	0	0	0	0	0	1	2	0	21	0	0	0
VGMS00109	0	21	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	4	0	0	0
VGMS00112	1	3	6	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	32	0	0	0
VGMS00121	0	12	2	0	1	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	0	0	0	34	0	0	0
VGMS00124	0	24	0	0	7	0	0	0	0	0	20	0	1	0	0	4	1	0	0	0	6	12	0	4	0	0	0
VGMS00126	0	38	1	0	0	0	0	0	0	0	0	1	3	0	10	0	0	0	0	0	0	0	0	1	0	0	0
VGMS00128	0	121	10	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	15	0	0	0
VGMS00162	0	11	14	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0
VGMS00177	0	3	12	0	0	0	0	0	0	3	0	0	0	0	5	0	0	0	0	0	0	0	0	37	0	0	0
VGMS00191	0	96	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	48	0	0	0	0
VGMS00206	0	72	4	0	1	0	0	0	0	0	1	0	1	0	90	0	0	0	0	0	28	0	0	1	0	0	0
VGMS00210	0	79	8	0	2	0	0	0	0	1	2	0	1	0	21	79	5	0	0	4	126	0	0	5	0	0	0
VGMS00247	0	11	11	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00252	0	15	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	4	0	0	0	0
VGMS00255	0	47	0	0	1	0	0	0	0	0	0	0	20	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00277	0	58	0	0	2	0	0	0	0	0	43	0	0	0	0	0	0	0	0	0	0	0	35	0	0	0	0
VGMS00306	0	59	28	0	3	0	0	2	3	72	0	14	0	31	64	5	0	0	0	9	88	0	0	10	0	0	0

	<i>Alisotrichia</i>	<i>Americabaetis</i>	<i>Anacroneria</i>	<i>Anchitrichia</i>	<i>Apobaetis</i>	<i>Askola</i>	<i>Asthenopus</i>	<i>Atanatolia</i>	<i>Atopsyche</i>	<i>Aturbina</i>	<i>Austrotinodes</i>	<i>Baetodes</i>	<i>Barypenthus</i>	<i>Caenis</i>	<i>Callibaetis</i>	<i>Camelobaetidius</i>	<i>Campsurus</i>	<i>Campylocia</i>	<i>Chimarra</i>	<i>Cloeodes</i>	<i>Cryptonympha</i>	<i>Cynelus</i>	<i>Farrodes</i>	<i>Grumichella</i>	<i>Gryopterix</i>	<i>Guajrolus</i>
VGMS00320	0	1	1	0	0	0	0	0	1	0	0	28	0	0	0	0	0	0	0	0	2	0	13	0	0	0
VGMS00380	0	14	0	0	1	0	0	0	1	28	0	0	0	0	0	0	0	0	0	0	2	0	23	0	0	0
VGMS00387	0	7	0	0	0	0	0	0	0	0	2	30	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00418	0	20	20	0	2	0	0	6	26	24	0	12	0	7	2	9	0	0	0	5	0	0	147	0	0	0
VGMS00433	0	1	26	0	0	0	0	0	4	0	1	1	0	0	0	0	0	0	0	0	0	0	25	0	0	0
VGMS00444	1	264	26	0	44	0	0	0	0	97	1	510	0	1	0	32	0	0	86	4	32	0	96	0	0	0
VGMS00447	0	26	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
VGMS00450	0	14	0	0	0	0	0	0	0	0	0	5	0	0	0	2	0	0	0	0	0	0	0	0	0	0
VGMS00511	0	24	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	4	0	0	0	0
VGMS00515	0	43	2	0	0	0	0	0	0	0	0	14	0	0	0	101	0	0	0	0	0	0	36	0	0	0
VGMS00558	0	58	0	0	0	0	0	0	0	0	0	205	0	0	0	0	0	0	9	0	0	0	0	0	0	0
VGMS00575	0	12	0	0	5	0	0	0	0	0	0	0	0	9	0	0	0	0	0	0	0	3	0	0	0	0
SSMS0001	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	4	0	0	0	0	0
SSMS0002	0	72	0	0	3	0	0	0	0	58	3	0	0	12	1	2	0	0	0	18	7	0	17	0	0	0
SSMS0008	0	61	2	0	19	0	0	0	0	0	1	4	0	32	14	6	0	0	0	25	1	0	2	0	0	0
SSMS0010	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	3	0	0	0
SSMS0014	0	8	1	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	2	0	0	6	0	0	0
SSMS0028	0	30	1	0	6	0	0	0	1	0	1	0	0	12	0	0	0	0	2	0	2	0	86	0	0	0
SSMS0029	0	1	0	0	0	0	0	0	0	1	3	2	0	4	0	0	0	0	0	0	0	4	0	0	0	0
SSMS0031	0	10	0	0	2	0	0	0	0	0	0	0	0	8	6	3	0	0	0	1	0	0	3	0	0	0
SSMS0033	0	28	1	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0035	0	2	0	0	0	0	0	0	0	0	0	4	0	0	1	15	0	0	1	3	1	0	12	0	0	0
SSMS0037	0	14	0	0	39	0	0	0	0	7	2	0	0	16	53	37	0	0	0	8	1	1	0	0	0	0
SSMS0038	0	8	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56	0	0	0	0
SSMS0044	0	21	5	0	12	0	0	0	0	1	0	0	0	7	0	0	0	0	1	3	5	0	30	0	0	0
SSMS0051	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0053	0	27	8	0	0	0	0	0	0	0	0	15	0	1	6	0	0	0	0	0	0	5	0	0	0	0
SSMS0057	0	35	9	0	0	0	0	0	0	2	0	4	0	33	0	0	0	0	32	15	0	0	77	0	0	0
SSMS0059	0	11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
SSMS0073	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0078	0	214	14	0	19	0	0	0	0	0	0	9	0	1	0	32	0	0	0	4	5	0	143	0	0	0
SSMS0094	0	25	16	0	0	0	0	0	0	1	0	61	0	1	0	1	0	0	0	6	15	0	28	0	0	0
SSMS0105	0	3	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	7	0	0	0	0

	<i>Alisotrichia</i>	<i>Americabaetis</i>	<i>Anacroneuria</i>	<i>Anchitrichia</i>	<i>Apobaetis</i>	<i>Askola</i>	<i>Asthenopus</i>	<i>Atanatolia</i>	<i>Atopsyche</i>	<i>Aturbina</i>	<i>Austrotinodes</i>	<i>Baetodes</i>	<i>Barypenthus</i>	<i>Caenis</i>	<i>Callibaetis</i>	<i>Camelobaetidius</i>	<i>Campsurus</i>	<i>Campylocia</i>	<i>Chimarra</i>	<i>Cloeodes</i>	<i>Cryptonympha</i>	<i>Cynelus</i>	<i>Farrodes</i>	<i>Grumichella</i>	<i>Grypopteryx</i>	<i>Guajrolus</i>
SSMS0126	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0129	0	17	1	0	2	0	0	0	0	1	0	0	0	17	0	0	0	0	0	0	0	0	30	0	0	0
SSMS0133	2	339	0	0	0	0	0	0	0	5	0	0	0	9	78	60	0	0	2	63	7	0	40	0	0	0
SSMS0144	0	9	1	0	9	0	0	0	0	0	0	3	0	7	2	9	0	0	0	1	8	0	5	0	0	0
SSMS0149	0	13	0	0	1	0	0	0	0	0	6	1	0	0	0	0	0	0	0	0	31	0	0	0	0	0
SSMS0150	0	10	8	0	1	0	0	0	0	0	1	14	0	0	0	1	0	0	0	0	7	0	55	0	0	0
SSMS0157	0	1	2	0	1	0	0	0	0	0	0	0	0	28	0	0	0	0	0	2	0	0	16	0	0	0
SSMS0175	0	44	144	0	0	0	0	0	0	6	0	341	0	1	5	8	0	0	182	43	0	0	46	0	0	0
SSMS0191	0	56	13	0	18	0	0	0	0	2	0	4	0	0	0	11	0	0	10	19	1	0	118	0	0	0
SSMS0193	0	50	4	0	6	0	0	0	0	0	0	0	0	153	0	0	0	0	0	0	0	159	0	0	5	
SSMS0199	0	3	0	0	5	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0	7	0	0	0	
SSMS0213	0	23	5	0	0	0	0	0	0	4	3	8	0	0	0	44	0	0	0	5	8	0	7	0	0	0
SSMS0351	0	41	11	0	0	0	0	0	0	1	1	0	0	1	2	41	0	0	7	1	0	0	107	0	0	0
SSMS0408	0	2	0	0	3	0	0	0	0	0	3	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0411	0	368	6	0	3	0	0	0	3	50	0	2	0	10	9	77	0	0	0	41	0	0	14	0	0	1
SSMS0447	0	13	0	0	3	0	0	0	0	1	0	0	0	1	1	8	0	0	0	2	1	0	22	0	0	0
SSMS1000	0	22	17	0	0	0	0	0	0	0	1	61	0	0	0	0	0	0	1	0	0	0	34	0	0	0
SSMS4173	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS4330	0	2	0	0	0	0	0	0	0	0	4	0	0	4	2	0	0	0	2	0	1	0	8	0	0	0
RENP0008	0	15	10	0	0	0	0	0	0	0	1	0	9	2	0	0	0	0	0	0	0	0	1	0	0	0
RENP0012	1	92	12	0	0	0	0	0	2	0	0	49	1	1	3	2	0	0	0	1	0	0	36	0	0	0
RENP0016	0	20	1	0	0	0	0	0	6	0	0	0	0	64	1	3	0	1	0	14	0	0	15	0	0	0
RENP0028	0	0	8	0	14	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	5	0	0	0	0	0
RENP0047	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RENP0052	0	95	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0	0	0	0	0
RENP0054	0	0	0	0	0	5	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
RENP0055	0	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	
RENP0075	0	45	36	0	2	0	0	0	8	5	3	18	0	3	3	5	0	3	0	15	2	0	14	0	0	0
RENP0092	0	4	1	0	0	1	0	0	0	0	0	0	0	33	0	0	0	0	0	0	0	1	0	0	0	0
RENP0095	0	0	0	0	0	6	0	0	0	0	0	0	0	22	0	0	0	0	0	0	0	2	0	0	0	0
RENP0096	0	5	23	0	14	0	0	0	1	0	0	0	4	1	0	0	0	0	0	0	0	5	0	0	0	0
RENP0097	0	8	0	0	0	0	0	0	0	0	0	24	0	0	0	1	0	0	1	0	0	16	0	0	0	0
RENP0100	0	60	14	0	0	0	0	0	4	1	0	0	2	97	6	0	0	0	0	1	24	0	17	0	0	0

	<i>Alisotrichia</i>	<i>Americabaetis</i>	<i>Anacroneria</i>	<i>Anchitrichia</i>	<i>Apobaetis</i>	<i>Askola</i>	<i>Asthenopus</i>	<i>Atanatria</i>	<i>Atopsyche</i>	<i>Aturbina</i>	<i>Austrotinodes</i>	<i>Baetodes</i>	<i>Barypenthus</i>	<i>Caenis</i>	<i>Callibaetis</i>	<i>Camelobaetidius</i>	<i>Campsurus</i>	<i>Campylocia</i>	<i>Chinarra</i>	<i>Cloeodes</i>	<i>Cryptonympha</i>	<i>Cymelus</i>	<i>Farrades</i>	<i>Grumichella</i>	<i>Gryopterix</i>	<i>Guajrolus</i>
REN0108	0	22	2	0	0	0	0	0	0	1	0	7	0	0	0	0	0	0	0	3	0	0	0	0	1	0
REN0110	0	65	7	0	0	0	0	0	0	0	0	48	0	0	0	3	0	0	2	7	0	0	3	0	0	0
REN0112	0	395	20	0	0	4	0	0	0	5	8	0	2	191	6	0	0	2	1	1	0	0	210	0	0	0
REN0128	0	16	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0
REN0132	0	2	2	0	0	0	0	0	0	1	0	1	4	4	1	0	0	0	0	0	0	0	34	0	1	0
REN0139	0	12	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0
REN0144	0	23	0	0	0	0	0	0	0	56	0	16	1	40	5	0	0	0	0	6	0	0	8	0	0	0
REN0187	0	17	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0
REN0192	0	26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REN0203	0	0	0	0	0	0	0	0	0	4	0	12	1	2	0	6	0	0	0	0	0	0	3	0	0	0
REN0228	1	11	3	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	3	0	9	0
REN0240	0	0	0	0	0	10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
REN0251	0	26	1	0	0	0	0	0	0	0	0	0	2	1	0	0	0	3	1	0	0	0	1	0	7	0
REN0287	0	9	7	0	0	0	0	0	0	0	0	0	0	368	155	0	0	0	2	5	0	0	75	0	0	0
REN0368	0	0	2	0	0	0	0	0	0	1	2	0	3	0	0	0	0	0	0	0	0	0	2	0	0	0
REN0375	0	34	11	1	7	1	0	0	5	0	1	8	0	5	42	0	0	0	0	8	1	0	1	0	0	0
REN0443	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0
REN0511	0	125	16	0	2	0	0	0	0	6	0	0	2	0	0	0	0	0	0	0	7	0	7	0	0	0
REN1524	0	1	107	0	0	6	0	0	0	0	0	0	0	4	0	0	0	0	0	0	29	0	4	0	0	0
REN2991	0	150	18	0	0	0	1	0	24	0	2	0	0	0	0	0	0	0	0	0	14	0	62	0	0	0
REN5612	0	0	0	0	0	2	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
REN7308	0	14	12	0	0	11	0	0	0	2	0	0	4	7	0	0	0	14	0	0	0	0	13	0	0	0
REN9611	0	5	5	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
REN9757	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REN12892	0	145	1	0	2	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	0	0
REN15048	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA02	0	554	0	0	0	0	0	0	21	0	0	0	0	0	0	0	0	0	0	25	26	0	21	31	0	0
RCA08	0	0	0	0	0	0	0	0	0	0	0	0	0	22	13	0	0	0	0	3	1	0	1	0	0	0
RCA22	0	20	0	0	0	1	0	0	3	0	1	0	0	24	0	0	0	4	0	9	50	0	16	1	0	0
RCA23	1	51	7	0	0	19	0	0	5	0	0	0	2	0	0	0	0	0	0	10	8	0	17	2	1	0
RCA30	2	40	0	0	0	0	0	0	0	2	0	7	4	2	0	1	0	6	0	23	6	0	3	31	1	0
RCA31	0	0	2	0	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
RCA44	0	8	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	11	0	0	0

	<i>Alisotrichia</i>	<i>Americabaetis</i>	<i>Anacronetria</i>	<i>Anchitrichia</i>	<i>Apobaetis</i>	<i>Askola</i>	<i>Asthenopus</i>	<i>Atanatolia</i>	<i>Atopsyche</i>	<i>Aturbina</i>	<i>Austrotinodes</i>	<i>Baetodes</i>	<i>Barypenthus</i>	<i>Caenis</i>	<i>Callibaetis</i>	<i>Camelobaetidius</i>	<i>Campsurus</i>	<i>Campylocia</i>	<i>Chimarra</i>	<i>Cloeodes</i>	<i>Cryptonympha</i>	<i>Cynelus</i>	<i>Farrodes</i>	<i>Grumichella</i>	<i>Grypopteryx</i>	<i>Guajirulus</i>
RCA48	0	5	59	0	0	0	0	0	1	0	4	2	0	0	0	6	0	0	0	0	0	0	12	0	0	0
RCA49	1	1	12	0	0	0	0	0	0	1	7	0	4	38	0	0	0	6	0	6	0	0	10	0	0	0
RCA50	0	2	0	0	0	0	0	0	0	0	1	0	0	5	0	0	0	2	0	5	1	0	0	0	0	0
RCA52	0	0	22	0	0	0	0	0	1	0	1	0	0	1	0	0	0	12	0	0	4	0	0	0	0	0
RCA53	1	0	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	4	2	0	0	0	0	0	0
RCA57	0	3	0	0	0	2	0	0	0	0	0	0	3	17	2	0	0	14	0	65	0	0	0	0	0	0
RCA58	1	0	1	0	0	0	0	0	6	0	0	0	0	2	0	0	0	23	0	0	7	0	5	0	0	0
RCA59	1	62	11	0	0	0	0	0	0	0	0	15	0	1	0	0	0	0	0	8	96	0	119	40	0	0
RCA60	1	106	5	0	0	0	0	0	2	0	0	32	0	0	0	0	0	0	0	0	6	0	48	336	0	0
RCA62	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0
RCA64	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
RCA65	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA66	0	1	1	0	0	0	0	0	0	0	1	0	4	68	0	0	0	0	0	1	0	0	0	0	0	0
RCA67	0	4	11	0	0	0	0	0	0	0	0	0	2	3	1	0	0	0	0	3	0	0	17	0	0	0
RCA68	0	6	17	0	0	0	0	0	0	0	1	4	0	10	0	0	0	12	0	2	0	0	29	0	0	0
RCA69	0	3	7	0	0	0	0	0	1	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA70	1	0	1	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA71	0	1	18	0	0	0	0	0	0	1	0	0	5	7	0	0	0	20	0	0	0	0	2	0	0	0
RCA72	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
RCA73	0	1	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA74	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	0	1	0	0	0
RCA90	0	4	0	0	1	0	0	0	0	0	0	0	2	1	0	6	0	0	0	0	2	0	1	0	0	0

	<i>Hagenulopsis</i>	<i>Helicopsyche</i>	<i>Hermanella</i>	<i>Hexagenia</i>	<i>Hydroptila</i>	<i>Hydrosmilodon</i>	<i>Itaura</i>	<i>Kempnyia</i>	<i>Latineosus</i>	<i>Leptohyphes</i>	<i>Leptohyphodes</i>	<i>Leptonema</i>	<i>Macronema</i>	<i>Macrostemum</i>	<i>Marilia</i>	<i>Massartella</i>	<i>Metrichia</i>	<i>Miroculis</i>	<i>Mortoniella</i>	<i>Nectopsyche</i>	<i>Neotrichia</i>	<i>Notalina</i>	<i>Nyctiophylax</i>	<i>Oecetis</i>	<i>Oxyetira</i>
TMMS0003	0	0	0	0	0	312	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0
TMMS0007	0	0	0	4	0	1	0	0	0	0	0	1	0	0	0	0	0	14	0	0	0	0	0	4	0
TMMS0009	1	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0	0	0	0	0	0	0	0	6
TMMS0027	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	3
TMMS0028	0	0	0	0	45	0	0	0	0	0	0	0	0	0	0	3	0	2	0	1	0	0	0	0	4
TMMS0033	0	0	0	0	0	0	0	0	0	0	0	0	1	0	4	15	0	15	0	0	0	0	0	3	0
TMMS0040	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	16	0	21	0	4	0	0	0	0	0
TMMS0043	0	9	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	14	0	6	0	0	0	0	1
TMMS0058	0	0	0	0	0	0	0	0	0	0	0	5	4	0	5	0	0	36	0	0	0	0	0	2	2
TMMS0072	0	0	0	0	5	0	0	0	0	0	0	7	0	0	6	0	0	0	0	0	0	0	0	0	3
TMMS0082	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0
TMMS0088	0	11	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	12	0	0	0	0	0	0	5
TMMS0090	0	0	0	0	1	0	0	0	0	0	0	0	0	0	6	0	0	45	0	0	0	0	0	0	3
TMMS0091	0	0	10	0	6	20	0	0	0	6	0	5	0	0	1	0	0	1	0	7	0	0	0	0	11
TMMS0106	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	0	0	0	0	0	0	0	0
TMMS0119	0	0	0	0	0	0	0	0	0	0	0	0	3	6	0	0	0	0	0	8	0	0	0	1	0
TMMS0126	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	16	0	8	0	0	0	1	0
TMMS0133	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	1	0	0	0	0	0	4	0
TMMS0134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	40	0	0	0	0	0	0	0
TMMS0137	1	0	0	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	0	0	0	0	0
TMMS0159	0	0	0	0	10	0	0	0	8	0	0	0	0	0	0	0	15	2	0	4	0	0	0	1	8
TMMS0171	0	2	16	0	2	12	0	0	0	0	0	2	0	0	1	0	2	0	0	0	0	0	0	0	2
TMMS0178	0	0	0	0	26	0	0	0	12	0	0	9	1	0	0	0	3	0	3	18	0	0	0	9	3
TMMS0183	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	1	2	0	4	0	0	0	4	2
TMMS0187	2	4	0	0	2	0	0	0	0	0	0	0	4	0	7	1	0	56	1	1	2	0	0	3	6
TMMS0193	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2	0	0	2	0	2	0	0	0	0	0
TMMS0209	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	
TMMS0214	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
TMMS0220	30	0	0	0	4	0	0	0	0	0	0	1	0	0	0	8	0	3	0	12	0	0	0	0	0
TMMS0279	0	0	0	2	9	1	0	0	0	0	0	7	0	0	0	0	0	1	0	0	0	0	0	0	1
TMMS0283	2	0	6	0	0	0	0	0	0	7	0	0	0	0	26	0	0	3	0	1	0	0	0	0	0
TMMS0290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TMMS0296	0	4	0	0	24	0	0	0	0	13	0	2	3	0	3	0	50	23	2	0	0	0	0	4	2

	<i>Hagenulopsis</i>	<i>Helicopsyche</i>	<i>Hermanella</i>	<i>Hexagenia</i>	<i>Hydroptila</i>	<i>Hydrosmilodon</i>	<i>Itaura</i>	<i>Kempnyia</i>	<i>Latineosus</i>	<i>Leptohyphes</i>	<i>Leptohyphodes</i>	<i>Leptonema</i>	<i>Macronema</i>	<i>Macrostemum</i>	<i>Marilia</i>	<i>Massartella</i>	<i>Metrichia</i>	<i>Miroculis</i>	<i>Mortoniella</i>	<i>Nectopsyche</i>	<i>Neotrichia</i>	<i>Notalina</i>	<i>Nyctiophylax</i>	<i>Oecetis</i>	<i>Oxyetira</i>	
TMMS0381	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
TMMS0391	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	2	0
TMMS0437	0	0	0	0	9	0	0	0	0	0	0	2	30	1	0	0	0	0	0	0	0	0	0	0	0	2
TMMS1865	2	0	0	0	0	0	0	0	0	0	0	0	9	0	7	0	0	0	0	1	0	0	0	0	0	3
TMMS3195	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0
TMMS3962	0	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	3	0	0	0	5	1	
VGMS00002	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
VGMS00004	92	0	0	0	77	0	2	0	0	147	0	1	0	0	2	0	1	0	0	4	0	0	0	1	0	0
VGMS00016	3	17	0	0	0	36	0	0	0	11	0	0	0	0	0	0	0	0	0	3	0	0	0	1	0	0
VGMS00018	0	0	0	0	0	0	0	0	0	2	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00022	2	0	0	0	0	0	9	0	0	7	0	0	0	0	0	0	4	0	0	0	0	0	0	1	0	0
VGMS00034	1	0	0	0	0	0	0	0	0	5	0	0	0	1	3	0	0	6	0	0	0	0	0	0	1	0
VGMS00037	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00044	8	0	0	0	0	0	11	0	0	0	0	2	1	0	17	0	0	51	0	1	0	0	0	0	2	0
VGMS00048	0	0	0	0	2	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	3	0
VGMS00080	2	1	0	0	0	4	2	0	0	5	0	3	0	0	0	0	0	0	0	1	0	0	0	0	1	0
VGMS00109	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
VGMS00112	3	1	4	0	0	5	0	0	0	20	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0
VGMS00121	7	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0
VGMS00124	0	0	0	0	0	0	8	0	0	0	0	0	0	0	4	0	0	6	0	0	2	0	0	0	0	0
VGMS00126	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	5	0
VGMS00128	0	0	0	0	0	0	0	0	0	0	0	0	1	0	3	0	0	2	0	0	0	0	0	0	0	0
VGMS00162	0	0	0	0	0	0	1	0	0	16	0	1	1	0	3	0	0	1	0	0	1	0	0	0	0	0
VGMS00177	0	0	0	0	0	0	0	0	0	19	0	0	0	0	0	0	0	0	0	0	10	0	0	0	3	0
VGMS00191	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00206	8	0	0	0	0	0	6	0	0	10	0	4	0	0	35	0	0	0	0	1	0	0	0	0	1	0
VGMS00210	3	0	0	0	0	0	5	0	0	12	0	0	0	0	6	0	1	0	0	1	0	0	0	0	0	0
VGMS00247	0	0	0	0	0	0	0	0	0	0	0	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0
VGMS00252	0	3	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0
VGMS00255	0	0	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00277	1	0	0	0	0	1	0	0	0	3	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
VGMS00306	6	0	0	0	0	2	121	0	0	34	0	2	0	0	2	0	0	2	0	4	0	0	0	0	0	1
VGMS00320	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0

	<i>Hagenulopsis</i>	<i>Helicopsyche</i>	<i>Hermanella</i>	<i>Hexagenia</i>	<i>Hydroptila</i>	<i>Hydrosmilodon</i>	<i>Itaura</i>	<i>Kempnyia</i>	<i>Latineosus</i>	<i>Leptohyphes</i>	<i>Leptohyphodes</i>	<i>Leptonema</i>	<i>Macronema</i>	<i>Macrostemum</i>	<i>Marilia</i>	<i>Massartella</i>	<i>Metrichia</i>	<i>Miroculis</i>	<i>Mortoniella</i>	<i>Nectopsyche</i>	<i>Neotrichia</i>	<i>Notalina</i>	<i>Nyctiophylax</i>	<i>Oecetis</i>	<i>Oxyetira</i>
VGMS00380	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	32	0	1	0	0	0	3	0
VGMS00387	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0
VGMS00418	23	0	0	0	0	0	42	0	0	38	0	6	0	0	5	0	0	80	0	0	1	0	0	1	0
VGMS00433	0	14	0	0	0	1	0	0	0	20	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
VGMS00444	13	3	0	0	0	10	13	0	0	380	0	17	0	0	1	0	0	0	0	13	1	0	0	1	0
VGMS00447	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00450	0	0	0	0	0	0	36	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
VGMS00511	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00515	8	0	0	0	0	4	21	0	0	7	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0
VGMS00558	0	0	0	0	0	0	0	0	0	0	0	36	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00575	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
SSMS0001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0
SSMS0002	0	1	0	0	1	0	0	0	5	0	0	0	6	0	1	0	0	151	0	35	0	0	2	1	0
SSMS0008	13	2	0	0	4	0	2	0	0	2	0	0	33	0	11	0	0	15	0	0	0	0	0	0	0
SSMS0010	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0014	0	0	0	0	0	0	9	0	0	0	0	0	0	1	0	0	0	0	2	0	0	0	0	0	0
SSMS0028	0	0	0	0	0	1	0	0	0	20	0	3	1	2	0	0	0	0	0	5	0	0	0	1	0
SSMS0029	5	1	0	0	0	0	0	0	1	4	0	0	0	0	0	0	0	1	0	3	0	0	0	1	0
SSMS0031	0	0	0	0	0	0	0	0	0	0	0	1	131	0	4	0	0	103	0	0	0	0	0	0	1
SSMS0033	0	0	0	0	22	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0035	0	0	5	0	0	9	0	0	0	1	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
SSMS0037	2	1	0	0	0	0	0	0	1	0	0	1	3	0	1	0	0	13	0	3	0	0	0	3	0
SSMS0038	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0044	46	6	0	0	0	7	0	0	0	7	0	0	5	0	0	0	0	8	0	1	0	0	0	2	0
SSMS0051	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	1	0	0	0	0	0
SSMS0053	0	1	0	0	1	0	1	0	0	0	0	2	15	0	0	0	0	14	0	0	0	0	0	0	0
SSMS0057	0	18	0	0	0	0	0	0	0	0	0	5	4	0	0	0	0	59	0	0	0	0	0	0	0
SSMS0059	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0073	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
SSMS0078	0	1	0	0	1	0	0	0	0	11	0	5	0	0	0	0	0	0	0	57	1	0	0	0	0
SSMS0094	4	2	0	0	0	2	12	0	0	2	0	2	1	4	0	0	0	8	0	2	0	0	0	1	0
SSMS0105	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	
SSMS0126	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

	<i>Hagenulopsis</i>	<i>Helicopsyche</i>	<i>Hermanella</i>	<i>Hexagenia</i>	<i>Hydroptila</i>	<i>Hydrosmilodon</i>	<i>Itaura</i>	<i>Kempnyia</i>	<i>Latineosus</i>	<i>Leptohyphes</i>	<i>Leptohyphodes</i>	<i>Leptonema</i>	<i>Macronema</i>	<i>Macrostemun</i>	<i>Marilia</i>	<i>Massartella</i>	<i>Metrichia</i>	<i>Miroculis</i>	<i>Mortoniella</i>	<i>Nectopsyche</i>	<i>Neotrichia</i>	<i>Notalina</i>	<i>Nyctiophylax</i>	<i>Oecetis</i>	<i>Oxyetira</i>
SSMS0129	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0133	0	14	13	0	160	2	0	0	1	0	0	0	6	0	2	0	0	16	0	5	0	0	3	2	21
SSMS0144	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
SSMS0149	0	5	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
SSMS0150	0	9	2	0	0	16	0	0	0	12	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0
SSMS0157	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	18	0	1	0	0	3	5	0
SSMS0175	6	3	1	0	0	0	0	0	0	164	0	12	0	0	0	0	0	25	0	0	0	0	3	0	0
SSMS0191	0	23	4	0	3	0	0	0	1	26	0	0	0	0	0	0	0	7	0	0	0	0	0	1	0
SSMS0193	0	0	5	0	0	1	0	0	1	0	0	4	0	0	0	0	0	0	0	0	1	0	0	1	0
SSMS0199	0	10	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0	34	0	1	0	0	0	2	0
SSMS0213	3	3	3	0	0	19	0	0	0	28	0	0	1	0	0	0	1	0	0	3	0	0	0	0	0
SSMS0351	0	7	0	0	2	23	0	0	1	26	0	13	0	0	0	0	2	2	0	1	0	0	0	0	0
SSMS0408	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0411	0	25	62	0	5	1	2	0	10	14	0	0	14	0	3	0	29	9	0	11	0	0	0	2	0
SSMS0447	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	1	0	0	0	0	0
SSMS1000	1	0	0	0	0	0	0	0	0	19	0	0	7	0	0	0	0	0	0	0	0	0	0	0	0
SSMS4173	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS4330	1	24	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	2	0	0	0	6	0
RENP0008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
RENP0012	0	0	0	0	6	0	1	0	0	1	0	9	0	3	0	0	0	0	0	0	0	0	0	0	8
RENP0016	19	0	0	0	6	0	0	0	0	0	0	1	0	0	3	0	1	13	0	0	2	0	0	0	6
RENP0028	0	0	0	0	2	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	1	0	0
RENP0047	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
RENP0052	0	0	0	0	0	0	4	1	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0
RENP0054	0	0	0	0	0	0	0	2	0	3	9	0	0	0	0	0	0	19	0	0	0	2	0	1	0
RENP0055	0	0	0	0	0	0	1	0	0	0	0	3	0	0	12	0	0	0	0	0	0	0	0	0	0
RENP0075	59	0	0	0	3	0	8	5	0	0	0	11	2	0	12	0	0	29	0	0	0	7	0	8	1
RENP0092	1	0	0	0	0	0	0	1	0	0	0	0	0	0	4	0	0	0	0	0	0	1	0	0	0
RENP0095	0	0	0	0	0	0	0	0	0	0	0	1	1	0	11	0	0	12	0	0	0	26	0	5	0
RENP0096	0	0	0	0	0	0	1	0	0	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0
RENP0097	0	0	0	0	0	0	2	0	0	18	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
RENP0100	58	0	0	0	0	0	51	1	0	0	0	2	0	0	6	0	0	17	0	11	0	0	0	0	3
RENP0108	0	0	0	0	0	0	0	0	0	0	0	27	0	0	4	0	0	0	0	0	0	1	0	0	0

	<i>Hagenulopsis</i>	<i>Helicopsyche</i>	<i>Hermanella</i>	<i>Hexagenia</i>	<i>Hydroptila</i>	<i>Hydrosmilodon</i>	<i>Itaura</i>	<i>Kempnyia</i>	<i>Latineosus</i>	<i>Leptohyphes</i>	<i>Leptohyphodes</i>	<i>Leptonema</i>	<i>Macronema</i>	<i>Macrostemun</i>	<i>Marilia</i>	<i>Massartella</i>	<i>Metrichia</i>	<i>Miroculis</i>	<i>Mortoniella</i>	<i>Nectopsyche</i>	<i>Neotrichia</i>	<i>Notalina</i>	<i>Nyctiophylax</i>	<i>Oecetis</i>	<i>Oxyetira</i>
REN0110	0	0	0	0	0	0	22	1	0	0	0	0	1	0	0	0	3	0	0	1	2	0	0	0	0
REN0112	24	0	0	0	0	0	0	3	0	0	0	6	0	0	3	5	0	68	0	0	4	2	0	0	0
REN0128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
REN0132	0	0	0	0	0	0	0	1	0	0	0	1	2	0	1	1	0	8	0	0	0	2	0	0	0
REN0139	0	0	0	0	0	0	0	0	0	0	0	10	0	0	1	0	0	0	0	0	0	0	0	0	0
REN0144	6	0	0	0	0	0	0	0	0	0	0	0	0	0	5	1	0	13	0	0	0	0	0	2	0
REN0187	0	0	0	0	0	0	2	0	0	0	0	1	0	0	4	0	0	0	0	0	0	0	0	0	0
REN0192	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REN0203	0	0	0	0	3	0	5	0	0	0	0	14	0	0	0	1	0	0	0	0	0	0	0	1	0
REN0228	0	0	0	0	0	0	0	1	0	0	0	1	0	0	3	0	0	2	0	0	0	1	0	0	0
REN0240	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
REN0251	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	7	2	0	0	0	0	0	0	0
REN0287	1	0	0	0	0	0	0	1	0	0	0	2	1	0	6	14	0	5	0	1	0	0	0	4	0
REN0368	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REN0375	11	0	0	0	0	2	17	1	0	0	0	4	0	0	0	0	0	0	0	0	0	1	0	0	0
REN0443	0	0	0	0	0	0	20	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
REN0511	0	0	0	0	13	0	119	0	0	0	0	0	0	0	0	0	0	0	1	3	0	1	0	9	0
REN1524	2	0	0	0	0	0	13	0	0	0	0	6	1	0	27	0	0	0	0	0	0	0	0	0	0
REN2991	0	0	0	0	2	0	27	0	0	3	0	1	0	0	3	0	0	0	0	0	0	0	0	2	0
REN5612	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
REN7308	8	0	0	0	0	0	0	2	0	0	7	2	0	1	1	23	0	26	0	0	0	1	0	0	0
REN9611	0	0	0	0	0	0	0	1	0	0	8	8	1	0	3	0	0	0	0	0	1	0	0	0	0
REN9757	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REN12892	0	0	0	0	2	0	0	0	0	0	0	0	0	0	13	0	0	0	0	0	0	0	0	0	128
REN15048	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA02	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	1	0	0	0	2
RCA08	0	1	0	0	0	0	0	4	0	0	0	0	0	0	0	1	0	1	0	0	0	6	0	1	0
RCA22	8	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	9	42	0	8	0	1	0	0	1
RCA23	4	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	94	8	0	0	1	1	0	0	1
RCA30	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	14	23	0	0	1	0	0	0	0
RCA31	0	1	0	0	0	0	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
RCA44	0	0	0	0	0	0	0	15	0	0	0	0	0	0	14	0	0	0	0	1	0	1	0	1	0
RCA48	82	1	0	0	2	0	35	1	0	0	0	4	3	5	173	0	0	0	0	171	9	0	0	0	0

	<i>Hagenulopsis</i>	<i>Helicopsyche</i>	<i>Hermanella</i>	<i>Hexagenia</i>	<i>Hydroptila</i>	<i>Hydrosmilodon</i>	<i>Itaura</i>	<i>Kempnya</i>	<i>Latineosus</i>	<i>Leptohyphes</i>	<i>Leptohyphodes</i>	<i>Leptonema</i>	<i>Macronema</i>	<i>Macrostemun</i>	<i>Marilia</i>	<i>Massartella</i>	<i>Metrichia</i>	<i>Miroculis</i>	<i>Mortoniella</i>	<i>Nectopsyche</i>	<i>Neotrichia</i>	<i>Notalina</i>	<i>Nyctiophylax</i>	<i>Oecetis</i>	<i>Oxyetira</i>
RCA49	8	0	0	0	0	0	1	1	0	0	0	1	9	3	7	1	8	17	0	0	0	5	0	0	0
RCA50	0	0	0	0	2	0	0	0	0	0	0	0	0	0	42	0	0	0	0	2	0	1	0	2	0
RCA52	31	0	0	0	8	0	5	13	0	0	0	1	0	0	69	0	0	9	0	2	0	2	0	2	0
RCA53	12	0	0	0	0	0	0	1	0	0	0	0	0	0	5	0	0	0	0	0	2	0	0	0	0
RCA57	5	2	0	0	0	0	0	0	0	0	8	0	7	0	4	0	0	62	0	0	0	23	0	0	0
RCA58	2	1	0	0	5	0	0	0	0	0	1	1	9	0	4	0	42	2	0	0	0	2	0	0	37
RCA59	0	0	20	0	7	0	0	0	0	0	0	13	0	1	0	0	12	0	0	3	7	0	0	0	17
RCA60	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	21	0	0	0	1	0	0	0	21
RCA62	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	108	0	0	0	0	0	26	0
RCA64	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0
RCA65	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA66	0	2	0	0	1	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	4	0	5	0
RCA67	4	0	0	0	0	0	6	2	0	0	0	0	0	0	1	0	0	1	0	0	2	9	0	3	0
RCA68	15	1	0	0	0	0	15	2	0	0	0	1	5	25	3	0	0	1	0	0	0	1	0	0	0
RCA69	7	0	0	0	0	2	6	1	0	0	0	0	0	2	8	0	2	0	0	0	0	0	0	0	0
RCA70	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA71	11	4	0	0	0	0	2	0	0	0	9	2	0	8	3	0	0	6	0	0	2	0	0	1	0
RCA72	0	0	0	0	0	0	0	0	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA73	10	0	1	0	0	0	8	1	0	0	0	1	0	3	10	0	0	0	0	0	0	0	0	0	0
RCA74	1	8	0	0	0	2	7	0	0	0	0	0	0	0	18	0	0	0	0	3	0	0	0	0	0
RCA90	1	0	0	0	0	0	32	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0

	<i>Paracloedes</i>	<i>Paragrypopteryx</i>	<i>Paramaka</i>	<i>Phylloicus</i>	<i>Polycentropus</i>	<i>Polyplectropus</i>	<i>Protoptila</i>	<i>Rivudiva</i>	<i>Simothraulopsis</i>	<i>Smicridea</i>	<i>Spiritiops</i>	<i>Terpides</i>	<i>Thraulodes</i>	<i>Traverhypes</i>	<i>Tricorythodes</i>	<i>Tricorythopsis</i>	<i>Triplectides</i>	<i>Tupiperla</i>	<i>Ulmeritoides</i>	<i>Varipes</i>	<i>Waltzophius</i>	<i>Wormaldia</i>	<i>Zelus</i>
TMMS0003	1	0	0	0	9	0	0	0	0	133	0	0	0	2	149	0	0	0	0	0	17	0	3
TMMS0007	2	0	0	0	6	1	0	0	1	4	0	0	0	0	0	0	0	0	1	0	3	0	4
TMMS0009	2	0	0	0	0	0	0	0	0	0	0	1	1	12	0	0	0	0	1	0	0	0	0
TMMS0027	1	0	0	0	3	1	0	0	0	1	0	0	0	9	0	0	0	0	0	0	16	0	0
TMMS0028	27	0	0	0	1	2	0	0	0	1	0	0	24	401	0	0	0	0	7	0	0	0	0
TMMS0033	8	0	0	0	0	5	0	0	1	0	0	0	7	0	0	0	0	0	16	0	1	0	16
TMMS0040	32	0	0	0	0	0	0	0	3	1	0	0	0	38	0	0	0	0	5	0	0	0	8
TMMS0043	18	0	0	0	0	0	0	0	1	0	0	0	0	10	1	1	0	0	34	0	11	0	2
TMMS0058	7	0	0	1	0	3	0	0	0	55	0	0	135	66	0	0	0	0	35	0	2	0	0
TMMS0072	0	0	0	1	0	6	0	0	0	84	0	0	9	27	0	0	0	0	1	0	0	0	0
TMMS0082	0	0	0	1	1	0	0	0	1	0	0	0	0	11	1	0	0	0	6	0	0	0	1
TMMS0088	0	0	0	0	0	0	0	0	0	0	0	0	0	73	3	2	0	0	63	0	0	0	0
TMMS0090	19	0	0	0	0	13	0	0	2	0	0	0	0	0	0	0	0	0	4	0	0	0	4
TMMS0091	20	0	0	0	0	0	0	0	0	26	0	0	170	85	2	1	0	0	1	0	0	0	0
TMMS0106	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	0	0
TMMS0119	0	0	0	0	0	0	0	0	0	60	0	0	0	0	0	0	0	0	0	0	2	0	1
TMMS0126	3	0	0	0	24	6	0	0	7	0	0	0	1	1	1	0	0	0	0	0	7	0	11
TMMS0133	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	2	0	7	0	0
TMMS0134	0	0	0	22	0	1	0	0	1	0	0	0	0	13	0	0	0	0	11	0	0	0	2
TMMS0137	0	0	0	0	2	0	0	0	3	0	0	0	0	21	0	0	5	0	22	0	1	0	3
TMMS0159	18	0	1	0	0	1	1	0	0	0	0	0	9	154	10	4	0	0	0	0	1	0	0
TMMS0171	0	0	5	0	0	0	0	0	2	47	0	0	69	180	7	3	0	0	4	0	0	0	0
TMMS0178	0	0	0	0	2	17	2	0	0	6	0	0	52	343	0	0	0	0	4	0	0	1	0
TMMS0183	0	0	0	0	6	0	0	0	2	1	0	0	0	75	0	0	0	0	0	0	2	0	0
TMMS0187	17	0	0	18	0	1	0	0	2	4	0	0	5	15	0	11	1	0	18	0	7	0	0
TMMS0193	0	0	0	0	4	2	0	0	0	1	0	0	0	24	0	0	1	0	0	0	13	0	0
TMMS0209	0	0	0	0	36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	12	0	0
TMMS0214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TMMS0220	0	0	0	0	1	7	0	0	0	55	0	0	92	869	0	0	2	0	4	0	0	0	0
TMMS0279	1	0	0	0	7	2	0	0	0	13	0	0	1	59	0	21	1	0	7	0	0	0	0
TMMS0283	0	0	0	0	0	1	0	0	0	8	8	0	4	12	0	2	0	0	0	0	0	0	0
TMMS0290	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TMMS0296	6	0	0	1	0	10	0	0	7	38	0	0	50	171	6	0	0	0	2	0	0	0	1

	<i>Paracloeodes</i>	<i>Paragrypopteryx</i>	<i>Paramaka</i>	<i>Phylloicus</i>	<i>Polycentropus</i>	<i>Polyplectropus</i>	<i>Protoptila</i>	<i>Rivulidra</i>	<i>Simothraulopsis</i>	<i>Smicridea</i>	<i>Spiritiops</i>	<i>Terpides</i>	<i>Thraulodes</i>	<i>Traverhypes</i>	<i>Tricorythodes</i>	<i>Tricorythopsis</i>	<i>Triplectides</i>	<i>Tupiperla</i>	<i>Ulmeritoides</i>	<i>Varipes</i>	<i>Waltzophius</i>	<i>Wormaldia</i>	<i>Zelus</i>
TMMS0381	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
TMMS0391	0	0	0	0	0	3	0	0	0	14	0	0	0	2	4	0	0	0	2	0	0	0	0
TMMS0437	0	0	0	0	2	0	0	0	2	37	0	0	0	14	14	0	0	0	4	0	198	0	4
TMMS1865	2	0	0	0	0	0	0	0	5	1	0	0	2	35	1	0	6	0	0	0	35	0	5
TMMS3195	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TMMS3962	0	0	0	0	11	13	0	0	0	0	0	0	0	7	0	0	0	0	7	0	4	0	2
VGMS00002	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	22	0	0
VGMS00004	0	0	0	6	0	0	5	0	0	51	0	14	84	15	4	0	1	0	47	0	3	0	142
VGMS00016	0	0	0	1	1	0	0	0	0	6	0	1	2	17	5	0	0	0	8	0	0	0	8
VGMS00018	0	0	0	4	7	0	0	0	0	4	0	0	0	16	0	0	0	0	1	0	2	0	0
VGMS00022	0	0	0	123	0	0	0	0	0	15	0	1	2	20	0	0	0	0	0	0	13	0	12
VGMS00034	2	0	0	34	0	0	0	0	0	22	0	0	0	48	4	0	0	0	3	0	2	0	1
VGMS00037	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
VGMS00044	22	0	0	12	0	0	1	3	0	9	0	27	12	7	10	0	0	0	83	0	16	0	27
VGMS00048	0	0	0	4	0	1	0	0	0	107	0	0	0	1	0	0	1	0	0	0	0	0	0
VGMS00080	2	0	0	4	0	0	1	0	0	7	0	0	0	4	8	2	1	0	0	0	1	0	17
VGMS00109	0	0	0	1	2	0	0	0	0	2	0	0	0	9	20	0	0	0	2	0	10	0	56
VGMS00112	0	0	0	0	1	0	0	0	0	16	0	1	1	0	2	0	0	0	0	0	5	0	12
VGMS00121	0	0	0	0	1	0	0	0	0	65	0	3	0	2	4	0	0	0	0	0	1	0	13
VGMS00124	56	0	0	0	0	0	0	1	0	3	0	2	8	7	0	0	0	0	13	0	10	0	4
VGMS00126	0	0	0	12	0	0	0	0	0	114	0	0	0	7	0	0	0	0	0	0	0	0	0
VGMS00128	1	0	0	0	0	0	0	0	0	10	0	0	0	0	2	1	0	0	0	0	21	0	49
VGMS00162	11	0	0	3	0	0	0	0	0	8	0	1	1	2	12	0	0	0	3	0	9	0	53
VGMS00177	0	0	0	0	4	0	0	0	0	105	0	0	0	5	0	0	0	0	0	0	1	0	1
VGMS00191	0	0	0	0	1	0	31	0	0	280	0	0	0	1	0	0	0	0	0	0	1	0	0
VGMS00206	1	0	0	93	0	0	0	0	0	90	0	1	31	90	0	0	0	0	0	0	0	0	4
VGMS00210	23	0	0	2	0	0	1	0	0	7	0	1	112	35	7	0	0	0	3	0	0	0	1
VGMS00247	0	0	0	0	0	0	0	0	0	1	0	0	0	21	1	0	1	0	0	0	3	0	10
VGMS00252	0	0	0	0	0	0	0	0	0	5	0	0	6	3	1	3	2	0	0	0	0	0	0
VGMS00255	2	0	0	0	2	0	5	0	0	2	0	0	0	13	2	0	0	0	0	0	0	0	1
VGMS00277	0	0	0	7	0	0	0	0	0	0	0	9	3	12	11	2	0	0	5	0	7	0	28
VGMS00306	14	0	0	3	0	0	8	0	0	18	0	12	583	26	49	2	0	0	19	0	0	0	6
VGMS00320	0	0	1	0	0	0	1	0	0	7	0	0	3	0	1	0	0	0	0	0	0	0	1

	<i>Paracloeodes</i>	<i>Paragrypopteryx</i>	<i>Paramaka</i>	<i>Phylloicus</i>	<i>Polycentropus</i>	<i>Polyplectropus</i>	<i>Protoptila</i>	<i>Rivulidra</i>	<i>Simothraulopsis</i>	<i>Smicridea</i>	<i>Spiritiops</i>	<i>Terpides</i>	<i>Thraulodes</i>	<i>Traverhypes</i>	<i>Tricorythodes</i>	<i>Tricorythopsis</i>	<i>Triplectides</i>	<i>Tupiperla</i>	<i>Ulmeritoides</i>	<i>Varipes</i>	<i>Waltzophius</i>	<i>Wormaldia</i>	<i>Zelus</i>
VGMS00380	35	0	0	6	4	0	2	0	0	2	0	3	1	38	12	1	0	0	43	0	9	0	8
VGMS00387	0	0	0	0	1	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	1
VGMS00418	7	0	0	5	2	0	0	0	0	19	0	6	58	44	78	0	0	0	0	0	25	0	6
VGMS00433	0	0	0	0	0	0	0	0	0	16	0	0	0	0	4	5	0	0	0	0	1	0	38
VGMS00444	11	0	0	0	0	0	32	0	0	97	0	10	236	115	3	5	0	0	2	0	4	0	3
VGMS00447	0	0	0	0	0	0	0	0	0	30	0	0	0	0	0	1	0	0	0	0	1	0	0
VGMS00450	0	0	0	0	0	0	0	0	0	6	0	0	0	0	3	0	0	0	0	0	0	0	0
VGMS00511	0	0	0	0	0	0	0	0	0	4	0	0	0	7	0	0	0	0	0	0	0	0	0
VGMS00515	0	0	0	5	0	0	8	1	0	21	0	0	11	1	0	3	0	0	0	0	0	0	0
VGMS00558	0	0	0	0	0	0	98	0	0	210	0	0	0	0	0	0	0	0	0	0	0	3	0
VGMS00575	2	0	0	14	0	0	5	0	0	5	0	1	2	11	2	0	0	0	0	0	3	0	9
SSMS0001	0	0	0	1	0	0	0	0	0	11	0	0	0	0	0	0	0	0	0	0	2	0	6
SSMS0002	51	0	0	52	0	4	0	2	0	1	0	41	7	126	0	3	0	0	11	0	19	0	111
SSMS0008	0	0	0	3	0	2	2	0	0	3	0	11	7	35	1	0	0	0	5	0	2	0	0
SSMS0010	1	0	0	0	0	0	0	0	0	6	0	0	0	1	0	0	0	0	0	0	5	0	0
SSMS0014	0	0	0	0	0	7	0	0	0	9	0	0	0	0	2	3	0	0	0	0	0	0	3
SSMS0028	0	0	0	3	0	0	1	0	0	43	0	0	1	180	1	1	0	0	1	0	2	0	31
SSMS0029	0	0	0	1	0	0	0	0	0	0	0	2	0	26	0	0	0	0	0	0	0	0	0
SSMS0031	4	0	0	0	3	0	0	0	0	3	0	0	0	0	0	0	0	0	18	0	141	0	68
SSMS0033	0	0	0	0	0	0	7	0	0	686	0	0	0	11	8	0	0	0	0	0	0	0	0
SSMS0035	0	0	0	0	0	0	7	6	0	3	0	0	1	0	1	1	0	0	0	0	0	0	0
SSMS0037	48	0	0	10	0	0	8	15	0	0	0	1	18	17	5	0	0	0	2	0	0	0	2
SSMS0038	0	0	0	0	0	0	0	0	0	13	0	0	0	1	3	0	0	0	0	0	0	0	7
SSMS0044	12	0	0	1	0	0	0	0	0	4	0	10	0	49	79	5	0	0	19	0	4	0	25
SSMS0051	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0
SSMS0053	3	0	0	7	0	4	0	18	0	6	0	6	0	2	0	0	0	0	0	0	5	0	0
SSMS0057	0	0	0	0	3	0	0	0	0	84	0	0	1	3	0	0	0	0	21	0	0	0	0
SSMS0059	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
SSMS0073	0	0	0	0	0	0	22	0	0	124	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS0078	123	0	0	2	0	0	1	2	0	93	0	0	0	9	0	0	0	0	0	0	0	0	0
SSMS0094	0	0	0	3	0	23	0	5	0	35	0	0	118	6	42	3	0	0	7	0	0	0	45
SSMS0105	0	0	0	0	0	0	0	0	0	17	0	0	1	0	0	0	0	0	0	0	0	0	2
SSMS0126	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

	<i>Paracloeodes</i>	<i>Paragrypopteryx</i>	<i>Paramaka</i>	<i>Phylloicus</i>	<i>Polycentropus</i>	<i>Polyplectropus</i>	<i>Protoptila</i>	<i>Rivudiva</i>	<i>Simothraulopsis</i>	<i>Smicridea</i>	<i>Spiritiops</i>	<i>Terpides</i>	<i>Thraulodes</i>	<i>Traverhypes</i>	<i>Tricorythodes</i>	<i>Tricorythopsis</i>	<i>Triplectides</i>	<i>Tupiperla</i>	<i>Ulmeritoides</i>	<i>Varipes</i>	<i>Waltzophius</i>	<i>Wormaldia</i>	<i>Zelus</i>
SSMS0129	5	0	0	0	0	1	0	0	0	1	0	0	0	5	5	0	0	0	0	0	0	0	2
SSMS0133	59	0	0	0	0	6	1	6	0	35	0	1	0	17	33	6	0	0	1	0	0	0	2
SSMS0144	0	0	0	2	1	3	1	0	0	0	0	0	0	16	2	0	0	0	0	0	2	0	5
SSMS0149	4	0	0	0	0	0	1	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0
SSMS0150	2	0	0	0	0	0	0	0	0	13	0	0	33	8	2	1	1	0	0	0	0	0	1
SSMS0157	0	0	0	66	7	1	0	0	0	7	0	0	0	9	0	0	3	0	6	0	2	0	13
SSMS0175	7	0	1	8	1	6	6	0	0	133	0	2	300	17	3	0	0	0	3	0	6	38	27
SSMS0191	39	0	0	0	0	0	1	14	0	7	0	0	12	7	42	2	0	0	5	0	6	1	62
SSMS0193	7	0	0	0	0	0	0	6	0	57	0	0	0	87	48	0	0	0	2	0	0	0	2
SSMS0199	0	0	0	1	4	0	0	0	0	0	0	1	0	1	0	2	0	0	5	0	1	0	11
SSMS0213	1	0	0	2	0	1	6	0	0	15	0	0	20	3	3	5	0	0	1	0	0	0	1
SSMS0351	21	0	1	3	0	1	4	0	0	30	0	10	141	47	5	4	0	0	2	0	0	1	1
SSMS0408	0	0	0	1	0	0	0	0	0	13	0	0	0	12	0	0	0	0	0	0	1	0	0
SSMS0411	57	0	0	2	0	1	4	7	0	24	0	0	69	78	9	0	0	0	12	0	2	0	6
SSMS0447	8	0	0	1	0	0	2	6	0	2	0	0	2	3	14	1	0	0	2	0	1	0	22
SSMS1000	0	0	0	0	0	0	0	0	0	20	0	1	35	23	0	0	0	0	0	0	3	0	4
SSMS4173	0	0	0	0	0	0	0	0	0	439	0	0	0	0	0	0	0	0	0	0	0	0	0
SSMS4330	1	0	0	3	0	0	1	0	0	18	0	0	0	52	0	0	0	0	13	0	0	0	1
RENP0008	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	41	0	0
RENP0012	6	3	0	2	0	4	0	0	0	31	0	0	2	389	0	73	0	5	0	0	0	0	0
RENP0016	9	0	0	1	0	8	0	0	1	0	0	0	153	22	0	88	0	0	2	0	2	0	0
RENP0028	2	0	0	0	0	1	0	0	0	5	0	0	17	14	0	11	1	1	2	0	1	0	2
RENP0047	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0
RENP0052	0	59	0	1	0	0	0	0	0	9	0	0	0	38	0	0	1	9	0	0	0	0	0
RENP0054	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	4	0	0	1	0	13
RENP0055	0	3	0	0	0	0	0	0	0	0	0	0	0	5	0	19	0	1	0	0	4	0	1
RENP0075	75	0	0	2	1	21	0	0	6	2	0	27	67	66	11	74	0	0	59	0	1	0	0
RENP0092	2	0	0	0	0	0	0	0	0	42	0	0	0	4	0	0	2	5	6	0	0	0	0
RENP0095	0	1	0	29	0	0	0	0	0	0	0	0	0	5	17	1	54	18	0	0	0	0	1
RENP0096	9	0	0	0	0	0	0	3	0	20	0	0	103	41	2	24	5	0	1	0	0	0	0
RENP0097	0	0	0	0	0	0	0	0	0	17	0	0	8	62	0	0	0	2	0	0	1	0	0
RENP0100	20	0	0	2	1	3	0	0	0	7	0	0	211	88	0	183	3	4	0	0	4	0	0
RENP0108	2	35	0	7	0	0	0	0	0	37	0	0	1	2	5	6	2	101	0	0	0	0	4

	<i>Paracloeodes</i>	<i>Paragrypopteryx</i>	<i>Paramaka</i>	<i>Phylloicus</i>	<i>Polycentropus</i>	<i>Polyplectropus</i>	<i>Protoptila</i>	<i>Rivudiva</i>	<i>Simothraulopsis</i>	<i>Smicridea</i>	<i>Spiritiops</i>	<i>Terpides</i>	<i>Thraulodes</i>	<i>Traverhypes</i>	<i>Tricorythodes</i>	<i>Tricorythopsis</i>	<i>Triplectides</i>	<i>Tupiperla</i>	<i>Ulmeritoides</i>	<i>Varipes</i>	<i>Waltzophius</i>	<i>Wormaldia</i>	<i>Zelus</i>
REN0110	9	0	0	1	0	0	1	0	0	22	0	0	0	40	6	9	0	6	0	0	0	0	2
REN0112	23	0	0	1	0	0	0	0	0	23	0	3	61	146	0	4	13	0	20	0	2	0	45
REN0128	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92	0	1	
REN0132	3	5	0	0	0	1	0	0	0	0	0	0	16	81	2	57	10	106	0	0	6	0	6
REN0139	1	0	0	0	0	0	0	0	0	7	0	0	0	5	0	2	0	0	3	0	5	0	8
REN0144	91	1	0	0	0	1	0	0	0	0	0	0	34	24	0	0	0	3	18	0	0	0	6
REN0187	2	4	0	0	0	0	0	0	0	3	0	0	0	21	0	35	0	1	0	0	0	0	0
REN0192	0	0	0	0	0	0	0	0	0	10	0	0	0	0	0	1	0	0	0	0	0	0	0
REN0203	1	0	0	0	1	2	2	0	0	0	0	0	1	637	0	219	1	7	0	0	0	0	0
REN0228	3	2	0	11	0	0	0	0	0	13	0	0	0	25	1	0	3	2	0	0	2	0	0
REN0240	0	0	0	6	0	0	0	0	0	4	0	0	0	0	0	0	0	0	1	0	0	0	0
REN0251	0	12	0	0	0	0	0	0	0	2	0	0	0	122	0	28	0	15	0	0	1	0	1
REN0287	34	7	0	17	0	0	0	0	0	56	0	0	0	0	0	0	8	113	13	0	1	0	25
REN0368	1	0	0	0	0	0	0	0	0	0	0	0	1	68	1	9	4	1	1	0	4	0	1
REN0375	17	0	0	1	0	0	0	0	0	11	0	0	303	23	0	136	0	1	0	0	0	0	1
REN0443	1	2	0	0	0	0	0	0	0	1	0	0	0	58	0	42	0	0	2	0	0	0	3
REN0511	12	0	0	1	0	0	64	1	0	14	0	0	3	91	1	88	1	0	9	4	1	0	1
REN1524	0	0	0	0	0	0	0	0	0	5	0	0	4	0	0	0	0	0	0	0	34	0	1
REN2991	26	0	0	0	0	0	0	0	0	13	0	0	30	68	0	7	0	0	4	0	14	0	1
REN5612	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
REN7308	0	3	0	13	0	0	0	0	0	25	0	0	0	21	0	10	42	25	59	0	0	0	13
REN9611	0	4	0	5	0	0	0	0	0	10	0	0	0	27	0	7	17	11	0	0	0	0	9
REN9757	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
REN12892	1	0	0	0	0	0	0	0	0	49	0	1	0	0	0	0	0	0	6	0	4	0	0
REN15048	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA02	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0
RCA08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	169	0	0	0	0
RCA22	38	0	0	0	2	2	0	0	0	0	0	0	0	2	1	11	1	0	0	0	0	0	0
RCA23	8	0	0	0	1	0	0	0	0	98	0	0	0	0	0	16	37	0	0	0	0	0	2
RCA30	8	0	0	1	1	0	0	0	0	1	0	0	0	0	3	21	0	0	0	0	0	0	2
RCA31	0	0	0	1	0	0	0	0	0	0	0	0	5	1	0	0	0	0	0	0	0	0	0
RCA44	0	0	0	4	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA48	0	0	0	0	0	2	0	0	0	171	0	0	109	137	0	39	0	0	0	0	0	0	0

	<i>Paracloeodes</i>	<i>Paragrypopteryx</i>	<i>Paramaka</i>	<i>Phylloicus</i>	<i>Polycentropus</i>	<i>Polyplectropus</i>	<i>Protoptila</i>	<i>Rivudiva</i>	<i>Simothraulopsis</i>	<i>Smicridea</i>	<i>Spiritiops</i>	<i>Terpides</i>	<i>Thraulodes</i>	<i>Traverhypes</i>	<i>Tricorythodes</i>	<i>Tricorythopsis</i>	<i>Triplectides</i>	<i>Tupiperla</i>	<i>Ulmeritoidea</i>	<i>Varipes</i>	<i>Waltzophyphus</i>	<i>Wormaldia</i>	<i>Zelus</i>
RCA49	0	0	0	12	0	0	0	0	0	77	0	0	0	85	0	34	1	10	11	0	7	0	2
RCA50	2	0	0	0	0	1	0	0	0	0	0	0	18	3	0	4	0	0	0	0	0	0	0
RCA52	2	0	0	0	2	17	0	0	0	37	0	0	159	22	0	108	2	0	0	0	0	3	0
RCA53	0	0	0	0	0	4	0	0	0	11	0	0	9	2	0	11	0	0	0	0	0	0	0
RCA57	38	0	0	5	0	2	0	0	0	0	0	0	0	1	0	20	0	0	0	0	0	0	0
RCA58	1	0	0	0	0	0	0	0	0	6	0	0	0	1	0	0	0	0	0	0	0	0	0
RCA59	13	30	0	0	0	0	0	0	0	71	0	0	0	1	0	61	0	1	0	0	0	0	0
RCA60	0	7	0	0	0	2	0	0	0	19	0	0	0	1	0	19	0	0	0	0	0	0	0
RCA62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RCA64	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	1	0	2	0	0	1	0
RCA65	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	11	0	0	0	0	0	0	0
RCA66	1	0	0	2	0	1	0	0	0	0	0	12	0	0	41	0	3	0	8	0	0	0	0
RCA67	1	0	0	4	0	2	0	0	0	8	0	13	0	40	0	4	6	1	14	0	2	0	0
RCA68	0	0	0	4	1	3	0	0	0	26	0	0	13	73	0	22	1	0	0	0	0	0	1
RCA69	0	0	0	3	0	0	0	0	0	16	0	1	6	16	0	8	2	2	0	0	1	0	0
RCA70	0	1	0	0	0	0	0	0	0	5	0	0	0	1	0	1	0	0	0	0	0	0	0
RCA71	0	2	0	8	0	1	0	0	0	24	0	0	0	29	0	18	7	1	51	0	0	0	3
RCA72	0	0	0	1	0	0	0	0	0	13	0	0	0	66	0	4	0	0	0	0	0	0	0
RCA73	0	0	0	0	0	2	0	0	0	20	0	0	37	14	0	3	0	0	0	0	0	0	0
RCA74	0	0	0	0	0	0	0	0	0	12	0	0	26	5	0	12	0	0	0	1	0	0	0
RCA90	2	0	0	0	0	0	2	0	0	1	0	0	8	5	0	22	1	0	0	0	0	0	0

Appendix 4: Abundance, count and average body size of each taxon measured in each sampling site.

Site	Taxon	Abundance	Count	Average size (cm)
TMMS0003	<i>Farrodes</i>	81	7	3.81
TMMS0003	<i>Hydrosmilodon</i>	312	69	3.84
TMMS0003	<i>Tricorythodes</i>	149	32	3.19
TMMS0007	<i>Hexagenia</i>	4	4	5.27
TMMS0009	<i>Cloeodes</i>	23	22	2.91
TMMS0028	<i>Caenis</i>	112	10	4.65
TMMS0028	<i>Farrodes</i>	35	19	2.57
TMMS0028	<i>Massartella</i>	3	3	7.66
TMMS0028	<i>Ulmeritoides</i>	7	3	5.60
TMMS0040	<i>Caenis</i>	66	23	2.48
TMMS0040	<i>Campylocia</i>	4	4	16.44
TMMS0040	<i>Cloeodes</i>	476	23	2.80
TMMS0040	<i>Massartella</i>	16	16	9.77
TMMS0040	<i>Miroculis</i>	21	10	3.19
TMMS0040	<i>Ulmeritoides</i>	5	3	8.33
TMMS0043	<i>Helicopsyche</i>	9	3	4.23
TMMS0043	<i>Miroculis</i>	14	7	2.99
TMMS0043	<i>Paracloeodes</i>	18	8	2.74
TMMS0043	<i>Ulmeritoides</i>	34	11	4.04
TMMS0058	<i>Americabaetis</i>	440	32	2.25
TMMS0058	<i>Apobaetis</i>	4	4	2.04
TMMS0058	<i>Caenis</i>	190	20	2.37
TMMS0058	<i>Chimarra</i>	26	22	5.82
TMMS0058	<i>Leptonema</i>	5	5	13.95
TMMS0058	<i>Smicridea</i>	55	36	4.97
TMMS0072	<i>Caenis</i>	53	18	2.64
TMMS0072	<i>Leptonema</i>	7	6	16.98
TMMS0072	<i>Oxyetira</i>	3	3	2.31
TMMS0072	<i>Polyplectropus</i>	6	4	7.40
TMMS0082	<i>Campsurus</i>	9	7	7.35
TMMS0088	<i>Callibaetis</i>	168	10	5.71
TMMS0088	<i>Helicopsyche</i>	11	5	3.72
TMMS0088	<i>Tricorythodes</i>	3	3	3.04
TMMS0088	<i>Tricorythopsis</i>	2	10	2.19
TMMS0090	<i>Campylocia</i>	17	16	7.84
TMMS0090	<i>Miroculis</i>	45	6	4.17
TMMS0090	<i>Paracloeodes</i>	19	4	2.68
TMMS0091	<i>Aturbina</i>	18	5	3.07
TMMS0091	<i>Callibaetis</i>	173	34	3.63
TMMS0091	<i>Leptohyphes</i>	6	6	2.95
TMMS0091	<i>Oxyetira</i>	11	6	1.83
TMMS0091	<i>Traverhyphes</i>	85	19	2.02
TMMS0119	<i>Asthenopus</i>	3	3	13.10
TMMS0119	<i>Macrostemun</i>	6	4	6.21
TMMS0126	<i>Zelus</i>	11	7	3.52
TMMS0134	<i>Miroculis</i>	40	8	2.86
TMMS0134	<i>Ulmeritoides</i>	11	5	2.80
TMMS0137	<i>Asthenopus</i>	22	16	5.40
TMMS0159	<i>Aturbina</i>	28	19	2.72
TMMS0159	<i>Callibaetis</i>	60	7	4.30
TMMS0159	<i>Latineosus</i>	8	7	2.74
TMMS0159	<i>Metrichia</i>	15	13	1.75
TMMS0159	<i>Oxyetira</i>	8	6	1.69
TMMS0171	<i>Hydrosmilodon</i>	12	10	2.99
TMMS0171	<i>Thraulodes</i>	69	25	2.59
TMMS0171	<i>Ulmeritoides</i>	4	3	4.89
TMMS0178	<i>Atopsyche</i>	20	3	4.31

Site	Taxon	Abundance	Count	Average size (cm)
TMMS0178	<i>Baetodes</i>	60	17	1.86
TMMS0178	<i>Cloeodes</i>	74	16	2.54
TMMS0178	<i>Farrodes</i>	34	19	2.26
TMMS0178	<i>Hydroptila</i>	26	5	2.07
TMMS0178	<i>Latineosus</i>	12	12	2.84
TMMS0178	<i>Metrichia</i>	3	3	1.69
TMMS0178	<i>Mortoniella</i>	3	3	1.97
TMMS0178	<i>Nectopsyche</i>	18	8	3.43
TMMS0178	<i>Thraulodes</i>	52	19	1.95
TMMS0178	<i>Traverhyphes</i>	343	84	2.66
TMMS0183	<i>Farrodes</i>	9	8	2.02
TMMS0183	<i>Hydrosmilodon</i>	6	4	2.40
TMMS0183	<i>Oecetis</i>	4	3	2.13
TMMS0183	<i>Polycentropus</i>	6	3	3.75
TMMS0187	<i>Asthenopus</i>	16	13	5.49
TMMS0187	<i>Cryptonympha</i>	17	8	2.66
TMMS0187	<i>Macronema</i>	4	3	12.10
TMMS0187	<i>Tricorythopsis</i>	11	9	1.88
TMMS0193	<i>Apobaetis</i>	1	3	3.03
TMMS0209	<i>Campsurus</i>	30	25	3.64
TMMS0209	<i>Polycentropus</i>	36	9	6.29
TMMS0220	<i>Cloeodes</i>	129	9	2.71
TMMS0220	<i>Smicridea</i>	55	36	3.35
TMMS0220	<i>Traverhyphes</i>	869	93	2.59
TMMS0279	<i>Polycentropus</i>	7	3	4.74
TMMS0279	<i>Tricorythopsis</i>	21	10	1.86
TMMS0283	<i>Americabaetis</i>	213	82	2.47
TMMS0283	<i>Atopsyche</i>	11	3	6.40
TMMS0283	<i>Farrodes</i>	11	8	3.26
TMMS0283	<i>Hermanella</i>	6	6	3.15
TMMS0283	<i>Leptohyphes</i>	7	5	2.50
TMMS0283	<i>Smicridea</i>	8	24	3.46
TMMS0296	<i>Caenis</i>	39	22	2.13
TMMS0296	<i>Campsurus</i>	15	12	8.30
TMMS0296	<i>Hydroptila</i>	24	8	1.69
TMMS0296	<i>Leptohyphes</i>	13	12	1.70
TMMS0296	<i>Metrichia</i>	50	39	1.36
TMMS0296	<i>Polyplectropus</i>	10	5	4.80
TMMS0296	<i>Smicridea</i>	38	20	4.33
TMMS0296	<i>Thraulodes</i>	50	28	2.18
TMMS0296	<i>Traverhyphes</i>	171	49	3.91
TMMS0296	<i>Tricorythodes</i>	6	4	3.83
TMMS0391	<i>Anchitrichia</i>	3	3	4.71
TMMS0391	<i>Cloeodes</i>	10	5	4.32
TMMS0437	<i>Americabaetis</i>	620	76	2.37
TMMS0437	<i>Apobaetis</i>	28	8	2.50
TMMS0437	<i>Asthenopus</i>	6	5	6.82
TMMS0437	<i>Campsurus</i>	32	19	7.02
TMMS0437	<i>Cyrnelus</i>	12	6	4.92
TMMS0437	<i>Farrodes</i>	31	8	2.88
TMMS0437	<i>Hydroptila</i>	9	7	2.08
TMMS0437	<i>Macronema</i>	30	11	12.12
TMMS0437	<i>Smicridea</i>	37	18	6.63
TMMS0437	<i>Waltzoyphius</i>	198	24	3.41
TMMS1865	<i>Asthenopus</i>	6	5	7.66
TMMS1865	<i>Callibaetis</i>	67	19	5.08
TMMS1865	<i>Simothraulopsis</i>	5	3	5.31
TMMS1865	<i>Waltzoyphius</i>	35	15	3.30
TMMS3962	<i>Caenis</i>	38	14	2.64

Site	Taxon	Abundance	Count	Average size (cm)
TMMS3962	<i>Oecetis</i>	5	5	4.34
TMMS3962	<i>Ulmeritoides</i>	7	3	5.80
VGMS0002	<i>Waltizoyphius</i>	22	5	3.26
VGMS0004	<i>Americabaetis</i>	347	31	3.03
VGMS0004	<i>Anacroneuria</i>	65	20	6.70
VGMS0004	<i>Austrotinodes</i>	8	8	3.75
VGMS0004	<i>Camelobaetidius</i>	47	4	3.29
VGMS0004	<i>Cloeodes</i>	8	4	1.96
VGMS0004	<i>Farrodes</i>	606	75	2.32
VGMS0004	<i>Hagenulopsis</i>	92	28	1.55
VGMS0004	<i>Hydroptila</i>	77	23	1.82
VGMS0004	<i>Leptohyphes</i>	147	24	2.39
VGMS0004	<i>Nectopsyche</i>	4	3	2.14
VGMS0004	<i>Thraulodes</i>	84	31	4.20
VGMS0004	<i>Ulmeritoides</i>	47	3	1.69
VGMS0004	<i>Zelus</i>	142	56	2.35
VGMS0016	<i>Americabaetis</i>	30	6	2.08
VGMS0016	<i>Leptohyphes</i>	11	3	2.60
VGMS0016	<i>Nectopsyche</i>	3	3	3.54
VGMS0016	<i>Traverhyphes</i>	17	13	2.31
VGMS0016	<i>Ulmeritoides</i>	8	6	5.32
VGMS0018	<i>Polycentropus</i>	7	6	4.15
VGMS0018	<i>Smicridea</i>	4	3	1.86
VGMS0018	<i>Traverhyphes</i>	16	5	3.83
VGMS0022	<i>Alisotrichia</i>	6	6	1.42
VGMS0022	<i>Metrichia</i>	4	4	1.95
VGMS0022	<i>Phylloicus</i>	123	75	3.59
VGMS0022	<i>Smicridea</i>	15	7	4.20
VGMS0022	<i>Traverhyphes</i>	20	13	2.83
VGMS0034	<i>Caenis</i>	73	35	2.83
VGMS0034	<i>Cloeodes</i>	34	8	2.19
VGMS0034	<i>Leptohyphes</i>	5	5	3.10
VGMS0034	<i>Phylloicus</i>	34	3	5.78
VGMS0034	<i>Smicridea</i>	22	14	3.30
VGMS0034	<i>Traverhyphes</i>	48	25	2.41
VGMS0044	<i>Itaura</i>	11	7	2.86
VGMS0044	<i>Marilia</i>	17	14	5.00
VGMS0044	<i>Miroculis</i>	51	27	4.23
VGMS0044	<i>Paracloeodes</i>	22	4	2.39
VGMS0044	<i>Phylloicus</i>	12	7	5.83
VGMS0044	<i>Rivudiva</i>	3	3	2.86
VGMS0044	<i>Terpides</i>	27	11	6.46
VGMS0044	<i>Traverhyphes</i>	7	5	3.24
VGMS0044	<i>Tricorythodes</i>	10	7	3.11
VGMS0044	<i>Ulmeritoides</i>	83	35	5.79
VGMS0048	<i>Anacroneuria</i>	36	13	4.66
VGMS0048	<i>Smicridea</i>	107	31	3.27
VGMS0080	<i>Americabaetis</i>	14	3	2.76
VGMS0109	<i>Polycentropus</i>	2	3	3.69
VGMS0109	<i>Tricorythodes</i>	20	10	2.27
VGMS0109	<i>Waltizoyphius</i>	10	4	2.92
VGMS0112	<i>Hermanella</i>	4	3	4.19
VGMS0112	<i>Leptohyphes</i>	20	13	2.64
VGMS0121	<i>Farrodes</i>	34	13	2.91
VGMS0121	<i>Hagenulopsis</i>	7	5	1.82
VGMS0124	<i>Aturbina</i>	20	13	2.90
VGMS0124	<i>Paracloeodes</i>	56	37	2.87
VGMS0124	<i>Smicridea</i>	3	3	4.70
VGMS0124	<i>Ulmeritoides</i>	13	6	1.84

Site	Taxon	Abundance	Count	Average size (cm)
VGMS0124	<i>Waltizoyphius</i>	10	4	5.29
VGMS0126	<i>Oecetis</i>	5	4	1.47
VGMS0126	<i>Phylloicus</i>	12	6	3.18
VGMS0162	<i>Atopsyche</i>	3	3	4.23
VGMS0162	<i>Leptohyphes</i>	16	9	2.21
VGMS0162	<i>Marilia</i>	3	3	4.68
VGMS0177	<i>Atopsyche</i>	3	3	4.81
VGMS0177	<i>Neotrichia</i>	10	3	1.23
VGMS0177	<i>Oecetis</i>	3	3	1.95
VGMS0177	<i>Polycentropus</i>	4	4	6.92
VGMS0191	<i>Americabaetis</i>	96	14	2.35
VGMS0191	<i>Smicridea</i>	280	12	2.63
VGMS0206	<i>Caenis</i>	90	41	2.37
VGMS0206	<i>Hagenulopsis</i>	8	4	1.97
VGMS0206	<i>Leptohyphes</i>	10	8	3.62
VGMS0206	<i>Marilia</i>	35	23	3.10
VGMS0206	<i>Phylloicus</i>	93	21	7.31
VGMS0206	<i>Traverhyphes</i>	90	25	2.90
VGMS0210	<i>Caenis</i>	21	13	2.57
VGMS0210	<i>Cloeodes</i>	126	18	2.47
VGMS0210	<i>Leptohyphes</i>	12	8	1.54
VGMS0210	<i>Traverhyphes</i>	35	9	2.30
VGMS0247	<i>Anacroneuria</i>	11	4	4.00
VGMS0255	<i>Traverhyphes</i>	13	7	2.42
VGMS0277	<i>Phylloicus</i>	7	6	8.34
VGMS0306	<i>Anacroneuria</i>	28	7	2.71
VGMS0306	<i>Atopsyche</i>	3	3	3.44
VGMS0306	<i>Aturbina</i>	72	24	2.44
VGMS0306	<i>Caenis</i>	31	16	3.13
VGMS0306	<i>Cloeodes</i>	88	8	2.29
VGMS0306	<i>Itaura</i>	121	24	2.23
VGMS0306	<i>Leptohyphes</i>	34	12	1.86
VGMS0306	<i>Nectopsyche</i>	4	4	3.38
VGMS0306	<i>Paracloeodes</i>	14	4	1.89
VGMS0306	<i>Thraulodes</i>	583	34	3.19
VGMS0306	<i>Tricorythodes</i>	49	10	3.12
VGMS0320	<i>Smicridea</i>	7	4	5.02
VGMS0380	<i>Miroculis</i>	32	13	2.80
VGMS0380	<i>Oecetis</i>	3	3	3.71
VGMS0380	<i>Phylloicus</i>	6	4	8.78
VGMS0380	<i>Traverhyphes</i>	38	26	3.26
VGMS0380	<i>Tricorythodes</i>	12	7	3.48
VGMS0380	<i>Ulmeritoides</i>	43	8	1.71
VGMS0387	<i>Baetodes</i>	30	14	1.72
VGMS0418	<i>Atanatolia</i>	6	5	3.58
VGMS0418	<i>Atopsyche</i>	26	19	3.54
VGMS0418	<i>Caenis</i>	7	3	2.37
VGMS0418	<i>Hagenulopsis</i>	23	3	2.77
VGMS0418	<i>Leptohyphes</i>	38	11	2.21
VGMS0418	<i>Marilia</i>	5	3	7.19
VGMS0418	<i>Phylloicus</i>	5	4	8.08
VGMS0418	<i>Tricorythodes</i>	78	31	1.92
VGMS0418	<i>Waltizoyphius</i>	25	3	2.49
VGMS0418	<i>Zelus</i>	6	3	4.50
VGMS0433	<i>Anacroneuria</i>	26	17	4.50
VGMS0433	<i>Atopsyche</i>	4	5	2.88
VGMS0433	<i>Zelus</i>	38	14	2.03
VGMS0444	<i>Anacroneuria</i>	26	4	1.40
VGMS0444	<i>Apobaetis</i>	44	18	2.56

Site	Taxon	Abundance	Count	Average size (cm)
VGMS0444	<i>Aturbina</i>	97	35	3.12
VGMS0444	<i>Baetodes</i>	510	39	1.79
VGMS0444	<i>Camelobaetidius</i>	32	4	2.35
VGMS0444	<i>Chimarra</i>	86	34	7.12
VGMS0444	<i>Leptohyphes</i>	380	80	2.14
VGMS0444	<i>Nectopsyche</i>	13	10	4.20
VGMS0444	<i>Protoptila</i>	32	15	2.64
VGMS0444	<i>Terpides</i>	10	5	3.78
VGMS0444	<i>Traverhyphes</i>	115	25	1.84
VGMS0444	<i>Waltzoyphius</i>	4	4	2.17
VGMS0511	<i>Americabaetis</i>	24	4	2.08
VGMS0515	<i>Itaura</i>	21	19	2.13
VGMS0515	<i>Protoptila</i>	8	4	2.47
VGMS0558	<i>Chimarra</i>	9	7	5.18
VGMS0558	<i>Leptonema</i>	36	6	14.51
VGMS0558	<i>Protoptila</i>	98	43	2.50
VGMS0558	<i>Smicridea</i>	210	38	3.50
VGMS0558	<i>Wormaldia</i>	3	3	6.70
VGMS0575	<i>Phylloicus</i>	14	7	3.99
SSMS0002	<i>Latineosus</i>	5	5	1.55
SSMS0002	<i>Nectopsyche</i>	35	4	2.90
SSMS0002	<i>Phylloicus</i>	52	19	3.79
SSMS0002	<i>Polypsectopus</i>	4	3	5.20
SSMS0002	<i>Ulmeritoides</i>	11	8	3.86
SSMS0008	<i>Hagenulopsis</i>	13	5	1.92
SSMS0008	<i>Hydroptila</i>	4	3	2.00
SSMS0008	<i>Macronema</i>	33	19	9.75
SSMS0008	<i>Marilia</i>	11	6	5.36
SSMS0008	<i>Terpides</i>	11	3	2.52
SSMS0008	<i>Traverhyphes</i>	35	12	3.21
SSMS0010	<i>Smicridea</i>	6	4	3.75
SSMS0014	<i>Itaura</i>	9	5	2.67
SSMS0028	<i>Caenis</i>	12	6	3.18
SSMS0028	<i>Leptonema</i>	3	3	12.89
SSMS0028	<i>Traverhyphes</i>	180	16	2.31
SSMS0029	<i>Austrotinodes</i>	3	3	2.51
SSMS0031	<i>Macronema</i>	131	13	9.79
SSMS0031	<i>Marilia</i>	4	3	5.81
SSMS0031	<i>Miroculis</i>	103	3	2.90
SSMS0031	<i>Polycentropus</i>	3	3	3.52
SSMS0031	<i>Waltzoyphius</i>	141	37	3.50
SSMS0031	<i>Zelus</i>	68	21	2.34
SSMS0033	<i>Protoptila</i>	7	4	2.85
SSMS0033	<i>Smicridea</i>	686	66	3.14
SSMS0035	<i>Mortoniella</i>	3	3	2.58
SSMS0035	<i>Rivulid</i>	6	5	3.28
SSMS0037	<i>Callibaetis</i>	53	23	3.80
SSMS0037	<i>Paracloeodes</i>	48	3	2.44
SSMS0037	<i>Phylloicus</i>	10	6	5.00
SSMS0037	<i>Protoptila</i>	8	6	2.21
SSMS0038	<i>Smicridea</i>	13	7	2.36
SSMS0044	<i>Caenis</i>	7	5	2.23
SSMS0053	<i>Americabaetis</i>	27	6	4.12
SSMS0053	<i>Anacronetia</i>	8	14	5.73
SSMS0053	<i>Polypsectopus</i>	4	3	4.13
SSMS0053	<i>Rivulid</i>	18	3	3.77
SSMS0057	<i>Baetodes</i>	4	3	1.58
SSMS0057	<i>Caenis</i>	33	5	3.40
SSMS0057	<i>Chimarra</i>	32	22	5.09

Site	Taxon	Abundance	Count	Average size (cm)
SSMS0057	<i>Polycentropus</i>	3	3	5.13
SSMS0057	<i>Smicridea</i>	84	29	3.91
SSMS0073	<i>Protoptila</i>	22	12	2.55
SSMS0073	<i>Smicridea</i>	124	31	3.61
SSMS0078	<i>Anacroneuria</i>	14	6	4.94
SSMS0078	<i>Leptonema</i>	5	3	16.80
SSMS0094	<i>Anacroneuria</i>	16	3	5.38
SSMS0094	<i>Itaura</i>	12	3	1.78
SSMS0094	<i>Polyplectropus</i>	23	18	4.94
SSMS0094	<i>Thraulodes</i>	118	22	3.01
SSMS0094	<i>Tricorythodes</i>	42	7	2.25
SSMS0129	<i>Caenis</i>	17	5	4.81
SSMS0133	<i>Helicopsyche</i>	14	8	3.15
SSMS0133	<i>Hydroptila</i>	160	57	1.85
SSMS0133	<i>Macronema</i>	6	4	4.74
SSMS0133	<i>Oxyetira</i>	21	16	1.81
SSMS0133	<i>Polyplectropus</i>	6	3	5.02
SSMS0133	<i>Rivulidva</i>	6	5	3.71
SSMS0133	<i>Smicridea</i>	35	21	4.03
SSMS0133	<i>Tricorythodes</i>	33	10	3.71
SSMS0133	<i>Tricorythopsis</i>	6	6	1.52
SSMS0144	<i>Polyplectropus</i>	3	3	6.02
SSMS0149	<i>Austrotinodes</i>	6	7	3.30
SSMS0149	<i>Helicopsyche</i>	5	3	4.80
SSMS0150	<i>Anacroneuria</i>	8	4	6.06
SSMS0150	<i>Leptohyphes</i>	12	3	3.58
SSMS0157	<i>Miroculis</i>	18	11	2.73
SSMS0157	<i>Nyctiophylax</i>	3	3	2.04
SSMS0157	<i>Phylloicus</i>	66	36	3.27
SSMS0157	<i>Polycentropus</i>	7	6	4.11
SSMS0157	<i>Tripletides</i>	3	3	2.55
SSMS0175	<i>Anacroneuria</i>	144	20	5.38
SSMS0175	<i>Baetodes</i>	341	13	1.45
SSMS0175	<i>Chimarra</i>	182	26	3.85
SSMS0175	<i>Farrodes</i>	46	14	2.67
SSMS0175	<i>Hagenulopsis</i>	6	4	1.93
SSMS0175	<i>Leptohyphes</i>	164	3	2.46
SSMS0175	<i>Leptonema</i>	12	3	15.07
SSMS0175	<i>Phylloicus</i>	8	5	3.82
SSMS0175	<i>Protoptila</i>	6	3	2.75
SSMS0175	<i>Smicridea</i>	133	18	3.08
SSMS0175	<i>Thraulodes</i>	300	18	3.42
SSMS0175	<i>Wormaldia</i>	38	28	1.87
SSMS0191	<i>Anacroneuria</i>	13	9	6.09
SSMS0191	<i>Chimarra</i>	10	9	3.76
SSMS0191	<i>Farrodes</i>	118	35	2.59
SSMS0191	<i>Helicopsyche</i>	23	6	4.25
SSMS0191	<i>Miroculis</i>	7	5	2.52
SSMS0191	<i>Traverhyphes</i>	7	6	2.56
SSMS0193	<i>Anacroneuria</i>	4	4	2.41
SSMS0193	<i>Caenis</i>	153	62	2.63
SSMS0193	<i>Leptonema</i>	4	3	16.00
SSMS0193	<i>Tikuna</i>	3	3	3.33
SSMS0193	<i>Traverhyphes</i>	87	33	2.52
SSMS0193	<i>Tricorythodes</i>	48	26	2.39
SSMS0199	<i>Helicopsyche</i>	10	4	3.22
SSMS0199	<i>Polycentropus</i>	4	4	4.01
SSMS0213	<i>Aturbina</i>	4	3	2.87
SSMS0213	<i>Camelobaetidius</i>	44	3	1.39

Site	Taxon	Abundance	Count	Average size (cm)
SSMS0213	<i>Hydrosmilodon</i>	19	6	2.51
SSMS0213	<i>Protophila</i>	6	3	2.45
SSMS0351	<i>Farrodes</i>	107	29	2.65
SSMS0351	<i>Helicopsyche</i>	7	6	2.76
SSMS0351	<i>Hydrosmilodon</i>	23	7	2.04
SSMS0351	<i>Leptonema</i>	13	5	13.86
SSMS0351	<i>Phylloicus</i>	3	3	10.97
SSMS0351	<i>Terpides</i>	10	6	4.67
SSMS0351	<i>Thraulodes</i>	141	11	3.13
SSMS0351	<i>Traverhyphes</i>	47	21	3.03
SSMS0408	<i>Smicridea</i>	13	4	5.78
SSMS0411	<i>Americabaetis</i>	368	41	1.82
SSMS0411	<i>Anacroneuria</i>	6	5	4.05
SSMS0411	<i>Aturbina</i>	50	18	2.42
SSMS0411	<i>Caenis</i>	10	7	3.72
SSMS0411	<i>Latineosus</i>	10	12	3.06
SSMS0411	<i>Leptohyphes</i>	14	10	2.21
SSMS0411	<i>Metrichia</i>	29	15	2.34
SSMS0411	<i>Nectopsyche</i>	11	8	2.81
SSMS0411	<i>Rivudiva</i>	7	26	3.23
SSMS0411	<i>Traverhyphes</i>	78	31	2.77
SSMS0411	<i>Ulmeritoides</i>	12	7	4.87
SSMS1000	<i>Baetodes</i>	61	7	1.81
SSMS1000	<i>Macronema</i>	7	4	2.52
SSMS1000	<i>Smicridea</i>	20	6	2.10
SSMS4173	<i>Smicridea</i>	439	66	4.27
SSMS4330	<i>Phylloicus</i>	3	3	9.87
SSMS4330	<i>Traverhyphes</i>	52	30	2.44
REN0008	<i>Anacroneuria</i>	10	5	10.60
REN0008	<i>Barypenthus</i>	9	8	8.80
REN0012	<i>Macrostemun</i>	3	4	9.93
REN0012	<i>Smicridea</i>	31	4	4.98
REN0012	<i>Tricorythopsis</i>	73	7	1.57
REN0016	<i>Atopsyche</i>	6	5	6.46
REN0016	<i>Farrodes</i>	15	9	3.14
REN0016	<i>Hydroptila</i>	6	4	1.86
REN0016	<i>Marilia</i>	3	3	5.38
REN0016	<i>Miroculis</i>	13	9	3.03
REN0016	<i>Polyplectropus</i>	8	6	5.22
REN0016	<i>Thraulodes</i>	153	77	3.53
REN0052	<i>Paragrypopteryx</i>	59	33	2.07
REN0052	<i>Tupiperla</i>	9	5	3.29
REN0054	<i>Leptohyphes</i>	3	4	4.99
REN0054	<i>Leptohyphodes</i>	9	8	5.44
REN0075	<i>Anacroneuria</i>	36	17	3.08
REN0075	<i>Atopsyche</i>	8	9	5.10
REN0075	<i>Campylocia</i>	3	3	16.21
REN0075	<i>Leptonema</i>	11	6	9.06
REN0075	<i>Marilia</i>	12	6	6.30
REN0075	<i>Polyplectropus</i>	21	9	6.20
REN0075	<i>Tricorythopsis</i>	74	13	1.71
REN0092	<i>Caenis</i>	33	9	2.76
REN0092	<i>Smicridea</i>	42	12	5.30
REN0095	<i>Marilia</i>	11	5	5.49
REN0095	<i>Phylloicus</i>	29	13	6.92
REN0095	<i>Tricorythodes</i>	17	16	2.80
REN0095	<i>Tupiperla</i>	18	4	4.02
REN0096	<i>Farrodes</i>	5	3	2.00
REN0096	<i>Smicridea</i>	20	8	4.20

Site	Taxon	Abundance	Count	Average size (cm)
REN0097	<i>Farrodes</i>	16	10	2.77
REN0100	<i>Callibaetis</i>	6	5	6.56
REN0100	<i>Farrodes</i>	17	11	2.74
REN0100	<i>Hagenulopsis</i>	58	38	3.67
REN0100	<i>Itaura</i>	51	22	1.87
REN0100	<i>Marilia</i>	6	3	5.07
REN0100	<i>Miroculis</i>	17	12	3.83
REN0100	<i>Nectopsyche</i>	11	6	4.15
REN0100	<i>Thraulodes</i>	211	17	3.06
REN0100	<i>Tupiperla</i>	4	3	4.60
REN0108	<i>Leptonema</i>	27	16	4.31
REN0108	<i>Paragrypopteryx</i>	35	20	2.05
REN0108	<i>Phylloicus</i>	7	6	6.10
REN0108	<i>Tricorythodes</i>	5	5	3.18
REN0108	<i>Tupiperla</i>	101	44	3.80
REN0110	<i>Americabaetis</i>	65	103	2.87
REN0110	<i>Neotrichia</i>	2	5	1.33
REN0112	<i>Anacroneuria</i>	20	7	2.96
REN0112	<i>Austrotinodes</i>	8	5	3.21
REN0112	<i>Caenis</i>	191	93	2.58
REN0112	<i>Callibaetis</i>	6	5	4.32
REN0112	<i>Traverhyphes</i>	146	55	2.85
REN0112	<i>Zelus</i>	45	7	3.79
REN0132	<i>Tupiperla</i>	106	77	3.44
REN0139	<i>Leptonema</i>	10	6	7.94
REN0139	<i>Smicridea</i>	7	3	2.34
REN0144	<i>Americabaetis</i>	23	11	2.01
REN0144	<i>Aturbina</i>	56	32	3.86
REN0144	<i>Baetodes</i>	16	13	1.67
REN0144	<i>Callibaetis</i>	5	4	4.57
REN0144	<i>Cloeodes</i>	6	4	3.35
REN0144	<i>Farrodes</i>	8	5	2.40
REN0144	<i>Marilia</i>	5	3	5.97
REN0144	<i>Miroculis</i>	13	8	3.54
REN0144	<i>Paracloeodes</i>	91	45	3.19
REN0144	<i>Tupiperla</i>	3	3	3.70
REN0144	<i>Zelus</i>	6	4	2.80
REN0187	<i>Paragrypopteryx</i>	4	3	1.92
REN0187	<i>Tricorythopsis</i>	35	4	1.91
REN0203	<i>Camelobaetidius</i>	6	3	3.75
REN0203	<i>Leptonema</i>	14	8	12.11
REN0203	<i>Traverhyphes</i>	637	148	2.78
REN0203	<i>Tricorythopsis</i>	219	73	1.93
REN0203	<i>Tupiperla</i>	7	3	2.21
REN0228	<i>Grypopteryx</i>	9	9	3.27
REN0240	<i>Askola</i>	10	9	4.04
REN0251	<i>Americabaetis</i>	26	5	1.99
REN0251	<i>Grypopteryx</i>	7	6	1.95
REN0251	<i>Kempnys</i>	3	3	7.12
REN0251	<i>Metrichia</i>	7	6	1.86
REN0251	<i>Paragrypopteryx</i>	12	11	1.62
REN0251	<i>Tupiperla</i>	15	3	2.05
REN0287	<i>Callibaetis</i>	155	40	4.89
REN0287	<i>Farrodes</i>	75	23	3.76
REN0287	<i>Massartella</i>	14	14	5.16
REN0287	<i>Miroculis</i>	5	3	5.63
REN0287	<i>Oecetis</i>	4	3	3.16
REN0287	<i>Paracloeodes</i>	34	6	2.81
REN0287	<i>Paragrypopteryx</i>	7	5	1.72

Site	Taxon	Abundance	Count	Average size (cm)
REN0287	<i>Phylloicus</i>	17	5	4.52
REN0287	<i>Smicridea</i>	56	23	4.88
REN0287	<i>Triplectides</i>	8	3	5.46
REN0287	<i>Tupiperla</i>	113	28	3.79
REN0375	<i>Atopsyche</i>	5	4	8.24
REN0375	<i>Hagenulopsis</i>	11	8	3.02
REN0375	<i>Smicridea</i>	11	5	4.58
REN0443	<i>Itaura</i>	20	8	2.09
REN0443	<i>Zelus</i>	3	3	2.63
REN0511	<i>Itaura</i>	119	22	2.24
REN0511	<i>Oecetis</i>	9	7	2.07
REN0511	<i>Protophila</i>	64	23	2.55
REN0511	<i>Tricorythopsis</i>	88	19	1.48
REN1524	<i>Askola</i>	6	6	3.08
REN1524	<i>Itaura</i>	13	5	2.38
REN1524	<i>Leptonema</i>	6	3	10.10
REN1524	<i>Marilia</i>	27	9	3.67
REN2991	<i>Americabaetis</i>	150	54	4.41
REN2991	<i>Atopsyche</i>	24	9	4.40
REN2991	<i>Cryptonympha</i>	14	3	3.42
REN2991	<i>Itaura</i>	27	13	1.88
REN2991	<i>Paracloeodes</i>	26	10	2.40
REN2991	<i>Waltzophius</i>	14	8	4.09
REN7308	<i>Askola</i>	11	4	3.17
REN7308	<i>Barypenthus</i>	4	3	11.05
REN7308	<i>Campylocia</i>	14	13	10.01
REN7308	<i>Farrodes</i>	13	6	3.25
REN7308	<i>Hagenulopsis</i>	8	4	3.92
REN7308	<i>Leptohyphodes</i>	7	6	7.10
REN7308	<i>Massartella</i>	23	20	7.00
REN7308	<i>Miroculis</i>	26	9	3.71
REN7308	<i>Phylloicus</i>	13	3	5.16
REN7308	<i>Triplectides</i>	42	4	8.11
REN7308	<i>Tupiperla</i>	25	16	3.50
REN7308	<i>Ulmeritoides</i>	59	41	3.83
REN9611	<i>Leptonema</i>	8	3	11.37
REN9611	<i>Phylloicus</i>	5	5	9.45
REN9611	<i>Triplectides</i>	17	6	10.89
REN9611	<i>Tupiperla</i>	11	6	6.12
REN12892	<i>Oxyetira</i>	128	41	2.60
REN12892	<i>Smicridea</i>	49	34	3.84

Appendix 5: Geographic coordinates (pseudo-mercator) of each sampling site.

	XN	YN
TMMS0003	-5004750	-2126023
TMMS0007	-4972390	-2145335
TMMS0009	-5072223	-2136948
TMMS0027	-5008322	-2091517
TMMS0028	-5087172	-2153538
TMMS0033	-5050820	-2182975
TMMS0040	-5084544	-2166847
TMMS0043	-5008248	-2084999
TMMS0058	-5028051	-2164074
TMMS0072	-5084166	-2088968
TMMS0082	-5059776	-2165143
TMMS0088	-5077452	-2101090
TMMS0090	-5032387	-2177727
TMMS0091	-5011468	-2098094
TMMS0106	-5025505	-2167614
TMMS0119	-4990320	-2123820
TMMS0126	-5010063	-2140963
TMMS0133	-5035765	-2181756
TMMS0134	-5011200	-2156475
TMMS0137	-5068465	-2129999
TMMS0159	-5009753	-2075817
TMMS0171	-5022241	-2076486
TMMS0178	-5037971	-2154479
TMMS0183	-4985081	-2135849
TMMS0187	-5022757	-2089236
TMMS0193	-5066444	-2192409
TMMS0209	-5056364	-2185712
TMMS0214	-5012401	-2164986
TMMS0220	-5080251	-2149399
TMMS0279	-4975397	-2159685
TMMS0283	-5010553	-2083446
TMMS0290	-5059075	-2176289
TMMS0296	-5080568	-2161000
TMMS0391	-4967616	-2148333
TMMS0437	-5070297	-2140772
TMMS1865	-5066888	-2128753
TMMS3195	-5032925	-2065596
TMMS3962	-5004644	-2111141
VGMS00002	-5326258	-2244702
VGMS00004	-5318625	-2287935
VGMS00016	-5340011	-2261589
VGMS00018	-5312304	-2248158
VGMS00022	-5306571	-2253297
VGMS00034	-5323168	-2243889
VGMS00037	-5345010	-2266346
VGMS00044	-5341554	-2252390
VGMS00048	-5356907	-2261993
VGMS00080	-5346036	-2263545
VGMS00109	-5322995	-2255848
VGMS00112	-5353010	-2263343
VGMS00121	-5332599	-2260880
VGMS00124	-5351154	-2247651
VGMS00126	-5313693	-2307859
VGMS00128	-5368684	-2258779
VGMS00162	-5321331	-2250967
VGMS00177	-5356053	-2271250
VGMS00191	-5323158	-2282967
VGMS00206	-5314518	-2293294
VGMS00210	-5320238	-2243733

	XN	YN
VGMS00247	-5310177	-2311374
VGMS00252	-5339644	-2265206
VGMS00255	-5317948	-2282474
VGMS00277	-5340319	-2267512
VGMS00306	-5321099	-2247594
VGMS00320	-5352835	-2248199
VGMS00380	-5353615	-2251879
VGMS00387	-5324336	-2308152
VGMS00418	-5319546	-2247685
VGMS00433	-5353179	-2269349
VGMS00444	-5339265	-2259219
VGMS00447	-5321195	-2280954
VGMS00450	-5311717	-2252843
VGMS00511	-5317390	-2284070
VGMS00515	-5318759	-2306905
VGMS00558	-5314345	-2298670
VGMS00575	-5315793	-2285833
SSMS0001	-5659094	-2124221
SSMS0002	-5515157	-2145194
SSMS0008	-5495045	-2079551
SSMS0010	-5603289	-2160963
SSMS0014	-5637589	-2121498
SSMS0028	-5541379	-2094286
SSMS0029	-5549126	-2131715
SSMS0031	-5631492	-2101506
SSMS0033	-5555716	-2158091
SSMS0035	-5639297	-2137661
SSMS0037	-5532310	-2134461
SSMS0038	-5571472	-2150876
SSMS0044	-5524368	-2078213
SSMS0051	-5569751	-2061765
SSMS0053	-5532425	-2151622
SSMS0057	-5556096	-2152442
SSMS0059	-5627459	-2081248
SSMS0073	-5524773	-2116908
SSMS0078	-5652950	-2121606
SSMS0094	-5639594	-2130108
SSMS0105	-5566612	-2135756
SSMS0126	-5631319	-2122483
SSMS0129	-5561747	-2159236
SSMS0133	-5525438	-2163278
SSMS0144	-5558142	-2072888
SSMS0149	-5541030	-2152985
SSMS0150	-5576997	-2145713
SSMS0157	-5511353	-2133206
SSMS0175	-5621549	-2107708
SSMS0191	-5639510	-2082252
SSMS0193	-5561676	-2159509
SSMS0199	-5576777	-2066224
SSMS0213	-5541996	-2149359
SSMS0351	-5625084	-2098036
SSMS0408	-5519969	-2108761
SSMS0411	-5607935	-2079929
SSMS0447	-5639767	-2085368
SSMS1000	-5522800	-2117123
SSMS4173	-5507053	-2150245
SSMS4330	-5508137	-2095185
RENPO008	-5292426	-2191103
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REN0028	-5256068	-2182408
REN0047	-5219796	-2207514
REN0052	-5304098	-2202266
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REN0055	-5217844	-2156991
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REN0092	-5260559	-2191396
REN0095	-5211962	-2186358
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REN0100	-5236062	-2179200
REN0108	-5245483	-2191019
REN0110	-5284615	-2230633
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REN0128	-5272763	-2157352
REN0132	-5230236	-2181848
REN0139	-5239032	-2147196
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REN12892	-5260215	-2190168
REN15048	-5290278	-2191936