

Input File: Workbook - [parametrosfarmacocineticos_atenololSPH58_08_ID.pwo]

Date: 2/12/2010
Time: 14:40:18

WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE
Version 5.2.1 Build 2008033011
Core Version 17Oct2006

Model Specification and User Settings

```
Dependent variable : Cmax
Transform : LN
Fixed terms : int+sequence+form+period
Random/repeated terms : sequence*subject
Maximum iterations : 50
Convergence Criterion : 1e-010
Singularity tolerance : 1e-010
Denominator df option : residual
```

Class variables and their levels

Using method of moments for starting values

Starting estimates of variance parameters:

Var(sequence*subject) 0.131534
 Var(Residual) 0.0552627

Diagnostics

Total Observations :	32
Observations Used :	32
Obs. Missing Model Terms :	0
Residual SS :	0.7736777
Residual df :	14
Residual Variance :	0.0552627

Breakout of variance structure

```
-----  
          Variance Index : 1  
          Source : Random  
          Type : Variance Components  
          Columns : sequence*subject  
          Parameters : Var(sequence*subject)
```

```
Variance Index : 2
    Source : Assumed
        Type : Identity
    Columns : None
Parameters : Var(Residual)
```

Variance parameter estimation at each iteration:

```

          Objective
Iteration    function Var(sequence*subject)  Var(Residual)
      0      -14.2823        0.131534        0.0552627

```

Newton's algorithm converged.

Final variance parameter estimates:

Var(sequence*subject)	0.131534
Var(Residual)	0.0552627
Intersubject CV	0.374935
Intrasubject CV	0.238366

REML log(likelihood) -11.448
 -2* REML log(likelihood) 22.8961
 Akaike Information Crit. 34.8961
 Schwarz Bayesian Crit. 42.8893

Ordered Final Hessian Eigenvalues:
 2370.3
 267.198

Solution

	Effect:Level	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
6.253	int	6.5602	0.143254	14	45.7942	0.0000	95	2.145
0.5809	sequence:RT	-0.139069	0.20602	14	-0.67503	0.5107	95	2.145
0.1698	sequence:TR	Not estimable						-
0.0828	form:R	0.0143156	0.0858391	14	0.166773	0.8699	95	2.145
	0.1984							-
	form:T	Not estimable						-
	period:1	0.10131	0.0858391	14	1.18023	0.2576	95	2.145
	0.2854							-
	period:2	Not estimable						-

Sequential Tests of Model Effects

Hypothesis	Numer_DF	Denom_DF	F_stat	P_value
int	1	14	4333.67	0.0000
sequence	1	14	0.455665	0.5107
form	1	14	0.0175538	0.8965
period	1	14	1.39293	0.2576

Sequential Sum of Squares

Hypothesis	DF	SS	MS	F_stat
sequence	1	0.145052	0.145052	0.455665
sequence*subject	14	4.45663	0.31833	5.76031
form	1	0.000970071	0.000970071	0.0175538
period	1	0.0769772	0.0769772	1.39293
Error	14	0.773677	0.0552627	

Partial Tests of Model Effects

Hypothesis	Numer_DF	Denom_DF	F_stat	P_value
int	1	14	4041.33	0.0000
sequence	1	14	0.455665	0.5107
form	1	14	0.0278131	0.8699
period	1	14	1.39293	0.2576

Partial Sum of Squares

Hypothesis	DF	SS	MS	F_stat
sequence	1	0.145052	0.145052	0.455665
sequence*subject	14	4.45663	0.31833	5.76031
form	1	0.00153703	0.00153703	0.0278131

0.8699
 0.2576

	period	1	0.0769772	0.0769772	1.39293			
	Error	14	0.773677	0.0552627				
Least squares means								
	form	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
-----	-----	-----	-----	-----	-----	-----	-----	-----
6.359	R	6.55564	0.111593	14	58.7457	0.0000	90	1.761
	T	6.54132	0.111593	14	58.6174	0.0000	90	1.761
6.345	6.738							
Differences between means								
	form	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
-----	-----	-----	-----	-----	-----	-----	-----	-----
0.1369	R - T	0.0143156	0.0858391	14	0.166773	0.8699	90	1.761
	0.1655							-
Bioequivalence Statistics								
User-Specified Confidence Level for CI's and Power = 90.0000								
Percent of Reference to Detect for 2-1 Tests and Power = 20.0%								
A.H.Lower = 0.800 A.H.Upper = 1.250								
Formulation variable: form								
Reference: R LSMean= 6.555638 SE= 0.111593 GeoLSM= 703.197624								
Test: T LSMean= 6.541322 SE= 0.111593 GeoLSM= 693.202624								
Difference = -0.0143, Diff_SE= 0.0858, df= 14.0								
Ratio(%Ref) = 98.5786								
Classical								
CI 80% = (87.8281, 110.6451) (88.4629, 111.5371)								
CI 90% = (84.7435, 114.6725) (84.9877, 115.0123)								
CI 95% = (81.9986, 118.5112) (81.7882, 118.2118)								
Average bioequivalence shown for confidence=90.00 and percent=20.0.								
Two One-Sided T-tests								
Prob(< 80%)=0.0145 Prob(> 125%)=0.0076 Max=0.0145 Total=0.0221								
Anderson-Hauck Procedure								
A.H. p-value = 0.006918								
Power of ANOVA for Confidence Level 90.00								
Power at 20% = 0.792223								

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Version 5.2.1 Build 2008033011
Core Version 17Oct2006

Model Specification and User Settings

```
Dependent variable : AUClast
        Transform : LN
      Fixed terms : int+sequence+form+period
Random/repeated terms : sequence*subject
  Maximum iterations : 50
Convergence Criterion : 1e-010
Singularity tolerance : 1e-010
Denominator df option : residual
```

Class variables and their levels

Using method of moments for starting values
Starting estimates of variance parameters:

Var(sequence*subject) 0.132386
 Var(Residual) 0.0220492

Diagnostics

```

      Total Observations : 32
      Observations Used : 32
Obs. Missing Model Terms : 0
                  Residual SS : 0.308689
                  Residual df : 14
      Residual Variance : 0.0220492

```

Breakout of variance structure

```
-----  
          Variance Index : 1  
          Source : Random  
          Type : Variance Components  
          Columns : sequence*subject  
          Parameters : Var(sequence*subject)  
-----  
          Variance Index : 2  
          Source : Assumed  
          Type : Identity  
          Columns : None  
          Parameters : Var(Residual)
```

Variance parameter estimation at each iteration:

	Objective		
Iteration	function	Var(sequence*subject)	Var(Residual)
0	-21.4436	0.132386	0.0220492

Newton's algorithm converged.

Final variance parameter estimates:

Var(sequence*subject)	0.132386
Var(Residual)	0.0220492
Intersubject CV	0.376229
Intrasubject CV	0.149312

REML log(likelihood) -4.28666
 -2* REML log(likelihood) 8.57332
 Akaike Information Crit. 20.5733
 Schwarz Bayesian Crit. 28.5665

Ordered Final Hessian Eigenvalues:
 14485.4
 338.311

Solution

	Effect:Level	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
8.353	int	8.62617	0.127195	14	67.8187	0.0000	95	2.145
0.4457	sequence:RT	-0.0262531	0.195558	14	-0.134247	0.8951	95	2.145
0.05579	sequence:TR	Not estimable						-
0.09603	form:R	0.0605059	0.0542208	14	1.11592	0.2832	95	2.145
0.09603	form:T	Not estimable						-
0.09603	period:1	0.0202652	0.0542208	14	0.373754	0.7142	95	2.145
0.09603	period:2	0.1366	Not estimable					-

Sequential Tests of Model Effects

	Hypothesis	Numer_DF	Denom_DF	F_stat	P_value
0.8951	int	1	14	8360.75	0.0000
0.0000	sequence	1	14	0.0180223	0.8951
0.3088	form	1	14	1.11516	0.3088
0.7142	period	1	14	0.139692	0.7142

Sequential Sum of Squares

	Hypothesis	DF	SS	MS	F_stat
	P_value				
0.8951	sequence	1	0.00516917	0.00516917	0.0180223
0.0000	sequence*subject	14	4.01549	0.286821	13.0082
0.3088	form	1	0.0245884	0.0245884	1.11516
0.7142	period	1	0.0030801	0.0030801	0.139692
0.7142	Error	14	0.308689	0.0220492	

Partial Tests of Model Effects

	Hypothesis	Numer_DF	Denom_DF	F_stat	P_value
0.8951	int	1	14	7832.26	0.0000
0.0000	sequence	1	14	0.0180223	0.8951
0.3088	form	1	14	1.24527	0.2832
0.7142	period	1	14	0.139692	0.7142

Partial Sum of Squares

	Hypothesis	DF	SS	MS	F_stat
	P_value				
0.8951	sequence	1	0.00516917	0.00516917	0.0180223
0.0000	sequence*subject	14	4.01549	0.286821	13.0082

0.2832	form	1	0.0274572	0.0274572	1.24527
0.7142	period	1	0.0030801	0.0030801	0.139692
	Error	14	0.308689	0.0220492	
Least squares means					
	form	Estimate	StdError	Denom_DF	T_stat
	Lower_CI	Upper_CI			

8.505	R	8.68368	0.101468	14	85.5809
8.862	T	8.62317	0.101468	14	84.9845
8.444	8.802				
Differences between means					
	form	Estimate	StdError	Denom_DF	T_stat
	Lower_CI	Upper_CI			

0.03499	R - T	0.0605059	0.0542208	14	1.11592
	0.156				

Bioequivalence Statistics

User-Specified Confidence Level for CI's and Power = 90.0000
Percent of Reference to Detect for 2-1 Tests and Power = 20.0%
A.H.Lower = 0.800 A.H.Upper = 1.250

Formulation variable: form
Reference: R LSMean= 8.683680 SE= 0.101468 GeoLSM= 5905.739690

Test: T LSMean= 8.623174 SE= 0.101468 GeoLSM= 5559.003095

Difference = -0.0605, Diff_SE= 0.0542, df= 14.0
Ratio(%Ref) = 94.1288

Classical Westlake
CI 80% = (87.5075, 101.2511) (89.6981, 110.3019)
CI 90% = (85.5535, 103.5637) (87.4284, 112.5716)
CI 95% = (83.7925, 105.7402) (85.4800, 114.5200)
Average bioequivalence shown for confidence=90.00 and percent=20.0.

Two One-Sided T-tests

Prob(< 80%)=0.0048 Prob(> 125%)=0.0001 Max=0.0048 Total=0.0048

Anderson-Hauck Procedure
A.H. p-value = 0.004717

Power of ANOVA for Confidence Level 90.00
Power at 20% = 0.983159

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Version 5.2.1 Build 2008033011
Core Version 17Oct2006

Model Specification and User Settings
Dependent variable : AUCINF_obs
Transform : LN
Fixed terms : int+sequence+form+period
Random/repeated terms : sequence*subject
Maximum iterations : 50
Convergence Criterion : 1e-010
Singularity tolerance : 1e-010
Denominator df option : residual

Class variables and their levels
form : R T
subject : 1 3 4 6 9 10 14 16 17 19 22
24 25 27 30 34
period : 1 2
sequence : RT TR

Using method of moments for starting values
Starting estimates of variance parameters:
Var(sequence*subject) 0.120611
Var(Residual) 0.0204339

Diagnostics
Total Observations : 32
Observations Used : 32
Obs. Missing Model Terms : 0
Residual SS : 0.286074
Residual df : 14
Residual Variance : 0.0204339

Breakout of variance structure

Variance Index : 1
Source : Random
Type : Variance Components
Columns : sequence*subject
Parameters : Var(sequence*subject)

Variance Index : 2
Source : Assumed
Type : Identity
Columns : None
Parameters : Var(Residual)

Variance parameter estimation at each iteration:
Objective
Iteration function Var(sequence*subject) Var(Residual)
0 -22.619 0.120611 0.0204339

Newton's algorithm converged.

Final variance parameter estimates:
Var(sequence*subject) 0.120611
Var(Residual) 0.0204339
Intersubject CV 0.358031
Intrasubject CV 0.14368

REML log(likelihood) -3.11128
 -2* REML log(likelihood) 6.22257
 Akaike Information Crit. 18.2226
 Schwarz Bayesian Crit. 26.2158

Ordered Final Hessian Eigenvalues:
 16869.5
 406.436

Solution

	Effect:Level	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
8.423	int	8.6843	0.121596	14	71.4192	0.0000	95	2.145
0.4299	sequence:RT	-0.0293221	0.186782	14	-0.156986	0.8775	95	2.145
0.05545	sequence:TR	0.3713	Not estimable					-
0.09625	form:R	0.0565018	0.0521969	14	1.08247	0.2973	95	2.145
	period:1	0.1685	Not estimable					-
	period:2	0.0157005	0.0521969	14	0.300794	0.7680	95	2.145
	period:2	0.1277	Not estimable					-

Sequential Tests of Model Effects

Hypothesis	Numer_DF	Denom_DF	F_stat	P_value
int	1	14	9276.76	0.0000
sequence	1	14	0.0246446	0.8775
form	1	14	1.08224	0.3158
period	1	14	0.0904768	0.7680

Sequential Sum of Squares

Hypothesis	DF	SS	MS	F_stat
sequence	1	0.00644839	0.00644839	0.0246446
sequence*subject	14	3.66318	0.261656	12.805
form	1	0.0221144	0.0221144	1.08224
period	1	0.00184879	0.00184879	0.0904768
Error	14	0.286074	0.0204339	

Partial Tests of Model Effects

Hypothesis	Numer_DF	Denom_DF	F_stat	P_value
int	1	14	8689.65	0.0000
sequence	1	14	0.0246446	0.8775
form	1	14	1.17175	0.2973
period	1	14	0.0904768	0.7680

Partial Sum of Squares

Hypothesis	DF	SS	MS	F_stat
sequence	1	0.00644839	0.00644839	0.0246446
sequence*subject	14	3.66318	0.261656	12.805

0.2973	form	1	0.0239434	0.0239434	1.17175			
0.7680	period	1	0.00184879	0.00184879	0.0904768			
	Error	14	0.286074	0.0204339				
Least squares means								
	form	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
-----	-----	-----	-----	-----	-----	-----	-----	-----
8.563	R	8.73399	0.096969	14	90.0699	0.0000	90	1.761
8.507	T	8.67749	0.096969	14	89.4872	0.0000	90	1.761
8.507	8.848							
Differences between means								
	form	Estimate	StdError	Denom_DF	T_stat	P_value	Conf	T_crit
	Lower_CI	Upper_CI						
-----	-----	-----	-----	-----	-----	-----	-----	-----
0.03543	R - T	0.0565018	0.0521969	14	1.08247	0.2973	90	1.761 -
	0.1484							

Bioequivalence Statistics

User-Specified Confidence Level for CI's and Power = 90.0000
Percent of Reference to Detect for 2-1 Tests and Power = 20.0%
A.H.Lower = 0.800 A.H.Upper = 1.250

Formulation variable: form
Reference: R LSMean= 8.733987 SE= 0.096969 GeoLSM= 6210.438391

Test: T LSMean= 8.677485 SE= 0.096969 GeoLSM= 5869.266875

Difference = -0.0565, Diff_SE= 0.0522, df= 14.0
Ratio(%Ref) = 94.5065

Classical Westlake
CI 80% = (88.0982, 101.3809) (90.2092, 109.7908)
CI 90% = (86.2036, 103.6091) (88.0135, 111.9865)
CI 95% = (84.4947, 105.7045) (86.1254, 113.8746)
Average bioequivalence shown for confidence=90.00 and percent=20.0.

Two One-Sided T-tests
Prob(< 80%)=0.0033 Prob(> 125%)=0.0001 Max=0.0033 Total=0.0033

Anderson-Hauck Procedure
A.H. p-value = 0.003208

Power of ANOVA for Confidence Level 90.00
Power at 20% = 0.987605