## Chapter 57

### The HPLMIXED Procedure

#### Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview: HPLMIXED Procedure</td>
<td>4618</td>
</tr>
<tr>
<td>PROC HPLMIXED Features</td>
<td>4619</td>
</tr>
<tr>
<td>Notation for the Mixed Model</td>
<td>4620</td>
</tr>
<tr>
<td>PROC HPLMIXED Contrasted with Other SAS Procedures</td>
<td>4621</td>
</tr>
<tr>
<td>Getting Started: HPLMIXED Procedure</td>
<td>4621</td>
</tr>
<tr>
<td>Mixed Model Analysis of Covariance with Many Groups</td>
<td>4621</td>
</tr>
<tr>
<td>Syntax: HPLMIXED Procedure</td>
<td>4624</td>
</tr>
<tr>
<td>PROC HPLMIXED Statement</td>
<td>4625</td>
</tr>
<tr>
<td>CLASS Statement</td>
<td>4630</td>
</tr>
<tr>
<td>ID Statement</td>
<td>4630</td>
</tr>
<tr>
<td>MODEL Statement</td>
<td>4630</td>
</tr>
<tr>
<td>OUTPUT Statement</td>
<td>4632</td>
</tr>
<tr>
<td>PARMS Statement</td>
<td>4633</td>
</tr>
<tr>
<td>PERFORMANCE Statement</td>
<td>4635</td>
</tr>
<tr>
<td>RANDOM Statement</td>
<td>4635</td>
</tr>
<tr>
<td>REPEATED Statement</td>
<td>4641</td>
</tr>
<tr>
<td>Details: HPLMIXED Procedure</td>
<td>4642</td>
</tr>
<tr>
<td>Linear Mixed Models Theory</td>
<td>4642</td>
</tr>
<tr>
<td>Matrix Notation</td>
<td>4642</td>
</tr>
<tr>
<td>Formulation of the Mixed Model</td>
<td>4643</td>
</tr>
<tr>
<td>Estimating Covariance Parameters in the Mixed Model</td>
<td>4648</td>
</tr>
<tr>
<td>Estimating Fixed and Random Effects in the Mixed Model</td>
<td>4649</td>
</tr>
<tr>
<td>Statistical Properties</td>
<td>4650</td>
</tr>
<tr>
<td>Computational Method</td>
<td>4651</td>
</tr>
<tr>
<td>Distributed Computing</td>
<td>4651</td>
</tr>
<tr>
<td>Multithreading</td>
<td>4651</td>
</tr>
<tr>
<td>Displayed Output</td>
<td>4652</td>
</tr>
<tr>
<td>Performance Information</td>
<td>4652</td>
</tr>
<tr>
<td>Model Information</td>
<td>4652</td>
</tr>
<tr>
<td>Class Level Information</td>
<td>4652</td>
</tr>
<tr>
<td>Dimensions</td>
<td>4652</td>
</tr>
<tr>
<td>Number of Observations</td>
<td>4652</td>
</tr>
<tr>
<td>Optimization Information</td>
<td>4653</td>
</tr>
<tr>
<td>Iteration History</td>
<td>4653</td>
</tr>
<tr>
<td>Convergence Status</td>
<td>4654</td>
</tr>
<tr>
<td>Covariance Parameter Estimates</td>
<td>4654</td>
</tr>
</tbody>
</table>
Overview: HPLMIXED Procedure

The HPLMIXED procedure fits a variety of mixed linear models to data and enables you to use these fitted models to make statistical inferences about the data. A mixed linear model is a generalization of the standard linear model used in the GLM procedure in SAS/STAT software; the generalization is that the data are permitted to exhibit correlation and nonconstant variability. Therefore, the mixed linear model provides you with the flexibility of modeling not only the means of your data (as in the standard linear model) but also their variances and covariances.

The primary assumptions underlying the analyses performed by PROC HPLMIXED are as follows:

- The data are normally distributed (Gaussian).
- The means (expected values) of the data are linear in terms of a certain set of parameters.
- The variances and covariances of the data are in terms of a different set of parameters, and they exhibit a structure that matches one of those available in PROC HPLMIXED.

Because Gaussian data can be modeled entirely in terms of their means and variances/covariances, the two sets of parameters in a mixed linear model actually specify the complete probability distribution of the data. The parameters of the mean model are referred to as fixed-effects parameters, and the parameters of the variance-covariance model are referred to as covariance parameters.

The fixed-effects parameters are associated with known explanatory variables, as in the standard linear model. These variables can be either qualitative (as in the traditional analysis of variance) or quantitative (as in standard linear regression). However, the covariance parameters are what distinguishes the mixed linear model from the standard linear model.

The need for covariance parameters arises quite frequently in applications; the following scenarios are the most typical:

- The experimental units on which the data are measured can be grouped into clusters, and the data from a common cluster are correlated. This scenario can be generalized to include one set of clusters nested within another. For example, if students are the experimental unit, they can be clustered into classes, which in turn can be clustered into schools. Each level of this hierarchy can introduce an additional source of variability and correlation.

- Repeated measurements are taken on the same experimental unit, and these repeated measurements are correlated or exhibit variability that changes. This scenario occurs in longitudinal studies, where repeated measurements are taken over time. Alternatively, the repeated measures could be spatial or multivariate in nature.
PROC HPLMIXED provides a variety of covariance structures to handle these two scenarios. The most common covariance structures arise from the use of random-effects parameters, which are additional unknown random variables that are assumed to affect the variability of the data. The variances of the random-effects parameters, commonly known as variance components, become the covariance parameters for this particular structure. Traditional mixed linear models contain both fixed- and random-effects parameters; in fact, it is the combination of these two types of effects that led to the name mixed model. PROC HPLMIXED fits not only these traditional variance component models but also numerous other covariance structures.

PROC HPLMIXED fits the structure you select to the data by using the method of restricted maximum likelihood (REML), also known as residual maximum likelihood. It is here that the Gaussian assumption for the data is exploited.

PROC HPLMIXED runs in either single-machine mode or distributed mode.

**NOTE:** Distributed mode requires SAS High-Performance Statistics.

**PROC HPLMIXED Features**

PROC HPLMIXED provides easy accessibility to numerous mixed linear models that are useful in many common statistical analyses.

Here are some basic features of PROC HPLMIXED:

- covariance structures, including variance components, compound symmetry, unstructured, AR(1), Toeplitz, and factor analytic
- **MODEL, RANDOM, and REPEATED** statements for model specification as in the HPLMIXED procedure
- appropriate standard errors, *t* tests, and *F* tests for all specified estimable linear combinations of fixed and random effects
- a subject effect that enables blocking
- REML and ML (maximum likelihood) estimation methods implemented with a variety of optimization algorithms
- capacity to handle unbalanced data
- special dense and sparse algorithms that take advantage of distributed and multicore computing environments

Because the HPLMIXED procedure is a high-performance analytical procedure, it also does the following:

- enables you to run in distributed mode on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode on the server where SAS is installed
- exploits all the available cores and concurrent threads, regardless of execution mode
For more information, see the section “Processing Modes” (Chapter 2, SAS/STAT User’s Guide: High-Performance Procedures).

PROC HPLMIXED uses the Output Delivery System (ODS), a SAS subsystem that provides capabilities for displaying and controlling the output from SAS procedures. ODS enables you to convert any output from PROC HPLMIXED into a SAS data set. See the section “ODS Table Names” on page 4655.

---

**Notation for the Mixed Model**

This section introduces the mathematical notation used throughout this chapter to describe the mixed linear model and assumes familiarity with basic matrix algebra (for an overview, see Searle 1982). A more detailed description of the mixed model is contained in the section “Linear Mixed Models Theory” on page 4642.

A statistical model is a mathematical description of how data are generated. The standard linear model, as used by the GLM procedure, is one of the most common statistical models:

\[
y = X\beta + \epsilon
\]

In this expression, \( y \) represents a vector of observed data, \( \beta \) is an unknown vector of fixed-effects parameters with a known design matrix \( X \), and \( \epsilon \) is an unknown random error vector that models the statistical noise around \( X\beta \). The focus of the standard linear model is to model the mean of \( y \) by using the fixed-effects parameters \( \beta \). The residual errors \( \epsilon \) are assumed to be independent and identically distributed Gaussian random variables with mean 0 and variance \( \sigma^2 \).

The mixed model generalizes the standard linear model as follows:

\[
y = X\beta + Z\gamma + \epsilon
\]

Here, \( \gamma \) is an unknown vector of random-effects parameters with a known design matrix \( Z \), and \( \epsilon \) is an unknown random error vector whose elements are no longer required to be independent and homogeneous.

To further develop this notion of variance modeling, assume that \( \gamma \) and \( \epsilon \) are Gaussian random variables that are uncorrelated, have expectations 0, and have variances \( G \) and \( R \), respectively. The variance of \( y \) is thus

\[
V = ZGZ' + R
\]

Note that when \( R = \sigma^2 I \) and \( Z = 0 \), the mixed model reduces to the standard linear model.

You can model the variance of the data \( y \) by specifying the structure of \( Z \), \( G \), and \( R \). The model matrix \( Z \) is set up in the same fashion as \( X \), the model matrix for the fixed-effects parameters. For \( G \) and \( R \), you must select some covariance structure. Possible covariance structures include the following:

- variance components
- compound symmetry (common covariance plus diagonal)
- unstructured (general covariance)
- autoregressive
- spatial
PROC HPLMIXED Contrasted with Other SAS Procedures

The RANDOM and REPEATED statements of the HPLMIXED procedure follow the convention of the same statements in the MIXED procedure in SAS/STAT software. For information about how these statements differ from RANDOM and REPEATED statements in the MIXED procedure, see the documentation for the MIXED procedure in the SAS/STAT User’s Guide.

The GLIMMIX procedure in SAS/STAT software fits generalized linear mixed models. Linear mixed models—where the data are normally distributed, given the random effects—are in the class of generalized linear mixed models. Therefore, PROC GLIMMIX accommodates nonnormal data with random effects.

Generalized linear mixed models have intrinsically nonlinear features because a nonlinear mapping (the link function) connects the conditional mean of the data (given the random effects) to the explanatory variables. The NLMIXED procedure also accommodates nonlinear structures in the conditional mean, but places no restrictions on the nature of the nonlinearity.

The HPMIXED procedure in SAS/STAT software is also termed a “high-performance” procedure, but it does not follow the general pattern of high-performance analytical procedures. The HPMIXED procedure does not take advantage of distributed or multicore computing environments; it derives high performance from applying sparse techniques to solving the mixed model equations. The HPMIXED procedure fits a small subset of the statistical models you can fit with the MIXED or HPLMIXED procedures and is particularly suited for problems in which the $\mathbf{X}^T \mathbf{X}$ crossproducts matrix is sparse.

The HPLMIXED procedure employs algorithms that are specialized for distributed and multicore computing environments. The HPLMIXED procedure does not support BY processing.

Getting Started: HPLMIXED Procedure

Mixed Model Analysis of Covariance with Many Groups

Suppose you are an educational researcher who studies how student scores on math tests change over time. Students are tested four times, and you want to estimate the overall rise or fall, accounting for correlation between test response behaviors of students in the same neighborhood and school. One way to model this correlation is by using a random-effects analysis of covariance, where the scores for students from the same neighborhood and school are all assumed to share the same quadratic mean test response function, the parameters of this response function being random. The following statements simulate a data set with this structure:

- general linear
- factor analytic

By appropriately defining the model matrices $\mathbf{X}$ and $\mathbf{Z}$ in addition to the covariance structure matrices $\mathbf{G}$ and $\mathbf{R}$, you can perform numerous mixed model analyses.
data SchoolSample;
  do SchoolID = 1 to 300;
    do nID = 1 to 25;
      Neighborhood = (SchoolID-1)*5 + nId;
      bInt = 5*ranuni(1);
      bTime = 5*ranuni(1);
      bTime2 = ranuni(1);
      do sID = 1 to 2;
        do Time = 1 to 4;
          Math = bInt + bTime*Time + bTime2*Time*Time + rannor(2);
          output;
        end;
      end;
    end;
  end;
run;

In this data, there are 300 schools and about 1,500 neighborhoods; neighborhoods are associated with more
than one school and vice versa. The following statements use PROC HPLMIXED to fit a mixed analysis
of covariance model to this data. To run these statements successfully, you need to set the macro variables
GRIDHOST and GRIDINSTALLLOC to resolve to appropriate values, or you can replace the references to
macro variables with appropriate values.

proc hplmixed data=SchoolSample;
  performance host="&GRIDHOST" install="&GRIDINSTALLLOC" nodes=20 nthreads=4;
  class Neighborhood SchoolID;
  model Math = Time Time*Time / solution;
  random int Time Time *Time / sub=Neighborhood(SchoolID) type=un;
run;

This model fits a quadratic mean response model with an unstructured covariance matrix to model the covari-
ance between the random parameters of the response model. With 7,500 neighborhood/school combinations,
this model can be computationally daunting to fit, but PROC HPLMIXED finishes quickly and displays the
results shown in Figure 57.1.

---

**Figure 57.1** Mixed Model Analysis of Covariance

<table>
<thead>
<tr>
<th>Performance Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Host Node</td>
</tr>
<tr>
<td>Install Location</td>
</tr>
<tr>
<td>Execution Mode</td>
</tr>
<tr>
<td>Number of Compute Nodes</td>
</tr>
<tr>
<td>Number of Threads per Node</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Data Access Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Engine Role Path</td>
</tr>
<tr>
<td>WORK.SCHOOLSAMPLE</td>
</tr>
</tbody>
</table>
Mixed Model Analysis of Covariance with Many Groups

Model Information

Data Set WORK.SCHOOLSAMPLE
Dependent Variable Math
Covariance Structure Unstructured
Subject Effect Neighborho(SchoolID)
Estimation Method Restricted Maximum Likelihood
Residual Variance Method Profile
Fixed Effects SE Method Model-Based
Degrees of Freedom Method Residual

Class Level Information

Class Levels Values
Neighborhood 1520 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 ...
SchoolID 300 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 ...

Dimensions

Covariance Parameters 7
Columns in Z per Subject 3
Subjects 7500
Max Obs per Subject 8

Number of Observations Read 60000
Number of Observations Used 60000
Number of Observations Not Used 0

Optimization Information

Optimization Technique Newton-Raphson with Ridging
Parameters in Optimization 6
Lower Boundaries 3
Upper Boundaries 0
Starting Values From Data

Convergence criterion (ABSGCONV=0.00001) satisfied.

Covariance Parameter Estimates

<table>
<thead>
<tr>
<th>Cov Parm</th>
<th>Subject</th>
<th>Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>UN(1,1)</td>
<td>Neighborho(SchoolID)</td>
<td>2.0902</td>
</tr>
<tr>
<td>UN(2,1)</td>
<td>Neighborho(SchoolID)</td>
<td>0.000349</td>
</tr>
<tr>
<td>UN(2,2)</td>
<td>Neighborho(SchoolID)</td>
<td>2.0517</td>
</tr>
<tr>
<td>UN(3,1)</td>
<td>Neighborho(SchoolID)</td>
<td>0.01448</td>
</tr>
<tr>
<td>UN(3,2)</td>
<td>Neighborho(SchoolID)</td>
<td>0.01599</td>
</tr>
<tr>
<td>UN(3,3)</td>
<td>Neighborho(SchoolID)</td>
<td>0.08047</td>
</tr>
<tr>
<td>Residual</td>
<td></td>
<td>1.0083</td>
</tr>
</tbody>
</table>

Fit Statistics

-2 Res Log Likelihood 225642
AIC (Smaller is Better) 225656
AICC (Smaller is Better) 225656
BIC (Smaller is Better) 225704
### Syntax: HPLMIXED Procedure

The following statements are available in PROC HPLMIXED.

```
PROC HPLMIXED <options> ;
  CLASS variables ;
  ID variables ;
  MODEL dependent = <fixed-effects> < / options > ;
  OUTPUT <OUT=SAS-data-set> <keyword = name > . . . <keyword = name > < / options > ;
  RANDOM random-effects < / options > ;
  REPEATED repeated-effect < / options > ;
  PARMS < (value-list) > . . . < / options > ;
  PERFORMANCE < options > ;
```

Items within angle brackets ( < > ) are optional. The RANDOM statement can appear multiple times. Other statements can appear only once.

The PROC HPLMIXED and MODEL statements are required, and the MODEL statement must appear after the CLASS statement if a CLASS statement is included. The RANDOM statement must follow the MODEL statement.

Table 57.1 summarizes the basic functions and important options of the PROC HPLMIXED statements. The syntax of each statement in Table 57.1 is described in the following sections in alphabetical order after the description of the PROC HPLMIXED statement.

### Table 57.1  Summary of PROC HPLMIXED Statements

<table>
<thead>
<tr>
<th>Statement</th>
<th>Description</th>
<th>Important Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>PROC HPLMIXED</td>
<td>Invokes the procedure</td>
<td>DATA= specifies the input data set; METHOD= specifies the estimation method.</td>
</tr>
<tr>
<td>CLASS</td>
<td>Declares qualitative variables that create indicator variables in X and Z matrices.</td>
<td>None</td>
</tr>
<tr>
<td>ID</td>
<td>Lists additional variables to be included in predicted values tables</td>
<td>None</td>
</tr>
<tr>
<td>MODEL</td>
<td>Specifies dependent variable and fixed effects, setting up X</td>
<td>S requests a solution for fixed-effects parameters.</td>
</tr>
</tbody>
</table>
Table 57.1 continued

<table>
<thead>
<tr>
<th>Statement</th>
<th>Description</th>
<th>Important Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>RANDOM</td>
<td>Specifies random effects, setting up $Z$ and $G$</td>
<td>$\text{SUBJECT=}=$ creates block-diagonality; $\text{TYPE=}=$ specifies the covariance structure; $S$ requests a solution for the random effects.</td>
</tr>
<tr>
<td>REPEATED</td>
<td>Sets up $R$</td>
<td>$\text{SUBJECT=}=$ creates block-diagonality; $\text{TYPE=}=$ specifies the covariance structure.</td>
</tr>
<tr>
<td>OUTPUT</td>
<td>Creates a data set that contains observationwise statistics</td>
<td>$\text{ALLSTATS}$ requests that all statistics be computed.</td>
</tr>
<tr>
<td>PARMS</td>
<td>Specifies a grid of initial values for the covariance parameters</td>
<td>$\text{HOLD=}=$ and $\text{NOITER}$ hold the covariance parameters or their ratios constant; $\text{PARMSDATA=}=$ reads the initial values from a SAS data set.</td>
</tr>
<tr>
<td>PERFORMANCE</td>
<td>Invokes the distributed computing connection</td>
<td>$\text{NODES=}=$ specifies the number of nodes to use.</td>
</tr>
</tbody>
</table>

**PROC HPLMIXED Statement**

```markdown
PROC HPLMIXED <options>;
```

The PROC HPLMIXED statement invokes the procedure. Table 57.2 summarizes important options in the PROC HPLMIXED statement by function. These and other options in the PROC HPLMIXED statement are then described fully in alphabetical order.

### Table 57.2 PROC HPLMIXED Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data set</td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies the estimation method</td>
</tr>
<tr>
<td>NAMELEN=</td>
<td>Limits the length of effect names</td>
</tr>
<tr>
<td>BLUP</td>
<td>Computes the best linear unbiased prediction</td>
</tr>
<tr>
<td><strong>Options Related to Output</strong></td>
<td></td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Suppresses the “Class Level Information” table completely or in parts</td>
</tr>
<tr>
<td>MAXCLPRINT=</td>
<td>Specifies the maximum levels of CLASS variables to print</td>
</tr>
<tr>
<td>RANKS</td>
<td>Displays the rank of design matrix $X$</td>
</tr>
<tr>
<td><strong>Optimization Options</strong></td>
<td></td>
</tr>
<tr>
<td>ABSCONV=</td>
<td>Tunes an absolute function convergence criterion</td>
</tr>
</tbody>
</table>

---

**Table 57.1 continued**

<table>
<thead>
<tr>
<th>Statement</th>
<th>Description</th>
<th>Important Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>RANDOM</td>
<td>Specifies random effects, setting up $Z$ and $G$</td>
<td>$\text{SUBJECT=}=$ creates block-diagonality; $\text{TYPE=}=$ specifies the covariance structure; $S$ requests a solution for the random effects.</td>
</tr>
<tr>
<td>REPEATED</td>
<td>Sets up $R$</td>
<td>$\text{SUBJECT=}=$ creates block-diagonality; $\text{TYPE=}=$ specifies the covariance structure.</td>
</tr>
<tr>
<td>OUTPUT</td>
<td>Creates a data set that contains observationwise statistics</td>
<td>$\text{ALLSTATS}$ requests that all statistics be computed.</td>
</tr>
<tr>
<td>PARMS</td>
<td>Specifies a grid of initial values for the covariance parameters</td>
<td>$\text{HOLD=}=$ and $\text{NOITER}$ hold the covariance parameters or their ratios constant; $\text{PARMSDATA=}=$ reads the initial values from a SAS data set.</td>
</tr>
<tr>
<td>PERFORMANCE</td>
<td>Invokes the distributed computing connection</td>
<td>$\text{NODES=}=$ specifies the number of nodes to use.</td>
</tr>
</tbody>
</table>
### Table 57.2 continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABSFCONV=</td>
<td>Tunes an absolute function difference convergence criterion</td>
</tr>
<tr>
<td>ABSGCONV=</td>
<td>Tunes the absolute gradient convergence criterion</td>
</tr>
<tr>
<td>FCN=</td>
<td>Tunes the relative function convergence criterion</td>
</tr>
<tr>
<td>GCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Chooses the maximum number of iterations in any optimization</td>
</tr>
<tr>
<td>MAXFUNC=</td>
<td>Specifies the maximum number of function evaluations in any optimization</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the upper limit on seconds of CPU time for any optimization</td>
</tr>
<tr>
<td>MINITER=</td>
<td>Specifies the minimum number of iterations in any optimization</td>
</tr>
<tr>
<td>TECHNIQUE=</td>
<td>Selects the optimization technique</td>
</tr>
<tr>
<td>XCONV=</td>
<td>Tunes the relative parameter convergence criterion</td>
</tr>
</tbody>
</table>

You can specify the following *options* in the PROC HPLMIXED statement.

**ABSCONV=**

specifies an absolute function convergence criterion. For minimization, termination requires \( f(\boldsymbol{\psi}^{(k)}) \leq r \), where \( \boldsymbol{\psi} \) is the vector of parameters in the optimization and \( f(\cdot) \) is the objective function. The default value of \( r \) is the negative square root of the largest double-precision value, which serves only as a protection against overflows.

**ABSFCONV=**

specifies an absolute function difference convergence criterion. For all techniques except Nelder–Mead simplex (NMSIMP), termination requires a small change of the function value in successive iterations:

\[
|f(\boldsymbol{\psi}^{(k-1)}) - f(\boldsymbol{\psi}^{(k)})| \leq r
\]

Here, \( \boldsymbol{\psi} \) denotes the vector of parameters that participate in the optimization and \( f(\cdot) \) is the objective function. The same formula is used for the NMSIMP technique, but \( \boldsymbol{\psi}^{(k)} \) is defined as the vertex with the lowest function value and \( \boldsymbol{\psi}^{(k-1)} \) is defined as the vertex with the highest function value in the simplex. The default value is \( r=0 \).

**ABSGCONV=**

specifies an absolute gradient convergence criterion. Termination requires the maximum absolute gradient element to be small:

\[
\max_j |g_j(\boldsymbol{\psi}^{(k)})| \leq r
\]

Here, \( \boldsymbol{\psi} \) denotes the vector of parameters that participate in the optimization and \( g_j(\cdot) \) is the gradient of the objective function with respect to the \( j \) parameter. This criterion is not used by the NMSIMP technique. The default value is \( r=1E-5 \).

**BLUP**(suboptions)**

requests that best linear unbiased predictions (BLUPs) for the random effects be displayed. To use this option, you must also use the PARMS statement to specify fixed values for the covariance parameters,
which means that the NOITER option in the PARMS statement will be implied by the BLUP option. Also, the iterations in the ODS Table IterHistory will refer to iterations used to compute the BLUP rather than optimization iterations.

The BLUP solution might be sensitive to the order of observations, and hence to how the data are distributed on the grid. If there are multiple measures of a repeated effect, then the BLUP solution is not unique. If the order of these multiple measures on the grid differs for different runs, then different BLUP solutions will result.

You can specify the following suboptions:

**ITPRINT=** specifies that the iteration history be displayed after every number of iterations. The default value is 10, which means the procedure displays the iteration history for every 10 iterations.

**MAXITER=** specifies the maximum number of iterations allowed. The default value is the number of parameters in the BLUP option plus 2.

**TOL=** specifies the tolerance value. The default value is the square root of machine precision.

**DATA=** names the SAS data set to be used as the input data set. The default is the most recently created data set.

**FCONV=** specifies a relative function convergence criterion. For all techniques except NMSIMP, termination requires a small relative change of the function value in successive iterations,

\[
\frac{|f(\psi^{(k)}) - f(\psi^{(k-1)})|}{|f(\psi^{(k-1)})|} \leq r
\]

Here, \(\psi\) denotes the vector of parameters that participate in the optimization and \(f(\cdot)\) is the objective function. The same formula is used for the NMSIMP technique, but \(\psi^{(k)}\) is defined as the vertex with the lowest function value and \(\psi^{(k-1)}\) is defined as the vertex with the highest function value in the simplex.

The default is \(r = 10^{-FDIGITS}\), where FDIGITS is \(-\log_{10}(\epsilon)\) and \(\epsilon\) is the machine precision.

**GCONV=** specifies a relative gradient convergence criterion. For all techniques except CONGRA and NMSIMP, termination requires that the normalized predicted function reduction be small,

\[
\frac{g(\psi^{(k)})' [H^{(k)}]^{-1} g(\psi^{(k)})}{|f(\psi^{(k)})|} \leq r
\]

Here, \(\psi\) denotes the vector of parameters that participate in the optimization, \(f(\cdot)\) is the objective function, and \(g(\cdot)\) is the gradient. For the CONGRA technique (where a reliable Hessian estimate \(H\) is not available), the following criterion is used:

\[
\| g(\psi^{(k)}) \|_2^2 \| s(\psi^{(k)}) \|_2 \leq r
\]

This criterion is not used by the NMSIMP technique. The default value is \(r=1E^{-8}\).
**MAXCLPRINT=number**
specifies the maximum levels of CLASS variables to print in the ODS table “ClassLevels.” The default value is 20. MAXCLPRINT=0 enables you to print all levels of each CLASS variable. However, the option NOCLPRINT takes precedence over MAXCLPRINT.

**MAXFUNC=n**
specifies the maximum number n of function calls in the optimization process. The default values are as follows, depending on the optimization technique:

- TRUREG, NRRIDG, NEWRAP: 125
- QUANEW, DBLDOG: 500
- CONGRA: 1,000
- NMSIMP: 3,000

The optimization can terminate only after completing a full iteration. Therefore, the number of function calls that are actually performed can exceed n. You can choose the optimization technique with the TECHNIQUE= option.

**MAXITER=n**
specifies the maximum number n of iterations in the optimization process. The default values are as follows, depending on the optimization technique:

- TRUREG, NRRIDG, NEWRAP: 50
- QUANEW, DBLDOG: 200
- CONGRA: 400
- NMSIMP: 1,000

These default values also apply when n is specified as a missing value. You can choose the optimization technique with the TECHNIQUE= option.

**MAXTIME=r**
specifies an upper limit of r seconds of CPU time for the optimization process. The default value is the largest floating-point double representation of your computer. The time specified by the MAXTIME= option is checked only once at the end of each iteration. Therefore, the actual running time can be longer than r.

**METHOD=REML**
**METHOD=ML**
specifies the estimation method for the covariance parameters. METHOD=REML performs residual (restricted) maximum likelihood; it is the default method. METHOD=ML performs maximum likelihood.

**MINITER=n**
specifies the minimum number of iterations. The default value is 0. If you request more iterations than are actually needed for convergence to a stationary point, the optimization algorithms can behave strangely. For example, the effect of rounding errors can prevent the algorithm from continuing for the required number of iterations.
**NAMELEN=number**  
specifies the length to which long effect names are shortened. The minimum value is 20, which is also the default.

**NOCLPRINT<=number>**  
suppresses the display of the “Class Level Information” table if you do not specify number. If you specify number, the values of the classification variables are displayed for only those variables whose number of levels is less than number. Specifying a number helps to reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

**NOPRINT**  
suppresses the generation of ODS output.

**RANKS**  
displays the rank of design matrix $X$.

**SINGCHOL=number**  
tunes the singularity criterion in Cholesky decompositions. The default is 1E4 times the machine epsilon; this product is approximately 1E–12 on most computers.

**SINGSWEEP=number**  
tunes the singularity criterion for sweep operations. The default is 1E4 times the machine epsilon; this product is approximately 1E–12 on most computers.

**SINGULAR=number**  
tunes the general singularity criterion applied by the HPLMIXED procedure in sweeps and inversions. The default is 1E4 times the machine epsilon; this product is approximately 1E–12 on most computers.

**TECHNIQUE=keyword**  
specifies the optimization technique for obtaining maximum likelihood estimates. You can specify any of the following keywords:

- **CONGRA** performs a conjugate-gradient optimization.
- **DBLDOG** performs a version of double-dogleg optimization.
- **NEWRAP** performs a Newton-Raphson optimization combining a line-search algorithm with ridging.
- **NMSIMP** performs a Nelder-Mead simplex optimization.
- **NONE** performs no optimization.
- **NRRIDG** performs a Newton-Raphson optimization with ridging.
- **QUANEW** performs a dual quasi-Newton optimization.
- **TRUREG** performs a trust-region optimization.

The default value is TECHNIQUE=NRRIDG.

**XCONV=r**  
specifies the relative parameter convergence criterion:
• For all techniques except NMSIMP, termination requires a small relative parameter change in subsequent iterations:

\[ \frac{\max_j |\psi_j^{(k)} - \psi_j^{(k-1)}|}{\max(|\psi_j^{(k)}|, |\psi_j^{(k-1)}|)} \leq r \]

• For the NMSIMP technique, the same formula is used, but \(\psi_j^{(k)}\) is defined as the vertex with the lowest function value and \(\psi_j^{(k-1)}\) is defined as the vertex with the highest function value in the simplex.

The default value is \(r = 1 \times 10^{-8}\) for the NMSIMP technique and \(r = 0\) otherwise.

**CLASS Statement**

```plaintext
CLASS variables ;
```

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. These variables enter the analysis not through their values, but through levels to which the unique values are mapped. For more information about these mappings, see the section “Levelization of Classification Variables” (Chapter 3, SAS/STAT User’s Guide: High-Performance Procedures).

If a CLASS statement is specified, it must precede the MODEL statement in high-performance analytical procedures that support a MODEL statement.

Levels of classification variables are ordered by their external formatted values, except for numeric variables with no explicit format, which are ordered by their unformatted (internal) values.

**ID Statement**

```plaintext
ID variables ;
```

The ID statement specifies which variables from the input data set are to be included in the OUT= data set that is created by the OUTPUT statement. If you do not specify an ID statement, then no variables from the input data set are included in the OUT= data set.

**MODEL Statement**

```plaintext
MODEL dependent = < fixed-effects > / options ;
```

The MODEL statement names a single dependent variable and the fixed effects, which determine the \(X\) matrix of the mixed model. (For more information, see the section “Specification and Parameterization of Model Effects” (Chapter 3, SAS/STAT User’s Guide: High-Performance Procedures). The MODEL statement is required.

An intercept is included in the fixed-effects model by default. If no fixed effects are specified, only this intercept term is fit. The intercept can be removed by using the NOINT option.
Table 57.3 summarizes options in the MODEL statement. These are subsequently discussed in detail in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model Building</td>
<td>Excludes the fixed-effect intercept from model</td>
</tr>
<tr>
<td>NOINT</td>
<td></td>
</tr>
<tr>
<td>Statistical Computations</td>
<td>Determines the confidence level (1 - ( \alpha )) for fixed effects</td>
</tr>
<tr>
<td>ALPHA=( \alpha )</td>
<td></td>
</tr>
<tr>
<td>DDFM=</td>
<td>Specifies the method for computing denominator degrees of freedom</td>
</tr>
<tr>
<td>Statistical Output</td>
<td>Displays confidence limits for fixed-effects parameter estimates</td>
</tr>
<tr>
<td>CL</td>
<td></td>
</tr>
<tr>
<td>SOLUTION</td>
<td>Displays fixed-effects parameter estimates</td>
</tr>
</tbody>
</table>

You can specify the following options in the MODEL statement after a slash (/).

**ALPHA=number**

sets the confidence level to be 1 - number for each confidence interval of the fixed-effects parameters. The value of number must be between 0 and 1; the default is 0.05.

**CL**

requests that \( t \)-type confidence limits be constructed for each of the fixed-effects parameter estimates. The confidence level is 0.95 by default; this can be changed with the ALPHA= option.

**DDFM=NONE | RESIDUAL**

specifies the method for computing the denominator degrees of freedom for the tests of fixed effects.

The DDFM=RESIDUAL option performs all tests by using the residual degrees of freedom, \( n - \text{rank}(X) \), where \( n \) is the number of observations used. It is the default degrees-of-freedom method.

DDFM=NONE specifies that no denominator degrees of freedom be applied. PROC HPLMIXED then essentially assumes that infinite degrees of freedom are available in the calculation of \( p \)-values. The \( p \)-values for \( t \) tests are then identical to \( p \)-values that are derived from the standard normal distribution. In the case of \( F \) tests, the \( p \)-values equal those of chi-square tests determined as follows: if \( F_{\text{obs}} \) is the observed value of the \( F \) test with \( l \) numerator degrees of freedom, then

\[
p = \Pr\{F_{l,\infty} > F_{\text{obs}}\} = \Pr\{x_{l}^{2} > lF_{\text{obs}}\}
\]

**NOINT**

requests that no intercept be included in the model. (An intercept is included by default.)
SOLUTION

requests that a solution for the fixed-effects parameters be produced. Using notation from the section “Linear Mixed Models Theory” on page 4642, the fixed-effects parameter estimates are $\hat{\beta}$ and their approximate standard errors are the square roots of the diagonal elements of $(X'\hat{V}^{-1}X)^{-}$. Along with the estimates and their approximate standard errors, a $t$ statistic is computed as the estimate divided by its standard error. The Pr $>|t|$ column contains the two-tailed $p$-value that corresponds to the $t$ statistic and associated degrees of freedom. You can use the CL option to request confidence intervals for all of the parameters; they are constructed around the estimate by using a radius that is the product of the standard error times a percentage point from the $t$ distribution.

OUTPUT Statement

```
OUTPUT <OUT=SAS-data-set> <keyword <=name>> ... <keyword <=name>> </options> ;
```

The OUTPUT statement creates a data set that contains predicted values and residual diagnostics, which are computed after the model is fit. The variables in the input data set are not included in the output data set, in order to avoid data duplication for large data sets; however, variables that are specified in the ID statement are included. By default, only predicted values are included in the output data set.

If the input data are in distributed form, in which access of data in a particular order cannot be guaranteed, the HPLMIXED procedure copies the distribution or partition key to the output data set so that its contents can be joined with the input data.

For example, suppose that the data set Scores contains the variables Score, Machine, and Person. The following statements fit a model that has fixed machine and random person effects and save the predicted and residual values to the data set IgausOut:

```
proc hplmixed data = Scores;
  class machine person score;
  model score = machine;
  random person;
  output out=igausout pred=p resid=r;
run;
```

You can specify the following syntax element in the OUTPUT statement:

OUT=SAS-data-set

specifies the name of the output data set. If the OUT= option is omitted, PROC HPLMIXED uses the DATA$n$ convention to name the output data set.

A keyword can appear multiple times in the OUTPUT statement. Table 57.4 lists the keywords and the default names that PROC HPLMIXED assigns if you do not specify a name. In this table, $y$ denotes the response variable.

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
<th>Expression</th>
<th>Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRED</td>
<td>Linear predictor</td>
<td>$\hat{y} = x'\hat{\beta} + z'\hat{\gamma}$</td>
<td>Pred</td>
</tr>
</tbody>
</table>
Table 57.4 (continued)

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
<th>Expression</th>
<th>Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>PREDPA</td>
<td>Marginal linear predictor</td>
<td>$\hat{\eta}_m = x^T \hat{\beta}$</td>
<td>PredPA</td>
</tr>
<tr>
<td>RESIDUAL</td>
<td>Residual</td>
<td>$r = y - \hat{\eta}$</td>
<td>Resid</td>
</tr>
<tr>
<td>RESIDUALPA</td>
<td>Marginal residual</td>
<td>$r_m = y - \hat{\eta}_m$</td>
<td>ResidPA</td>
</tr>
</tbody>
</table>

The marginal linear predictor and marginal residual are also referred to as the predicted population average (PREDPA) and residual population average (RESIDUALPA), respectively. You can use the following shortcuts to request statistics: PRED for PREDICTED and RESID for RESIDUAL.

You can specify the following option in the OUTPUT statement after a slash (/):

**ALLSTATS**

requests that all statistics be computed. If you do not use a keyword to assign a name, PROC HPLMIXED uses the default name.

---

**PARMS Statement**

```plaintext
PARMS < (value-list) . . . > < / options > ;
```

The PARMS statement specifies initial values for the covariance parameters, or it requests a grid search over several values of these parameters. You must specify the values in the order in which they appear in the “Covariance Parameter Estimates” table.

The **value-list** specification can take any of several forms:

- $m$ a single value
- $m_1, m_2, \ldots, m_n$ several values
- $m$ to $n$ a sequence in which $m$ equals the starting value, $n$ equals the ending value, and the increment equals 1
- $m$ to $n$ by $i$ a sequence in which $m$ equals the starting value, $n$ equals the ending value, and the increment equals $i$
- $m_1, m_2$ to $m_3$ mixed values and sequences

You can use the PARMS statement to input known parameters.

If you specify more than one set of initial values, PROC HPLMIXED performs a grid search of the likelihood surface and uses the best point on the grid for subsequent analysis. Specifying a large number of grid points can result in long computing times.

The results from the PARMS statement are the values of the parameters on the specified grid (denoted by CovP1 through CovP$n$), the residual variance (possibly estimated) for models with a residual variance parameter, and various functions of the likelihood.

If there are multiple PARMS statements, the first one is used and the rest are ignored.

You can specify the following options in the PARMS statement after a slash (/).
**HOLD=all**

specifies that all parameter values be held to equal the specified values.

For example, the following statement constrains all covariance parameters to equal 5, 3, 2, and 3:

```
parms (5) (3) (2) (3) / hold=all;
```

**LOWERB=value-list**

enables you to specify lower boundary constraints on the covariance parameters. The *value-list* specification is a list of numbers or missing values (.) separated by commas. You must list the numbers in the order that PROC HPLMIXED uses for the covariance parameters, and each number corresponds to the lower boundary constraint. A missing value instructs PROC HPLMIXED to use its default constraint. If you do not specify numbers for all of the covariance parameters, PROC HPLMIXED assumes the remaining ones are missing.

This option is useful when you want to constrain the \( G \) matrix to be positive definite in order to avoid the more computationally intensive algorithms that would be required when \( G \) becomes singular. The corresponding statements for a random coefficients model are as follows:

```
proc hplmixed;
   class person;
   model y = time;
   random int time / type=fa0(2) sub=person;
   parms / lowerb=1e-4,.,1e-4;
run;
```

The **TYPE=FA0(2)** structure specifies a Cholesky root parameterization for the \( 2 \times 2 \) unstructured blocks in \( G \). This parameterization ensures that the \( G \) matrix is nonnegative definite, and the PARMS statement then ensures that it is positive definite by constraining the two diagonal terms to be greater than or equal to 1E–4.

**NOITER**

requests that no optimization iterations be performed and that PROC HPLMIXED use the best value from the grid search to perform inferences. By default, iterations begin at the best value from the PARMS grid search. The NOITER option will be implied by the specification of the BLUP option in the HPLMIXED statement.

**PARMSDATA=SAS-data-set**

**PDATA=SAS-data-set**

reads in covariance parameter values from a SAS data set. The data set should contain the Est or Covp1 through Covpn variables.

**UPPERB=value-list**

enables you to specify upper boundary constraints on the covariance parameters. The *value-list* specification is a list of numbers or missing values (.) separated by commas. You must list the numbers in the order that PROC HPLMIXED uses for the covariance parameters, and each number corresponds to the upper boundary constraint. A missing value instructs PROC HPLMIXED to use its default constraint. If you do not specify numbers for all of the covariance parameters, PROC HPLMIXED assumes that the remaining ones are missing.
PERFORMANCE Statement

PERFORMANCE < performance-options> ;

The PERFORMANCE statement defines performance parameters for multithreaded and distributed computing, passes variables about the distributed computing environment, and requests detailed results about the performance characteristics of a SAS high-performance analytical procedure.

You can also use the PERFORMANCE statement to control whether a SAS high-performance analytical procedure executes in single-machine mode or distributed mode.


RANDOM Statement

RANDOM random-effects / options ;

The RANDOM statement defines the random effects that constitute the $\mathbf{y}$ vector in the mixed model. You can use this statement to specify traditional variance component models and to specify random coefficients. The random effects can be classification or continuous, and multiple RANDOM statements are possible.

Using notation from the section “Linear Mixed Models Theory” on page 4642, the purpose of the RANDOM statement is to define the $\mathbf{Z}$ matrix of the mixed model, the random effects in the $\mathbf{y}$ vector, and the structure of $\mathbf{G}$. The $\mathbf{Z}$ matrix is constructed exactly as the $\mathbf{X}$ matrix for the fixed effects is constructed, and the $\mathbf{G}$ matrix is constructed to correspond with the effects that constitute $\mathbf{Z}$. The structure of $\mathbf{G}$ is defined by using the TYPE= option.

You can specify INTERCEPT (or INT) as a random effect to indicate the intercept. PROC HPLMIXED does not include the intercept in the RANDOM statement by default as it does in the MODEL statement.

Table 57.5 summarizes important options in the RANDOM statement. All options are subsequently discussed in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SUBJECT=</td>
<td>Identifies the subjects in the model</td>
</tr>
<tr>
<td>TYPE=</td>
<td>Specifies the covariance structure</td>
</tr>
<tr>
<td>ALPHA=(\alpha)</td>
<td>Determines the confidence level ((1 - \alpha))</td>
</tr>
<tr>
<td>CL</td>
<td>Requests confidence limits for predictors of random effects</td>
</tr>
<tr>
<td>SOLUTION</td>
<td>Displays solutions (\hat{\mathbf{y}}) of the random effects</td>
</tr>
</tbody>
</table>

You can specify the following options in the RANDOM statement after a slash (/).
**ALPHA=number**

sets the confidence level to be $1 - number$ for each confidence interval of the random-effects estimates. The value of number must be between 0 and 1; the default is 0.05.

**CL**

requests that $t$-type confidence limits be constructed for each of the random-effect estimates. The confidence level is 0.95 by default; this can be changed with the ALPHA= option.

**SOLUTION**

requests that the solution for the random-effects parameters be produced. Using notation from the section “Linear Mixed Models Theory” on page 4642, these estimates are the empirical best linear unbiased predictors (EBLUPs), $\hat{y} = \hat{G}Z'\hat{V}^{-1}(y - X\hat{\beta})$. They can be useful for comparing the random effects from different experimental units and can also be treated as residuals in performing diagnostics for your mixed model.

The numbers displayed in the SE Pred column of the “Solution for Random Effects” table are not the standard errors of the $\hat{y}$ displayed in the Estimate column; rather, they are the standard errors of predictions $\hat{y}_i - y_i$, where $\hat{y}_i$ is the $i$th EBLUP and $y_i$ is the $i$th random-effect parameter.

**SUBJECT=effect**

identifies the subjects in your mixed model. Complete independence is assumed across subjects; thus, for the RANDOM statement, the SUBJECT= option produces a block-diagonal structure in $G$ with identical blocks. In fact, specifying a subject effect is equivalent to nesting all other effects in the RANDOM statement within the subject effect.

When you specify the SUBJECT= option and a classification random effect, computations are usually much quicker if the levels of the random effect are duplicated within each level of the SUBJECT= effect.

**TYPE=covariance-structure**

specifies the covariance structure of $G$. Valid values for covariance-structure and their descriptions are listed in Table 57.6. Although a variety of structures are available, most applications call for either TYPE=VC or TYPE=UN. The TYPE=VC (variance components) option is the default structure, and it models a different variance component for each random effect.

The TYPE=UN (unstructured) option is useful for correlated random coefficient models. For example, the following statement specifies a random intercept-slope model that has different variances for the intercept and slope and a covariance between them:

```plaintext
random intercept age / type=un subject=person;
```

You can also use TYPE=FA0(2) here to request a $G$ estimate that is constrained to be nonnegative definite.

If you are constructing your own columns of $Z$ with continuous variables, you can use the TYPE=TOEP(1) structure to group them together to have a common variance component. If you want to have different covariance structures in different parts of $G$, you must use multiple RANDOM statements with different TYPE= options.
Table 57.6 Covariance Structures

<table>
<thead>
<tr>
<th>Structure</th>
<th>Description</th>
<th>Parms</th>
<th>(i, j) element</th>
</tr>
</thead>
<tbody>
<tr>
<td>ANTE(1)</td>
<td>Antedependence</td>
<td>$2t - 1$</td>
<td>$\sigma_i \sigma_j \prod_{k=1}^{t} \rho_k$</td>
</tr>
<tr>
<td>AR(1)</td>
<td>Autoregressive(1)</td>
<td>2</td>
<td>$\sigma^2 \rho_{i-j}$</td>
</tr>
<tr>
<td>ARH(1)</td>
<td>Heterogeneous AR(1)</td>
<td>$t + 1$</td>
<td>$\sigma_i \sigma_j \rho_{i-j}$</td>
</tr>
<tr>
<td>ARMA(1,1)</td>
<td>Autoregressive moving average(1,1)</td>
<td>3</td>
<td>$\sigma^2 [\gamma \rho_{i-j} - 11(i \neq j) + 1(i = j)]$</td>
</tr>
<tr>
<td>CS</td>
<td>Compound symmetry</td>
<td>2</td>
<td>$\sigma_1 + \sigma^2 1(i = j)$</td>
</tr>
<tr>
<td>CSH</td>
<td>Heterogeneous compound symmetry</td>
<td>$t + 1$</td>
<td>$\sigma_i \sigma_j [\rho_1(i \neq j) + 1(i = j)]$</td>
</tr>
<tr>
<td>FA(q)</td>
<td>Factor analytic</td>
<td>$\frac{q}{2}(2t - q + 1) + t$</td>
<td>$\sum_{k=1}^{\min(i,j,q)} \lambda_{ik} \lambda_{jk} + \sigma^2 1(i = j)$</td>
</tr>
<tr>
<td>FA0(q)</td>
<td>No diagonal FA</td>
<td>$\frac{q}{2}(2t - q + 1)$</td>
<td>$\sum_{k=1}^{\min(i,j,q)} \lambda_{ik} \lambda_{jk}$</td>
</tr>
<tr>
<td>FA1(q)</td>
<td>Equal diagonal FA</td>
<td>$\frac{q}{2}(2t - q + 1) + 1$</td>
<td>$\sum_{k=1}^{\min(i,j,q)} \lambda_{ik} \lambda_{jk} + \sigma^2 1(i = j)$</td>
</tr>
<tr>
<td>HF</td>
<td>Huynh-Feldt</td>
<td>$t + 1$</td>
<td>$(\sigma_i^2 + \sigma_j^2)/2 + \lambda 1(i \neq j)$</td>
</tr>
<tr>
<td>SIMPLE</td>
<td>An alias for VC</td>
<td>$q$</td>
<td>$\sigma^2 1(i = j)$ for the kth effect</td>
</tr>
<tr>
<td>TOEP</td>
<td>Toeplitz</td>
<td>$t$</td>
<td>$\sigma_{</td>
</tr>
<tr>
<td>TOEP(q)</td>
<td>Banded Toeplitz</td>
<td>$q$</td>
<td>$\sigma_{</td>
</tr>
<tr>
<td>TOEPH</td>
<td>Heterogeneous TOEP</td>
<td>$2t - 1$</td>
<td>$\sigma_i \sigma_j \rho_{i-j}$</td>
</tr>
<tr>
<td>TOEPH(q)</td>
<td>Banded heterogeneous TOEP</td>
<td>$t + q - 1$</td>
<td>$\sigma_i \sigma_j \rho_{i-j}(i - j) &lt; q$</td>
</tr>
<tr>
<td>UN</td>
<td>Unstructured</td>
<td>$t(t + 1)/2$</td>
<td>$\sigma_{ij}$</td>
</tr>
<tr>
<td>UN(q)</td>
<td>Banded</td>
<td>$\frac{q}{2}(2t - q + 1)$</td>
<td>$\sigma_{ij} 1(</td>
</tr>
<tr>
<td>UNR</td>
<td>Unstructured correlation</td>
<td>$t(t + 1)/2$</td>
<td>$\sigma_i \sigma_j \rho_{\max(i,j)\min(i,j)}$</td>
</tr>
<tr>
<td>UNR(q)</td>
<td>Banded correlations</td>
<td>$\frac{q}{2}(2t - q + 1)$</td>
<td>$\sigma_i \sigma_j \rho_{\max(i,j)\min(i,j)}$</td>
</tr>
<tr>
<td>VC</td>
<td>Variance components</td>
<td>$q$</td>
<td>$\sigma^2 1(i = j)$ for the kth effect</td>
</tr>
</tbody>
</table>

In Table 57.6, the Parms column represents the number of covariance parameters in the structure, $t$ is the overall dimension of the covariance matrix, and $1(A)$ equals 1 when $A$ is true and 0 otherwise. For example, $1(i = j)$ equals 1 when $i = j$ and 0 otherwise, and $1(|i - j| < q)$ equals 1 when $|i - j| < q$ and 0 otherwise. For the TYPE=TOEPH structures, $\rho_0 = 1$; for the TYPE=UNR structures, $\rho_{ij} = 1$ for all $i$.

Table 57.7 lists some examples of the structures in Table 57.6.

Table 57.7 Covariance Structure Examples

<table>
<thead>
<tr>
<th>Description</th>
<th>Structure</th>
<th>Example</th>
</tr>
</thead>
</table>
| Variance components| VC (default)  | \[
\begin{bmatrix}
    \sigma_B^2 & 0 & 0 & 0 \\
    0 & \sigma_B^2 & 0 & 0 \\
    0 & 0 & \sigma_{AB}^2 & 0 \\
    0 & 0 & 0 & \sigma_{AB}^2
\end{bmatrix}
\] |
<table>
<thead>
<tr>
<th>Description</th>
<th>Structure</th>
<th>Example</th>
</tr>
</thead>
</table>
| Compound symmetry                 | CS          | \[
\begin{bmatrix}
\sigma^2 + \sigma_1 & \sigma_1 & \sigma_1 & \sigma_1 \\
\sigma_1 & \sigma^2 + \sigma_1 & \sigma_1 & \sigma_1 \\
\sigma_1 & \sigma_1 & \sigma^2 + \sigma_1 & \sigma_1 \\
\sigma_1 & \sigma_1 & \sigma_1 & \sigma^2 + \sigma_1 \\
\end{bmatrix}
\] |
| Unstructured                      | UN          | \[
\begin{bmatrix}
\sigma_1^2 & \sigma_1 \sigma_2 & \sigma_1 \sigma_3 & \sigma_1 \\
\sigma_1 \sigma_2 & \sigma_2^2 & \sigma_2 \sigma_3 & \sigma_2 \sigma_4 \\
\sigma_1 \sigma_3 & \sigma_2 \sigma_3 & \sigma_3^2 & \sigma_3 \sigma_4 \\
\sigma_1 & \sigma_2 \sigma_4 & \sigma_2 \sigma_4 & \sigma_4^2 \\
\end{bmatrix}
\] |
| Banded main diagonal              | UN(1)       | \[
\begin{bmatrix}
\sigma_1^2 & 0 & 0 & 0 \\
0 & \sigma_2^2 & 0 & 0 \\
0 & 0 & \sigma_3^2 & 0 \\
0 & 0 & 0 & \sigma_4^2 \\
\end{bmatrix}
\] |
| First-order autoregressive        | AR(1)       | \[
\begin{bmatrix}
\sigma^2 & 1 & \rho & \rho^2 & \rho^3 \\
\rho & 1 & \rho & \rho^2 & \rho \\
\rho^2 & \rho & 1 & \rho & 1 \\
\rho^3 & \rho^2 & \rho & 1 & \mathbf{I}
\end{bmatrix}
\] |
| Toeplitz                          | TOEP        | \[
\begin{bmatrix}
\sigma_1 & \sigma_2 & \sigma_3 \\
\sigma_2 & \sigma_1 & \sigma_2 \\
\sigma_3 & \sigma_2 & \sigma_1 \\
\end{bmatrix}
\] |
| Toeplitz with two bands           | TOEP(2)     | \[
\begin{bmatrix}
\sigma_1 & 0 & 0 \\
\sigma_1 & \sigma_2 & 0 \\
0 & \sigma_1 & \sigma_2 \\
0 & 0 & \sigma_1 \\
\end{bmatrix}
\] |
| Heterogeneous autoregressive(1)   | ARH(1)      | \[
\begin{bmatrix}
\sigma_1^2 & \sigma_1 \sigma_2 \rho & \sigma_1 \sigma_3 \rho^2 & \sigma_1 \sigma_4 \rho^3 \\
\sigma_2 \sigma_1 \rho & \sigma_2^2 & \sigma_2 \sigma_3 \rho & \sigma_2 \sigma_4 \rho^2 \\
\sigma_3 \sigma_1 \rho^2 & \sigma_3 \sigma_2 \rho & \sigma_3^2 & \sigma_3 \sigma_4 \rho \\
\sigma_4 \sigma_1 \rho^3 & \sigma_4 \sigma_2 \rho^2 & \sigma_4 \sigma_3 \rho & \sigma_4^2 \\
\end{bmatrix}
\] |
| First-order autoregressive moving average | ARMA(1,1) | \[
\begin{bmatrix}
1 & \gamma & \gamma \rho & \gamma \rho^2 \\
\gamma & 1 & \gamma & \gamma \rho \\
\gamma \rho & \gamma & 1 & \gamma \\
\gamma \rho^2 & \gamma \rho & \gamma & 1
\end{bmatrix}
\] |
| Heterogeneous compound symmetry   | CSH         | \[
\begin{bmatrix}
\lambda_1^2 + d_1 & \lambda_1 \lambda_2 & \lambda_1 \lambda_3 & \lambda_1 \lambda_4 \\
\lambda_2 \lambda_1 & \lambda_2^2 + d_2 & \lambda_2 \lambda_3 & \lambda_2 \lambda_4 \\
\lambda_3 \lambda_1 & \lambda_3 \lambda_2 & \lambda_3^2 + d_3 & \lambda_3 \lambda_4 \\
\lambda_4 \lambda_1 & \lambda_4 \lambda_2 & \lambda_4 \lambda_3 & \lambda_4^2 + d_4
\end{bmatrix}
\] |
Table 57.7 continued

<table>
<thead>
<tr>
<th>Description</th>
<th>Structure</th>
<th>Example</th>
</tr>
</thead>
</table>
| Huynh-Feldt                     | HF        | $\begin{bmatrix}
\sigma_1^2 & \frac{\sigma_1^2 + \sigma_2^2}{2} - \lambda & \frac{\sigma_1^2 + \sigma_2^2}{2} - \lambda \\
\frac{\sigma_1^2 + \sigma_2^2}{2} - \lambda & \sigma_2^2 & \frac{\sigma_1^2 + \sigma_2^2}{2} - \lambda \\
\frac{\sigma_1^2 + \sigma_2^2}{2} - \lambda & \frac{\sigma_1^2 + \sigma_2^2}{2} - \lambda & \sigma_2^2
\end{bmatrix}$ |
| First-order antedependence      | ANTE(1)   | $\begin{bmatrix}
\sigma_1^2 & \sigma_1 \sigma_2 \rho_1 & \sigma_1 \sigma_3 \rho_1 \rho_2 \\
\sigma_2 \sigma_1 \rho_1 & \sigma_2^2 & \sigma_2 \sigma_3 \rho_2 \\
\sigma_3 \sigma_1 \rho_2 \rho_1 & \sigma_3 \sigma_2 \rho_2 & \sigma_3^2
\end{bmatrix}$ |
| Heterogeneous Toeplitz          | TOEPH     | $\begin{bmatrix}
\sigma_1^2 & \sigma_1 \sigma_2 \rho_1 & \sigma_1 \sigma_3 \rho_1 \rho_2 & \sigma_1 \sigma_4 \rho_3 \\
\sigma_2 \sigma_1 \rho_1 & \sigma_2^2 & \sigma_2 \sigma_3 \rho_1 \rho_2 & \sigma_2 \sigma_4 \rho_2 \\
\sigma_3 \sigma_1 \rho_2 & \sigma_3 \sigma_2 \rho_2 & \sigma_3^2 & \sigma_3 \sigma_4 \rho_1 \\
\sigma_4 \sigma_1 \rho_3 & \sigma_4 \sigma_2 \rho_2 & \sigma_4 \sigma_3 \rho_1 & \sigma_4^2
\end{bmatrix}$ |
| Unstructured correlations       | UNR       | $\begin{bmatrix}
\sigma_1^2 & \sigma_1 \sigma_2 \rho_1 & \sigma_1 \sigma_3 \rho_1 & \sigma_1 \sigma_4 \rho_1 \\
\sigma_2 \sigma_1 \rho_1 & \sigma_2^2 & \sigma_2 \sigma_3 \rho_1 & \sigma_2 \sigma_4 \rho_2 \\
\sigma_3 \sigma_1 \rho_2 & \sigma_3 \sigma_2 \rho_2 & \sigma_3^2 & \sigma_3 \sigma_4 \rho_1 \\
\sigma_4 \sigma_1 \rho_3 & \sigma_4 \sigma_2 \rho_2 & \sigma_4 \sigma_3 \rho_1 & \sigma_4^2
\end{bmatrix}$ |

The following list provides some further information about these covariance structures:

**TYPE=ANTE(1)** specifies the first-order antedependence structure (Kenward 1987; Patel 1991; Macchiavelli and Arnold 1994). In Table 57.6, $\sigma_i^2$ is the $i$ variance parameter, and $\rho_k$ is the $k$ autocorrelation parameter that satisfies $|\rho_k| < 1$.

**TYPE=AR(1)** specifies a first-order autoregressive structure. PROC HPLMIXED imposes the constraint $|\rho| < 1$ for stationarity.

**TYPE=ARH(1)** specifies a heterogeneous first-order autoregressive structure. As with TYPE=AR(1), PROC HPLMIXED imposes the constraint $|\rho| < 1$ for stationarity.

**TYPE=ARMA(1,1)** specifies the first-order autoregressive moving average structure. In Table 57.6, $\rho$ is the autoregressive parameter, $\gamma$ models a moving average component, and $\sigma^2$ is the residual variance. In the notation of Fuller (1976, p. 68), $\rho = \theta_1$ and

$$\gamma = \frac{(1 + b_1 \theta_1)(\theta_1 + b_1)}{1 + b_1^2 + 2b_1 \theta_1}$$

The example in Table 57.7 and $|b_1| < 1$ imply that

$$b_1 = \frac{\beta - \sqrt{\beta^2 - 4\alpha^2}}{2\alpha}$$

where $\alpha = \gamma - \rho$ and $\beta = 1 + \rho^2 - 2\gamma \rho$. PROC HPLMIXED imposes the constraints $|\rho| < 1$ and $|\gamma| < 1$ for stationarity, although the resulting covariance matrix is not positive definite for some values of $\rho$ and $\gamma$ in this region. When the estimated value of $\rho$ becomes negative, the computed covariance is multiplied by $\cos(\pi d_{ij})$ to account for the negativity.
Chapter 57: The HPLMIXED Procedure

**TYPE=CS** specifies the compound-symmetry structure, which has constant variance and constant covariance.

**TYPE=CSH** specifies the heterogeneous compound-symmetry structure. This structure has a different variance parameter for each diagonal element, and it uses the square roots of these parameters in the off-diagonal entries. In Table 57.6, \( \sigma_i^2 \) is the \( i \) variance parameter, and \( \rho \) is the correlation parameter that satisfies \( |\rho| < 1 \).

**TYPE=FA\((q)\)** specifies the factor-analytic structure with \( q \) factors (Jennrich and Schluchter 1986). This structure is of the form \( \Lambda \Lambda' + D \), where \( \Lambda \) is a \( t \times q \) rectangular matrix and \( D \) is a \( t \times t \) diagonal matrix with \( t \) different parameters. When \( q > 1 \), the elements of \( \Lambda \) in its upper right corner (that is, the elements in the \( i \) row and \( j \) column for \( j > i \)) are set to zero to fix the rotation of the structure.

**TYPE=FA0\((q)\)** is similar to the \( FA(q) \) structure except that no diagonal matrix \( D \) is included. When \( q < t \) (that is, when the number of factors is less than the dimension of the matrix), this structure is nonnegative definite but not of full rank. In this situation, you can use this structure for approximating an unstructured \( G \) matrix in the RANDOM statement. When \( q = t \), you can use this structure to constrain \( G \) to be nonnegative definite in the RANDOM statement.

**TYPE=FA1\((q)\)** is similar to the \( TYPE=FA(q) \) structure except that all of the elements in \( D \) are constrained to be equal. This offers a useful and more parsimonious alternative to the full factor-analytic structure.

**TYPE=HF** specifies the Huynh-Feldt covariance structure (Huynh and Feldt 1970). This structure is similar to the \( TYPE=CSH \) structure in that it has the same number of parameters and heterogeneity along the main diagonal. However, it constructs the off-diagonal elements by taking arithmetic means rather than geometric means.

You can perform a likelihood ratio test of the Huynh-Feldt conditions by running PROC HPLMIXED twice, once with \( TYPE=HF \) and once with \( TYPE=UN \), and then subtracting their respective values of \(-2 \) times the maximized likelihood.

If PROC HPLMIXED does not converge under your Huynh-Feldt model, you can specify your own starting values with the PARMS statement. The default MIVQUE(0) starting values can sometimes be poor for this structure. A good choice for starting values is often the parameter estimates that correspond to an initial fit that uses \( TYPE=CS \).

**TYPE=SIMPLE** is an alias for \( TYPE=VC \).

**TYPE=TOEP\(<(q)>\)** specifies a banded Toeplitz structure. This can be viewed as a moving average structure with order equal to \( q - 1 \). The \( TYPE=TOEP \) option is a full Toeplitz matrix, which can be viewed as an autoregressive structure with order equal to the dimension of the matrix. The specification \( TYPE=TOEP(1) \) is the same as \( \sigma^2 I \), where \( I \) is an identity matrix, and it can be useful for specifying the same variance component for several effects.

**TYPE=TOEPH\(<(q)>\)** specifies a heterogeneous banded Toeplitz structure. In Table 57.6, \( \sigma_i^2 \) is the \( i \) variance parameter and \( \rho_{ij} \) is the \( j \) correlation parameter that satisfies \( |\rho_{ij}| < 1 \). If you specify the order parameter \( q \), then PROC HPLMIXED estimates only the first \( q \) bands of the matrix, setting all higher bands equal to 0. The option \( TOEPH(1) \) is equivalent to both the \( TYPE=UN(1) \) and \( TYPE=UNR(1) \) options.
TYPE=UN\((q)\) specifies a completely general (unstructured) covariance matrix that is parameterized directly in terms of variances and covariances. The variances are constrained to be nonnegative, and the covariances are unconstrained. This structure is not constrained to be nonnegative definite in order to avoid nonlinear constraints. However, you can use the TYPE=FA0 structure if you want this constraint to be imposed by a Cholesky factorization. If you specify the order parameter \(q\), then PROC HPLMIXED estimates only the first \(q\) bands of the matrix, setting all higher bands equal to 0.

TYPE=UNR\((q)\) specifies a completely general (unstructured) covariance matrix that is parameterized in terms of variances and correlations. This structure fits the same model as the TYPE=UN\((q)\) option but with a different parameterization. The \(i\) variance parameter is \(\sigma_i^2\). The parameter \(\rho_{jk}\) is the correlation between the \(j\) and \(k\) measurements; it satisfies \(|\rho_{jk}| < 1\). If you specify the order parameter \(r\), then PROC HPLMIXED estimates only the first \(q\) bands of the matrix, setting all higher bands equal to zero.

TYPE=VC specifies standard variance components. This is the default structure for both the RANDOM and REPEATED statements. In the RANDOM statement, a distinct variance component is assigned to each effect.

Jennrich and Schluchter (1986) provide general information about the use of covariance structures, and Wolfinger (1996) presents details about many of the heterogeneous structures.

### REPEATED Statement

```
REPEATED repeated-effect < / options > ;
```

The REPEATED statement specifies the \(R\) matrix in the mixed model. If no REPEATED statement is specified, \(R\) is assumed to be equal to \(\sigma^2 I\). For this release, you can use the REPEATED statement only with the BLUP option. The statement is ignored when no BLUP option is specified.

The `repeated-effect` is required, because the order of the input data is not necessarily reproducible in a distributed environment. The `repeated-effect` must contain only classification variables. Make sure that the levels of the `repeated-effect` are different for each observation within a subject; otherwise, PROC HPLMIXED constructs identical rows in \(R\) that correspond to the observations with the same level. This results in a singular \(R\) matrix and an infinite likelihood.

Table 57.8 summarizes important options in the REPEATED statement. All options are subsequently discussed in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SUBJECT=</td>
<td>Identifies the subjects in the R-side model</td>
</tr>
<tr>
<td>TYPE=</td>
<td>Specifies the R-side covariance structure</td>
</tr>
</tbody>
</table>
You can specify the following options in the REPEATED statement after a slash (/).

**SUBJECT=** *effect*

identifies the subjects in your mixed model. Complete independence is assumed across subjects; therefore, the SUBJECT= option produces a block-diagonal structure in $R$ with identical blocks. When the SUBJECT= effect consists entirely of classification variables, the blocks of $R$ correspond to observations that share the same level of that effect. These blocks are sorted according to this effect as well.

If you want to model nonzero covariance among all of the observations in your SAS data set, specify SUBJECT=Dummy_Intercept to treat the data as if they are all from one subject. You need to create this Dummy_Intercept variable in the data set. However, be aware that in this case PROC HPLMIXED manipulates an $R$ matrix with dimensions equal to the number of observations.

**TYPE=** *covariance-structure*

specifies the covariance structure of the $R$ matrix. The SUBJECT= option defines the blocks of $R$, and the TYPE= option specifies the structure of these blocks. The default structure is VC. You can specify any of the covariance structures that are described in the TYPE= option in the RANDOM statement.

---

**Details: HPLMIXED Procedure**

**Linear Mixed Models Theory**

This section provides an overview of a likelihood-based approach to linear mixed models. This approach simplifies and unifies many common statistical analyses, including those that involve repeated measures, random effects, and random coefficients. The basic assumption is that the data are linearly related to unobserved multivariate normal random variables. For extensions to nonlinear and nonnormal situations, see the documentation of the GLIMMIX and NLMIXED procedures in the *SAS/STAT User’s Guide*. Additional theory and examples are provided in Littell et al. (2006); Verbeke and Molenberghs (1997, 2000); and Burdick and Graybill (1992).

**Matrix Notation**

Suppose that you observe $n$ data points $y_1, \ldots, y_n$ and that you want to explain them by using $n$ values for each of $p$ explanatory variables $x_{11}, \ldots, x_{1p}, x_{21}, \ldots, x_{2p}, \ldots, x_{n1}, \ldots, x_{np}$. The $x_{ij}$ values can be either regression-type continuous variables or dummy variables that indicate class membership. The standard linear model for this setup is

$$y_i = \sum_{j=1}^{p} x_{ij} \beta_j + \epsilon_i \quad i = 1, \ldots, n$$

where $\beta_1, \ldots, \beta_p$ are unknown fixed-effects parameters to be estimated and $\epsilon_1, \ldots, \epsilon_n$ are unknown independent and identically distributed normal (Gaussian) random variables with mean 0 and variance $\sigma^2$. 
The preceding equations can be written simultaneously by using vectors and a matrix, as follows:

\[
\begin{bmatrix}
  y_1 \\
y_2 \\
  \vdots \\
y_n
\end{bmatrix}
= 
\begin{bmatrix}
x_{11} & x_{12} & \ldots & x_{1p} \\
x_{21} & x_{22} & \ldots & x_{2p} \\
  \vdots & \vdots & \ddots & \vdots \\
x_{n1} & x_{n2} & \ldots & x_{np}
\end{bmatrix}
\begin{bmatrix}
  \beta_1 \\
  \beta_2 \\
  \vdots \\
  \beta_p
\end{bmatrix}
+ 
\begin{bmatrix}
  \epsilon_1 \\
  \epsilon_2 \\
  \vdots \\
  \epsilon_n
\end{bmatrix}
\]

For convenience, simplicity, and extendability, this entire system is written as

\[ y = X\beta + \epsilon \]

where \( y \) denotes the vector of observed \( y_i \)'s, \( X \) is the known matrix of \( x_{ij} \)'s, \( \beta \) is the unknown fixed-effects parameter vector, and \( \epsilon \) is the unobserved vector of independent and identically distributed Gaussian random errors.

In addition to denoting data, random variables, and explanatory variables in the preceding fashion, the subsequent development makes use of basic matrix operators such as transpose (\( ' \)), inverse (\( ^{-1} \)), generalized inverse (\( \cdot^-1 \)), determinant (\( | \cdot | \)), and matrix multiplication. See Searle (1982) for details about these and other matrix techniques.

**Formulation of the Mixed Model**

The previous general linear model is certainly a useful one (Searle 1971), and it is the one fitted by the GLM procedure. However, many times the distributional assumption about \( \epsilon \) is too restrictive. The mixed model extends the general linear model by allowing a more flexible specification of the covariance matrix of \( \epsilon \). In other words, it allows for both correlation and heterogeneous variances, although you still assume normality.

The mixed model is written as

\[ y = X\beta + Z\gamma + \epsilon \]

where everything is the same as in the general linear model except for the addition of the known design matrix, \( Z \), and the vector of unknown random-effects parameters, \( \gamma \). The matrix \( Z \) can contain either continuous or dummy variables, just like \( X \). The name mixed model comes from the fact that the model contains both fixed-effects parameters, \( \beta \), and random-effects parameters, \( \gamma \). See Henderson (1990) and Searle, Casella, and McCulloch (1992) for historical developments of the mixed model.

A key assumption in the foregoing analysis is that \( \gamma \) and \( \epsilon \) are normally distributed with

\[
\mathbb{E}\left[ \begin{bmatrix} \gamma \\ \epsilon \end{bmatrix} \right] = \begin{bmatrix} 0 \\ 0 \end{bmatrix}
\]

\[
\text{Var}\left[ \begin{bmatrix} \gamma \\ \epsilon \end{bmatrix} \right] = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix}
\]

Therefore, the variance of \( y \) is \( V = ZGZ' + R \). You can model \( V \) by setting up the random-effects design matrix \( Z \) and by specifying covariance structures for \( G \) and \( R \).

Note that this is a general specification of the mixed model, in contrast to many texts and articles that discuss only simple random effects. Simple random effects are a special case of the general specification with \( Z \) containing dummy variables, \( G \) containing variance components in a diagonal structure, and \( R = \sigma^2 I_n \), where \( I_n \) denotes the \( n \times n \) identity matrix. The general linear model is a further special case with \( Z = 0 \) and \( R = \sigma^2 I_n \).

The following two examples illustrate the most common formulations of the general linear mixed model.
Example: Growth Curve with Compound Symmetry

Suppose that you have three growth curve measurements for $s$ individuals and that you want to fit an overall linear trend in time. Your $X$ matrix is as follows:

$$
X = \begin{bmatrix}
1 & 1 \\
1 & 2 \\
1 & 3 \\
\vdots & \vdots \\
1 & 1 \\
1 & 2 \\
1 & 3
\end{bmatrix}
$$

The first column (coded entirely with 1s) fits an intercept, and the second column (coded with series of 1, 2, 3) fits a slope. Here, $n = 3s$ and $p = 2$.

Suppose further that you want to introduce a common correlation among the observations from a single individual, with correlation being the same for all individuals. One way of setting this up in the general mixed model is to eliminate the $Z$ and $G$ matrices and let the $R$ matrix be block-diagonal with blocks corresponding to the individuals and with each block having the compound-symmetry structure. This structure has two unknown parameters, one modeling a common covariance and the other modeling a residual variance. The form for $R$ would then be

$$
R = \begin{bmatrix}
\sigma_1^2 + \sigma^2 & \sigma_1^2 & \sigma_1^2 \\
\sigma_1^2 & \sigma_1^2 + \sigma^2 & \sigma_1^2 \\
\sigma_1^2 & \sigma_1^2 & \sigma_1^2 + \sigma^2 \\
& \ddots & \ddots \\
\sigma_1^2 & \sigma_1^2 & \sigma_1^2 \\
\sigma_1^2 & \sigma_1^2 + \sigma^2 & \sigma_1^2 \\
\sigma_1^2 & \sigma_1^2 & \sigma_1^2 + \sigma^2
\end{bmatrix}
$$

where blanks denote zeros. There are $3s$ rows and columns altogether, and the common correlation is $\sigma_1^2/(\sigma_1^2 + \sigma^2)$.

The following PROC HPLMIXED statements fit this model:

```sas
proc hplmixed;
  class indiv;
  model y = time;
  repeated morder/ type=cs subject=indiv;
run;
```

Here, INDIV is a classification variable that indexes individuals. The MODEL statement fits a straight line for TIME; the intercept is fit by default just as in PROC GLM. The REPEATED statement models the $R$ matrix: TYPE=CS specifies the compound symmetry structure, and SUBJECT=INDIV specifies the blocks of $R$, and MORDER is the repeated effect that records the order of the measurements for each individual.
An alternative way of specifying the common intra-individual correlation is to let

\[
Z = \begin{bmatrix}
1 \\
1 \\
1 \\
1 \\
1 \\
\vdots \\
1 \\
1 \\
1 \\
\end{bmatrix}
\]

\[
G = \begin{bmatrix}
\sigma_1^2 \\
\sigma_1^2 \\
\vdots \\
\sigma_1^2 \\
\end{bmatrix}
\]

and \( R = \sigma^2 I_n \). The \( Z \) matrix has \( 3s \) rows and \( s \) columns, and \( G \) is \( s \times s \).

You can set up this model in PROC HPLMIXED in two different but equivalent ways:

```plaintext
proc hplmixed;
  class indiv;
  model y = time;
  random indiv;
run;

proc hplmixed;
  class indiv;
  model y = time;
  random intercept / subject=indiv;
run;
```

Both of these specifications fit the same model as the previous one that used the REPEATED statement. However, the RANDOM specifications constrain the correlation to be positive, whereas the REPEATED specification leaves the correlation unconstrained.
Example: Split-Plot Design

The split-plot design involves two experimental treatment factors, A and B, and two different sizes of experimental units to which they are applied (Winer 1971; Snedecor and Cochran 1980; Milliken and Johnson 1992; Steel, Torrie, and Dickey 1997). The levels of A are randomly assigned to the larger-sized experimental units, called whole plots, whereas the levels of B are assigned to the smaller-sized experimental units, the subplots. The subplots are assumed to be nested within the whole plots, so that a whole plot consists of a cluster of subplots and a level of A is applied to the entire cluster.

Such an arrangement is often necessary by nature of the experiment; the classical example is the application of fertilizer to large plots of land and different crop varieties planted in subdivisions of the large plots. For this example, fertilizer is the whole-plot factor A and variety is the subplot factor B.

The first example is a split-plot design for which the whole plots are arranged in a randomized block design. The appropriate PROC HPLMIXED statements are as follows:

``` Sas
proc hplmixed;
  class a b block;
  model y = a b a*b;
  random block a*block;
run;
```

Here

\[ R = \sigma^2 I_{24} \]

and X, Z, and G have the following form:
\[
X = \begin{bmatrix}
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
\vdots & \vdots & \vdots & \vdots \\
1 & 1 & 1 & 1 \\
\end{bmatrix}
\]

\[
Z = \begin{bmatrix}
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
1 & 1 & 1 & 1 \\
\vdots & \vdots & \vdots & \vdots \\
1 & 1 & 1 & 1 \\
\end{bmatrix}
\]

\[
G = \begin{bmatrix}
\sigma^2_B & \sigma^2_B & \sigma^2_B & \sigma^2_B \\
\sigma^2_B & \sigma^2_B & \sigma^2_B & \sigma^2_B \\
\sigma^2_B & \sigma^2_B & \sigma^2_B & \sigma^2_B \\
\sigma^2_B & \sigma^2_B & \sigma^2_B & \sigma^2_B \\
\sigma^2_B & \sigma^2_B & \sigma^2_B & \sigma^2_B \\
\vdots & \vdots & \vdots & \vdots \\
\sigma^2_B & \sigma^2_B & \sigma^2_B & \sigma^2_B \\
\end{bmatrix}
\]
where $\sigma^2_B$ is the variance component for Block and $\sigma^2_{AB}$ is the variance component for A*Block. Changing the \texttt{RANDOM} statement as follows fits the same model, but with Z and G sorted differently:

\begin{verbatim}
random int a / subject=block;
\end{verbatim}

\begin{figure}
\centering
\includegraphics[width=\textwidth]{matrix}
\caption{Matrix Representation}
\end{figure}

\begin{verbatim}
\end{verbatim}

\section*{Estimating Covariance Parameters in the Mixed Model}

Estimation is more difficult in the mixed model than in the general linear model. Not only do you have $\beta$ as in the general linear model, but you also have unknown parameters in $y$, $G$, and $R$. Least squares is no longer the best method. Generalized least squares (GLS) is more appropriate, minimizing

\[(y - X\beta)'V^{-1}(y - X\beta)\]
However, GLS requires knowledge of \( V \) and therefore knowledge of \( G \) and \( R \). Lacking such information, one approach is to use an *estimated* GLS, in which you insert some reasonable estimate for \( V \) into the minimization problem. The goal thus becomes finding a reasonable estimate of \( G \) and \( R \).

In many situations, the best approach is to use likelihood-based methods, exploiting the assumption that \( \gamma \) and \( \epsilon \) are normally distributed (Hartley and Rao 1967; Patterson and Thompson 1971; Harville 1977; Laird and Ware 1982; Jennrich and Schluchter 1986). PROC HPLMIXED implements two likelihood-based methods: maximum likelihood (ML) and restricted (residual) maximum likelihood (REML). A favorable theoretical property of ML and REML is that they accommodate data that are missing at random (Rubin 1976; Little 1995).

PROC HPLMIXED constructs an objective function associated with ML or REML and maximizes it over all unknown parameters. Using calculus, it is possible to reduce this maximization problem to one over only the parameters in \( G \) and \( R \). The corresponding log-likelihood functions are as follows:

\[
\text{ML} : \quad l(G, R) = -\frac{1}{2} \log |V| - \frac{1}{2} r' V^{-1} r - \frac{n}{2} \log(2\pi) \\
\text{REML} : \quad l_R(G, R) = -\frac{1}{2} \log |V| - \frac{1}{2} \log |X' V^{-1} X| - \frac{1}{2} r' V^{-1} r - \frac{n - p}{2} \log(2\pi)
\]

where \( r = y - X(X' V^{-1} X)^{-1} X' V^{-1} y \) and \( p \) is the rank of \( X \). By default, PROC HPLMIXED actually minimizes a normalized form of \(-2\) times these functions by using a ridge-stabilized Newton-Raphson algorithm by default. Lindstrom and Bates (1988) provide reasons for preferring Newton-Raphson to the expectation-maximum (EM) algorithm described in Dempster, Laird, and Rubin (1977) and Laird, Lange, and Stram (1987), in addition to analytical details for implementing a QR-decomposition approach to the problem. Wolfinger, Tobias, and Sall (1994) present the sweep-based algorithms that are implemented in PROC HPLMIXED. You can change the optimization technique with the \textsc{technique=} option in the PROC HPLMIXED statement.

One advantage of using the Newton-Raphson algorithm is that the second derivative matrix of the objective function evaluated at the optima is available upon completion. Denoting this matrix \( H \), the asymptotic theory of maximum likelihood (Serfling 1980) shows that \( 2H^{-1} \) is an asymptotic variance-covariance matrix of the estimated parameters of \( G \) and \( R \). Thus, tests and confidence intervals based on asymptotic normality can be obtained. However, these can be unreliable in small samples, especially for parameters such as variance components that have sampling distributions that tend to be skewed to the right.

If a residual variance \( \sigma^2 \) is a part of your mixed model, it can usually be *profiled* out of the likelihood. This means solving analytically for the optimal \( \sigma^2 \) and plugging this expression back into the likelihood formula (Wolfinger, Tobias, and Sall 1994). This reduces the number of optimization parameters by 1 and can improve convergence properties. PROC HPLMIXED profiles the residual variance out of the log likelihood.

**Estimating Fixed and Random Effects in the Mixed Model**

ML and REML methods provide estimates of \( G \) and \( R \), which are denoted \( \hat{G} \) and \( \hat{R} \), respectively. To obtain estimates of \( \beta \) and predicted values of \( \gamma \), the standard method is to solve the *mixed model equations* (Henderson 1984):

\[
\begin{bmatrix}
X' \hat{R}^{-1} X & X' \hat{R}^{-1} Z \\
Z' \hat{R}^{-1} X & Z' \hat{R}^{-1} Z + \hat{G}^{-1}
\end{bmatrix}
\begin{bmatrix}
\hat{\beta} \\
\hat{\gamma}
\end{bmatrix} =
\begin{bmatrix}
X' \hat{R}^{-1} y \\
Z' \hat{R}^{-1} y
\end{bmatrix}
\]
The solutions can also be written as

\[
\hat{\beta} = (X'\hat{V}^{-1}X)^{-1}X'\hat{V}^{-1}y \\
\hat{\gamma} = \hat{G}Z'\hat{V}^{-1}(y - X\hat{\beta})
\]

and have connections with empirical Bayes estimators (Laird and Ware 1982; Carlin and Louis 1996). Note that the \( \gamma \) are random variables and not parameters (unknown constants) in the model. Technically, determining values for \( \gamma \) from the data is thus a prediction task, whereas determining values for \( \hat{\beta} \) is an estimation task.

The mixed model equations are extended normal equations. The preceding expression assumes that \( \hat{G} \) is nonsingular. For the extreme case where the eigenvalues of \( \hat{G} \) are very large, \( \hat{G}^{-1} \) contributes very little to the equations and \( \hat{\gamma} \) is close to what it would be if \( \gamma \) actually contained fixed-effects parameters. On the other hand, when the eigenvalues of \( \hat{G} \) are very small, \( \hat{G}^{-1} \) dominates the equations and \( \hat{\gamma} \) is close to 0. For intermediate cases, \( \hat{G}^{-1} \) can be viewed as shrinking the fixed-effects estimates of \( \gamma \) toward 0 (Robinson 1991).

If \( \hat{G} \) is singular, then the mixed model equations are modified (Henderson 1984) as follows:

\[
\begin{bmatrix}
X'\hat{R}^{-1}X & X'\hat{R}^{-1}\hat{Z}\hat{G} \\
\hat{G}'Z'\hat{R}^{-1}X & \hat{G}'Z'\hat{R}^{-1}\hat{Z}\hat{G} + \hat{G}
\end{bmatrix}
\begin{bmatrix}
\hat{\beta} \\
\hat{\gamma}
\end{bmatrix}
= 
\begin{bmatrix}
X'\hat{R}^{-1}y \\
\hat{G}'Z'\hat{R}^{-1}y
\end{bmatrix}
\]

Denote the generalized inverses of the nonsingular \( \hat{G} \) and singular \( \hat{G} \) forms of the mixed model equations by \( C \) and \( M \), respectively. In the nonsingular case, the solution \( \hat{\gamma} \) estimates the random effects directly. But in the singular case, the estimates of random effects are achieved through a back-transformation \( \hat{\gamma} = \hat{G}\hat{\tau} \) where \( \hat{\tau} \) is the solution to the modified mixed model equations. Similarly, while in the nonsingular case \( C \) itself is the estimated covariance matrix for \( (\hat{\beta}, \hat{\gamma}) \), in the singular case the covariance estimate for \( (\hat{\beta}, \hat{G}\hat{\tau}) \) is given by \( PMP \) where

\[
P = \begin{bmatrix} I \\ \hat{G} \end{bmatrix}
\]

An example of when the singular form of the equations is necessary is when a variance component estimate falls on the boundary constraint of 0.

**Statistical Properties**

If \( G \) and \( R \) are known, \( \hat{\beta} \) is the best linear unbiased estimator (BLUE) of \( \beta \), and \( \hat{\gamma} \) is the best linear unbiased predictor (BLUP) of \( \gamma \) (Searle 1971; Harville 1988, 1990; Robinson 1991; McLean, Sanders, and Stroup 1991). Here, “best” means minimum mean squared error. The covariance matrix of \( (\hat{\beta} - \beta, \hat{\gamma} - \gamma) \) is

\[
C = \begin{bmatrix} X'\hat{R}^{-1}X & X'\hat{R}^{-1}Z \\
Z'\hat{R}^{-1}X & Z'\hat{R}^{-1}Z + \hat{G}^{-1}
\end{bmatrix}^{-1}
\]

where \( - \) denotes a generalized inverse (Searle 1971).

However, \( G \) and \( R \) are usually unknown and are estimated by using one of the aforementioned methods. These estimates, \( \hat{G} \) and \( \hat{R} \), are therefore simply substituted into the preceding expression to obtain

\[
\hat{C} = \begin{bmatrix} X'\hat{R}^{-1}X & X'\hat{R}^{-1}Z \\
Z'\hat{R}^{-1}X & Z'\hat{R}^{-1}Z + \hat{G}^{-1}
\end{bmatrix}^{-1}
\]
as the approximate variance-covariance matrix of \((\hat{\beta} - \beta, \hat{\gamma} - \gamma)\). In this case, the BLUE and BLUP acronyms no longer apply, but the word *empirical* is often added to indicate such an approximation. The appropriate acronyms thus become EBLUE and EBLUP.

McLean and Sanders (1988) show that \(\hat{C}\) can also be written as

\[
\hat{C} = \begin{bmatrix}
\hat{C}_{11} & \hat{C}_{21} \\
\hat{C}_{21} & \hat{C}_{22}
\end{bmatrix}
\]

where

\[
\hat{C}_{11} = (X'\hat{V}^{-1}X)^{-1}
\]
\[
\hat{C}_{21} = -\hat{G}Z'\hat{V}^{-1}X\hat{C}_{11}
\]
\[
\hat{C}_{22} = (Z'\hat{R}^{-1}Z + \hat{G}^{-1})^{-1} - \hat{C}_{21}X'\hat{V}^{-1}Z\hat{G}
\]

Note that \(\hat{C}_{11}\) is the familiar estimated generalized least squares formula for the variance-covariance matrix of \(\hat{\beta}\).

---

**Computational Method**

**Distributed Computing**

Distributed computing refers to the use of multiple autonomous computers that communicate through a secure network. Distributed computing solves computational problems by dividing them into many tasks, each of which is solved by one or more computers. Each computer in this distributed environment is referred to as a node.

You can specify the number of nodes to use with the NODES= option in the PERFORMANCE statement. Specify NODES=0 to force the execution to be done locally (often referred to as single-machine mode).

**Multithreading**

Threading refers to the organization of computational work into multiple tasks (processing units that can be scheduled by the operating system). A task is associated with a thread. Multithreading refers to the concurrent execution of threads. When multithreading is possible, substantial performance gains can be realized compared to sequential (single-threaded) execution.

The number of threads spawned by the HPLMIXED procedure is determined by the number of CPUs on a machine and can be controlled in the following ways:

You can specify the NTHREADS= option in the PERFORMANCE statement to determine the number of threads. This specification overrides the system option. Specify NTHREADS=1 to force single-threaded execution.

The number of threads per machine is displayed in the “Performance Information” table, which is part of the default output. The HPLMIXED procedure allocates two threads per CPU.

The tasks multithreaded by the HPLMIXED procedure are primarily defined by dividing the data processed on a single machine among the threads—that is, the HPLMIXED procedure implements multithreading through a data-parallel model. For example, if the input data set has 1,000 observations and you are running
with four threads, then 250 observations are associated with each thread. All operations that require access to
the data are then multithreaded. These operations include the following:

- variable levelization
- effect levelization
- formation of the crossproducts matrix
- the log-likelihood computation

In addition, operations on matrices such as sweeps might be multithreaded if the matrices are of sufficient
size to realize performance benefits from managing multiple threads for the particular matrix operation.

Displayed Output

The following sections describe the output produced by PROC HPLMIXED. The output is organized into
various tables, which are discussed in the order of their appearance.

Performance Information

The “Performance Information” table is produced by default. It displays information about the execution
mode. For single-machine mode, the table displays the number of threads used. For distributed mode, the
table displays the grid mode (symmetric or asymmetric), the number of compute nodes, and the number of
threads per node.

If you specify the DETAILS option in the PERFORMANCE statement, PROC HPLMIXED also produces a
“Timing” table that displays elapsed times (absolute and relative) for the main tasks of the procedure.

Model Information

The “Model Information” table describes the model, some of the variables it involves, and the method used in
fitting it. The “Model Information” table also has a row labeled Fixed Effects SE Method. This row describes
the method used to compute the approximate standard errors for the fixed-effects parameter estimates and
related functions of them.

Class Level Information

The “Class Level Information” table lists the levels of every variable specified in the CLASS statement.

Dimensions

The “Dimensions” table lists the sizes of relevant matrices. This table can be useful in determining the
requirements for CPU time and memory.

Number of Observations

The “Number of Observations” table shows the number of observations read from the data set and the number
of observations used in fitting the model.
**Optimization Information**

The “Optimization Information” table displays important details about the optimization process.

The number of parameters that are updated in the optimization equals the number of parameters in this table minus the number of equality constraints. The number of constraints is displayed if you fix covariance parameters with the **HOLD=** option in the **PARMS** statement. The **HPLMIXED** procedure also lists the number of upper and lower boundary constraints. **PROC HPLMIXED** might impose boundary constraints for certain parameters, such as variance components and correlation parameters. If you specify the **HOLD=** option in the **PARMS** statement, covariance parameters have an upper and lower boundary equal to the parameter value.

**Iteration History**

The “Iteration History” table describes the optimization of the restricted log likelihood or log likelihood. The function to be minimized (the **objective function**) is $-2l$ for ML and $-2l_R$ for REML; the column name of the objective function in the “Iteration History” table is “-2 Log Like” for ML and “-2 Res Log Like” for REML. The minimization is performed by using a ridge-stabilized Newton-Raphson algorithm, and the rows of this table describe the iterations that this algorithm takes in order to minimize the objective function.

The Evaluations column of the “Iteration History” table tells how many times the objective function is evaluated during each iteration.

The Criterion column of the “Iteration History” table is, by default, a relative Hessian convergence quantity given by

$$
\frac{g_k^T H_k^{-1} g_k}{|f_k|}
$$

where $f_k$ is the value of the objective function at iteration $k$, $g_k$ is the gradient (first derivative) of $f_k$, and $H_k$ is the Hessian (second derivative) of $f_k$. If $H_k$ is singular, then **PROC HPLMIXED** uses the following relative quantity:

$$
\frac{g_k^T g_k}{|f_k|}
$$

To prevent division by $|f_k|$, specify the **ABSGCONV** option in the **PROC HPLMIXED** statement. To use a relative function or gradient criterion, specify the **FCONV** or **GCONV** option, respectively.

The Hessian criterion is considered superior to function and gradient criteria because it measures orthogonality rather than lack of progress (Bates et al. 1987). Provided that the initial estimate is feasible and the maximum number of iterations is not exceeded, the Newton-Raphson algorithm is considered to have converged when the criterion is less than the tolerance specified with the **FCONV** or **GCONV** option in the **PROC HPLMIXED** statement. The default tolerance is $1E^{-8}$. If convergence is not achieved, **PROC HPLMIXED** displays the estimates of the parameters at the last iteration.

A convergence criterion that is missing indicates that a boundary constraint has been dropped; it is usually not a cause for concern.
Convergence Status

The “Convergence Status” table displays the status of the iterative estimation process at the end of the optimization. The status appears as a message in the listing, and this message is repeated in the log. The ODS object “ConvergenceStatus” also contains several nonprinting columns that can be helpful in checking the success of the iterative process, in particular during batch processing. The Status variable takes on the value 0 for a successful convergence (even if the Hessian matrix might not be positive definite). The values 1 and 2 of the Status variable indicate lack of convergence and infeasible initial parameter values, respectively. The variable pdG can be used to check whether the G matrix is positive definite.

For models that are not fit iteratively, such as models without random effects or when the NOITER option is in effect, the “Convergence Status” is not produced.

Covariance Parameter Estimates

The “Covariance Parameter Estimates” table contains the estimates of the parameters in G and R. (See the section “Estimating Covariance Parameters in the Mixed Model” on page 4648.) Their values are labeled in the table along with Subject information if applicable. The estimates are displayed in the Estimate column and are the results of either the REML or the ML estimation method.

Fit Statistics

The “Fit Statistics” table provides some statistics about the estimated mixed model. Expressions for $-2$ times the log likelihood are provided in the section “Estimating Covariance Parameters in the Mixed Model” on page 4648. If the log likelihood is an extremely large number, then PROC HPLMIXED has deemed the estimated V matrix to be singular. In this case, all subsequent results should be viewed with caution.

In addition, the “Fit Statistics” table lists three information criteria: AIC, AICC, and BIC. All these criteria are in smaller-is-better form and are described in Table 57.9.

<table>
<thead>
<tr>
<th>Table 57.9</th>
<th>Information Criteria</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Criterion</strong></td>
<td><strong>Formula</strong></td>
</tr>
<tr>
<td>AIC</td>
<td>$-2\ell + 2d$</td>
</tr>
<tr>
<td>AICC</td>
<td>$-2\ell + 2dn^<em>/(n^</em> - d - 1)$</td>
</tr>
<tr>
<td>BIC</td>
<td>$-2\ell + d \log n$ for $n &gt; 0$</td>
</tr>
</tbody>
</table>

Here $\ell$ denotes the maximum value of the (possibly restricted) log likelihood; $d$ is the dimension of the model; and $n$ equals the number of effective subjects as displayed in the “Dimensions” table, unless this value equals 1, in which case $n$ equals the number of levels of the first random effect specified in the first RANDOM statement or the number of levels of the interaction of the first random effect with noncommon subject effect specified in the first RANDOM statement. If the number of effective subjects equals 1 and you have no RANDOM statements, then $n$ equals the number of valid observations for maximum likelihood estimation and $n - p$ for restricted maximum likelihood estimation, where $p$ equals the rank of $X$. For AICC (a finite-sample corrected version of AIC), $n^*$ equals the number of valid observations for maximum likelihood estimation and $n - p$ equals the number of valid observations for restricted maximum likelihood estimation, unless this number is less than $d + 2$, in which case it equals $d + 2$. When $n = 0$, the value of the BIC is $-2\ell$. For restricted likelihood estimation, $d$ equals $q$, the effective number of estimated covariance parameters. For maximum likelihood estimation, $d$ equals $q + p$. 
Timing Information

If you specify the DETAILS option in the PERFORMANCE statement, the procedure also produces a “Timing” table in which the elapsed time for each main task of the procedure is displayed.

ODS Table Names

Each table created by PROC HPLMIXED has a name associated with it, and you must use this name to refer to the table when you use ODS statements. These names are listed in Table 57.10.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ClassLevels</td>
<td>Level information from the CLASS statement</td>
<td>Default output</td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Convergence status</td>
<td>Default output</td>
</tr>
<tr>
<td>CovParms</td>
<td>Estimated covariance parameters</td>
<td>Default output</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Dimensions of the model</td>
<td>Default output</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default output</td>
</tr>
<tr>
<td>IterHistory</td>
<td>Iteration history</td>
<td>Default output</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Model information</td>
<td>Default output</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used</td>
<td>Default output</td>
</tr>
<tr>
<td>OptInfo</td>
<td>Optimization information</td>
<td>Default output</td>
</tr>
<tr>
<td>ParmSearch</td>
<td>Parameter search values</td>
<td>PARMS</td>
</tr>
<tr>
<td>PerformanceInfo</td>
<td>Information about high-performance computing environment</td>
<td>Default output</td>
</tr>
<tr>
<td>Ranks</td>
<td>Rank of designed matrix X</td>
<td>PROC HPLMIXED RANKS</td>
</tr>
<tr>
<td>SolutionF</td>
<td>Fixed-effects solution vector</td>
<td>MODEL / S</td>
</tr>
<tr>
<td>SolutionR</td>
<td>Random-effects solution vector</td>
<td>RANDOM / S</td>
</tr>
<tr>
<td>Timing</td>
<td>Timing breakdown by task</td>
<td>DETAILS option in the PERFORMANCE statement</td>
</tr>
</tbody>
</table>

Examples: HPLMIXED Procedure

Example 57.1: Computing BLUPs for a Large Number of Subjects

Suppose you are using health measurements on patients treated by each medical center to monitor the performance of those centers. Different measurements within each patient are correlated, and there is enough data to fit the parameters of an unstructured covariance model for this correlation. In fact, long experience with historical data provides you with values for the covariance model that are essentially known, and the task is to apply these known values in order to compute best linear unbiased predictors (BLUPs) of the random
effect of medical center. You can use these BLUPs to determine the best and worst performing medical centers, adjusting for other factors, on a weekly basis. Another reason why you want to do this with fixed values for the covariance parameters is to make the week-to-week BLUPs more comparable.

Although you cannot use the REPEATED statement in PROC HPLMIXED to fit models in this release, you can use it to compute BLUPs for such models with known values of the variance parameters. For illustration, the following statements create a simulated data set of a given week’s worth of patient health measurements across 100 different medical centers. Measurements at three different times are simulated for each patient, and each center has about 50 patients. The simulated model includes a fixed gender effect, a random effect due to center, and covariance between different measurements on the same patient.

```plaintext
%let NCenter = 100;
%let NPatient = %eval(&NCenter*50);
%let NTime = 3;
%let SigmaC = 2.0;
%let SigmaP = 4.0;
%let SigmaE = 8.0;
%let Seed = 12345;

data WeekSim;
  keep Gender Center Patient Time Measurement;
  array PGender{&NPatient};
  array PCenter{&NPatient};
  array PEffect{&NPatient};
  array CEffect{&NCenter};
  array GEffect{2};
  do Center = 1 to &NCenter;
    CEffect{Center} = sqrt(&SigmaC)*rannor(&Seed);
  end;
  GEffect{1} = 10*ranuni(&Seed);
  GEffect{2} = 10*ranuni(&Seed);
  do Patient = 1 to &NPatient;
    PGender{Patient} = 1 + int(2 *ranuni(&Seed));
    PCenter{Patient} = 1 + int(&NCenter*ranuni(&Seed));
    PEffect{Patient} = sqrt(&SigmaP)*rannor(&Seed);
  end;
  do Patient = 1 to &NPatient;
    Gender = PGender{Patient};
    Center = PCenter{Patient};
    Mean = 1 + GEffect{Gender} + CEffect{Center} + PEffect{Patient};
    do Time = 1 to &NTime;
      Measurement = Mean + sqrt(&SigmaE)*rannor(&Seed);
      output;
    end;
  end;
run;
```
Example 57.1: Computing BLUPs for a Large Number of Subjects

Suppose that the known values for the covariance parameters are

\[
\begin{align*}
\text{Var}(\text{Center}) & = 1.7564 \\
\text{Cov}(\text{Patient}) & = \begin{bmatrix}
11.4555 & 3.6883 & 4.5951 \\
3.6883 & 11.2071 & 3.6311 \\
4.5951 & 3.6311 & 12.1050
\end{bmatrix}
\end{align*}
\]

Incidentally, these are not precisely the same estimates you would get if you estimated these parameters based on the preceding data (for example, with the HPLMIXED procedure).

The following statements use PROC HPLMIXED to compute the BLUPs for the random medical center effect. Instead of simply displaying them (as PROC HPMIXED does), PROC HPLMIXED sorts them and displays the five highest and lowest values. To run these statements successfully, you need to set the macro variables GRIDHOST and GRIDINSTALLLOC to resolve to appropriate values, or you can replace the references to macro variables with appropriate values.

```latex
ods exclude all;
proc hplmixed data=WeekSim blup;
    performance host="&GRIDHOST" install="&GRIDINSTALLLOC" nodes=20;
    class Gender Center Patient Time;
    model Measurement = Gender;
    random Center / s;
    repeated Time / sub=Patient type=un;
    ods output SolutionR=BLUPs;
run;
ods exclude none;
proc sort data=BLUPs;
    by Estimate;
run;
data BLUPs; set BLUPs;
    Rank = _N_; run;
proc print data=BLUPs;
    where ((Rank <= 5) | (Rank >= 96));
    var Center Estimate;
run;
```

Three parts of the PROC HPLMIXED syntax are required in order to compute BLUPs for this model: the BLUP option in the HPLMIXED statement, the REPEATED statement, and the PARMS statement with fixed values for all parameters. The resulting values of the best and worst performing medical centers for this week are shown in Output 57.1.1. Apparently, for this week’s data, medical center 54 had the most decreasing effect, and medical center 48 the most increasing effect, on patient measurements overall.
Output 57.1.1 Highest and Lowest Medical Center BLUPs

<table>
<thead>
<tr>
<th>Obs</th>
<th>Center</th>
<th>Estimate</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>54</td>
<td>-2.9369</td>
</tr>
<tr>
<td>2</td>
<td>7</td>
<td>-2.4614</td>
</tr>
<tr>
<td>3</td>
<td>50</td>
<td>-2.2467</td>
</tr>
<tr>
<td>4</td>
<td>51</td>
<td>-2.2281</td>
</tr>
<tr>
<td>5</td>
<td>93</td>
<td>-2.1644</td>
</tr>
<tr>
<td>96</td>
<td>26</td>
<td>2.1603</td>
</tr>
<tr>
<td>97</td>
<td>99</td>
<td>2.2718</td>
</tr>
<tr>
<td>98</td>
<td>44</td>
<td>2.4222</td>
</tr>
<tr>
<td>99</td>
<td>60</td>
<td>2.6089</td>
</tr>
<tr>
<td>100</td>
<td>48</td>
<td>2.6443</td>
</tr>
</tbody>
</table>

References


Subject Index

2D geometric anisotropic structure
  HPLMIXED procedure, 4636

Akaike’s information criterion
  HPLMIXED procedure, 4654
Akaike’s information criterion (finite sample corrected version)
  HPLMIXED procedure, 4654

alpha level
  HPLMIXED procedure, 4631, 4636

ANTE(1) structure
  HPLMIXED procedure, 4636

anteredependence structure
  HPLMIXED procedure, 4636

AR(1) structure
  HPLMIXED procedure, 4636

autoregressive moving-average structure
  HPLMIXED procedure, 4636

autoregressive structure
  HPLMIXED procedure, 4636

banded Toeplitz structure
  HPLMIXED procedure, 4636

BLUE
  HPLMIXED procedure, 4650

BLUP
  HPLMIXED procedure, 4650

boundary constraints
  HPLMIXED procedure, 4634

class level
  HPLMIXED procedure, 4629, 4652

compound symmetry structure
  example (HPLMIXED), 4644
  HPLMIXED procedure, 4636

computational method
  HPLMIXED procedure, 4651

constraints
  boundary (HPLMIXED), 4634

convergence criterion
  HPLMIXED procedure, 4626, 4627, 4653

convergence status
  HPLMIXED procedure, 4654

covariance parameter estimates
  HPLMIXED procedure, 4654

covariance structure
  antedependence (HPLMIXED), 4639
  autoregressive (HPLMIXED), 4639

autoregressive moving average (HPLMIXED), 4639

banded (HPLMIXED), 4640

compound symmetry (HPLMIXED), 4640
equi-correlation (HPLMIXED), 4640
equivalence (HPLMIXED), 4637

factor-analytic (HPLMIXED), 4640

heterogeneous autoregressive (HPLMIXED), 4639

heterogeneous compound symmetry
  (HPLMIXED), 4640

generalized heterogeneous compound symmetry (HPLMIXED), 4640

Heterogeneous Toeplitz (HPLMIXED), 4640

Huynh-Feldt (HPLMIXED), 4640

simple (HPLMIXED), 4640

toepplitz (HPLMIXED), 4640

unstructured (HPLMIXED), 4641

unstructured, correlation (HPLMIXED), 4641

variance components (HPLMIXED), 4641

degrees of freedom
  HPLMIXED procedure, 4631

infinite (HPLMIXED), 4631

method (HPLMIXED), 4631

residual method (HPLMIXED), 4631

dimension information
  HPLMIXED procedure, 4652

direct product structure
  HPLMIXED procedure, 4636

displayed output
  HPLMIXED procedure, 4652

distributed computing
  HPLMIXED procedure, 4651

effect
  name length (HPLMIXED), 4629

estimation
  mixed model (HPLMIXED), 4648

estimation methods
  HPLMIXED procedure, 4628

examples, HPLMIXED
  compound symmetry, G-side setup, 4645

compound symmetry, R-side setup, 4644

holding covariance parameters fixed, 4634

specifying lower bounds, 4634

split-plot design, 4646

subject and no-subject formulation, 4645

unstructured covariance, G-side, 4636
factor analytic structures
HPLMIXED procedure, 4636
fixed effects
HPLMIXED procedure, 4620
fixed-effects parameters
HPLMIXED procedure, 4643
G matrix
HPLMIXED procedure, 4620, 4635, 4643, 4644
general linear covariance structure
HPLMIXED procedure, 4636
generalized inverse, 4650
gradient
growth curve analysis
example (HPLMIXED), 4644
Hessian matrix
HPLMIXED procedure, 4653
heterogeneous
AR(1) structure (HPLMIXED), 4636
compound-symmetry structure (HPLMIXED), 4636
covariance structure (HPLMIXED), 4641
toeplitz structure (HPLMIXED), 4636
HPLMIXED procedure, 4618
2D geometric anisotropic structure, 4636
Akaike’s information criterion, 4654
Akaike’s information criterion (finite sample corrected version), 4654
alpha level, 4631, 4636
ANTE(1) structure, 4636
antedependence structure, 4636
AR(1) structure, 4636
ARMA structure, 4636
autoregressive moving-average structure, 4636
autoregressive structure, 4636
banded toeplitz structure, 4636
BLUE, 4626, 4650
BLUP, 4626, 4650
boundary constraints, 4634
chi-square test, 4631
class level, 4629, 4652
compound symmetry structure, 4636, 4644
computational method, 4651
confidence interval, 4636
confidence limits, 4631, 4636
covariance criterion, 4626, 4627, 4653
covariance structure, 4620, 4636, 4637
degrees of freedom, 4631
dimension information, 4652
direct product structure, 4636
displayed output, 4652
distributed computing, 4651
EBLUPs, 4636, 4651
effect name length, 4629
estimation methods, 4628
factor analytic structures, 4636
fitting information, 4654
fixed effects, 4620
fixed-effects parameters, 4632, 4643
function-based convergence criteria, 4626, 4627
G matrix, 4620, 4635, 4643, 4644
general linear covariance structure, 4636
generalized inverse, 4650
gradient, 4653
gradient-based convergence criteria, 4626, 4627
grid search, 4633
growth curve analysis, 4644
Hessian matrix, 4653
heterogeneous AR(1) structure, 4636
heterogeneous compound-symmetry structure, 4636
heterogeneous covariance structures, 4641
heterogeneous Toeplitz structure, 4636
Huynh-Feldt structure, 4636
infinite degrees of freedom, 4631
infinite likelihood, 4641
initial values, 4633
input data sets, 4627
intercept effect, 4631, 4635
iteration history, 4653
iterations, 4653
Kronecker product structure, 4636
linear covariance structure, 4636
Matérn covariance structure, 4636
matrix notation, 4642
mixed model, 4643
mixed model equations, 4649
mixed model theory, 4642
model information, 4652
multi-threading, 4635
multithreading, 4651
Newton-Raphson algorithm, 4649
number of observations, 4652
ODS table names, 4655
optimization information, 4653
parameter constraints, 4633
parameter-based convergence criteria, 4629
performance information, 4652
R matrix, 4620, 4641, 4643, 4644
random effects, 4620, 4635
random-effects parameters, 4636, 4643
repeated measures, 4641
residual method, 4631
restricted maximum likelihood (REML), 4619
Newton-Raphson algorithm  
HPLMIXED procedure, 4649
number of observations  
HPLMIXED procedure, 4652
objective function  
mixed model (HPLMIXED), 4653
optimization information  
HPLMIXED procedure, 4653
options summary  
MODEL statement (HPLMIXED), 4631
PROC HPLMIXED statement, 4625
RANDOM statement (HPLMIXED), 4635
REPEATED statement (HPLMIXED), 4641

parameter constraints  
HPLMIXED procedure, 4633
performance information  
HPLMIXED procedure, 4652

R matrix  
HPLMIXED procedure, 4620, 4641, 4643, 4644
random effects  
HPLMIXED procedure, 4620, 4635
random-effects parameters  
HPLMIXED procedure, 4643
repeated measures  
HPLMIXED procedure, 4641
residual maximum likelihood (REML)  
HPLMIXED procedure, 4649
restricted maximum likelihood  
HPLMIXED procedure, 4619
restricted maximum likelihood (REML)  
HPLMIXED procedure, 4649

ridging  
HPLMIXED procedure, 4649

Schwarz’s Bayesian information criterion  
HPLMIXED procedure, 4654
spatial anisotropic exponential structure  
HPLMIXED procedure, 4636
split-plot design  
HPLMIXED procedure, 4646
standard linear model  
HPLMIXED procedure, 4620
statement positions  
HPLMIXED procedure, 4624
subject effect  
HPLMIXED procedure, 4636, 4642
summary of commands  
HPLMIXED procedure, 4624
table names  
HPLMIXED procedure, 4655
timing  
HPLMIXED procedure, 4655

Toeplitz structure  
HPLMIXED procedure, 4636
HPLMIXED procedure, 4636
unstructured correlations
   HPLMIXED procedure, 4636
unstructured covariance matrix
   HPLMIXED procedure, 4636
variance components
   HPLMIXED procedure, 4636
variance ratios
   HPLMIXED procedure, 4633
## Syntax Index

- **ABSCONV option**
  - PROC HPLMIXED statement, 4626

- **ABSFCONV option**
  - PROC HPLMIXED statement, 4626

- **ABSGCONV option**
  - PROC HPLMIXED statement, 4626

- **ABSGTOL option**
  - PROC HPLMIXED statement, 4626

- **ABSOLUTE option**
  - PROC HPLMIXED statement, 4653

- **ABSTOL option**
  - PROC HPLMIXED statement, 4626

- **ALLSTATS option**
  - OUTPUT statement (HPLMIXED), 4633

- **ALPHA= option**
  - RANDOM statement (HPLMIXED), 4636

- **BLUP option**
  - PROC HPLMIXED statement, 4626

- **CL option**
  - MODEL statement (HPLMIXED), 4631
  - RANDOM statement (HPLMIXED), 4636

- **CLASS statement**
  - HPLMIXED procedure, 4630, 4652

- **CONVF option**
  - PROC HPLMIXED statement, 4653

- **CONVG option**
  - PROC HPLMIXED statement, 4653

- **CONVH option**
  - PROC HPLMIXED statement, 4653

- **DATA= option**
  - PROC HPLMIXED statement, 4627

- **DDFM= option**
  - MODEL statement (HPLMIXED), 4631

- **EQCONS= option**
  - PARMS statement (HPLMIXED), 4634

- **FCONV option**
  - PROC HPLMIXED statement, 4627

- **FTOL option**
  - PROC HPLMIXED statement, 4627

- **GCONV option**
  - PROC HPLMIXED statement, 4627

- **GTOL option**
  - PROC HPLMIXED statement, 4627

- **HOLD= option**
  - PARMS statement (HPLMIXED), 4634

- **HPLMIXED procedure**
  - ID statement, 4630
  - OUTPUT statement, 4632
  - PERFORMANCE statement, 4635
  - PROC HPLMIXED statement, 4625

- **HPLMIXED procedure, CLASS statement**
  - 4630, 4652

- **HPLMIXED procedure, ID statement**
  - 4630

- **HPLMIXED procedure, MODEL statement**
  - 4630

- **HPLMIXED procedure, OUTPUT statement**
  - 4632

- **HPLMIXED procedure, PERFORMANCE statement**
  - 4635

- **HPLMIXED procedure, PROC HPLMIXED statement**
  - ABSCONV option, 4626
  - ABSFCONV option, 4626
  - ABSFTOL option, 4626
  - ABSGCONV option, 4626
  - ABSGTOL option, 4626
  - ABSOLUTE option, 4653
  - ABSTOL option, 4626
  - BLUP option, 4626
  - CL option, 4631
  - DDFM= option, 4631
  - NOINT option, 4631
  - SOLUTION option, 4632
  - EQCONS= option, 4633
  - HOLD= option, 4634
  - LOWERB= option, 4634
  - NOITER option, 4634
  - PARMSDATA= option, 4634
  - PDATA= option, 4634
  - UPPERB= option, 4634
  - BLUP option, 4626
  - CONVF option, 4653
  - CONVG option, 4653
  - CONVH option, 4653
  - DATA= option, 4627
  - DDFM= option, 4631
  - MODEL statement (HPLMIXED), 4631
  - EQCONS= option, 4634
  - PARMS statement (HPLMIXED), 4634
  - FCONV option, 4627
  - FTOL option, 4627
  - GCONV option, 4627
  - GTOL option, 4627
  - MAXCLPRINT= option, 4628
  - MAXFUNC= option, 4628
  - MAXITER= option, 4628
HPLMIXED procedure, RANDOM statement, 4635
   ALPHA= option, 4636
   CL option, 4636
   SOLUTION option, 4636
   SUBJECT= option, 4636
   TYPE= option, 4636
HPLMIXED procedure, REPEATED statement, 4641
   SUBJECT= option, 4642
   TYPE= option, 4642
HPLMIXEDC procedure, PROC HPLMIXED statement, 4625

ID statement
   HPLMIXED procedure, 4630

LOWERB= option
   PARMS statement (HPLMIXED), 4634

MAXCLPRINT= option
   PROC HPLMIXED statement, 4628
MAXFUNC= option
   PROC HPLMIXED statement, 4628
MAXITER= option
   PROC HPLMIXED statement, 4628
MAXTIME= option
   PROC HPLMIXED statement, 4628
METHOD= option
   PROC HPLMIXED statement, 4628
MODEL statement
   HPLMIXED procedure, 4630
NAMELEN= option
   PROC HPLMIXED statement, 4629
NOCLPRINT option
   PROC HPLMIXED statement, 4629
NOINT option
   MODEL statement (HPLMIXED), 4631
NOITER option
   PARMS statement (HPLMIXED), 4634
NOPRINT option
   PROC HPLMIXED statement, 4629

OUT= option
   OUTPUT statement (HPLMIXED), 4632
   OUTPUT statement
   HPLMIXED procedure, 4632
PARMS statement
   HPLMIXED procedure, 4633
PARMSDATA= option
   PARMS statement (HPLMIXED), 4634
PDATA= option
   PARMS statement (HPLMIXED), 4634
PERFORMANCE statement
   HPLMIXED procedure, 4635
PROC HPLMIXED statement, see HPLMIXED procedure
   HPLMIXED procedure, 4625
RANDOM statement
   HPLMIXED procedure, 4635
RANKS option
   PROC HPLMIXED statement, 4629
REPEATED statement
   HPLMIXED procedure, 4641
   SINGCHOL= option
   PROC HPLMIXED statement, 4629
SINGSWEEP= option
   PROC HPLMIXED statement, 4629
SINGULAR= option
   PROC HPLMIXED statement, 4629
SOLUTION option
   MODEL statement (HPLMIXED), 4632
   RANDOM statement (HPLMIXED), 4636
   SUBJECT= option
   RANDOM statement (HPLMIXED), 4636
   REPEATED statement (HPLMIXED), 4636
   TECHNIQUE= option
   PROC HPLMIXED statement, 4629
   TYPE= option
   RANDOM statement (HPLMIXED), 4636
   REPEATED statement (HPLMIXED), 4642
UPPERB= option
   PARMS statement (HPLMIXED), 4634
XCONV option
   PROC HPLMIXED statement, 4629
XTOL option
   PROC HPLMIXED statement, 4629