Bayesian, MCMC, and Multilevel Modeling (a foray into the subjective)

Christopher David Desjardins
http://cddesjardins.wordpress.com

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Outline

Bayesian toolbox for multilevel modeling

- MCMC software
  - JAGS. `JAGS` is cross-platform, actively developed, and can be called directly from `R` via the `rjags` library. It can run any model as long as you can program it!
    - It is CLI only
  - WinBUGS and/or OpenBUGS for PC. `OpenBUGS` is supposedly cross-platform. Similar to `JAGS` but more tested and with a large, active support community.
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  - MCMCglmm. This can do LMM and GLMM, meta-analyses, and more. Excellent vignette! Also Jarrod Hadfield is super nice!!!
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  - MCMC diagnostics, the coda package.
- CRAN task view: Bayesian!

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Thomas Bayes

A Presbyterian minister with an itch for gambling, who now rests in Bunhill Fields.

What is Bayesian?

- A statistical paradigm that defines probability as a measure of the state of knowledge, i.e. a 'personal probability'.
- In contrast, traditional frequentist statistics defines probability as the long running frequency of an event.
- Rooted in Bayes theorem
- All parameters in Bayesian are treated as random
- Inferences based on posterior distribution
  - In contrast, frequentist uses maximum likelihood

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Reasons for Bayesian inference (Berger 1985)

- You can use prior knowledge.
- Inferences are based only on the data, i.e. doesn't violate likelihood principle.
- Reason for stopping the experiment doesn't affect your inferences (Carlin & Louis, 2009).
- Easier to interpret.
- More coherent as all analyses are made based on the posterior.
- Any question can be answered through Bayesian analysis.
- Bayes procedures possess numerous optimality properties.
  - Can calculate actual probability of null hypothesis being true.
  - Ability to test logical hypotheses.
  - Ability to solve more complex models.

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Likelihood vs. posterior distribution

- Assume we have a normal distribution, with a mean (μ) and variance (σ^2) and some data.
- The likelihood is defined as the probability of the data given the parameters, $Pr(\mathbf{y}|\mu, \sigma^2)$
- This is a conditional distribution, we conditioned on the model parameters which are taken as fixed and known.
- Isn't this odd? We've already observed the data, and we don't know what the parameter values are. How can they be fixed and known?
- Aren't we really interested in conditioning the parameters on the data because the parameters aren't observed?
- In Bayesian, we are interested in the posterior distribution, $Pr(\mu, \sigma^2|\mathbf{y})$
- Looks simple right?

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Bayes theorem

Mathematically

$$Pr(\mu, \sigma^2|\mathbf{y}) = \frac{Pr(\mathbf{y}|\mu,\sigma^2)Pr(\mu,\sigma^2)}{Pr(\mathbf{y})}$$

Conceptually

$$\text{Posterior} = \frac{\text{Likelihood} * \text{Prior}}{\text{Marginal}}$$

Fortunately for us it simplifies ... a little

$$Pr(\mu, \sigma^2|\mathbf{y}) \propto Pr(\mathbf{y}|\mu, \sigma^2)Pr(\mu, \sigma^2)$$

- So ... what is the elephant in the room?

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The elephant is ...

Prior distribution

$$Pr(\mu, \sigma^2)$$

Why?
What is this?
How do we handle this?
How do we get rid of this?
Do we want to get rid of this?
Does it have any use?
Does it have any harm?
How can we marginalize this?
Is it useful?

Oh what a prior!

- Bayes thereom, and by extension Bayesian, forces us to incorporate priors
- Priors can be very useful
  - Imagine your study is only one of a 1000 studies on topic X.
  - You can formally synthesize all these results into your models.
  - Gives you a 'stronger model' because it's based on 1000+1 studies not just 1!?!
  - Is it cheating?
  - Philsophically, doesn't science build on science? Our very hypotheses on previous studies? Our models and our data are not isolated, objective icebergs!

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Oh no ... what a prior!

- If our results are truly unique and we incorporate previous data into our priors we might not see this in our results.
- Priors are subjective!
- With a small sample size, priors have a large effect on our results.
- Choice of your priors can have a profound impact on your inferences
- MLE estimates are 'more objective'
- Aren't economists Bayesian? Oh no ...

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Oh wait ... it is a wonderful prior!

- Confession: I would describe myself as a subjective Bayesian!
  - I believe priors should be informative and guide our models.
  - Bayesian is accepted in ecology.
  - However, I'm not foolish!
- Priors need to be based on sound evidence and must be justifiable.
- When in doubt, use non-informative, uniform priors
  - Estimates are similar to MLE in most instances.
- Guess what ... you're already using Bayesian!
  - Estimation of random effects in longitudinal analyses and HLM, BIC, IRT!

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The legendary R. A. Fischer on probability

"The probability of any event is the ratio between the value at which an expectation depending on the happening of the event ought to be computed, and the value of the thing expected upon its happening." (In Aldrich, 2008)

- But then again, Fischer didn't believe smoking caused cancer.

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How can prior distributions affect our results?

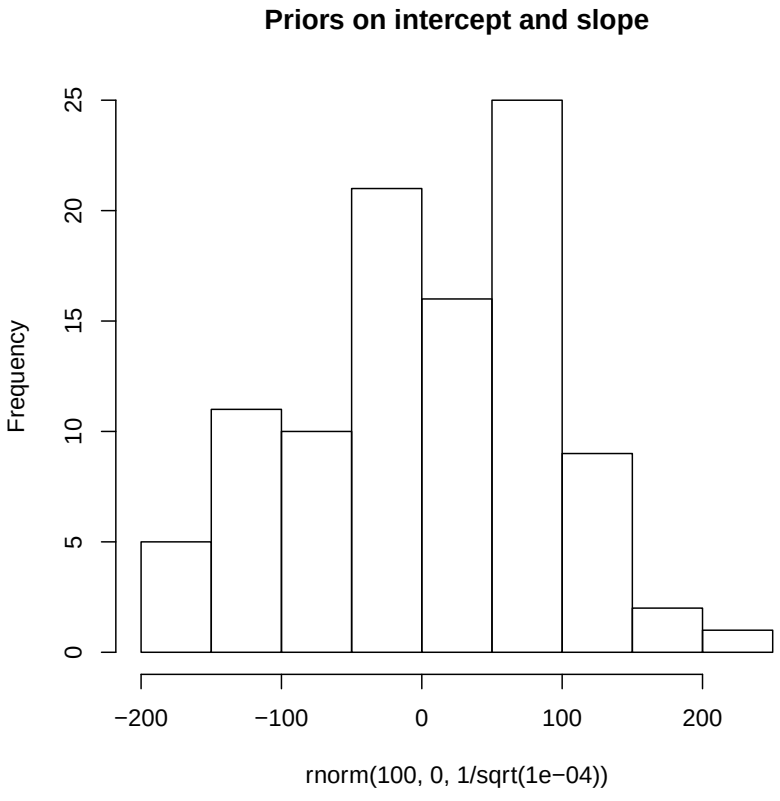
Let's take a look at `rjags`

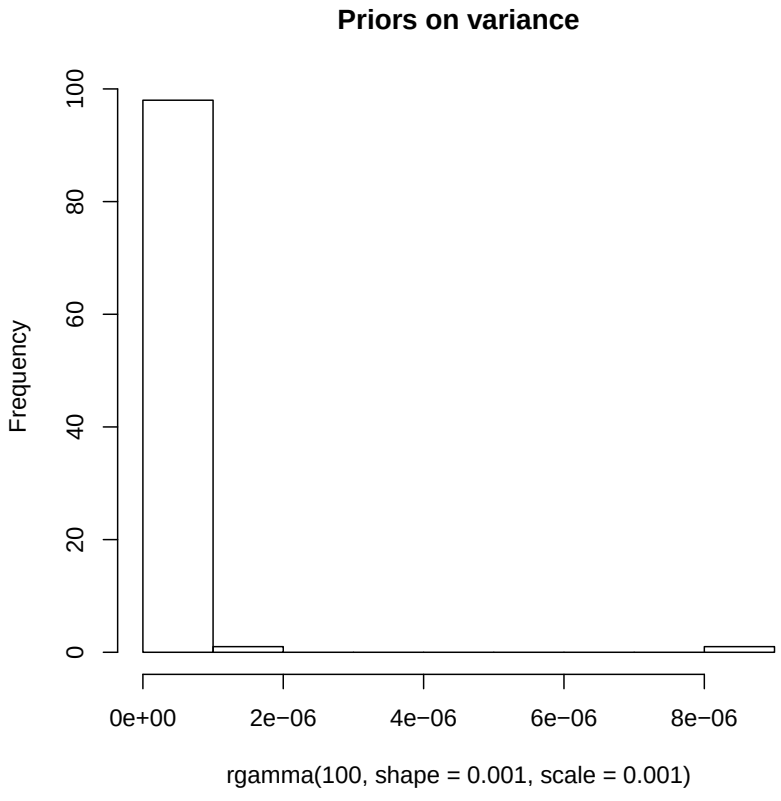
```
> require(rjags)
> dat0 <- na.omit(dat0)
> N <- nrow(dat0)
> Y <- dat0$ACT_ENGL
> x <- dat0$ACT_MATH
> dump(list=c("N","Y","x"),file="lr.data")
> datalr <- read.data(file="lr.data",format="jags")
> datalr

$x
 [1] 14 19 26 15 19 18 17 13 15 16 22 21 19 18 19 16 19 20 22 25 21 19 21 12 18
[26] 21 20 20 26 21 21 24 20 20 22 23 17 18 20 19 16 19 15 29 26 17 18 20 17 16
[51] 20 17 16 15 17 16 28 20 25 22 26 18 25 18 22 19 26

$Y
 [1] 16 25 24 21 17 13 18 19 16 19 17 19 15 23 21 20 16 22 18 18 14 19 22 10 13
[26] 21 18 18 16 18 24 28 25 16 16 17 14 15 18 22 15 18 10 23 19 22 20 21 16 19
[51] 18 15 12 16 19 19 27 16 23 16 23 19 25 19 25 19 20

$N
[1] 67
```

Exploring priors

```
> print(m1 <- jags.model(file="lr8920prior1.bug",data=datalr))

Compiling model graph
   Resolving undeclared variables
   Allocating nodes
   Graph Size: 197

JAGS model:

model {
    for (i in 1:N) {
          Y[i]   ~ dnorm(mu[i], tau)
          mu[i] <- alpha + beta * (x[i] - x.bar)
    }
  x.bar <- mean(x)
  alpha ~ dnorm(0.0, 1.0E-4)
  beta ~ dnorm(0.0, 1.0E-4)
  sigma <- 1.0/sqrt(tau)
  tau ~ dgamma(1.0E-3, 1.0E-3)
}

Fully observed variables:
 N Y x
```

What do these priors look like?





Posterior distribution from prior 1

```
> prior1 <- coda.samples(m1,variable.names=c("alpha","beta","sigma","tau"),n.iter=5000,thin=10)

 |**************************************************| 100%

> summary(prior1)

Iterations = 10:5000
Thinning interval = 10
Number of chains = 1
Sample size per chain = 500

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean      SD  Naive SE Time-series SE
alpha 18.73395 0.42902 0.0191865      0.0221243
beta   0.51495 0.12166 0.0054406      0.0051588
sigma  3.42628 0.63731 0.0285015      0.0247560
tau    0.08829 0.01595 0.0007132      0.0006959

2. Quantiles for each variable:

          2.5%      25%     50%      75%   97.5%
alpha 17.82418 18.47420 18.7603 18.98205 19.5555
beta   0.27909  0.44618  0.5155  0.58573  0.7579
sigma  2.88946  3.19051  3.3846  3.59386  4.0401
tau    0.06127  0.07742  0.0873  0.09824  0.1198
```

Maximum likelihood estimates

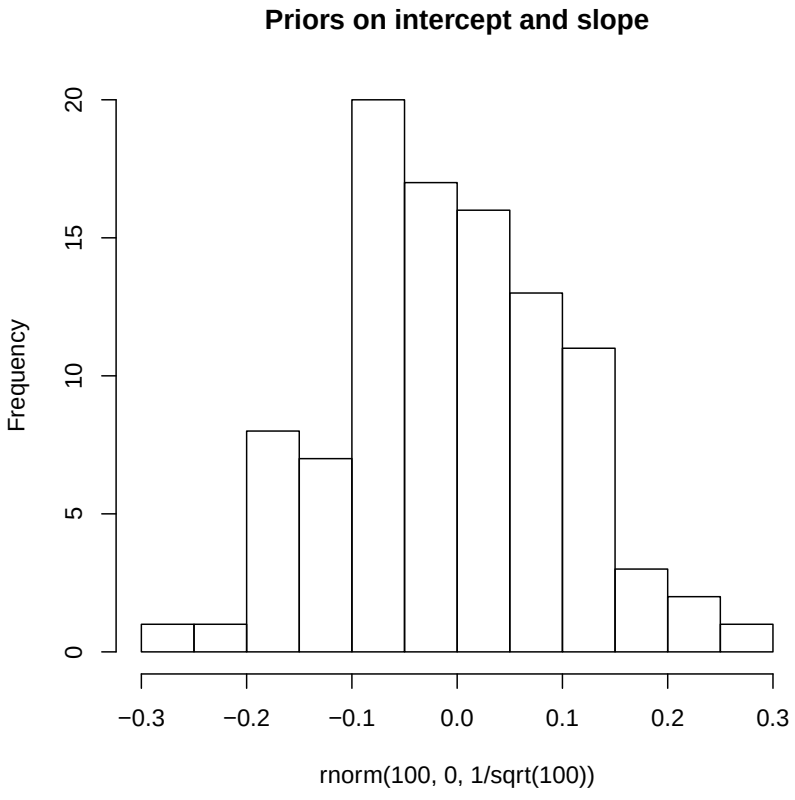
```
> coef(lm(Y ~ 1 + x))

(Intercept)           x
  8.5493151   0.5172069
```

The posterior distribution estimate of the slope is nearly identical to the maximum likelihood estimate. But the intercept is a little different. What happens if we decrease the variance?

Alternate priors with small variances

```
>  print(m2 <- jags.model(file="lr8920prior2.bug",data=datalr))

Compiling model graph
   Resolving undeclared variables
   Allocating nodes
   Graph Size: 197

JAGS model:

model {
    for (i in 1:N) {
          Y[i]   ~ dnorm(mu[i], tau)
          mu[i] <- alpha + beta * (x[i] - x.bar)
    }
  x.bar <- mean(x)
  alpha ~ dnorm(0.0, 100)
  beta ~ dnorm(0.0, 100)
  sigma <- 1.0/sqrt(tau)
  tau ~ dgamma(1.0E-3, 1.0E-3)
}

Fully observed variables:
 N Y x
```

What do these alternate priors look like?



I bet this will have an enormous impact!

Posterior distribution from prior 2

```
> prior2 <- coda.samples(m2,variable.names=c("alpha","beta","sigma","tau"),n.iter=5000,thin=10)

  |**************************************************| 100%

> summary(prior2)

Iterations = 10:5000
Thinning interval = 10
Number of chains = 1
Sample size per chain = 500

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

           Mean       SD  Naive SE Time-series SE
alpha  0.045119 0.341613 1.528e-02      1.453e-02
beta   0.013496 0.105259 4.707e-03      4.841e-03
sigma 19.366620 1.742587 7.793e-02      7.326e-02
tau    0.002731 0.000495 2.214e-05      2.127e-05

2. Quantiles for each variable:

           2.5%       25%       50%       75%     97.5%
alpha -0.165544 -0.034142  0.031131  0.093523  0.230392
beta  -0.193316 -0.055528  0.009584  0.082081  0.211800
sigma 16.482919 18.133185 19.282952 20.382879 22.999065
tau    0.001891  0.002407  0.002689  0.003041  0.003681
```

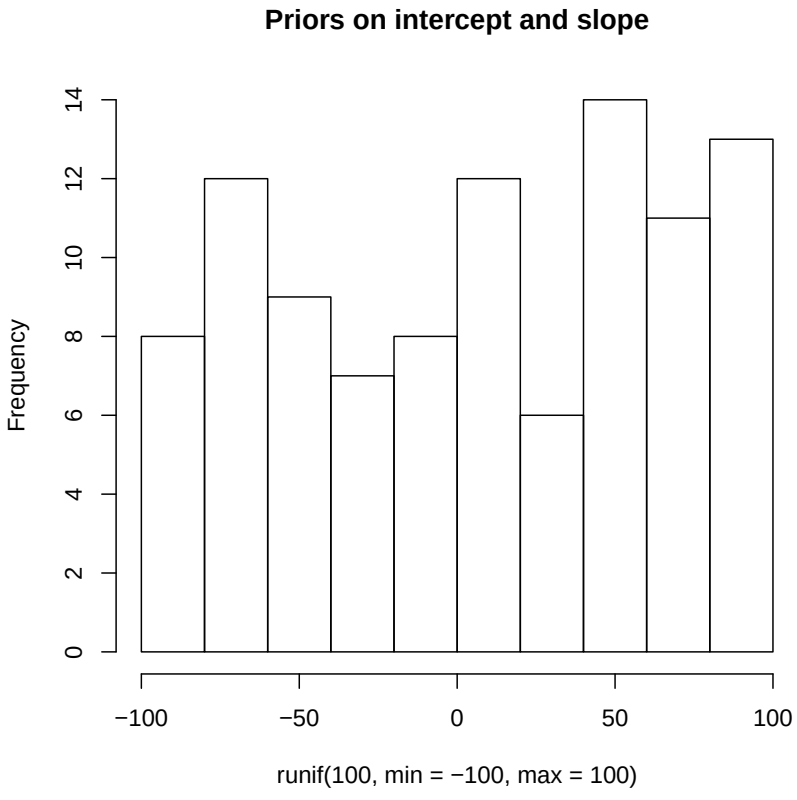
alpha and beta got pulled towards zero and sigma balloned!

This time with uniform priors

This time lets set set the priors on alpha and beta to be uniform.

```
> print(m3 <- jags.model(file="lr8920prior3.bug",data=datalr))

Compiling model graph
   Resolving undeclared variables
   Allocating nodes
   Graph Size: 197
JAGS model:

model {
    for (i in 1:N) {
          Y[i]   ~ dnorm(mu[i], tau)
          mu[i] <- alpha + beta * (x[i] - x.bar)
    }
  x.bar <- mean(x)
  alpha ~ dunif(-100, 100)
  beta ~ dunif(-100, 100)
  sigma <- 1.0/sqrt(tau)
  tau ~ dgamma(1.0E-3, 1.0E-3)
}

Fully observed variables:
 N Y x
```

3rd priors



What do you think the posterior distribution will look like?

Posterior distribution from prior 3

```
> prior3 <- coda.samples(m3,variable.names=c("alpha","beta","sigma","tau"),n.iter=5000,thin=10)

  |**************************************************| 100%

> summary(prior3)

Iterations = 1010:6000
Thinning interval = 10
Number of chains = 1
Sample size per chain = 500

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean     SD Naive SE Time-series SE
alpha 18.73255 0.4101 0.018342      0.0171511
beta   0.51656 0.1133 0.005069      0.0047222
sigma  3.37070 0.3047 0.013626      0.0131941
tau    0.09015 0.0161 0.000720      0.0007335

2. Quantiles for each variable:

          2.5%      25%      50%      75%   97.5%
alpha 17.96480 18.43754 18.74745 19.02622 19.4980
beta   0.30025  0.44335  0.51497  0.59273  0.7369
sigma  2.81918  3.18651  3.33087  3.56174  4.0542
tau    0.06084  0.07883  0.09013  0.09848  0.1258
```

Very similar to MLE

Your turn to run priors!

- I'd like you guys to break up into groups of 3.
- Using my code and data, tweak the model, and run it!
- Run `jags.model()` then `coda.samples()`
- Try it with a few different priors and `repeat the process for the same priors.`
- What were your priors? How did they affect your estimates? Do you get the same estimates when you ran the same priors again? What if you used `set.seed()`?

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What are the lessons from priors?

- Priors can greatly affect your estimates, especially the choice of the variance!
- When n increases, the influence of priors goes down
  - How big does n need to be? Bigger than 67 apparently ...
  - For "fixed effects" estimates, n doesn't need to be as big as it does for variance and "random effects".
- Should examine posterior modes, posterior means, and Bayesian confidence intervals. If these are similar to MLE then you are good to go! If not worry?
- Can also do sensitivity analysis of posterior distribution under different prior specifications.
- For GLMM and LMM, when in doubt use non-informative uniform priors on fixed effects and non-informative inverse Wishart on residuals & random effects (discussed later). Results will be similar to MLE.

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How do we estimate posterior distributions?

Recall for a simple linear regressioen of a normally distributed variable...

Bayes Theorem

$$Pr(\mu, \sigma^2|\mathbf{y}) \propto Pr(\mathbf{y}|\mu, \sigma^2)Pr(\mu, \sigma^2)$$

- In order to calculate the posterior distribution often requires integrating out many variables, taking integrals of integrals.
  - Imagine the case of a GLMM, where you have to estimate your fixed effects, variances, and random effects.
  - This can not be derived analytically and requires approximation.
- MCMC provides a way to estimate the posterior distribution.
- It can "find" the posterior distribution within MCMC error.
- MCMC works by walking stochastically through space, the Monte Carlo part, and hopefully from areas of low to high probability of where our parameters are living.

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Starting values

- The first thing that you need for MCMC are starting values
- This will help to speed up convergence and reduce wasted wandering
- All estimated parameters require starting values
- These may be generated by the program
- Or supplied by the user
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Metropolis-Hastings

- After we've initialized our chain we need to decide where to go next and start sampling from our posterior distribution!
- To do this we generate a candidate destination and decide whether we should move there or stay put.
- One way to do this is using a Metropolis-Hastings (MH) algorithm.
- During the first iteration, a random set of coordinates are picked from a multivariate normal distribution and compared to the intial coordinates.
- If the posterior probability is greater for the new coordinates, than we move to the new coordinates.

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Metropolis-Hastings continued

- If the posterior probability is lower, than we may stay or we may go.
- Once this iteration is complete, we repeat this again with our coordinates at the end of the last iteration becoming our base line coordinates.
- We repeat this over and over again depending upon how many iterations we've specified.
- Iterations are saved and we examine them when we look at the posterior distribution.
- Pros: Easy to write your own algorithms, less mathematical
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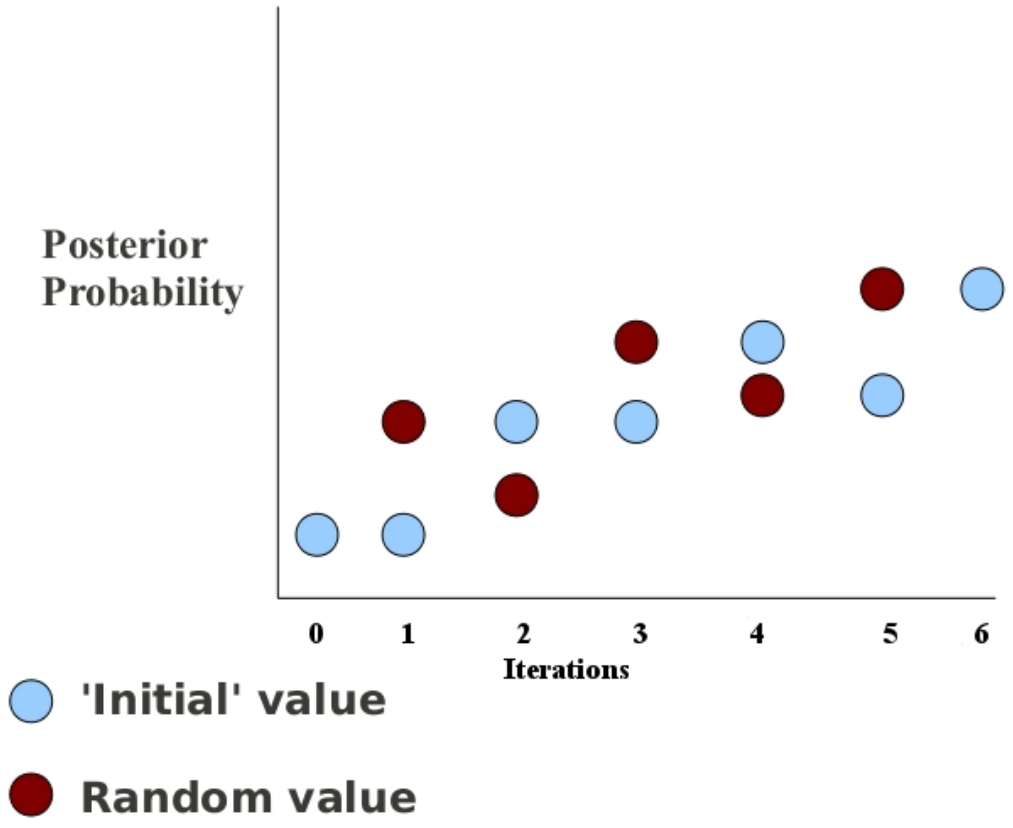
MH conceptually



Gibbs sampling

- A special case of MH
- In MH, we could move in multiple directions simulatenously, i.e. we moved for both μ and σ^2.
- However, we could have moved in just one direction at a time, for example move in the direction of μ conditioned on some value of σ^2 say 1.
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- First, let's move in the direction of μ conditioned on some value of σ^2
- We could generate a new candidate randomly and ask if it's posterior probability is higher but ...
- We often know the equation for this conditional distribution, this is Gibbs Sampling
- We know we're at $\sigma^2 = 1$, so why don't we just calculate μ directly.
- Repeat this process for σ^2 conditioning on the new value of μ and so on.
- Pro: Converges much faster!
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- First thing you should look at our trace plots.
  - They should be free from pattern
  - Each plot should have roughly a horizontal line with no ascending/descending pattern
- Next you should look at autocorrelation between iterations.
  - Iterations have a tendency to be autocorrelated and are not independent.
  - Should examine this empirically and thin out your chain.
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- Researchers have reported that MCMC needs some time to 'warm' up to remove autocorrelation, i.e. to reach convergence.
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    - Bayesian outshines traditional statistics here.
  - Developer extremely helpful and active on r-sig-mixed models mailing list.
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  - Very slow with large data sets. My data set can take 24 hours to run!
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  - Doesn't give frequentist p-values, no t-value
  - A little harder to program than lme4

Pros/Cons MCMCglmm

- Pros
  - Can estimate very complex models.
  - Lots of diagnostic tools available via coda package.
    - Bayesian outshines traditional statistics here.
  - Developer extremely helpful and active on r-sig-mixed models mailing list.
  - Can calculate actual p-values, 95% Bayesian confidence intervals, Deviance information criterion.
- Cons
  - Very slow with large data sets. My data set can take 24 hours to run!
  - Requires specification of priors and starting values
  - Doesn't give frequentist p-values, no t-value
  - A little harder to program than lme4

Specifying a MCMCglmm() model

Default arguments to MCMCglmm()

MCMCglmm(fixed, random=NULL, rcov= units, family="gaussian", mev=NULL, data,start=NULL, prior=NULL, tune=NULL, pedigree=NULL, nodes="ALL", scale=TRUE, nitt=13000, thin=10, burnin=3000, pr=FALSE, pl=FALSE, verbose=TRUE, DIC=TRUE, singular.ok=FALSE, saveX=FALSE, saveZ=FALSE, slice=FALSE)

fixed and **random** fixed and random effects formulae; **rcov** residual Cov structure; **family** probability family; **mev** specify measurement error (meta-analysis); **data** data; **start** starting values; **prior** the priors; **tune** Cov matrix for proposed latent variable; **pedigree**, **nodes**, and **scale** useful for genetics; **nitt** # of iterations; **thin** thinning interval; **burnin** # of burn-ins; **pr** and **pl** save posterior of random effects and latent variables; **verbose** get output; **DIC** Deviance information criterion; **singular.ok** when false linear dependencies in fixed effects are removed; **saveX** and **saveZ** save fixed effects and random effects matrix; **slice** use slice sampling (type of MCMC).

Labdosage data set

We'll use the labdosage.txt file. I believe you all are familiar with it?

```
> head(dos)
```

	id	group	time	count
1.1	1	2mg	1	5
1.2	1	2mg	2	2
1.3	1	2mg	3	2
1.4	1	2mg	4	5
1.5	1	2mg	5	2
1.6	1	2mg	6	4

Specifying priors on a random intercepts model with Poisson data

First, we need to specify the priors

- *B-structure* priors on 'fixed effects'; *G-structure* priors on 'random effects'; *R-structure* priors on residual variance.
- Default B is $\mu = 0$, V=I*1e+10, G and R are nu=0, V=1, alpha.mu=1, and alpha.V=0.
- B is multivariate normal; G and R are inverse Wishart with Cauchy parameter expansion (Gelman, 2006)
- Default B is weak and essentially uniformative, G and R are both weakly informative.

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Specifying a random intercepts model continued

```
> prior<-list(R=list(V=1, nu=0.002), G=list(G1=list(V=1, nu=0.002)))
```

These are essentially the same priors used for the the JAGS model.

```
> m1 <- MCMCglmm(count ~ 1 + time, random=~id, prior=prior,family="poisson",
                 data=dos)

                      MCMC iteration = 0
  Acceptance ratio for latent scores = 0.000396
                      MCMC iteration = 1000
  Acceptance ratio for latent scores = 0.424758
                       .....................
                      MCMC iteration = 13000
  Acceptance ratio for latent scores = 0.391338
```

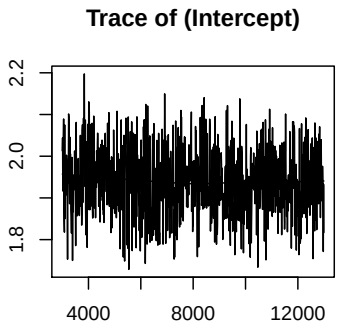
Summary statistics - Fixed effects

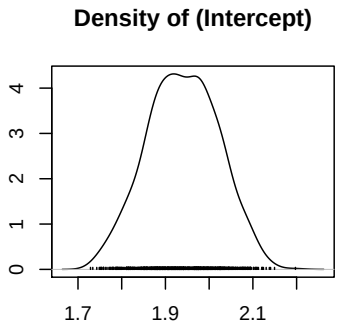
```
> # Summary of 'Fixed Effects'
> summary(m1$Sol)

Iterations = 3001:12991
Thinning interval = 10
Number of chains = 1
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:
               Mean       SD  Naive SE Time-series SE
(Intercept)  1.93977 0.080995 0.0025613      0.0030749
time        -0.05646 0.006811 0.0002154      0.0002181

2. Quantiles for each variable:
               2.5%      25%      50%      75%    97.5%
(Intercept)  1.78134  1.88190  1.93970  1.99740  2.09185
time        -0.06871 -0.06132 -0.05666 -0.05219 -0.04249


> HPDinterval(m1$Sol)

                 lower       upper
(Intercept)  1.78774756  2.09483939
time        -0.06889096 -0.04286956
attr(,"Probability")
[1] 0.95
```

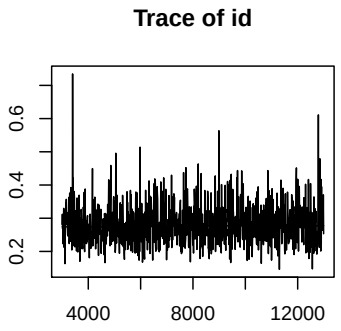
Summary statistics - Random effects

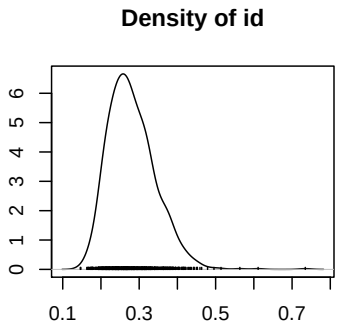
```
> # Summary of 'Random Effects
> summary(m1$VCV)

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

        Mean      SD  Naive SE Time-series SE
id    0.2815 0.06264 0.0019809       0.001970
units 0.2424 0.02490 0.0007873       0.001281

2. Quantiles for each variable:

        2.5%    25%    50%    75%  97.5%
id    0.1865 0.2372 0.2727 0.3174 0.4166
units 0.1997 0.2248 0.2410 0.2577 0.2959

> HPDinterval(m1$VCV)

          lower     upper
id    0.1728576 0.3990647
units 0.1967859 0.2921864
attr(,"Probability")
[1] 0.95
```

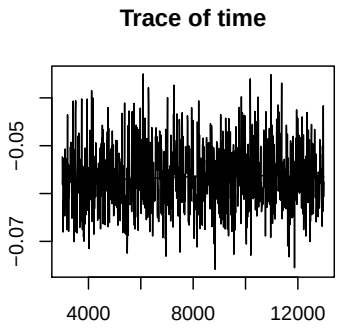
Trace plots of 'fixed' and 'random' effects

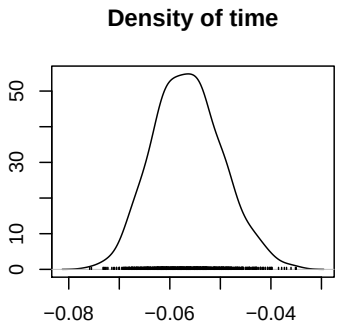


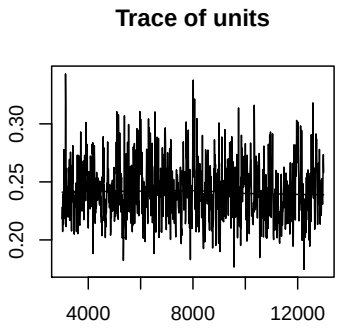


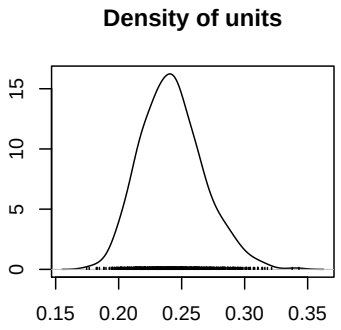












Autocorrelations of iterations

```
> autocorr(m1$Sol)

, , (Intercept)

         (Intercept)        time
Lag 0     1.00000000 -0.49419125
Lag 10    0.08802531 -0.07252791
Lag 50    0.06445487 -0.04806522
Lag 100  -0.02629911  0.06327561
Lag 500   0.03672346 -0.04482030

, , time

         (Intercept)        time
Lag 0    -0.49419125  1.00000000
Lag 10    0.02048099  0.04815938
Lag 50   -0.04384447  0.03041308
Lag 100  -0.01538620 -0.03313733
Lag 500  -0.00999942  0.02657281
```

How does this compare with glmer()

```
> m1.glmer <- glmer(count ~ 1 + time + (1 | id), family="poisson",data=dos)
```

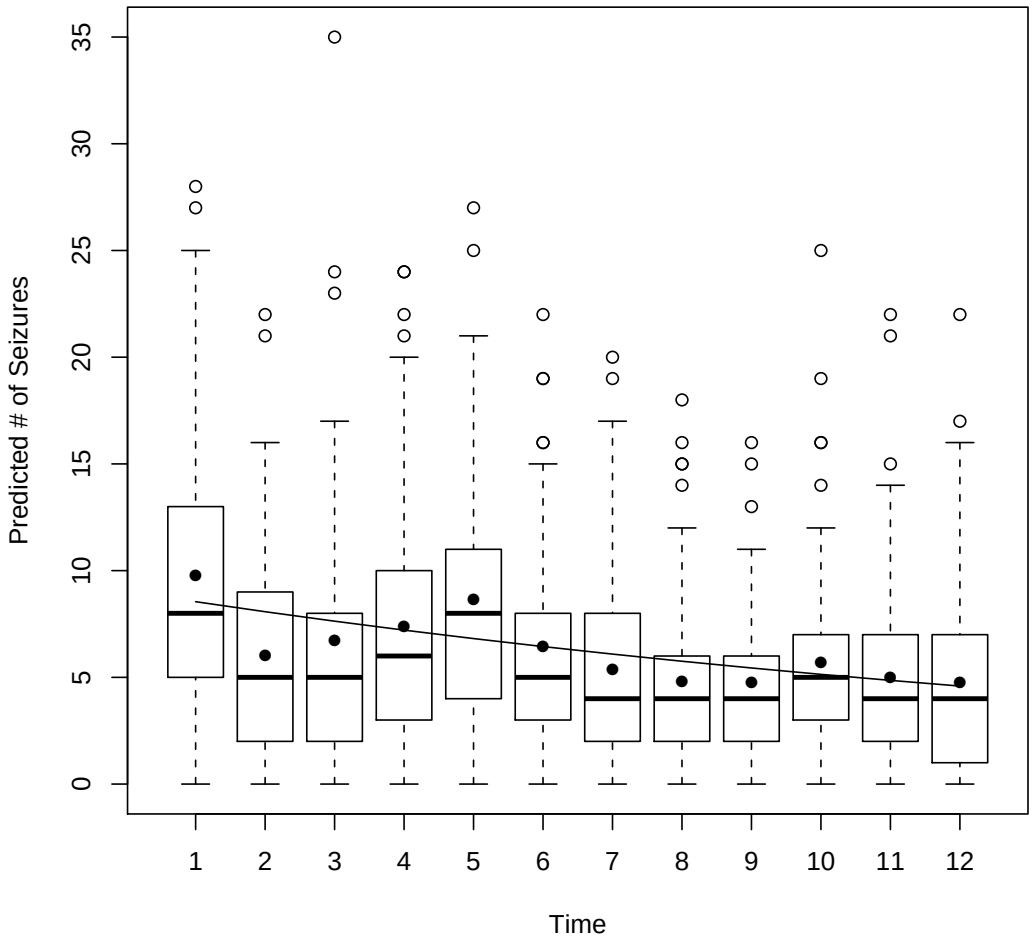
Effect	MCMCglmm	lme4
Intercept	1.9398	2.0389
Time	-0.0565	-0.0546
id	0.2815	0.2652

Very similar! This is great! Additionally, the standard errors were similar too with MCMCglmm being slightly smaller.

Predicted growth curve from MCMCglmm syntax

```
> beta<-colMeans(m1$Sol)
> pred<-beta[1]+beta[2]*I(1:12)
> plot(dos$count~as.factor(dos$time),xlab="Time",
  ylab="Predicted # of Seizures")
> points(tapply(dos$count, as.factor(dos$time), mean)~I(1:12),pch=16)
> lines(exp(pred+0.5*mean(rowSums(m1$VCV)))~I(1:12))
```

Predicted growth curve



Random slopes MCMCglmm model

```
> m2 <- MCMCglmm(count ~ 1 + time, random=~id + time, prior=prior,
                 family="poisson",data=dos, verbose=FALSE)
```

Which model is better: Random intercepts or random slope?

```
> m1$DIC;m2$DIC
```

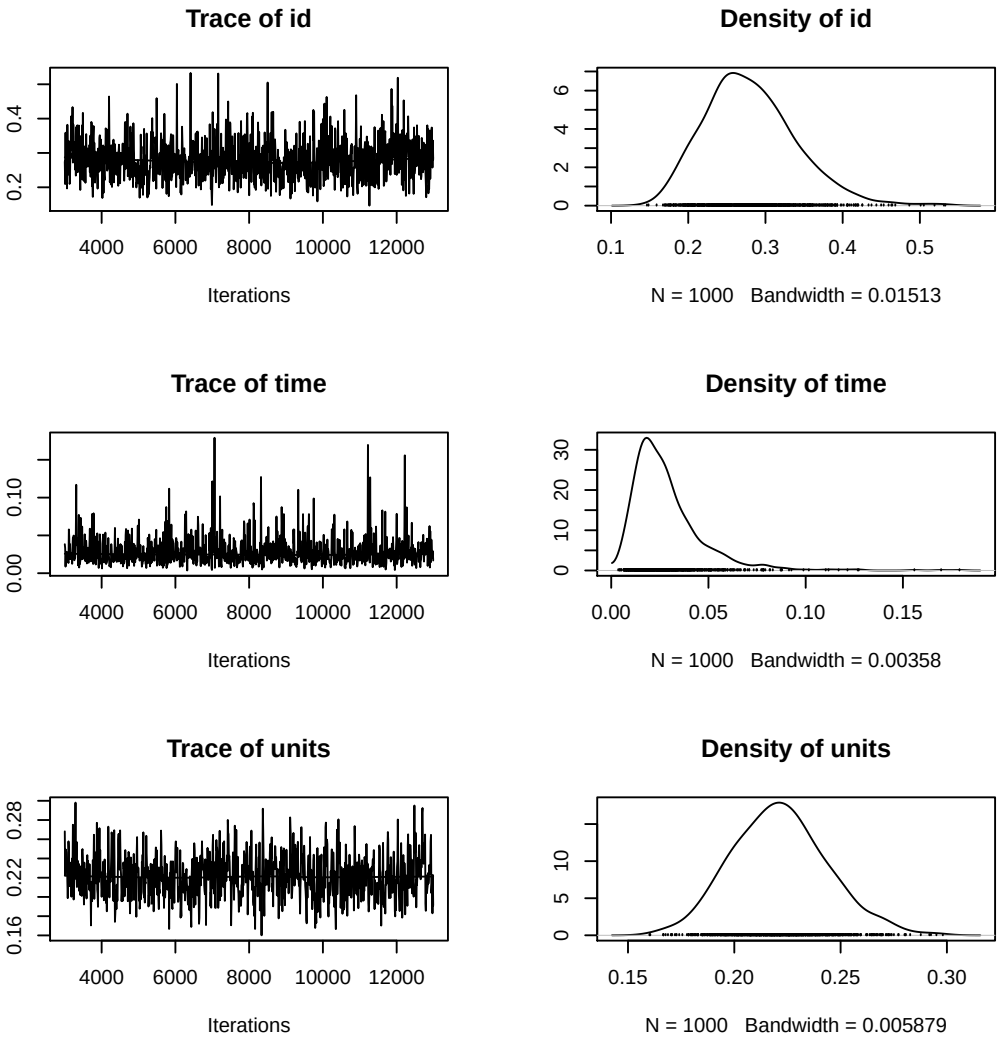
```
[1] 3871.923
```

```
[1] 3861.976
```

Random slopes model

```
> summary(m2$VCV)

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

          Mean      SD  Naive SE Time-series SE
id     0.28073 0.05920 0.0018722      0.0022649
time   0.02867 0.01890 0.0005977      0.0007020
units  0.22134 0.02244 0.0007097      0.0009372

2. Quantiles for each variable:

           2.5%     25%     50%     75%   97.5%
id     0.181775 0.24027 0.27404 0.31639 0.41390
time   0.007685 0.01663 0.02452 0.03464 0.07818
units  0.180095 0.20586 0.22075 0.23545 0.26900
```

Trace plots of random slopes model



Random slopes model with a static predictor

```
> m3 <- MCMCglmm(count ~ 1 + time + group, random=~id + time,
                 prior=prior, family="poisson",data=dos,
                 verbose=FALSE)
> m2$DIC; m3$DIC

[1] 3861.976

[1] 3860.961
```

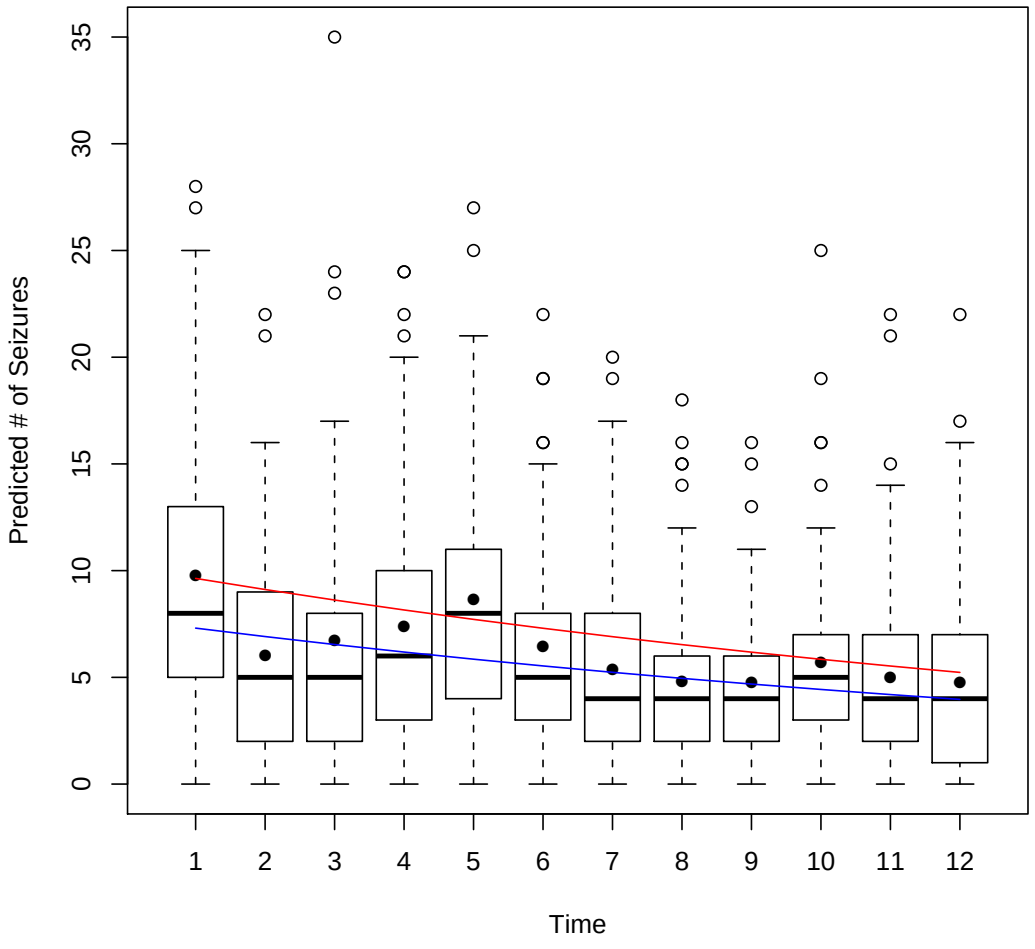
Summary statistics: Fixed effects

```
> summary(m3$Sol)

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                Mean      SD  Naive SE Time-series SE
(Intercept)  2.05451 0.14353 0.0045389      0.0050984
time        -0.05584 0.01520 0.0004808      0.0005261
group2mg    -0.27097 0.14036 0.0044387      0.0043285

2. Quantiles for each variable:

                2.5%     25%      50%      75%    97.5%
(Intercept)  1.75796  1.9676  2.05187  2.14983  2.33057
time        -0.08692 -0.0651 -0.05606 -0.04607 -0.02599
group2mg    -0.53615 -0.3666 -0.27407 -0.17733  0.00905
```

Predicted growth curves syntax

```
> beta<-colMeans(m3$Sol)
> pred.t<-beta[1]+beta[2]*I(1:12)+beta[3]
> pred.b<-beta[1]+beta[2]*I(1:12)
> plot(dos$count~as.factor(dos$time),xlab="Time",
+   ylab="Predicted # of Seizures")
> points(tapply(dos$count, as.factor(dos$time),
        mean)~I(1:12),pch=16)
> lines(exp(pred.t+0.5*mean(rowSums(m3$VCV)))~I(1:12),
       col="blue")
> lines(exp(pred.b+0.5*mean(rowSums(m3$VCV)))~I(1:12),
       col="red")
```

Growth curve



m3 with different priors

Let's set some pretty illogical priors

```
> priors2 <- list(B=list(mu=10,V=1),
                  R=list(V=1, nu=0.002),
                  G=list(G1=list(V=0, nu=10),
                         G2=list(V=1,nu=0.002)))
> m4 <- MCMCglmm(count ~ 1 + time + group, random=~id + time,
                 prior=prior2, family="poisson",data=dos,
                 verbose=FALSE)
```

And the results ...

Effects	Uninformative priors	Crazy priors
Intercept	2.055	2.061
Time	-0.056	-0.056
Group	-0.271	-0.270
Random Intercept	0.264	0.266
Random Slope	0.029	0.0274

With 780 data points, the likelihood already swamps the prior!

Running MCMCglmm() in your group

- Spend some time now in a group running different priors and different models on the data set.
- Maybe try specifying starting values?
  - `start <- list(B=2.05,-0.06,-0.27)`
  - `m3a <- MCMCglmm(count ~ 1 + time + group, random=~id + time,family="poisson",data=dos, prior=prior,start=start,verbose=FALSE)`
  - I don't recommend starting values for G and R
- If you need help with syntax please ask.
- Did you find anything interesting?

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To Bayesian or not to Bayesian ...

- In my opinion, it's useful to know Bayesian methods as ML approaches & least squares approaches don't always work.
- I believe that Bayesian methods will become more and more important as computers become more and more powerful.
- Bayesian frees you from the awkwardness of frequentist statistics and creates the opportunity to include prior information.
- But ... like everything there are costs to Bayesian.
- Hopefully I've give you just enough information to be dangerous

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Thanks!