Statistical Analysis
Text Output

Statistical Analysis Text Output

```
Input File: Workbook - [\\Travis...\PK Params_11-657-T1.pwo]

                                                    Date:   11/12/2003
                                                    Time:     11:33:44

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Non-Transformed Parameters


Model Specification and User Settings
       Dependent variable : Cmax
                Transform : None
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
             Treatment_ID :    A   B
                  Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                   Period :    1   2
                 Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)      78539.4
       Var(Residual)      12757.4

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :       548568
              Residual df :           43
        Residual Variance :      12757.4

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      505.174        78539.4         12757.4
Newton's algorithm converged.
```

```
Final variance parameter estimates:
    Var(Sequence*Subject)      78539.4
            Var(Residual)      12757.4

     REML log(likelihood)     -584.203
 -2* REML log(likelihood)      1168.41
 Akaike Information Crit.      1180.41
   Schwarz Bayesian Crit.      1195.13

Ordered Final Hessian Eigenvalues:
1.32866e-007
2.96441e-009

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int    364.193   64.3214  49.1   5.66208    0.0000   95   2.009
234.9    493.4
   Sequence:AB   -42.5617   86.9023    43 -0.489765    0.6268   95   2.017   -
217.8    132.7
   Sequence:BA   Not estimable
Treatment_ID:A    78.8863   23.8175    43   3.31211    0.0019   95   2.017
30.85    126.9
Treatment_ID:B   Not estimable
      Period:1    18.4482   23.8175    43  0.774562    0.4428   95   2.017   -
29.58    66.48
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                 int           1          43     81.0592      0.0000
            Sequence           1          43     0.23987      0.6268
        Treatment_ID           1          43     11.0899      0.0018
              Period           1          43    0.599946      0.4428

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                 int           1          43     81.2152      0.0000
            Sequence           1          43     0.23987      0.6268
        Treatment_ID           1          43     10.9701      0.0019
              Period           1          43    0.599946      0.4428

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
             A    431.022   45.0535  49.4    9.5669    0.0000   90   1.676
355.5    506.5
             B    352.136   45.0535  49.4   7.81595    0.0000   90   1.676
276.6    427.7

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
         A - B    78.8863   23.8175    43   3.31211    0.0019   90   1.681
38.85    118.9
```

```
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 =  1.200

Formulation variable: Treatment_ID
Reference: B   LSMean=  352.136140  SE=   45.053518
---------------------------------------------------------------------------

Test:      A   LSMean=  431.022432  SE=   45.053518

    Difference =    78.8863,  Diff_SE=   23.8175,  df= 43.0
    Ratio(%Ref) =   122.4022

                        Classical                Westlake
    CI  80% = (  113.5976,  131.2068)  (   71.8482,  128.1518)
    CI  90% = (  111.0294,  133.7751)  (   68.7944,  131.2056)
    CI  95% = (  108.7587,  136.0457)  (   66.2275,  133.7725)
    Failed to show average bioequivalence for confidence=90.00 and
percent=20.0.

                        Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 120%)=0.6379  Max=0.6379  Total=0.6379

                       Anderson-Hauck Procedure
    A.H. p-value = 0.637897

                Power of ANOVA for Confidence Level 90.00
    Power at 20% = 0.895526


Input File: Workbook - [\\Travis...\PK Params_11-657-T1.pwo]

                                                Date:   11/12/2003
                                                Time:     11:33:45

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Non-Transformed Parameters


Model Specification and User Settings
       Dependent variable : AUClast
                Transform : None
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
             Treatment_ID :    A   B
                  Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                   Period :    1   2
                 Sequence :    AB   BA
```

```
Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)       907104
       Var(Residual)      12707.5

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :       546421
              Residual df :           43
        Residual Variance :      12707.5

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      556.164         907104        12707.5
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)       907104
            Var(Residual)      12707.5

     REML log(likelihood)     -635.193
 -2* REML log(likelihood)      1270.39
 Akaike Information Crit.      1282.39
   Schwarz Bayesian Crit.      1297.11

Ordered Final Hessian Eigenvalues:
 1.3315e-007
2.57656e-011

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int    719.282   204.443  43.6   3.51825    0.0010   95   2.016
307.1     1131
   Sequence:AB    126.528    285.02    43  0.443926    0.6593   95   2.017   -
448.3    701.3
   Sequence:BA   Not estimable
Treatment_ID:A    5.69396   23.7709    43  0.239535    0.8118   95   2.017   -
42.24    53.63
Treatment_ID:B   Not estimable
      Period:1   -32.8267   23.7709    43  -1.38096    0.1744   95   2.017   -
80.77    15.11
```

```
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------------
                 int           1          43     29.2375      0.0000
            Sequence           1          43     0.19707      0.6593
        Treatment_ID           1          43   0.0436387      0.8355
              Period           1          43     1.90706      0.1744

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------------
                 int           1          43     29.1165      0.0000
            Sequence           1          43     0.19707      0.6593
        Treatment_ID           1          43   0.0573772      0.8118
              Period           1          43     1.90706      0.1744

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-----------------------------------------------------------------------------
-------------
             A    771.826   143.005  43.6   5.39721    0.0000   90   1.681
531.5     1012
             B    766.132   143.005  43.6   5.35739    0.0000   90   1.681
525.8     1006

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-----------------------------------------------------------------------------
-------------
         A - B    5.69396   23.7709    43  0.239535    0.8118   90   1.681   -
34.27    45.65

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 =  1.200

Formulation variable: Treatment_ID
Reference: B   LSMean=  766.132308  SE=  143.004727
-----------------------------------------------------------------------------

Test:      A   LSMean=  771.826272  SE=  143.004727

    Difference =     5.6940,  Diff_SE=   23.7709,  df= 43.0
    Ratio(%Ref) =   100.7432

                      Classical                Westlake
    CI  80% = (   96.7043,  104.7821)  (   95.8480,  104.1520)
    CI  90% = (   95.5262,  105.9603)  (   94.6424,  105.3576)
    CI  95% = (   94.4846,  107.0019)  (   93.5789,  106.4211)
    Average bioequivalence shown for confidence=90.00 and percent=20.0.

                      Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 120%)=0.0000  Max=0.0000  Total=0.0000

                     Anderson-Hauck Procedure
    A.H. p-value = 0.000000
```

```
                Power of ANOVA for Confidence Level 90.00
    Power at 20% = 0.999989


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     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Non-Transformed Parameters


Model Specification and User Settings
       Dependent variable : AUCINF_obs
                Transform : None
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
              Treatment_ID :    A   B
                   Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                    Period :    1   2
                  Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)       943849
       Var(Residual)      14003.2

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :       602136
              Residual df :           43
        Residual Variance :      14003.2

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      559.114          943849        14003.2
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)        943849
            Var(Residual)       14003.2

     REML log(likelihood)      -638.143
 -2* REML log(likelihood)       1276.29
 Akaike Information Crit.       1288.29
   Schwarz Bayesian Crit.       1303.01

Ordered Final Hessian Eigenvalues:
 1.0965e-007
2.37788e-011

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int    726.267   208.626  43.6   3.48119    0.0011   95   2.016
305.7     1147
   Sequence:AB     135.25   290.795    43  0.465104    0.6442   95   2.017   -
451.2    721.7
   Sequence:BA   Not estimable
Treatment_ID:A    1.30072   24.9534    43 0.0521259    0.9587   95   2.017   -
49.02    51.62
Treatment_ID:B   Not estimable
      Period:1   -35.9992   24.9534    43  -1.44266    0.1564   95   2.017   -
86.32    14.32
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                int           1          43      28.649      0.0000
           Sequence           1          43    0.216322      0.6442
        Treatment_ID          1          43 0.000402874      0.9841
              Period          1          43     2.08127      0.1564

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                int           1          43     28.5244      0.0000
           Sequence           1          43    0.216322      0.6442
        Treatment_ID          1          43  0.00271711      0.9587
              Period          1          43     2.08127      0.1564

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
             A    777.193   145.932  43.6   5.32572    0.0000   90   1.681
531.9     1022
             B    775.893   145.932  43.6   5.31681    0.0000   90   1.681
530.6     1021

Differences between means
```

```
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
         A - B    1.30072   24.9534    43 0.0521259    0.9587   90   1.681   -
40.65    43.25

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 =  1.200

Formulation variable: Treatment_ID
Reference: B   LSMean=  775.892506  SE=  145.931937
-----------------------------------------------------------------------------

Test:      A   LSMean=  777.193222  SE=  145.931937

    Difference =     1.3007,  Diff_SE=   24.9534,  df= 43.0
    Ratio(%Ref) =   100.1676

                      Classical                Westlake
    CI  80% = (   95.9812,  104.3541)  (   95.8085,  104.1915)
    CI  90% = (   94.7600,  105.5753)  (   94.5865,  105.4135)
    CI  95% = (   93.6803,  106.6550)  (   93.5059,  106.4941)
    Average bioequivalence shown for confidence=90.00 and percent=20.0.

                       Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 120%)=0.0000  Max=0.0000  Total=0.0000

                      Anderson-Hauck Procedure
    A.H. p-value = 0.000000

               Power of ANOVA for Confidence Level 90.00
    Power at 20% = 0.999977


Input File: Workbook - [\\Travis...\PK Params_11-657-T1.pwo]

                                                Date:   11/12/2003
                                                Time:     11:33:46

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Non-Transformed Parameters


Model Specification and User Settings
       Dependent variable : Tmax
                Transform : None
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
             Treatment_ID :    A   B
```

```
                    Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                     Period :    1   2
                   Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)      0.860413
       Var(Residual)       0.58167

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :      25.0118
              Residual df :           43
        Residual Variance :      0.58167

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      49.2811       0.860413        0.58167
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)      0.860413
            Var(Residual)      0.58167

     REML log(likelihood)      -128.31
 -2* REML log(likelihood)       256.62
 Akaike Information Crit.       268.62
   Schwarz Bayesian Crit.      283.346

Ordered Final Hessian Eigenvalues:
      68.851
     14.9718

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int    2.80464  0.254901  62.6   11.0029    0.0000   95   1.999
2.295    3.314
   Sequence:AB -0.0215976  0.319975    43 -0.067498    0.9465   95   2.017  -
0.6669   0.6237
```

```
   Sequence:BA   Not estimable
Treatment_ID:A  -0.227974  0.160825    43  -1.41753    0.1635   95   2.017  -
0.5523  0.09636
Treatment_ID:B   Not estimable
      Period:1  -0.121156  0.160825    43  -0.75334    0.4554   95   2.017  -
0.4455   0.2032
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                 int           1          43     268.118      0.0000
            Sequence           1          43  0.00455598      0.9465
        Treatment_ID           1          43     2.05814      0.1586
              Period           1          43    0.567521      0.4554

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                 int           1          43     268.035      0.0000
            Sequence           1          43  0.00455598      0.9465
        Treatment_ID           1          43     2.00938      0.1635
              Period           1          43    0.567521      0.4554

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
---------------------------------------- ------------- -------------------
-------------
            A    2.50529  0.179059  63.4   13.9914    0 0000   90   1.669
2.206    2.804
            B    2.73326  0.179059  63.4   15.2646    0.0000   90   1.669
2.434    3.032

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
---------------------------------------------------- ------------------------
-------------
         A - B  -0.227974  0.160825    43  -1.41753    0.1635   90   1.681  -
0.4983  0.04238

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 =  1.200

Formulation variable: Treatment_ID
Reference: B   LSMean=    2.733264  SE=    0.179059
-----------------------------------------------------------------------

Test:      A   LSMean=    2.505290  SE=    0.179059

    Difference =    -0.2280,  Diff_SE=    0.1608,  df= 43.0
    Ratio(%Ref) =    91.6593

                      Classical                Westlake
    CI  80% = (   83.9999,   99.3187)  (   86.6507,  113.3493)
    CI  90% = (   81.7656,  101.5529)  (   83.9981,  116.0019)
    CI  95% = (   79.7903,  103.5282)  (   81.7664,  118.2336)
    Average bioequivalence shown for confidence=90.00 and percent=20.0.
```

```
                    Two One-Sided T-tests

    Prob(< 80%)=0.0270  Prob(> 120%)=0.0000  Max=0.0270  Total=0.0270

                    Anderson-Hauck Procedure
    A.H. p-value = 0.026966

              Power of ANOVA for Confidence Level 90.00
    Power at 20% = 0.953472


Input File: Workbook - [\\Travis...\PK Params_11-657-T1.pwo]

                                                  Date:   11/12/2003
                                                  Time:     11:33:46

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Non-Transformed Parameters


Model Specification and User Settings
       Dependent variable : Lambda_z
                Transform : None
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
             Treatment_ID :    A   B
                  Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                   Period :    1   2
                 Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)    0.0539605
       Var(Residual)    0.0336701

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :      1.44781
              Residual df :           43
        Residual Variance :    0.0336701

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     -71.9381      0.0539605       0.0336701
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)    0.0539605
            Var(Residual)    0.0336701

     REML log(likelihood)     -7.09065
 -2* REML log(likelihood)      14.1813
 Akaike Information Crit.      26.1813
   Schwarz Bayesian Crit.      40.9074

Ordered Final Hessian Eigenvalues:
     20324.2
     4002.79

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int   0.774019 0.0628485  61.6   12.3156    0.0000   95   1.999
0.6484   0.8997
   Sequence:AB -0.0259119 0.0793476    43 -0.326562    0.7456   95   2.017  -
0.1859   0.1341
   Sequence:BA   Not estimable
Treatment_ID:A   0.113596 0.0386935    43   2.93578    0.0053   95   2.017
0.03556   0.1916
Treatment_ID:B   Not estimable
      Period:1   0.102044 0.0386935    43   2.63724    0.0116   95   2.017
0.02401   0.1801
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat      P_value
-----------------------------------------------------------------------
                 int           1          43     479.559       0.0000
            Sequence           1          43    0.106643       0.7456
        Treatment_ID           1          43     8.97077       0.0045
              Period           1          43     6.95504       0.0116

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat      P_value
-----------------------------------------------------------------------
                 int           1          43      479.64       0.0000
            Sequence           1          43    0.106643       0.7456
        Treatment_ID           1          43      8.6188       0.0053
              Period           1          43     6.95504       0.0116

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
```

```
            A   0.925681 0.0441396  62.4   20.9716    0.0000   90    1.67
0.852   0.9994
            B   0.812085 0.0441396  62.4   18.3981    0.0000   90    1.67
0.7384   0.8858

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
         A - B   0.113596 0.0386935    43   2.93578    0.0053   90   1.681
0.04855   0.1786

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 =  1.200

Formulation variable: Treatment_ID
Reference: B   LSMean=    0.812085  SE=    0.044140
-----------------------------------------------------------------------------

Test:      A   LSMean=    0.925681  SE=    0.044140

    Difference =     0.1136,  Diff_SE=    0.0387,  df= 43.0
    Ratio(%Ref) =   113.9881

                      Classical                Westlake
    CI  80% = (  107.7857,  120.1905)  (   81.9616,  118.0384)
    CI  90% = (  105.9765,  121.9997)  (   79.8104,  120.1896)
    CI  95% = (  104.3770,  123.5993)  (   78.0021,  121.9979)
    Failed to show average bioequivalence for confidence=90.00 and
percent=20.0.

                       Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 120%)=0.1069  Max=0.1069  Total=0.1069

                      Anderson-Hauck Procedure
    A.H. p-value = 0.106920

               Power of ANOVA for Confidence Level 90.00
    Power at 20% = 0.992160


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                                                Date:   11/12/2003
                                                Time:     11:33:46

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Non-Transformed Parameters


Model Specification and User Settings
       Dependent variable : HL_Lambda_z
                Transform : None
             Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
```

```
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
              Treatment_ID :    A   B
                   Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                    Period :    1   2
                  Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)    0.0960521
       Var(Residual)      1.08743

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :      46.7594
              Residual df :           43
        Residual Variance :      1.08743

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      50.1017      0.0960521        1.08743
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)    0.0960521
            Var(Residual)      1.08743

     REML log(likelihood)      -129.13
 -2* REML log(likelihood)      258.261
 Akaike Information Crit.      270.261
   Schwarz Bayesian Crit.      284.987

Ordered Final Hessian Eigenvalues:
     70.2467
     13.5959

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
```

```
-----------------------------------------------------------------------------
-------------
           int      1.174  0.229608  85.1   5.11304    0.0000   95   1.988
0.7175    1.631
   Sequence:AB   0.319538  0.238529    43   1.33962    0.1874   95   2.017  -
0.1615   0.8006
   Sequence:BA   Not estimable
Treatment_ID:A  -0.331322  0.219895    43  -1.50673    0.1392   95   2.017  -
0.7748   0.1121
Treatment_ID:B   Not estimable
      Period:1  -0.307282  0.219895    43   -1.3974    0.1695   95   2.017  -
0.7507   0.1362
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-------------------------------------------------------------------
                 int           1          43     72.8952      0.0000
            Sequence           1          43     1.79458      0.1874
        Treatment_ID           1          43     2.36593      0.1313
              Period           1          43     1.95273      0.1695

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-------------------------------------------------------------------
                 int           1          43     72.3519      0.0000
            Sequence           1          43     1.79458      0.1874
        Treatment_ID           1          43     2.27022      0.1392
              Period           1          43     1.95273      0.1695

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-----------------------------------------------------------------------------
-------------
             A   0.848803  0.162211  85.4   5.23269    0.0000   90   1.663
0.5791    1.119
             B    1.18012  0.162211  85.4   7.27522    0.0000   90   1.663
0.9104     1.45

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-----------------------------------------------------------------------------
-------------
         A - B  -0.331322  0.219895    43  -1.50673    0.1392   90   1.681   -
0.701  0.03834

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 =  1.200

Formulation variable: Treatment_ID
Reference: B   LSMean=    1.180125  SE=    0.162211
-----------------------------------------------------------------------

Test:      A   LSMean=    0.848803  SE=    0.162211

    Difference =    -0.3313,  Diff_SE=    0.2199,  df= 43.0
    Ratio(%Ref) =    71.9248
```

```
                    Classical                Westlake
CI  80% = (   47.6693,   96.1804)  (   56.0729,  143.9271)
CI  90% = (   40.5940,  103.2556)  (   47.6676,  152.3324)
CI  95% = (   34.3387,  109.5110)  (   40.5984,  159.4016)
Failed to show average bioequivalence for confidence=90.00 and
percent=20.0.

                    Two One-Sided T-tests

Prob(< 80%)=0.6665  Prob(> 120%)=0.0067  Max=0.6665  Total=0.6732

                    Anderson-Hauck Procedure
A.H. p-value = 0.659857

            Power of ANOVA for Confidence Level 90.00
Power at 20% = 0.277448
```

```
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                                                Date:   11/12/2003
                                                Time:     11:34:33

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Ln-Transformed Parameters


Model Specification and User Settings
       Dependent variable : Cmax
                Transform : LN
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
             Treatment_ID :    A   B
                  Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                   Period :    1   2
                 Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)     0.333982
       Var(Residual)    0.0954787

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :      4.10558
              Residual df :           43
        Residual Variance :    0.0954787

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     -13.3035       0.333982       0.0954787
Newton's algorithm converged.
```

```
Final variance parameter estimates:
    Var(Sequence*Subject)      0.333982
            Var(Residual)     0.0954787

     REML log(likelihood)      -65.7252
 -2* REML log(likelihood)        131.45
 Akaike Information Crit.        143.45
   Schwarz Bayesian Crit.       158.177

Ordered Final Hessian Eigenvalues:
     2397.75
     145.133

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int      5.687  0.139379  53.1   40.8023    0.0000   95   2.006
5.407    5.967
   Sequence:AB  -0.214008  0.184249    43  -1.16152    0.2518   95   2.017  -
0.5856   0.1576
   Sequence:BA   Not estimable
Treatment_ID:A   0.265799 0.0651582    43   4.07929    0.0002   95   2.017
0.1344   0.3972
Treatment_ID:B   Not estimable
      Period:1  0.0555445 0.0651582    43  0.852456    0.3987   95   2.017 -
0.07586   0.1869
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------------
                 int           1          43     3881.78      0.0000
            Sequence           1          43     1.34912      0.2518
        Treatment_ID           1          43     16.8038      0.0002
              Period           1          43    0.726681      0.3987

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------------
                 int           1          43     3883.08      0.0000
            Sequence           1          43     1.34912      0.2518
        Treatment_ID           1          43     16.6406      0.0002
              Period           1          43    0.726681      0.3987

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
             A    5.87357 0.0977154  53.6   60.1089    0.0000   90   1.674
5.71     6.037
             B    5.60777 0.0977154  53.6   57.3888    0.0000   90   1.674
5.444    5.771

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
         A - B   0.265799 0.0651582    43   4.07929    0.0002   90   1.681
0.1563   0.3753
```

```
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: Treatment_ID
Reference: B   LSMean=    5.607767  SE=    0.097715  GeoLSM=  272.534948
-------------------------------------------------------------------------

Test:      A   LSMean=    5.873566  SE=    0.097715  GeoLSM=  355.514573

    Difference =     0.2658,  Diff_SE=    0.0652,  df= 43.0
    Ratio(%Ref) =   130.4473

                        Classical                Westlake
    CI  80% = (  119.8392,  141.9945)  (   62.1235,  137.8764)
    CI  90% = (  116.9106,  145.5515)  (   58.0072,  141.9928)
    CI  95% = (  114.3810,  148.7704)  (   54.4521,  145.5479)
    Failed to show average bioequivalence for confidence=90.00 and
percent=20.0.

                        Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 125%)=0.7419  Max=0.7419  Total=0.7419

                        Anderson-Hauck Procedure
    A.H. p-value = 0.741910

                Power of ANOVA for Confidence Level 90.00
    Power at 20% = 0.955780


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                                                Time:     11:34:34

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Ln-Transformed Parameters


Model Specification and User Settings
       Dependent variable : AUClast
                Transform : LN
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
              Treatment_ID :    A   B
                   Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                    Period :    1   2
                  Sequence :    AB   BA
```

```
Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)      0.557953
       Var(Residual)     0.0141813

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :     0.609794
              Residual df :           43
        Residual Variance :    0.0141813

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     -45.8711       0.557953      0.0141813
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)     0.557953
            Var(Residual)    0.0141813

     REML log(likelihood)     -33.1576
 -2* REML log(likelihood)      66.3153
 Akaike Information Crit.      78.3153
   Schwarz Bayesian Crit.      93.0414

Ordered Final Hessian Eigenvalues:
      106925
     67.3297

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
           int    6.30668  0.161221    44   39.1183    0.0000   95   2.015
5.982    6.632
   Sequence:AB -0.0752554  0.224167    43 -0.335711    0.7387   95   2.017  -
0.5273   0.3768
   Sequence:BA   Not estimable
Treatment_ID:A   0.048729 0.0251115    43    1.9405    0.0589   95   2.017-
0.001913  0.09937
Treatment_ID:B   Not estimable
      Period:1  -0.014606 0.0251115    43 -0.581646    0.5638   95   2.017 -
0.06525  0.03604
```

```
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------------
                 int           1          43     3146.15      0.0000
            Sequence           1          43    0.112702      0.7387
        Treatment_ID           1          43     3.71739      0.0605
              Period           1          43    0.338312      0.5638

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------------
                 int           1          43     3145.43      0.0000
            Sequence           1          43    0.112702      0.7387
        Treatment_ID           1          43     3.76555      0.0589
              Period           1          43    0.338312      0.5638

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
            A    6.31047  0.112785  44.1   55.9515    0.0000   90    1.68
6.121      6.5
            B    6.26174  0.112785  44.1   55.5195    0.0000   90    1.68
6.072    6.451

Differences between means
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
         A - B   0.048729 0.0251115    43    1.9405    0.0589   90   1.681
0.006515  0.09094

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: Treatment_ID
Reference: B   LSMean=    6.261745  SE=    0.112785  GeoLSM=  524.132602
-----------------------------------------------------------------------

Test:      A   LSMean=    6.310474  SE=    0.112785  GeoLSM=  550.305569

    Difference =     0.0487,  Diff_SE=    0.0251,  df= 43.0
    Ratio(%Ref) =   104.9936

                      Classical                Westlake
    CI  80% = (  101.6170,  108.4824)  (   92.7410,  107.2590)
    CI  90% = (  100.6526,  109.5217)  (   91.5181,  108.4819)
    CI  95% = (   99.8077,  110.4489)  (   90.4793,  109.5207)
    Average bioequivalence shown for confidence=90.00 and percent=20.0.

                       Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 125%)=0.0000  Max=0.0000  Total=0.0000

                      Anderson-Hauck Procedure
    A.H. p-value = 0.000000
```

```
                Power of ANOVA for Confidence Level 90.00
    Power at 20% = 1.000000


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                                                    Date:   11/12/2003
                                                    Time:     11:34:34

     WINNONLIN LINEAR MIXED EFFECTS MODELING / BIOEQUIVALENCE (V4.0)

Ln-Transformed Parameters


Model Specification and User Settings
       Dependent variable : AUCINF_obs
                Transform : LN
              Fixed terms : int+Sequence+Treatment_ID+Period
    Random/repeated terms : Sequence*Subject
       Maximum iterations : 50
    Convergence Criterion :       1e-010
    Singularity tolerance :       1e-010
    Denominator df option : satterthwaite

Class variables and their levels
              Treatment_ID :    A   B
                   Subject :    1   2   3   4   5   7   8   9   10   11   12
13   14   15   16   18   19   20   21   22   23   24   25   26   27   28   29
30   31   32   33   34   35   36   37   38   39   40   41   42   43   44   45
47   48
                    Period :    1   2
                  Sequence :    AB   BA

Using method of moments for starting values
Starting estimates of variance parameters:
Var(Sequence*Subject)       0.5606
       Var(Residual)    0.0138758

Diagnostics
       Total Observations :           90
        Observations Used :           90
    Observations Excluded :            0
              Residual SS :     0.596658
              Residual df :           43
        Residual Variance :    0.0138758

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     -46.2446          0.5606       0.0138758
Newton's algorithm converged.

Final variance parameter estimates:
    Var(Sequence*Subject)        0.5606
            Var(Residual)     0.0138758

     REML log(likelihood)      -32.7842
 -2* REML log(likelihood)       65.5683
 Akaike Information Crit.       77.5683
   Schwarz Bayesian Crit.       92.2944

Ordered Final Hessian Eigenvalues:
      111683
     66.7397

Solution
   Effect:Level  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
            int    6.31408  0.161551    44    39.084    0.0000   95   2.015
5.988     6.64
   Sequence:AB -0.0711431  0.224661    43 -0.316668    0.7530   95   2.017  -
0.5242   0.3819
   Sequence:BA   Not estimable
Treatment_ID:A  0.0448577 0.0248396    43   1.80589    0.0779   95   2.017-
0.005236  0.09495
Treatment_ID:B   Not estimable
      Period:1  -0.017063 0.0248396    43 -0.686929    0.4958   95   2.017 -
0.06716  0.03303
      Period:2   Not estimable

Sequential Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                 int           1          43     3138.64      0.0000
            Sequence           1          43    0.100279      0.7530
        Treatment_ID           1          43     3.20794      0.0803
              Period           1          43    0.471872      0.4958

Partial Tests of Model Effects
          Hypothesis    Numer_DF    Denom_DF      F_stat     P_value
-----------------------------------------------------------------
                 int           1          43     3137.88      0.0000
            Sequence           1          43    0.100279      0.7530
        Treatment_ID           1          43     3.26125      0.0779
              Period           1          43    0.471872      0.4958

Least squares means
  Treatment_ID   Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
             A    6.31483  0.113015  44.1    55.876    0.0000   90    1.68
6.125    6.505
             B    6.26997  0.113015  44.1    55.479    0.0000   90    1.68
6.08     6.46

Differences between means
```

```
   Treatment_ID  Estimate  StdError Denom_DF T_stat   P_value Conf  T_crit
Lower_CI Upper_CI
-------------------------------------------------------------------------------
-------------
         A - B  0.0448577 0.0248396    43   1.80589    0.0779   90   1.681
0.003101  0.08661

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: Treatment_ID
Reference: B   LSMean=    6.269973  SE=    0.113015  GeoLSM=  528.463113
-----------------------------------------------------------------------------

Test:      A   LSMean=    6.314831  SE=    0.113015  GeoLSM=  552.708477

    Difference =     0.0449,  Diff_SE=    0.0248,  df= 43.0
    Ratio(%Ref) =   104.5879

                      Classical                Westlake
    CI  80% = (  101.2602,  108.0250)  (   93.1801,  106.8199)
    CI  90% = (  100.3096,  109.0487)  (   91.9755,  108.0245)
    CI  95% = (   99.4766,  109.9618)  (   90.9523,  109.0477)
    Average bioequivalence shown for confidence=90.00 and percent=20.0.

                      Two One-Sided T-tests

    Prob(< 80%)=0.0000  Prob(> 125%)=0.0000  Max=0.0000  Total=0.0000

                      Anderson-Hauck Procedure
    A.H. p-value = 0.000000

              Power of ANOVA for Confidence Level 90.00
    Power at 20% = 1.000000
```

The MEANS Procedure

Analysis Variable : Tmax

Treatment_ ID	N Obs	N	Median	Minimum	Maximum
A	45	45	2.3300000	1.0000000	6.0000000
B	45	45	2.6700000	1.0000000	5.5000000

The UNIVARIATE Procedure
Variable: Diff

Moments

N	45	Sum Weights	45
Mean	-0.2306667	Sum Observations	-10.38
Std Deviation	1.07327002	Variance	1.15190854
Skewness	-0.172274	Kurtosis	-0.1786583
Uncorrected SS	53.0782958	Corrected SS	50.6839758
Coeff Variation	-465.29047	Std Error Mean	0.15999365

Basic Statistical Measures

Location		Variability	
Mean	-0.23067	Std Deviation	1.07327
Median	-0.33000	Variance	1.15191
Mode	0.00000	Range	4.38670
		Interquartile Range	1.00000

Tests for Location: Mu0=0

Test	-Statistic-		-----p Value------	
Student's t	t	-1.44172	Pr > |t|	0.1565
Sign	M	-5	Pr >= |M|	0.1433
Signed Rank	S	-103	Pr >= |S|	0.1365

Quantiles (Definition 5)

Quantile	Estimate
100% Max	1.7167
99%	1.7167
95%	1.6700
90%	1.3400
75% Q3	0.3300
50% Median	-0.3300
25% Q1	-0.6700
10%	-1.6700
5%	-2.0000
1%	-2.6700
0% Min	-2.6700

Extreme Observations

----Lowest----		-----Highest----	
Value	Obs	Value	Obs
-2.67	16	1.3400	19
-2.33	41	1.5000	17
-2.00	37	1.6700	13
-2.00	27	1.6700	43
-1.67	14	1.7167	32

Obs	tmax_A	tmax_B	Min_A	Max_A	Min_B	Max_B	wilcoxon	Wil_ pvalue

1	2.33	2.67	1.00	6.00	1.00	5.50	-103.0	0.1365