Introducing the **BGLIMM** Procedure for **B**ayesian **G**eneralized **Li**near **M**ixed **M**odels

Amy Shi and Fang Chen
SAS Institute
fangk.chen@sas.com

BASUG, September 2019

1. PROC BGLIMM Overview
2. Procedure Details
3. Examples
   - Logistic Regression
   - Logistic Random-Effects Model
   - Repeated Measurements with Heterogeneity

Mixed Models

A mixed model contains fixed and random effects.

Mixed Models

A mixed model contains fixed and random effects.

First consider a normal linear mixed model,

$$\begin{aligned} \mathbf{Y} &= \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\epsilon} \\ \boldsymbol{\gamma} &\sim N(\mathbf{0}, \mathbf{G}) \\ \boldsymbol{\epsilon} &\sim N(\mathbf{0}, \mathbf{R}) \end{aligned}$$

where $\boldsymbol{\beta}$ is fixed effects and $\boldsymbol{\gamma}$ is random effects.

Mixed Models

A mixed model contains fixed and random effects.

First consider a normal linear mixed model,

$$\begin{aligned} \mathbf{Y} &= \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma} + \boldsymbol{\epsilon} \\ \boldsymbol{\gamma} &\sim N(\mathbf{0}, \mathbf{G}) \\ \boldsymbol{\epsilon} &\sim N(\mathbf{0}, \mathbf{R}) \end{aligned}$$

where $\boldsymbol{\beta}$ is fixed effects and $\boldsymbol{\gamma}$ is random effects.

- G-side matrix, $\mathbf{G}$, is the covariance matrix of the random effects.
- R-side matrix, $\mathbf{R}$, is the covariance matrix of the residuals.

GLMM Models

A generalized linear mixed model (GLMM) consists of the following:

GLMM Models

A generalized linear mixed model (GLMM) consists of the following:

- a linear predictor $\boldsymbol{\eta} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma}$
- a link function

$$\mathrm{E}[Y|\boldsymbol{\beta}, \boldsymbol{\gamma}] = g^{-1}(\boldsymbol{\eta}) = g^{-1}(\mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\boldsymbol{\gamma})$$

- a response distribution in the exponential family (binary, binomial, Poisson, normal, gamma, negative binomial, ...).

Bayesian Approach

The Bayesian paradigm: $p(\boldsymbol{\theta}|\mathbf{Y}) \propto \pi(\boldsymbol{\theta}) \cdot L(\mathbf{Y};\boldsymbol{\theta})$

Bayesian Approach

The Bayesian paradigm: $p(\boldsymbol{\theta}|\mathbf{Y}) \propto \pi(\boldsymbol{\theta}) \cdot L(\mathbf{Y};\boldsymbol{\theta})$

- uses the same likelihood function $L(\mathbf{Y};\boldsymbol{\theta})$

Bayesian Approach

The Bayesian paradigm: $p(\boldsymbol{\theta}|\mathbf{Y}) \propto \pi(\boldsymbol{\theta}) \cdot L(\mathbf{Y};\boldsymbol{\theta})$

- uses the same likelihood function $L(\mathbf{Y};\boldsymbol{\theta})$
- needs a prior for each set of parameters

$$\begin{aligned} \boldsymbol{\beta} &\sim \pi(\boldsymbol{\beta}) \\ \boldsymbol{\gamma} &\sim N(\mathbf{0}, \mathbf{G}) \\ \mathbf{G} &\sim \pi(\mathbf{G}) \\ \mathbf{R} &\sim \pi(\mathbf{R}) \end{aligned}$$

Bayesian Approach

The Bayesian paradigm: $p(\boldsymbol{\theta}|\mathbf{Y}) \propto \pi(\boldsymbol{\theta}) \cdot L(\mathbf{Y};\boldsymbol{\theta})$

- uses the same likelihood function $L(\mathbf{Y};\boldsymbol{\theta})$
- needs a prior for each set of parameters

$$\begin{aligned} \boldsymbol{\beta} &\sim \pi(\boldsymbol{\beta}) \\ \boldsymbol{\gamma} &\sim N(\mathbf{0}, \mathbf{G}) \\ \mathbf{G} &\sim \pi(\mathbf{G}) \\ \mathbf{R} &\sim \pi(\mathbf{R}) \end{aligned}$$

- treats every parameter, fixed effect or random effect, as a random variable.

Bayesian Approach

The Bayesian paradigm: $p(\boldsymbol{\theta}|\mathbf{Y}) \propto \pi(\boldsymbol{\theta}) \cdot L(\mathbf{Y};\boldsymbol{\theta})$

- uses the same likelihood function $L(\mathbf{Y};\boldsymbol{\theta})$
- needs a prior for each set of parameters

$$\begin{aligned} \boldsymbol{\beta} &\sim \pi(\boldsymbol{\beta}) \\ \boldsymbol{\gamma} &\sim N(\mathbf{0}, \mathbf{G}) \\ \mathbf{G} &\sim \pi(\mathbf{G}) \\ \mathbf{R} &\sim \pi(\mathbf{R}) \end{aligned}$$

- treats every parameter, fixed effect or random effect, as a random variable.
- estimates the joint posterior of $p(\boldsymbol{\beta}, \boldsymbol{\gamma}, \mathbf{R}, \mathbf{G}|\mathbf{Y})$ and infers from the marginal posteriors.

Advantages of Bayesian Analysis

1. Bayes theorem is a formula for learning, hence provides updates information in a natural way.

Advantages of Bayesian Analysis

1. Bayes theorem is a formula for learning, hence provides updates information in a natural way.
2. Bayesian inference does not require large sample theory.

Advantages of Bayesian Analysis

1. Bayes theorem is a formula for learning, hence provides updates information in a natural way.
2. Bayesian inference does not require large sample theory.
3. It estimates any functions of parameters directly, without using the "plug-in" method.

Advantages of Bayesian Analysis

1. Bayes theorem is a formula for learning, hence provides updates information in a natural way.
2. Bayesian inference does not require large sample theory.
3. It estimates any functions of parameters directly, without using the "plug-in" method.
4. In addition to a point estimate, it can give the probability distribution.

Advantages of Bayesian Analysis

1. Bayes theorem is a formula for learning, hence provides updates information in a natural way.
2. Bayesian inference does not require large sample theory.
3. It estimates any functions of parameters directly, without using the "plug-in" method.
4. In addition to a point estimate, it can give the probability distribution.
5. It provides a convenient setting for a wide range of complex models, such as hierarchical models and missing data problems.

Version Information

PROC BGLIMM is new in SAS/STAT 15.1 (SAS 9.4m6).

To find out your version:

```
proc product_status;
   run;
```

which produces something like:

```
...
For SAS/STAT ...
   Custom version information: 15.1
...
```

Feature: Simple Syntax

Transition from PROC MIXED or PROC GLIMMIX to PROC BGLIMM is straightforward.

Feature: Simple Syntax

Transition from PROC MIXED or PROC GLIMMIX to PROC BGLIMM is straightforward.

The essential statements:

- MODEL statement: specifies the response (Y), fixed effects (X), response distribution, and link function.

Feature: Simple Syntax

Transition from PROC MIXED or PROC GLIMMIX to PROC BGLIMM is straightforward.

The essential statements:

- MODEL statement: specifies the response (Y), fixed effects (X), response distribution, and link function.
- RANDOM statement: specifies the random effects (Z) and the **G**-side matrix.

Feature: Simple Syntax

Transition from PROC MIXED or PROC GLIMMIX to PROC BGLIMM is straightforward.

The essential statements:

- MODEL statement: specifies the response (Y), fixed effects (X), response distribution, and link function.
- RANDOM statement: specifies the random effects (Z) and the **G**-side matrix.
- REPEATED statement: specifies the **R**-side matrix.

Feature: Simple Syntax

Transition from PROC MIXED or PROC GLIMMIX to PROC BGLIMM is straightforward.

The essential statements:

- MODEL statement: specifies the response (Y), fixed effects (X), response distribution, and link function.
- RANDOM statement: specifies the random effects (Z) and the **G**-side matrix.
- REPEATED statement: specifies the **R**-side matrix.
- ESTIMATE statement: computes linear combination of parameters

Additional Features of PROC BGLIMM

- suite of covariance structures (for both **G**-side and **R**-side)

Additional Features of PROC BGLIMM

- suite of covariance structures (for both **G**-side and **R**-side)
- covariance heterogeneity modeling

Additional Features of PROC BGLIMM

- suite of covariance structures (for both **G**-side and **R**-side)
- covariance heterogeneity modeling
- built-in priors

Additional Features of PROC BGLIMM

- suite of covariance structures (for both **G**-side and **R**-side)
- covariance heterogeneity modeling
- built-in priors
- model comparison via DIC

Additional Features of PROC BGLIMM

- suite of covariance structures (for both **G**-side and **R**-side)
- covariance heterogeneity modeling
- built-in priors
- model comparison via DIC
- parallel computing combined with optimal sampling

PROC BGLIMM Syntax

PROC BGLIMM Statement

PROC BGLIMM Syntax

PROC BGLIMM Statement

This statement includes these commonly used options:

DATA=	names the input data set
SEED=	random seed for simulation
OUTPOST=	creates a data set to contain posterior samples

PROC BGLIMM Syntax

PROC BGLIMM Statement

This statement includes these commonly used options:

DATA=	names the input data set
SEED=	random seed for simulation
OUTPOST=	creates a data set to contain posterior samples
NBI=	number of burn-in iterations
NMC=	number of Markov chain iterations, excluding the burn-ins
NTHREADS=	number of CPUs to run simulations simultaneously on

PROC BGLIMM Syntax

PROC BGLIMM Statement

This statement includes these commonly used options:

DATA=	names the input data set
SEED=	random seed for simulation
OUTPOST=	creates a data set to contain posterior samples
NBI=	number of burn-in iterations
NMC=	number of Markov chain iterations, excluding the burn-ins
NTHREADS=	number of CPUs to run simulations simultaneously on
STATS=	posterior statistics (mean, std, credible intervals, covariance, correlation, percentiles)
DIAG=	convergence diagnostics (autocorrelation, ESS, Geweke, Heidelberger, MCSE, Raftery, ...)
PLOTS=	plotting (trace, autocorrelation, density plots)

PROC BGLIMM Syntax

MODEL *response* = *fixed-effects* / DIST= LINK= ...;

PROC BGLIMM Syntax

MODEL *response* = *fixed-effects* / DIST= LINK= ...;

- Response
- Fixed effects

PROC BGLIMM Syntax

MODEL *response* = *fixed-effects* / DIST= LINK= ...;

- Response
- Fixed effects
- 9 response distributions:
  - binary, binomial, exponential, gamma, geometric, inverse Gaussian, negative binomial, normal, Poisson

PROC BGLIMM Syntax

MODEL *response* = *fixed-effects* / DIST= LINK= ...;

- Response
- Fixed effects
- 9 response distributions:
  - binary, binomial, exponential, gamma, geometric, inverse Gaussian, negative binomial, normal, Poisson
- 8 link functions:
  - log, logit, probit, inverse, identity, pow(-2), loglog, complementary loglog

Simple Linear Regression with Class Variable

```
proc bglimm data=Sashelp.Class seed=436792;
   class sex;
   model Weight = Height Age Sex / dist=normal
         coeffprior=normal(var=1e6);
run;
```

Simple Linear Regression with Class Variable

```
proc bglimm data=Sashelp.Class seed=436792;
   class sex;
   model Weight = Height Age Sex / dist=normal
         coeffprior=normal(var=1e6);
run;
```

- Normal is the default distribution for a continuous response.

Simple Linear Regression with Class Variable

```
proc bglimm data=Sashelp.Class seed=436792;
   class sex;
   model Weight = Height Age Sex / dist=normal
         coeffprior=normal(var=1e6);
run;
```

- Normal is the default distribution for a continuous response.
- COEFFPRIOR= specifies the prior of β. The default is the flat prior.

Simple Linear Regression with Class Variable

```
proc bglimm data=Sashelp.Class seed=436792;
   class sex;
   model Weight = Height Age Sex / dist=normal
         coeffprior=normal(var=1e6);
run;
```

- Normal is the default distribution for a continuous response.
- COEFFPRIOR= specifies the prior of β. The default is the flat prior.
- SCALEPRIOR= specifies the prior of the scale parameter ϕ. The default is inverse gamma.

Poisson Regression

```
proc bglimm data=LipCancer seed=10571042;
   class County;
   model Observed = x County / dist=poisson
         link=loglog offset=LogN;
run;
```

Poisson Regression

```
proc bglimm data=LipCancer seed=10571042;
   class County;
   model Observed = x County / dist=poisson
         link=loglog offset=LogN;
run;
```

- The default link for Poisson is the log function.

Poisson Regression

```
proc bglimm data=LipCancer seed=10571042;
   class County;
   model Observed = x County / dist=poisson
         link=loglog offset=LogN;
run;
```

- The default link for Poisson is the log function.
- OFFSET= adds an offset variable to the linear predictor.

Binomial with Probit Link

```
proc bglimm data=MultiCenter seed=976352;
   class Center Group;
   model SideEffect/N = Group / link=probit noint;
run;
```

Binomial with Probit Link

```
proc bglimm data=MultiCenter seed=976352;
   class Center Group;
   model SideEffect/N = Group / link=probit noint;
run;
```

- The default link for the binomial distribution is the logit function.
- NOINT excludes the intercept from the model.

PROC BGLIMM Syntax

RANDOM *random-effects* **/ SUB= GROUP= TYPE= ...;**

Defines **Z** and the **G**-side matrix.

PROC BGLIMM Syntax

RANDOM *random-effects* / SUB= GROUP= TYPE= ...;

Defines **Z** and the **G**-side matrix.

- SUB= identifies the subjects for the random effects. A set of random effects is estimated for each subject level.

PROC BGLIMM Syntax

RANDOM *random-effects* / SUB= GROUP= TYPE= ...;

Defines **Z** and the **G**-side matrix.

- SUB= identifies the subjects for the random effects. A set of random effects is estimated for each subject level.
- GROUP= specifies groups by which to vary the covariance parameters; each new level of the grouping effect produces a new set of covariance parameters.

PROC BGLIMM Syntax

RANDOM *random-effects* / SUB= GROUP= TYPE= ...;

Defines **Z** and the **G**-side matrix.

- SUB= identifies the subjects for the random effects. A set of random effects is estimated for each subject level.
- GROUP= specifies groups by which to vary the covariance parameters; each new level of the grouping effect produces a new set of covariance parameters.
- TYPE= defines the type of the **G**-side matrix.

PROC BGLIMM Syntax

RANDOM *random-effects* / SUB= GROUP= TYPE= ...;

Defines **Z** and the **G**-side matrix.

- SUB= identifies the subjects for the random effects. A set of random effects is estimated for each subject level.
- GROUP= specifies groups by which to vary the covariance parameters; each new level of the grouping effect produces a new set of covariance parameters.
- TYPE= defines the type of the **G**-side matrix.
  - 13 choices: VC, CS, AR, ARMA, TOEP, UN, ...

Logistic Random-Effects Model

```
proc bglimm data=MultiCenter seed=976352;
   class Center Group;
   model SideEffect/N = Group / noint;
   random int / sub = Center;
run;
```

Logistic Random-Effects Model

```
proc bglimm data=MultiCenter seed=976352;
   class Center Group;
   model SideEffect/N = Group / noint;
   random int / sub = Center;
run;
```

The random effects are assumed to be normally distributed:

$$\gamma_i \sim N(0, \mathbf{G_i})$$

Multiple RANDOM Statements

You can add multiple random effects to the model.

```
proc bglimm data=a;
   class Analyst Run Plate;
   model log_assay = Analyst;
   random int conc / sub=run(analyst)
     covprior=uniform(lower=0, upper=2);
   random int conc / sub=plate(run*analyst)
     covprior=halfnormal(var=4);
run;
```

Multiple RANDOM Statements

You can add multiple random effects to the model.

```
proc bglimm data=a;
   class Analyst Run Plate;
   model log_assay = Analyst;
   random int conc / sub=run(analyst)
     covprior=uniform(lower=0, upper=2);
   random int conc / sub=plate(run*analyst)
     covprior=halfnormal(var=4);
run;
```

The random effects can be nested or nonnested.

Multiple RANDOM Statements

You can add multiple random effects to the model.

```
proc bglimm data=a;
   class Analyst Run Plate;
   model log_assay = Analyst;
   random int conc / sub=run(analyst)
     covprior=uniform(lower=0, upper=2);
   random int conc / sub=plate(run*analyst)
     covprior=halfnormal(var=4);
run;
```

The random effects can be nested or nonnested.

The COVPRIOR= option specifies the prior for the **G**-side matrix.

PROC BGLIMM Syntax

REPEATED *repeated-effect* / **SUB=** **GROUP=** **TYPE=** **...;**

Specifies the **R**-side matrix.

PROC BGLIMM Syntax

REPEATED *repeated-effect* **/ SUB= GROUP= TYPE= ...;**

Specifies the **R**-side matrix.

- A *repeated-effect* is required to define the proper location of the repeated responses.

PROC BGLIMM Syntax

REPEATED *repeated-effect* / SUB= GROUP= TYPE= ...;

Specifies the **R**-side matrix.

- A *repeated-effect* is required to define the proper location of the repeated responses.
- SUB= groups repeated measures together for the same subject.

PROC BGLIMM Syntax

REPEATED *repeated-effect* **/ SUB= GROUP= TYPE= ...;**

Specifies the **R**-side matrix.

- A *repeated-effect* is required to define the proper location of the repeated responses.
- SUB= groups repeated measures together for the same subject.
- GROUP= specifies groups by which to vary the covariance parameters; each new level of the grouping effect produces a new set of covariance parameters.

PROC BGLIMM Syntax

REPEATED *repeated-effect* / **SUB=** **GROUP=** **TYPE=** **...;**

Specifies the **R**-side matrix.

- A *repeated-effect* is required to define the proper location of the repeated responses.
- SUB= groups repeated measures together for the same subject.
- GROUP= specifies groups by which to vary the covariance parameters; each new level of the grouping effect produces a new set of covariance parameters.
- TYPE= defines the type of the **R**-side matrix.

PROC BGLIMM Syntax

REPEATED *repeated-effect* / SUB= GROUP= TYPE= ...;

Specifies the **R**-side matrix.

- A *repeated-effect* is required to define the proper location of the repeated responses.
- SUB= groups repeated measures together for the same subject.
- GROUP= specifies groups by which to vary the covariance parameters; each new level of the grouping effect produces a new set of covariance parameters.
- TYPE= defines the type of the **R**-side matrix.
  - 13 choices: VC, CS, AR, ARMA, TOEP, UN, ...

Repeated Measures Model

```
proc bglimm data=Fev nmc=10000 seed=44672057
      outpost=FevOut;
   class Drug Patient Hour;
   model FEV = BaseVal Drug Hour;
   random int / sub=Patient;
   repeated Hour / sub=Patient(Drug) type=un;
run;
```

Repeated Measures Model

```
proc bglimm data=Fev nmc=10000 seed=44672057
      outpost=FevOut;
   class Drug Patient Hour;
   model FEV = BaseVal Drug Hour;
   random int / sub=Patient;
   repeated Hour / sub=Patient(Drug) type=un;
run;
```

- Repeated measurements can be balanced or unbalanced.

Repeated Measures Model

```
proc bglimm data=Fev nmc=10000 seed=44672057
      outpost=FevOut;
   class Drug Patient Hour;
   model FEV = BaseVal Drug Hour;
   random int / sub=Patient;
   repeated Hour / sub=Patient(Drug) type=un;
run;
```

- Repeated measurements can be balanced or unbalanced.
- The REPEATED statement is available only for the normal distribution with the identity link in SAS/STAT 15.1.

Model Heterogeneity

The GROUP= option models different covariance matrices for different groups:

```
proc bglimm data=pr seed=475193 outpost=pr_out;
   class Person Gender Time;
   model Distance = Age|Gender;
   repeated Time / type=un sub=Person group=Gender;
run;
```

ESTIMATE Statement

ESTIMATE "*label*" *estimate-specification* < / *options*>;

This provides a mechanism for computing linear combinations of the parameters $\mathrm{L}'\boldsymbol{\theta}$ and $\boldsymbol{\theta}' = (\boldsymbol{\beta}'\,\boldsymbol{\gamma}')$.

ESTIMATE Statement

ESTIMATE "*label*" *estimate-specification* < / *options*>;

This provides a mechanism for computing linear combinations of the parameters $L'\boldsymbol{\theta}$ and $\boldsymbol{\theta}' = (\boldsymbol{\beta}' \boldsymbol{\gamma}')$.

Example: To compare the first level with the second level for the effect A:

```
estimate 'A 1 vs 2' A 1 -1 0;
```

ESTIMATE Statement

ESTIMATE "*label*" *estimate-specification* < / *options*>;

This provides a mechanism for computing linear combinations of the parameters $L'\theta$ and $\theta' = (\beta' \gamma')$.

Example: To compare the first level with the second level for the effect A:

```
estimate 'A 1 vs 2' A 1 -1 0;
```

Random effects are added after the vertical bar:

```
estimate 'A 1 vs 2' A 1 -1 0 | A*Block .25 .25 .25 .25 -.25 -.25 -.25 -.25 / e;
```

Outline

Sampling

PROC BGLIMM updates parameters conditionally and sequentially through Gibbs sampling.

Sampling

PROC BGLIMM updates parameters conditionally and sequentially through Gibbs sampling.

1. The fixed-effects parameters are drawn together first at each iteration.
2. The random-effect parameters are updated by subjects.
3. The G-side covariance parameters are then sampled.
4. Last, the R-side covariance parameters are updated.
5. If present, missing response values are treated as parameters and are thus also sampled.

Conditional Posteriors

$$\log(p(\boldsymbol{\beta}|\gamma, \mathbf{y}, \mathbf{R})) = \log(\pi(\boldsymbol{\beta})) + \sum_{\mathbf{i=1}}^{\mathbf{n}} \log(\mathbf{f}(\mathbf{y_i}|\boldsymbol{\beta}, \gamma, \mathbf{R}))$$

$$\log(p(\gamma_j|\boldsymbol{\theta}, \mathbf{y})) = \log(\pi(\gamma_j|\mathbf{G})) + \sum_{\mathbf{i}\in\{\mathbf{j}\ \text{cluster}\}} \log(\mathbf{f}(\mathbf{y_i}|\boldsymbol{\beta}, \boldsymbol{\gamma_j}, \mathbf{R}))$$

$$\log(p(\mathbf{G}|\gamma)) = \log(\pi(\mathbf{G}))) + \sum_{\mathbf{j}} \log(\pi(\boldsymbol{\gamma_j}|\mathbf{G}))$$

$$\log(p(\mathbf{R}|\gamma, \mathbf{y}, \boldsymbol{\beta})) = \log(\pi(\mathbf{R})) + \sum_{\mathbf{i=1}}^{\mathbf{n}} \log(\mathbf{f}(\mathbf{y_i}|\boldsymbol{\beta}, \gamma, \mathbf{R}))$$

Sampling Algorithms

- Conjugate sampler
  - for β, γ_i in normal distribution when there is conjugacy
  - for a covariance matrix with conjugacy
- Gamerman algorithm
  - a variation of Metropolis sampling, more efficient for GLMMs
  - for β, γ_i when the response distribution is not normal
- No-U-Turn (NUTS) algorithm
  - Hamiltonian Monte Carlo sampling with autotuning
  - for a covariance matrix when there is no conjugacy
- Direct sampler
  - sample directly from the likelihood distribution for missing responses

Prior Distribution: $\boldsymbol{\beta}$

- flat/constant prior: $\pi(\boldsymbol{\beta}) \propto 1$ (the default)

```
model y = x / ... coeffprior=constant;
```

Prior Distribution: $\boldsymbol{\beta}$

- flat/constant prior: $\pi(\boldsymbol{\beta}) \propto 1$ (the default)

```
model y = x / ... coeffprior=constant;
```

- normal prior:

Prior Distribution: $\boldsymbol{\beta}$

- flat/constant prior: $\pi(\boldsymbol{\beta}) \propto 1$ (the default)

```
model y = x / ... coeffprior=constant;
```

- normal prior:
  - $\boldsymbol{\beta} \sim N(0, \sigma^2 \mathrm{I})$

```
model y = x / ... coeffprior=normal(var=1e4);
```

Prior Distribution: $\boldsymbol{\beta}$

- flat/constant prior: $\pi(\boldsymbol{\beta}) \propto 1$ (the default)

```
model y = x / ... coeffprior=constant;
```

- normal prior:
  - $\boldsymbol{\beta} \sim N(0, \sigma^2 \mathrm{I})$

```
model y = x / ... coeffprior=normal(var=1e4);
```

  - $\boldsymbol{\beta} \sim N(\boldsymbol{\mu}, \Sigma)$ (via a SAS data set)

```
model y = x / ... coeffprior=normal(input=MyPrior);
```

Prior Distribution: Scale Parameter ϕ

1. Normal: variance
2. Inverse Gaussian: variance
3. Gamma: shape parameter
4. Negative binomial: number of non-events

Prior Distribution: Scale Parameter ϕ

1. Normal: variance
2. Inverse Gaussian: variance
3. Gamma: shape parameter
4. Negative binomial: number of non-events

- Inverse gamma prior

```
model y = x / ... scaleprior=igamma(shape=a, scale=b);
```

- Gamma prior

```
model y = x / ... scaleprior=gamma(shape=a, iscale=b);
```

- Improper prior: $\pi(\phi) \propto \phi^{-1}$

```
model y = x / ... scaleprior=improper;
```

Prior Distribution: G-Side Cov

Specify this in the RANDOM statement, for UN, UN(1), VC, and TOEP(1) types:

```
random z / subject=id covprior=iwishart(df=a, scale=b);

random z / subject=id covprior=igamma(shape=a, scale=b);

random z / subject=id covprior=uniform(lower=, upper=);

random z / subject=id covprior=halfcauchy(scale=a);

random z / subject=id covprior=halfnormal(var=a);

random z / subject=id covprior=siwishart(df=a, scale=b, var=c);
```

Prior Distribution: R-Side Cov

Specify this in the REPEATED statement, for UN, UN(1), VC, and TOEP(1) types:

```
repeated Time / subject=id covprior=iwishart(df=a, scale=b);

repeated Time / subject=id covprior=igamma(shape=a, scale=b);
```

Outline

PROC BGLIMM: Logistic Regression Example

Consider a study of the analgesic effects of treatments on elderly patients with neuralgia.

- Two test treatments and a placebo are compared
- The response variable is whether the patient reported pain or not
- Covariates include the age and gender of 60 patients and the duration of complaint before the treatment began

The Data

A subset of the data:

```
Data Neuralgia;
   input Treatment $ Sex $ Age Duration Pain $ @@;
   datalines;
P  F  68   1  No   B  M  74  16  No  P  F  67  30  No
P  M  66  26  Yes  B  F  67  28  No  B  F  77  16  No
A  F  71  12  No   B  F  72  50  No  B  F  76   9  Yes
...
P  M  67  17  Yes  B  M  70  22  No  A  M  65  15  No
P  F  67   1  Yes  A  M  67  10  No  P  F  72  11  Yes
A  F  74   1  No   B  M  80  21  Yes A  F  69   3  No
;
```

Treatment: A, B, P

Sex: F, M

Pain: Yes, No

The Model

A logistic regression is considered for this data set:

$$
\begin{aligned}
\text{pain}_i &\sim \text{binary}(p_i) \\
p_i &= \text{logit}(\beta_0 + \beta_1 \cdot \text{Sex}_{\text{F},i} + \beta_2 \cdot \text{Treatment}_{\text{A},i} \\
&\quad + \beta_3 \cdot \text{Treatment}_{\text{B},i} + \beta_4 \cdot \text{Sex}_{\text{F},i} \cdot \text{Treatment}_{\text{A},i} \\
&\quad + \beta_5 \cdot \text{Sex}_{\text{F},i} \cdot \text{Treatment}_{\text{B},i} + \beta_6 \cdot \text{Age} + \beta_7 \cdot \text{Duration})
\end{aligned}
$$

where Sex_F, $\text{Treatment}_\text{A}$, and $\text{Treatment}_\text{B}$ are dummy variables for the categorical predictors.

The Model

A logistic regression is considered for this data set:

$$\begin{aligned} \text{pain}_i &\sim \text{binary}(p_i) \\ p_i &= \text{logit}(\beta_0 + \beta_1 \cdot \text{Sex}_{\text{F},i} + \beta_2 \cdot \text{Treatment}_{\text{A},i} \\ &\quad + \beta_3 \cdot \text{Treatment}_{\text{B},i} + \beta_4 \cdot \text{Sex}_{\text{F},i} \cdot \text{Treatment}_{\text{A},i} \\ &\quad + \beta_5 \cdot \text{Sex}_{\text{F},i} \cdot \text{Treatment}_{\text{B},i} + \beta_6 \cdot \text{Age} + \beta_7 \cdot \text{Duration}) \end{aligned}$$

where Sex_F, $\text{Treatment}_\text{A}$, and $\text{Treatment}_\text{B}$ are dummy variables for the categorical predictors.

You might want to consider a normal prior with large variance as a noninformative prior distribution on all the regression coefficients:

$$\pi(\beta_0, \cdots, \beta_7) \sim \text{normal}(0, \text{var} = 1e6)$$

Logistic Regression with Fixed Effects

The following statements fit a Bayesian logistic regression model in PROC BGLIMM:

```
proc bglimm data=neuralgia seed=7896 nbi=1000 nmc=20000
          thin=2 outpost=SampOut;
   class Treatment(ref="P") Sex(ref="M") / param = ref;
   model Pain = sex|treatment Age Duration / dist=bin
      coeffprior=normal(var=1e6);
run;
```

- This code models the probability of *no pain* (Pain = No). To change this to model the probability of *pain* (Pain = Yes), you can specify the DESCENDING keyword after the response in the MODEL statement.
- The REFERENCE coding is used increating the design matrix (categorical variables).

PROC BGLIMM Output

The BGLIMM Procedure

Model Information	
Data Set	WORK.NEURALGIA
Response Variable	Pain
Distribution	Binary
Link Function	Logit
Fixed Effects Included	Yes
Random Effects Included	No
Sampling Algorithm	Gamerman
Burn-In Size	1000
Simulation Size	20000
Thinning	2
Random Number Seed	7896
Number of Threads	1

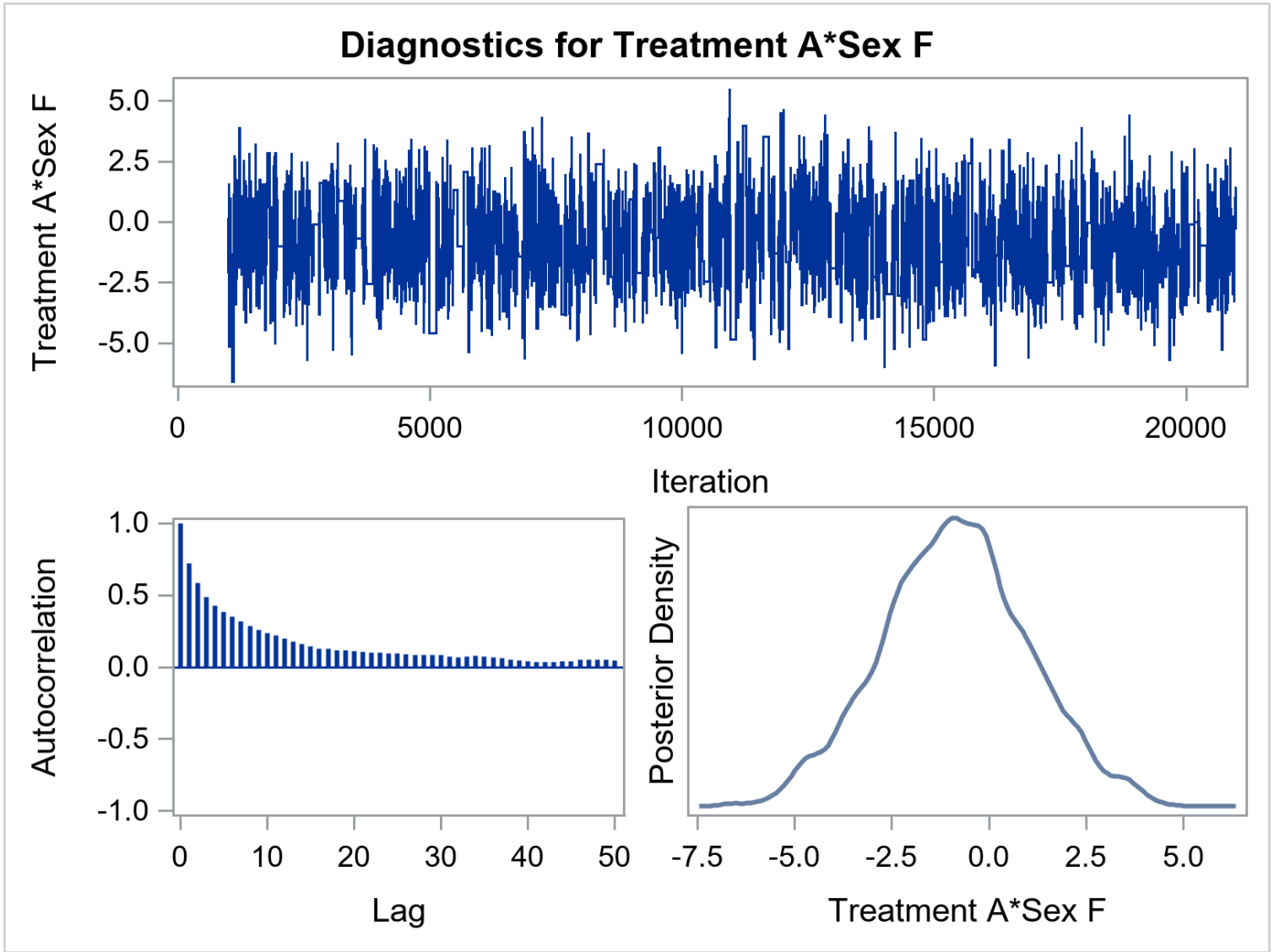
Posterior Summary Statistics

Posterior Summaries and Intervals

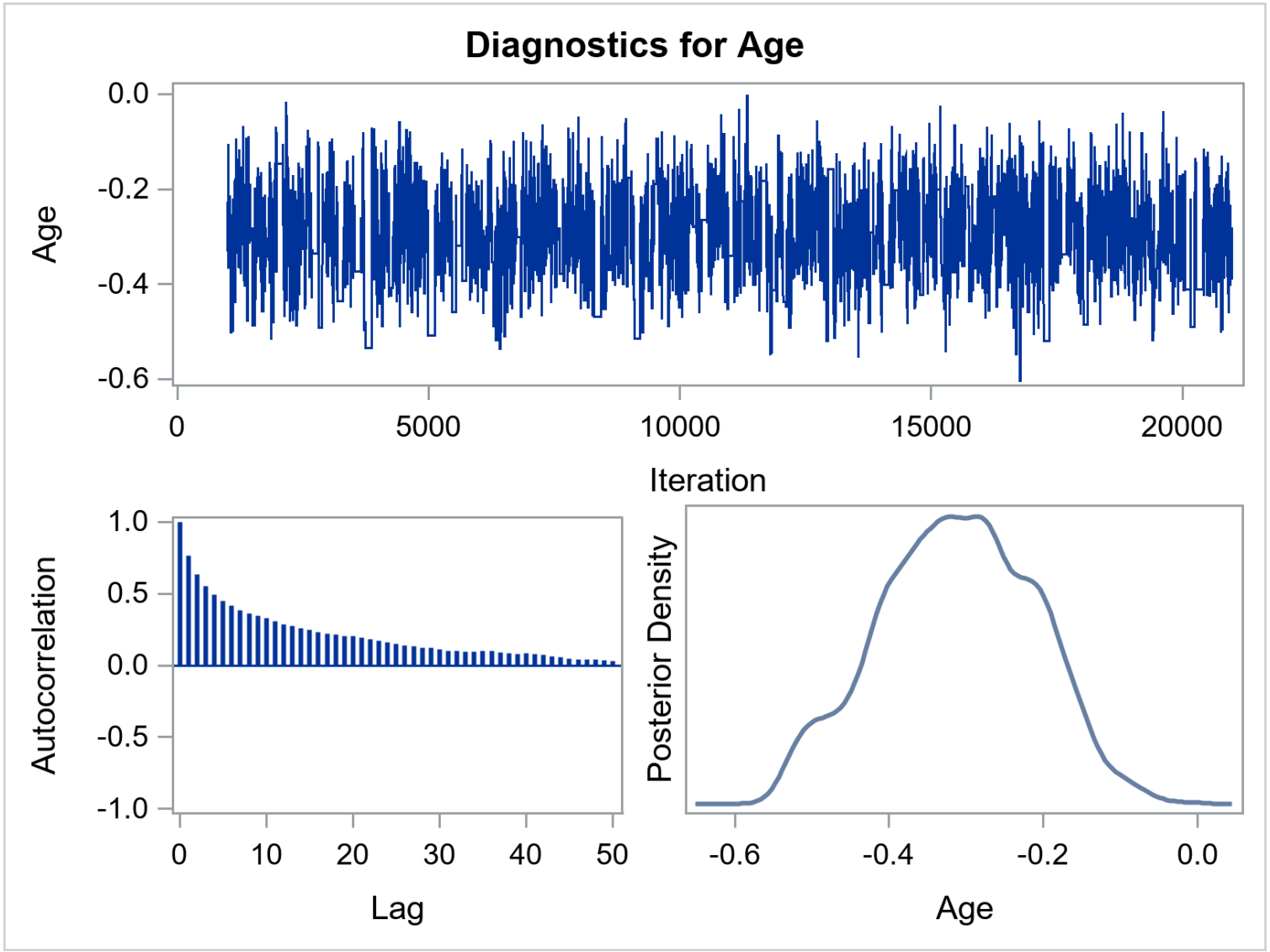
Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Intercept	10000	18.3156	6.7527	5.6462	30.3823
Sex F	10000	2.5533	1.3674	-0.0862	5.2098
Treatment A	10000	4.1330	1.4634	0.9898	6.8380
Treatment B	10000	4.5530	1.5439	1.5893	7.7565
Treatment A*Sex F	10000	-0.8679	1.8766	-4.8454	2.4119
Treatment B*Sex F	10000	-0.3217	1.9256	-3.9514	3.1730
Age	10000	-0.3116	0.0996	-0.5147	-0.1420
Duration	10000	0.00673	0.0345	-0.0518	0.0811

Compare to page 41

TAD (Trace, Autocorrelation, Density) Plots



TAD (Trace, Autocorrelation, Density) Plots



Odds Ratio

In the logistic model, the log odds function, $\text{logit}(X)$, is given by:

$$\text{logit}(X) \equiv \log\left(\frac{\Pr(Y = 1 \mid X)}{\Pr(Y = 0 \mid X)}\right) = \beta_0 + X\beta_1$$

Odds Ratio

In the logistic model, the log odds function, $\text{logit}(X)$, is given by:

$$\text{logit}(X) \equiv \log\left(\frac{\Pr(Y = 1 \mid X)}{\Pr(Y = 0 \mid X)}\right) = \beta_0 + X\beta_1$$

Suppose that you are interested in calculating the ratio of the odds for the female patients ($\text{Sex}_\text{F} = 1$) to the male patients ($\text{Sex}_\text{F} = 0$). The log of the odds ratio is the following:

$$\begin{aligned}
\log(\psi) &\equiv \log(\psi(\text{Sex}_\text{F} = 1, \text{Sex}_\text{F} = 0)) \\
&= \text{logit}(\text{Sex}_\text{F} = 1) - \text{logit}(\text{Sex}_\text{F} = 0) \\
&= (\beta_0 + 1 \times \beta_1) - (\beta_0 + 0 \times \beta_1) \\
&= \beta_1
\end{aligned}$$

Odds Ratio

In the logistic model, the log odds function, $\text{logit}(X)$, is given by:

$$\text{logit}(X) \equiv \log\left(\frac{\Pr(Y = 1 \mid X)}{\Pr(Y = 0 \mid X)}\right) = \beta_0 + X\beta_1$$

Suppose that you are interested in calculating the ratio of the odds for the female patients ($\text{Sex}_\text{F} = 1$) to the male patients ($\text{Sex}_\text{F} = 0$). The log of the odds ratio is the following:

$$\begin{aligned}
\log(\psi) &\equiv \log(\psi(\text{Sex}_\text{F} = 1, \text{Sex}_\text{F} = 0)) \\
&= \text{logit}(\text{Sex}_\text{F} = 1) - \text{logit}(\text{Sex}_\text{F} = 0) \\
&= (\beta_0 + 1 \times \beta_1) - (\beta_0 + 0 \times \beta_1) \\
&= \beta_1
\end{aligned}$$

It follows that the odds ratio is:

$$\psi = \exp(\beta_1)$$

ESTIMATE Statement

Use the ESTIMATE statement to get the log of the odds ratio between the female group and male group conditional on treatment A:

```
proc bglimm data=neuralgia seed=7896 nbi=1000 nmc=20000
            thin=2 outpost=SampOut;
   class Treatment(ref="P") Sex(ref="M");
   model Pain= sex|treatment Age Duration / dist=bin
         coeffprior=normal(var=1e6);
   estimate "F vs M, at Trt=A" sex 1 -1
            treatment*sex 1 -1 0 0 0 0 / e;
run;
```

ESTIMATE Statement

Use the ESTIMATE statement to get the log of the odds ratio between the female group and male group conditional on treatment A:

```
proc bglimm data=neuralgia seed=7896 nbi=1000 nmc=20000
            thin=2 outpost=SampOut;
   class Treatment(ref="P") Sex(ref="M");
   model Pain= sex|treatment Age Duration / dist=bin
         coeffprior=normal(var=1e6);
   estimate "F vs M, at Trt=A" sex 1 -1
            treatment*sex 1 -1 0 0 0 0 / e;
run;
```

sex 1 -1 : estimates the difference between β_1 and β_2, which under the default GLM parametrization, is equal to β_1

ESTIMATE Statement

Use the ESTIMATE statement to get the log of the odds ratio between the female group and male group conditional on treatment A:

```
proc bglimm data=neuralgia seed=7896 nbi=1000 nmc=20000
            thin=2 outpost=SampOut;
   class Treatment(ref="P") Sex(ref="M");
   model Pain= sex|treatment Age Duration / dist=bin
         coeffprior=normal(var=1e6);
   estimate "F vs M, at Trt=A" sex 1 -1
            treatment*sex 1 -1 0 0 0 0 / e;
run;
```

sex 1 -1 : estimates the difference between β_1 and β_2, which under the default GLM parametrization, is equal to β_1

treatment * sex ... : assigns **1** to the interaction where "treatment=A" and "sex=F", and -**1** to the interaction where "treatment=A" and "sex=M"

ESTIMATE Statement

Use the ESTIMATE statement to get the log of the odds ratio between the female group and male group conditional on treatment A:

```
proc bglimm data=neuralgia seed=7896 nbi=1000 nmc=20000
            thin=2 outpost=SampOut;
   class Treatment(ref="P") Sex(ref="M");
   model Pain= sex|treatment Age Duration / dist=bin
         coeffprior=normal(var=1e6);
   estimate "F vs M, at Trt=A" sex 1 -1
            treatment*sex 1 -1 0 0 0 0 / e;
run;
```

sex 1 -1 : estimates the difference between β_1 and β_2, which under the default GLM parametrization, is equal to β_1

treatment * sex ... : assigns **1** to the interaction where "treatment=A" and "sex=F", and **-1** to the interaction where "treatment=A" and "sex=M"

e : requests that the **L** matrix coefficients be displayed

L Matrix Coefficients

Coefficients for F vs M, at Trt=A	
Parameter	**Row**
Intercept	
Sex F	1
Sex M	-1
Treatment A	
Treatment B	
Treatment P	
Treatment A*Sex F	1
Treatment A*Sex M	-1
Treatment B*Sex F	
Treatment B*Sex M	
Treatment P*Sex F	
Treatment P*Sex M	
Age	
Duration	

Posterior Summary Statistics (GLM Parametrization)

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Intercept	10000	18.3156	6.7527	5.6462	30.3823
Sex F	10000	2.5533	1.3674	-0.0862	5.2098
Sex M	0	.	.	.	.
Treatment A	10000	4.1330	1.4634	0.9898	6.8380
Treatment B	10000	4.5530	1.5439	1.5893	7.7565
Treatment P	0	.	.	.	.
Treatment A*Sex F	10000	-0.8679	1.8766	-4.8454	2.4119
Treatment A*Sex M	0	.	.	.	.
Treatment B*Sex F	10000	-0.3217	1.9256	-3.9514	3.1730
Treatment B*Sex M	0	.	.	.	.
Treatment P*Sex F	0	.	.	.	.
Treatment P*Sex M	0	.	.	.	.
Age	10000	-0.3116	0.0996	-0.5147	-0.1420
Duration	10000	0.00673	0.0345	-0.0518	0.0811

Compare to page 35

Results from ESTIMATE Statement

The log odds ratio between the female group and male group conditional on treatment A:

Results from ESTIMATE Statements

Label	Mean	Standard Deviation	95% HPD Interval	
F vs M, at Trt=A	1.6855	1.2913	-0.7977	4.3331

Functions of Parameters

Use the DATA step to compute the odds ratio by taking exponential of the ESTIMATE statement variable whose posterior samples are saved in the SampOut data set.

```
data ORSamp;
  set SampOut;
  OddsRatio=exp(F_vs_M__at_Trt_A);
run;

%sumint(data=ORSamp,var=OddsRatio)
```

Functions of Parameters

Use the DATA step to compute the odds ratio by taking exponential of the ESTIMATE statement variable whose posterior samples are saved in the SampOut data set.

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
OddsRatio	10000	12.1075	22.5590	0.1646	43.9975

```
data ORSamp;
  set SampOut;
  OddsRatio=exp(F_vs_M__at_Trt_A);
run;

%sumint(data=ORSamp,var=OddsRatio)
```

Functions of Parameters

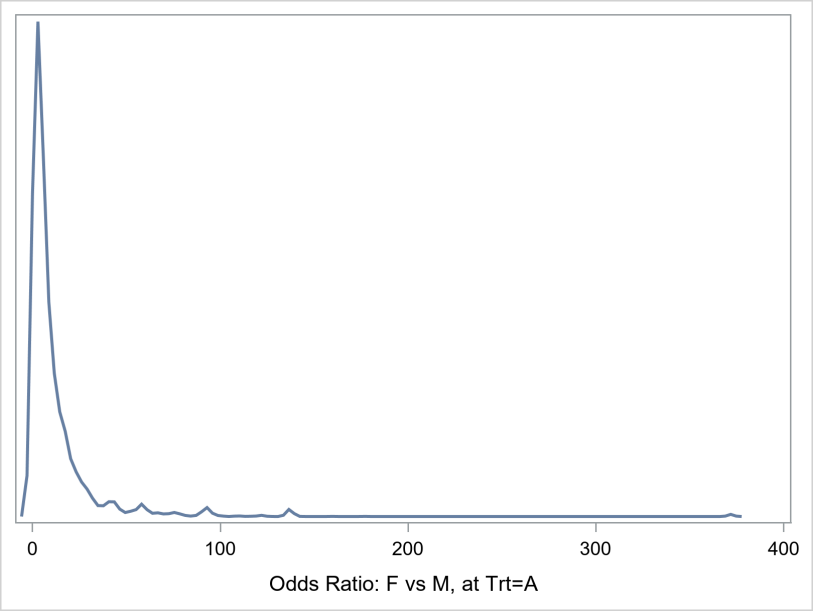
Use the DATA step to compute the odds ratio by taking exponential of the ESTIMATE statement variable whose posterior samples are saved in the SampOut data set.

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
OddsRatio	10000	12.1075	22.5590	0.1646	43.9975

```
data ORSamp;
  set SampOut;
  OddsRatio=exp(F_vs_M__at_Trt_A);
run;

%sumint(data=ORSamp,var=OddsRatio)
```



Built-In Bayesian Macros

%ESS	Effective sample sizes
%GEWEKE	Geweke diagnostic
%HEIDEL	Heidelberger-Welch diagnostic
%MCSE	Monte Carlo standard errors
%POSTACF	Autocorrelation
%POSTCOR	Correlation matrix
%POSTCOV	Covariance matrix
%POSTINT	Equal-tail and HPD intervals
%POSTSUM	Mean, std, and quantiles
%RAFTERY	Raftery diagnostic
%SUMINT	Mean, std, and HPD intervals
%TADPLOT	Trace plot, AC plot, and density plot

Outline

Logistic Regression with Random Intercepts

Researchers investigated two medical procedures.

- 15 centers were randomly selected.
- Patients were assigned to two treatment groups, A or B.
- N is number of patients who received a given procedure.
- Sideeffect is the number of patients who reported side effects.

Logistic Regression with Random Intercepts

Researchers investigated two medical procedures.

- 15 centers were randomly selected.
- Patients were assigned to two treatment groups, A or B.
- N is number of patients who received a given procedure.
- Sideeffect is the number of patients who reported side effects.

```
data MultiCenter;
   input Center Group$ N SideEffect @@;
   datalines;
 1  A  32  14   1  B  33  18
 2  A  30   4   2  B  28   8
 3  A  23  14   3  B  24   9
 4  A  22   7   4  B  22  10
 5  A  20   6   5  B  21  12
 6  A  19   1   6  B  20   3
 7  A  17   2   7  B  17   6
 8  A  16   7   8  B  15   9
 9  A  13   1   9  B  14   5
10  A  13   3  10  B  13   1
11  A  11   1  11  B  12   2
12  A  10   1  12  B   9   0
13  A   9   2  13  B   9   6
14  A   8   1  14  B   8   1
15  A   7   1  15  B   8   0
;
```

Logistic Regression with Random Intercepts

- The response is sample proportions of side effects as binomial ratios
- The fixed effect is Group
- The random effect cluster is Center

```
proc bglimm data=MultiCenter nmc=10000 thin=2 seed=976352
   outpost=CenterOut plots=all;
   class Center Group;
   model SideEffect/N = Group / noint;
   random int / sub = Center;
run;
```

PROC BGLIMM Output

The BGLIMM Procedure

Model Information	
Data Set	WORK.MULTICENTER
Response Variable	SideEffect
Distribution	Binomial
Link Function	Logit
Fixed Effects Included	Yes
Random Effects Included	Yes
Sampling Algorithm	Gamerman, Conjugate
Burn-In Size	500
Simulation Size	10000
Thinning	2
Random Number Seed	976352
Number of Threads	1

Posterior Summary Statistics

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Group A	5000	-1.3895	0.3102	-2.0071	-0.7956
Group B	5000	-0.8839	0.2968	-1.4819	-0.3186
Random Var	5000	0.9184	0.4198	0.3024	1.7515

Posterior Summary Statistics

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Group A	5000	-1.3895	0.3102	-2.0071	-0.7956
Group B	5000	-0.8839	0.2968	-1.4819	-0.3186
Random Var	5000	0.9184	0.4198	0.3024	1.7515

- Group A vs. Group B

Posterior Summary Statistics

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Group A	5000	-1.3895	0.3102	-2.0071	-0.7956
Group B	5000	-0.8839	0.2968	-1.4819	-0.3186
Random Var	5000	0.9184	0.4198	0.3024	1.7515

- Group A vs. Group B
- 'Random Var' measures variability of center-level intercepts.

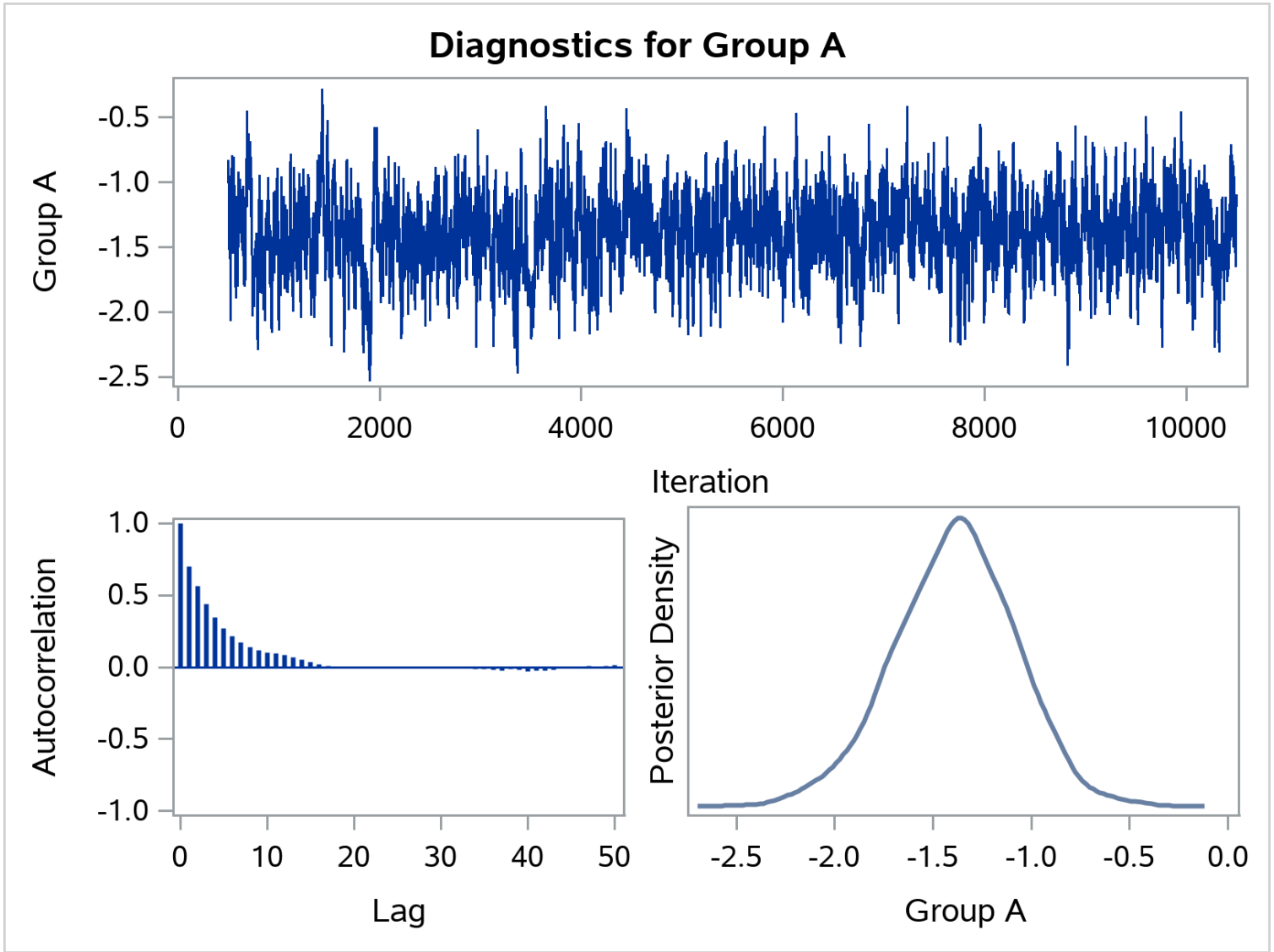
Posterior Summary Statistics

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
Group A	5000	-1.3895	0.3102	-2.0071	-0.7956
Group B	5000	-0.8839	0.2968	-1.4819	-0.3186
Random Var	5000	0.9184	0.4198	0.3024	1.7515

- Group A vs. Group B
- 'Random Var' measures variability of center-level intercepts.
- Each center's intercept can be printed with MONITOR option in the RANDOM statement.

TAD Plots (Trace, Auto-correlation, Density plots)



Functions of Parameters

Example: probability difference between A and B:

$$\text{pDiff} = \frac{\exp(\beta_b)}{1+\exp(\beta_b)} - \frac{\exp(\beta_a)}{1+\exp(\beta_a)}$$

```
data prob;
   set CenterOut;
   pDiff = logistic(group_b)
         - logistic(group_a);
run;

%sumint(data=prob, var=pDiff)
```

Functions of Parameters

Example: probability difference between A and B:

$$\text{pDiff} = \frac{\exp(\beta_b)}{1+\exp(\beta_b)} - \frac{\exp(\beta_a)}{1+\exp(\beta_a)}$$

```
data prob;
   set CenterOut;
   pDiff = logistic(group_b)
           - logistic(group_a);
run;

%sumint(data=prob, var=pDiff)
```

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
pDiff	5000	0.0920	0.0395	0.0195	0.1750

Functions of Parameters

Example: probability difference between A and B:

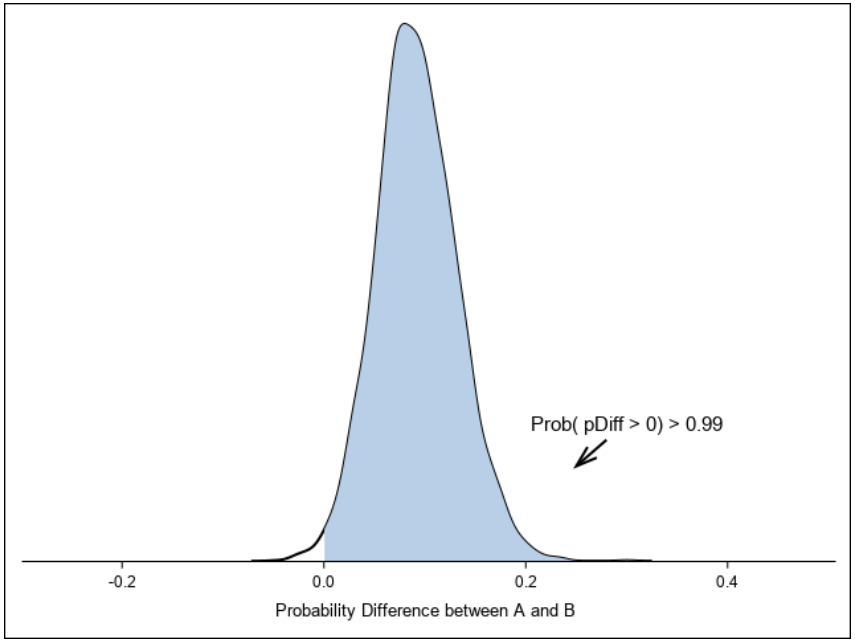
$$\text{pDiff} = \frac{\exp(\beta_b)}{1+\exp(\beta_b)} - \frac{\exp(\beta_a)}{1+\exp(\beta_a)}$$

```
data prob;
   set CenterOut;
   pDiff = logistic(group_b)
         - logistic(group_a);
run;

%sumint(data=prob, var=pDiff)
```

Posterior Summaries and Intervals

Parameter	N	Mean	Standard Deviation	95% HPD Interval	
pDiff	5000	0.0920	0.0395	0.0195	0.1750



Outline

Repeated Measurements with Heterogeneity

Repeated Measurements with Heterogeneity

- A two-treatment trial for patients with rheumatoid arthritis
- 67 subjects enrolled
- Subjects were followed up three times
- A grip strength measurement was taken at each follow-up visit
- A baseline grip strength (in mmHg) was measured at the start

```
data GripData;
input Subject Baseline Treat Gender$ Time Grip;
datalines;
26  175  1  M  1  161
26  175  1  M  2  210
26  175  1  M  3  230
27  165  1  M  1  215
27  165  1  M  2  245
27  165  1  M  3  265
...

71  104  2  F  1  107
71  104  2  F  2  .
71  104  2  F  3  .
72   60  2  F  1   60
72   60  2  F  2   55
72   60  2  F  3   58
;
```

Model Details

A reasonable initial model should involve fairly general specifications for both the mean and the variance-covariance structure (Littell et al. 2006).

- The mean includes three-way interactions of the variables Gender,Treat, and Time and the Baseline measure.
- To allow general within-subject heterogeneity, the unstructured type is used in the R-side covariance matrix.
  - An advantage of considering this most general covariance type is to inspect the estimates for heterogeneous patterns in both the variances and correlations.

Repeated Measurements using PROC BGLIMM

- The fixed effects contain 12 cell means: 2 treatments by 2 genders by 3 visits.
- The REPEATED statement specifies that the repeated measurements be taken over the Time variable and are grouped according to the Subject variable.

```
proc bglimm data=GripData seed=475193;
   class Subject Treat Gender Time;
   model Grip = Gender*Treat*Time Baseline / noint;
   repeated Time / sub=Subject type=un r rcorr;
   run;
```

Posterior R-Side Covariance and Correlation Matrices

Requested via the options `r` and `rcorr`.

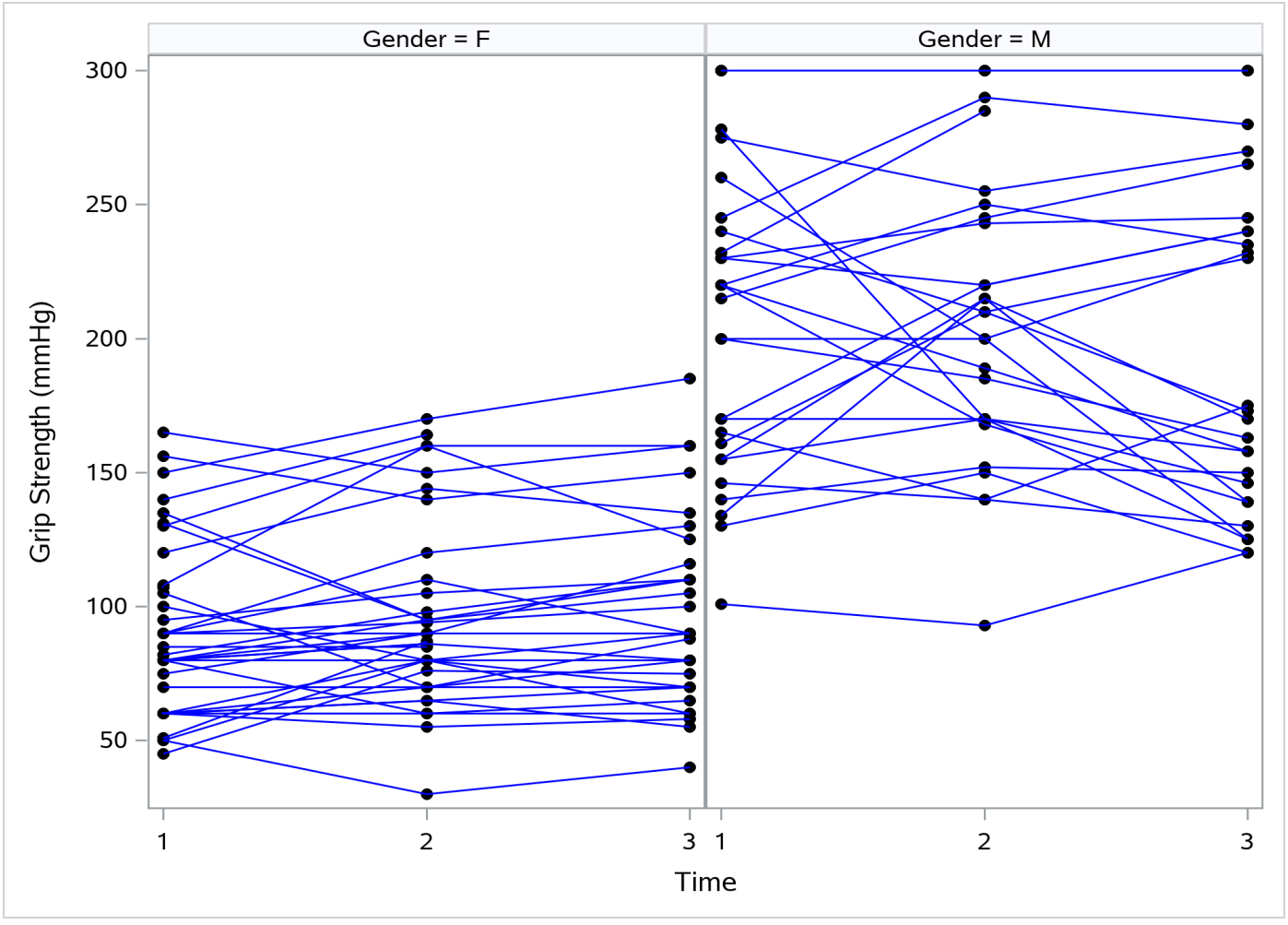
Estimated R Matrix

Row	Col 1	Col 2	Col 3
1	604.96	308.00	288.96
2	308.00	950.48	885.65
3	288.96	885.65	1304.71

Estimated R Correlation Matrix

Row	Col 1	Col 2	Col 3
1	1.0000	0.4062	0.3252
2	0.4062	1.0000	0.7953
3	0.3252	0.7953	1.0000

Grip Strength Measurements over Time by Gender



Between-Subject Heterogeneity by Gender

To account for distinct covariance structures of the two gender groups, you can fit the model by adding the option GROUP=GENDER to the REPEATED statement:

```
proc bglimm data=GripData seed=475193;
   class Subject Treat Gender Time;
   model Grip = Gender*Treat*Time Baseline / noint;
   repeated Time / sub=Subject type=un group=Gender r rcorr;
run;
```

R-Side Covariance Matrices by Gender

The BGLIMM Procedure

Estimated R Matrix

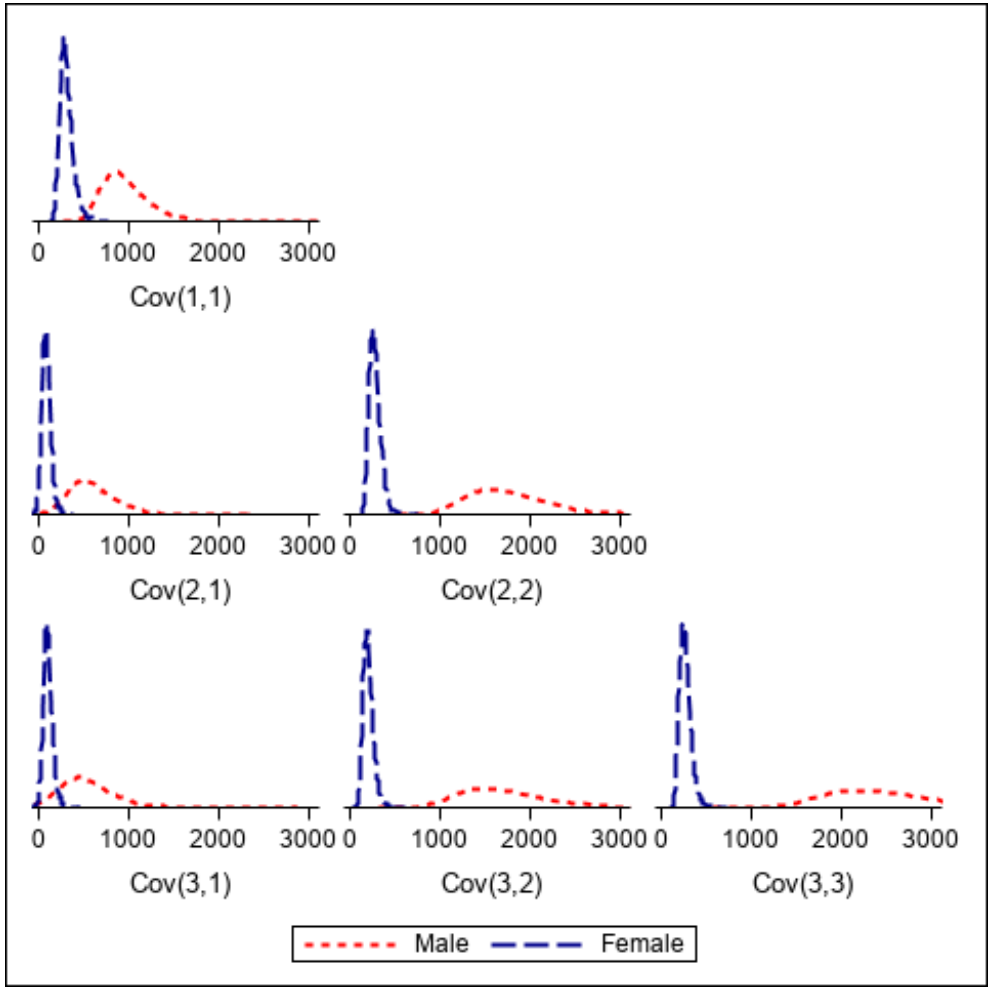
Group	Row	Col 1	Col 2	Col 3
Gender F	1	300.08	77.2769	95.2165
Gender F	2	77.2769	267.23	195.20
Gender F	3	95.2165	195.20	257.48
Gender M	1	960.37	591.43	528.93
Gender M	2	591.43	1773.63	1710.94
Gender M	3	528.93	1710.94	2504.11

R-Side Covariance Matrices by Gender

The BGLIMM Procedure

Estimated R Matrix

Group	Row	Col 1	Col 2	Col 3
Gender F	1	300.08	77.2769	95.2165
Gender F	2	77.2769	267.23	195.20
Gender F	3	95.2165	195.20	257.48
Gender M	1	960.37	591.43	528.93
Gender M	2	591.43	1773.63	1710.94
Gender M	3	528.93	1710.94	2504.11



Between-Subject Heterogeneity in Random effects

You can account for more between-subject heterogeneity by adding a random statement.

```
proc bglimm data=GripData seed=475193 nmc=20000 thin=4;
   class Subject Treat Gender Time;
   model Grip = Gender*Treat*Time Baseline / noint;
   random int / sub=Subject group=Gender covprior=uniform;
   repeated Time / sub=Subject type=un group=Gender r rcorr
            covprior=iw(scale=500);
run;
```

Finishing Thoughts

- These development represents part of SAS' continuing effort to add Bayesian capability to the software.

Finishing Thoughts

- These development represents part of SAS' continuing effort to add Bayesian capability to the software.
- We are interested in
  - establishing knowledge base and providing how-tos to our users who are interested in Bayesian GLMMs
  - identifying key areas where we can make improvements and enhancements to our procedures, e.g. PROC MCMC, PROC BGLIMM, etc

Finishing Thoughts

- These development represents part of SAS' continuing effort to add Bayesian capability to the software.
- We are interested in
  - establishing knowledge base and providing how-tos to our users who are interested in Bayesian GLMMs
  - identifying key areas where we can make improvements and enhancements to our procedures, e.g. PROC MCMC, PROC BGLIMM, etc
- More features and improvements on the way.

For More Information

See the 2019 SAS Global Forum paper 'Introducing the BGLIMM Procedure for Bayesian Generalized Linear Mixed Models'.

PROC BGLIMM requires SAS/STAT 15.1 (SAS 9.4M6). Complete documentation of the procedure can be found at http://support.sas.com/documentation/onlinedoc/stat/151/bglimm.pdf.

You can find additional coding examples at http://support.sas.com/rnd/app/examples/STATexamples.html.