Mixed Models with R:
Generalized Linear Mixed Models

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- Generalized Linear Mixed Models (**GLMM**s) generalize Generalized Linear Models (**GLM**s) to Mixed Models as
  Linear Mixed Models (**LMM**s, **HLM**s) generalize Linear Models (**LM**s) to Mixed Models.

- They allow modeling a non-normal response with a model that incorporates random effects.
- However, the ratio of complexity $\frac{\text{GLMM}}{\text{GLM}}$ is much greater than that of $\frac{\text{LMM}}{\text{LM}}$
- The reason is that integrating out the unseen random effects in the LMM is relatively easy thanks to the good behaviour of the normal distribution.

- Except in a few special cases the random effects don't integrate out easily in GLMMs and various approximations need to be used. This is an active area of research and good practice is far from settled.

There are many functions in R that can be used for GLMMs. Some key ones:

Function	Approach
glmmPQL in MASS, nlme	A marriage of glm and lme using Penalized Quasi Likelihood: easy to use with familiar syntax of glm and lme. Based on PQL algorithm which is robust but breaks down with small clusters of binary data with probabilities near 0 or 1. Can use both R side and G side models.
lmer in lme4	Newer package by Doug Bates especially strong with crossed random (not necessarily nested) random effects. Uses Gauss-Hermite quadrature considered more accurate than PQL. No R side. Simpler G structures than in glmmPQL (lme)
MCMCglmm in MCMCglmm	Uses faster Markov Chain Monte Carlo. Fits censored and zero-inflated model. R and G side.

The matrix formulation:

GLM	$\mathbf{y} \sim G_\phi(\boldsymbol{\mu})\ g(\boldsymbol{\mu}) = \boldsymbol{\eta}\ \ \boldsymbol{\eta} = \mathbf{X}\boldsymbol{\beta}$	
GLMM for Hier-archical Data	$\mathbf{y}_j \sim G_\phi(\boldsymbol{\mu}_j)\ g(\boldsymbol{\mu}_j) = \boldsymbol{\eta}_j$ $\boldsymbol{\eta}_j = \mathbf{X}_j\boldsymbol{\gamma} + \mathbf{Z}_j\mathbf{u}_j$ $\mathbf{u}_j \sim N(\mathbf{0}, \mathbf{G})$	$\mathbf{y}_j = \begin{bmatrix} y_{j1} \\ y_{j2} \\ \vdots \\ y_{jn_j} \end{bmatrix}$ Observations in **j**th cluster (students in **j**th school)

- If G is an exponential family with link function *g*, then the GLMM for hierarchical data is a 'true' model with a likelihood.
- The ML solution for the GLM can be found easily with **I**teratively **R**e**W**eighted **L**east-**S**quares (**IRWLS**).
- However the ML solution for the hierarchical GLMM requires integrating over the unobserved random effects $\mathbf{u}_j$ – relatively easy with a Gaussian model, much harder in general. In practice, we use various approximations. We will look at glmmPQL, glmer and MCMCglmm.
- Some approaches, e.g. MCMCglmm, add an $\boldsymbol{\varepsilon}_j \sim N(0, R_j)$ which doesn't seem to fit with GLMs but can be a real boon.

Methods for fitting GLMMs: (from glmm.wikidot.com/faq)

(adapted from Bolker et al TREE 2009)

Penalized quasi-likelihood	Flexible, widely implemented	Likelihood inference may be inappropriate; biased for large variance or small means PROC GLIMMIX (SAS), GLMM (GenStat), glmmPQL (R:MASS), ASREML-R
Laplace approximation	More accurate than PQL	Slower and less flexible than PQL glmer (R:lme4,lme4a), glmm.admb (R:glmmADMB), AD Model Builder, HLM
Gauss-Hermite quadrature	More accurate than Laplace	Slower than Laplace; limited to 2-3 random effects PROC NLMIXED (SAS), glmer (R:lme4, lme4a), glmmML (R:glmmML), xtlogit (Stata)

Markov chain Monte Carlo	Highly flexible, arbitrary number of random effects; accurate	Very slow, technically challenging, Bayesian framework MCMCglmm (R:MCMCglmm), MCMCpack (R), WinBUGS/OpenBUGS (R interface: BRugs/R2WinBUGS), JAGS (R interface: rjags/R2jags), AD Model Builder (R interface: R2admb), glmm.admb[1] (R:glmmADMB)

glmmPQL

- Advantages: easy syntax like lme:

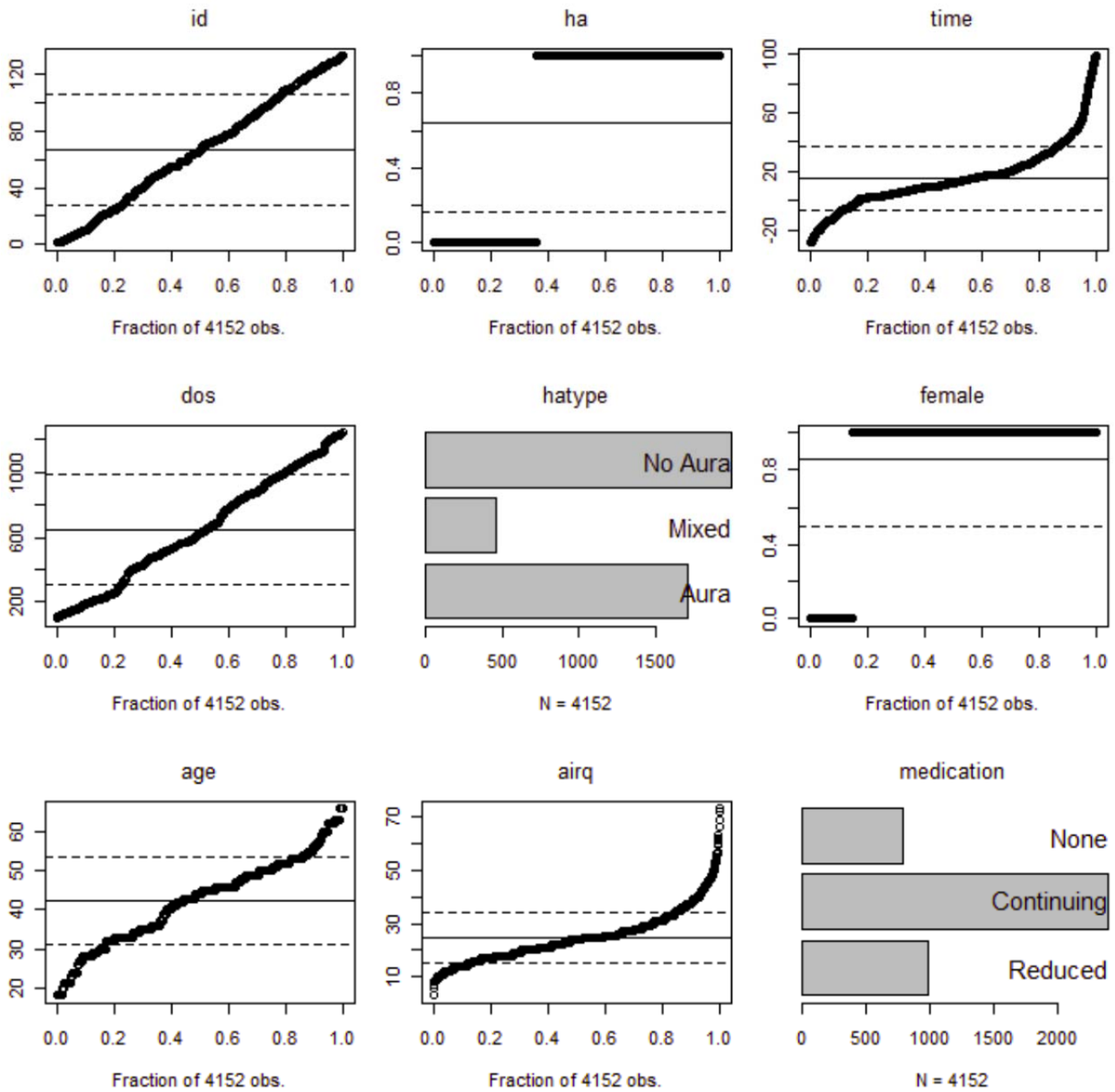
```
fit <- glmmPQL( y ~ x + z, data = dd,
      family = binomial,
      random = ~ 1 + x | id)
```

converges relatively easily, easy Wald tests for linear parameters, generalizes to GLMM for Longitudinal Data.
The syntax is exactly the same as for lme except for the family argument.

- Disadvantage: Performs poorly with small binary clusters. Other methods take more time but may be more accurate. Solution is not a maximum likelihood.

Consider 4,152 daily records of headache logs kept by 133 patients in a treatment program in which bio-feedback was used to attempt to reduce migraine frequency and severity. Patients entered the program at different times over a period of about 3 years. Patients were encouraged to begin their logs four weeks before the onset of treatment and to continue for one month afterwards, but only 55 patients have data preceding the onset of treatment.

```
Usage:  > library( spidadev ) # loads MASS and nlme for glmmPQL
        > data( migraines )
        > ?migraines
        > ds <- migraines
        > xqplot(ds)
```


id
ha
time
dos
hatype
female
age
airq
medication
No Aura
Mixed
Aura
None
Continuing
Reduced
Fraction of 4152 obs.
N = 4152

```
> ds$treat <- (ds$time > 0)*1

> fit <- glmmPQL ( ha ~ treat, data = ds,
+              random = ~ 1 | id,
+              family = binomial)
iteration 1
. . .
iteration 5
> summary(fit)
Linear mixed-effects model fit by maximum likelihood
 Data: ds
  AIC BIC logLik
   NA  NA     NA

Random effects:
 Formula: ~1 | id
        (Intercept)  Residual
StdDev:    1.479865 0.9410313

Variance function:
 Structure: fixed weights
 Formula: ~invwt
```

Create a dummy variable for treatment

NAs warn you that the fit is not really maximum likelihood

```
Fixed effects: ha ~ treat
                 Value Std.Error   DF   t-value p-value
(Intercept)  0.8477543 0.1621571 4018  5.227980  0.0000
treat       -0.0164957 0.1038301 4018 -0.158872  0.8738

. . .

Number of Observations: 4152
Number of Groups: 133
```

The model used is a GLM with family = binomial, i.e. a logistic regression.

$$\text{logit}(\Pr(ha)) = 0.84 - 0.016 \times treat$$

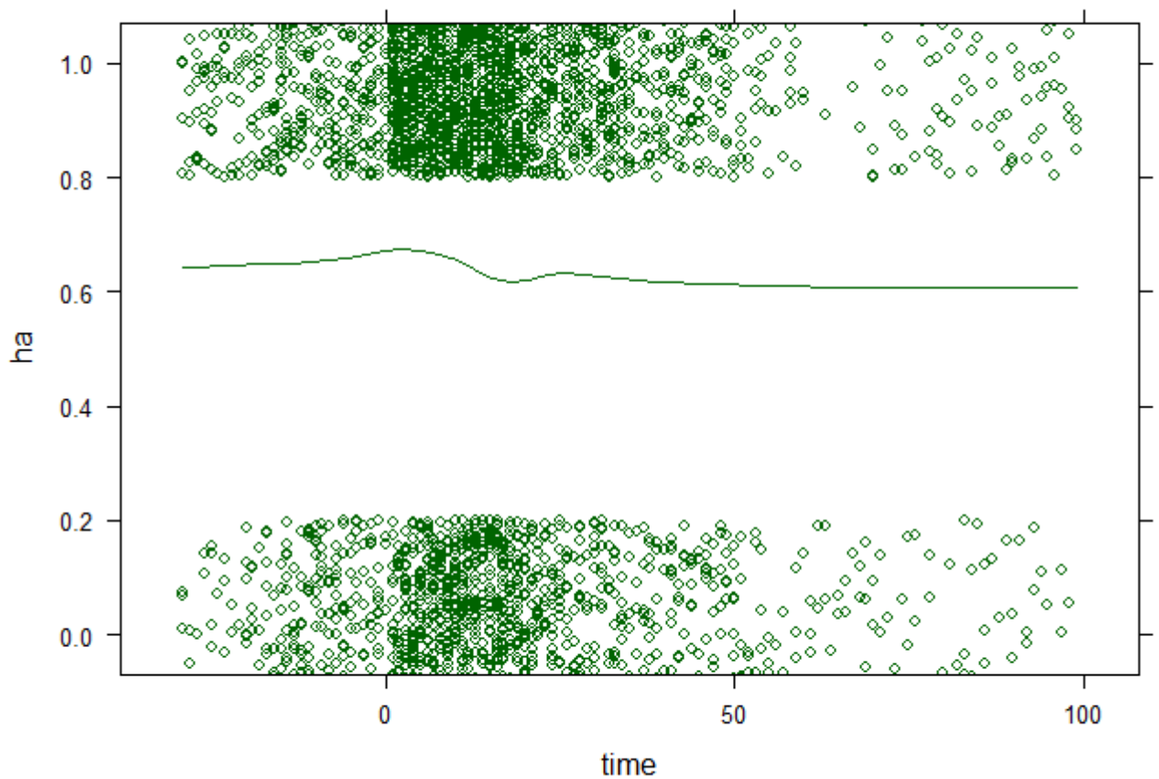
So the treatment reduces odds of headache to

$$\exp(-0.016) = 0.984 = 98\%,$$

i.e. a reduction of 2%

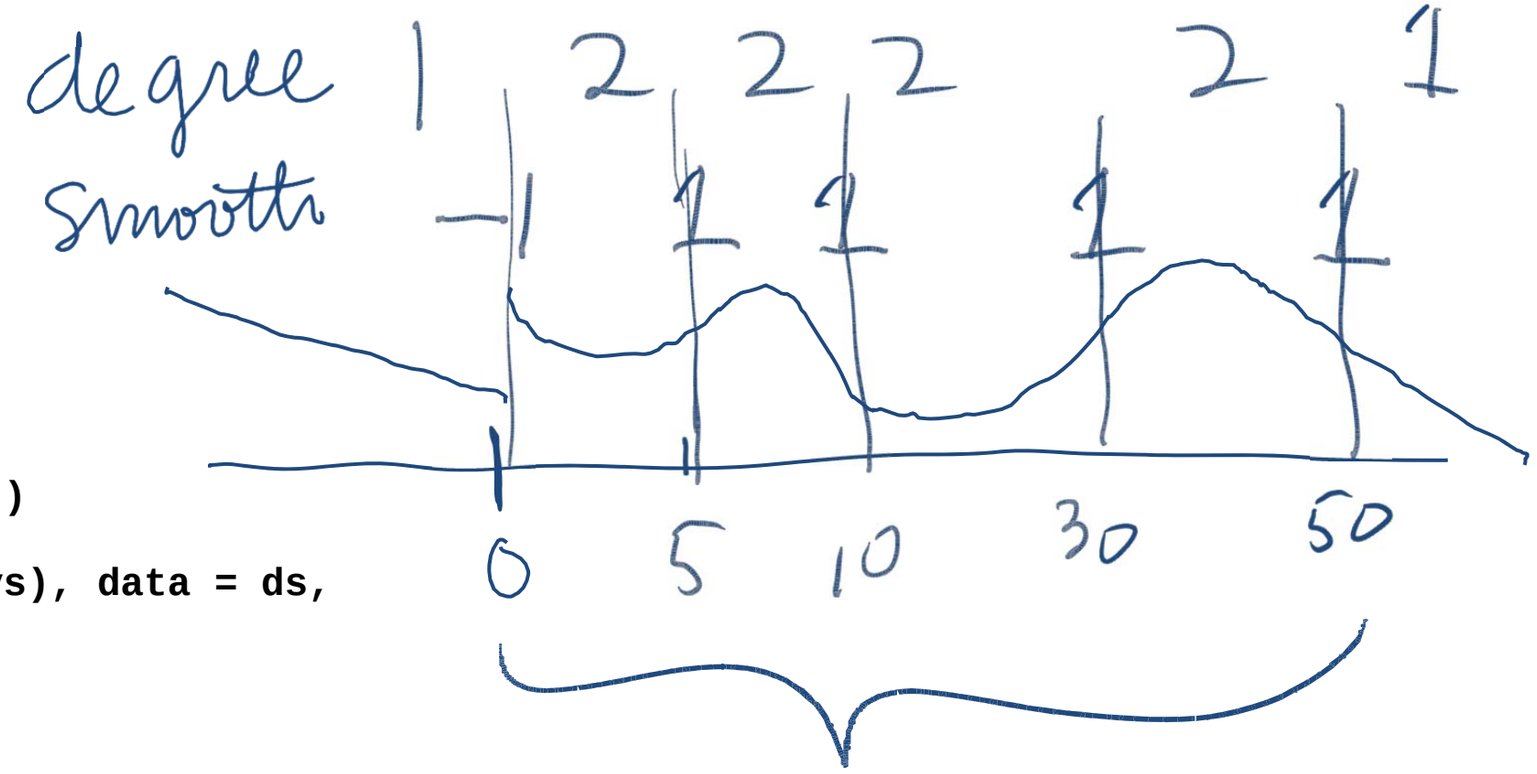
Overall view of the effect of treatment

```
xyplot( ha ~ time, ds, panel = function(x, y, ...) {
        panel.xyplot( x, jitter(y),...)
        panel.loess( x, y, ..., family = 'gaussian')})
```



Seems to make people worse before they get better (slightly)
Maybe it’s short-term pain for long-term gain.

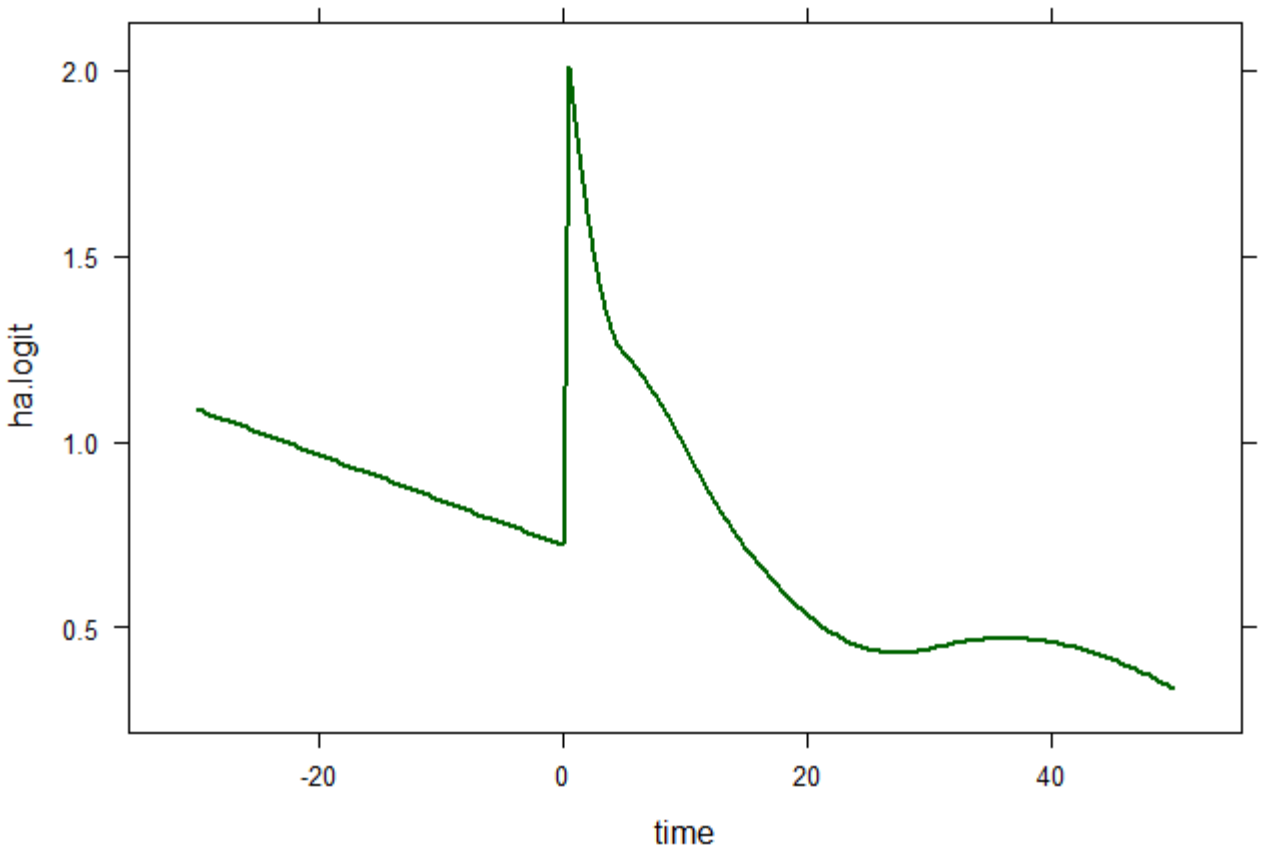
```
> ds$tdays <- ds$time / 10
>
> # create a spline function:

> sp <- function(x) gsp( x,
+ knots =   c(0,5,10,30,50)/10,
+ degree = c(1,2,2, 2, 2 ,1),
+    smooth =  c(-1,1,1, 1,  1))

> fit <- glmmPQL ( ha ~ sp(tdays), data = ds,
+ random = ~ 1 | id,
+ family = binomial)
iteration 1
iteration 2
iteration 3
iteration 4
iteration 5
> summary(fit)
Linear mixed-effects model fit by maximum likelihood
 Data: ds
  AIC BIC logLik
   NA  NA     NA

Random effects:
 Formula: ~1 | id
        (Intercept)  Residual
StdDev:    1.568552 0.9406108
```



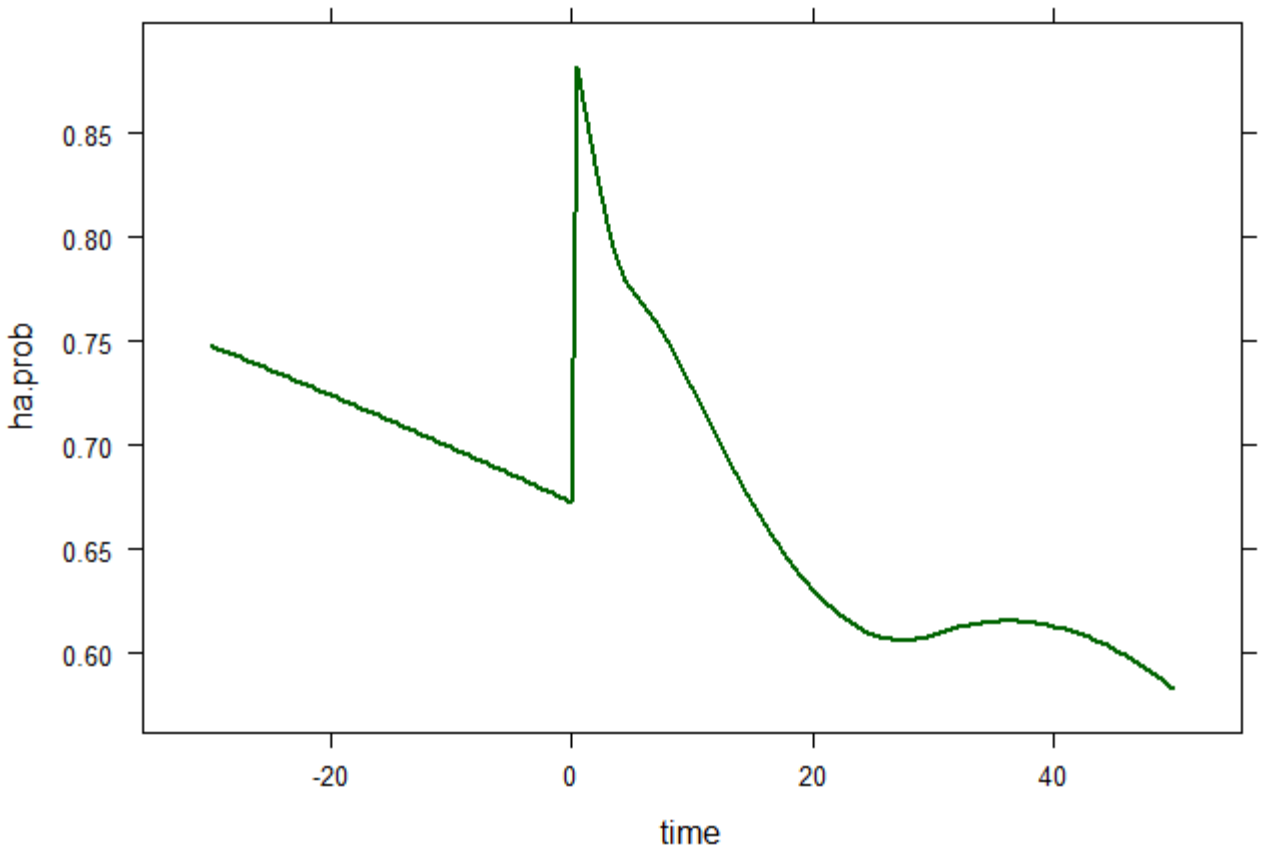
Spline :- polynomial in each interval
- constraints at knots

-1 : discontinuous
0 : continuous but kinky
1 : smooth
etc. ...

```
Variance function:
 Structure: fixed weights
 Formula: ~invwt
Fixed effects: ha ~ sp(tdays)
                     Value Std.Error   DF   t-value p-value
(Intercept)       0.720987  0.211794 4012  3.404190  0.0007
sp(tdays)D1(0)   -0.122074  0.110583 4012 -1.103906  0.2697
sp(tdays)C(0).0   1.448669  0.429678 4012  3.371521  0.0008
sp(tdays)C(0).1  -3.241710  2.275235 4012 -1.424780  0.1543
sp(tdays)C(0).2   5.976928  5.544150 4012  1.078060  0.2811
sp(tdays)C(0.5).2 -6.482328  6.792881 4012 -0.954283  0.3400
sp(tdays)C(1).2   0.863025  1.594558 4012  0.541231  0.5884
sp(tdays)C(3).2  -0.498702  0.213875 4012 -2.331749  0.0198


Number of Observations: 4152
Number of Groups: 133


> pred <- expand.grid( time = seq(-30,50,.5))

> pred$tdays <- pred$time / 10

> pred$ha.logit <- predict( fit, pred, level = 0)

> xyplot( ha.logit ~ time, pred, type = 'l')
```




```
> pred$ha.prob <- 1/(1+exp( -pred$ha.logit))

> xyplot( ha.prob ~ time, pred, type = 'l')
```



Is there a significant difference between, say, -10 days, and 30 days?

```
sc(sp, x, D = 0, type = 1)

generates a portion of an L matrix.
  sp – spline
  x  - where spline should be evaluated
  D  - what to evaluate:
         0:  value
         1:  slope
         2:  curvature, etc.
  type – at a knot:
           type = 0: on the left,
           type = 1: on the right,
           type = 2: ‘saltus’: right – left
```

```
> Lp <- sc(sp,x = c(-10,30)/10, D = 0)
> Lp
      D1(0) C(0).0 C(0).1 C(0).2 C(0.5).2 C(1).2 C(3).2
g(-1)    -1      0      0    0.0    0.000      0      0
g(3+)     3      1      3    4.5    3.125      2      0

> wald(fit)
 numDF denDF  F.value p.value
     8  4012 15.43282 <.00001

Coefficients          Estimate Std.Error   DF   t-value p-value
  (Intercept)         0.720987  0.211590 4012  3.407474 0.00066
  sp(tdays)D1(0)     -0.122074  0.110477 4012 -1.104971 0.26924
  sp(tdays)C(0).0     1.448669  0.429264 4012  3.374774 0.00075
  sp(tdays)C(0).1    -3.241710  2.273042 4012 -1.426155 0.15390
  sp(tdays)C(0).2     5.976928  5.538806 4012  1.079100 0.28061
  sp(tdays)C(0.5).2  -6.482328  6.786334 4012 -0.955203 0.33953
  sp(tdays)C(1).2     0.863025  1.593021 4012  0.541754 0.58802
  sp(tdays)C(3).2    -0.498702  0.213669 4012 -2.333998 0.01964

> Lm <- cbind(0,Lp)
> Ldiff <- rbind( Lm, diff= Lm[2,] - Lm[1,])
```

```
>  Ldiff
             D1(0) C(0).0 C(0).1 C(0).2 C(0.5).2  C(1).2  C(3).2
g(-1)        0     -1       0       0     0.0     0.000        0       0
g(3+)        0      3       1       3     4.5     3.125        2       0
 diff        0      4       1       3     4.5     3.125        2       0

> wald(fit, Ldiff)
  numDF  denDF   F.value  p.value
1     2   4012  5.930952  0.00268

          Estimate Std.Error   DF   t-value p-value
  g(-1)  0.122074  0.110477 4012  1.104971 0.26924
  g(3+) -0.277731  0.183149 4012 -1.516422 0.12949
  diff  -0.399805  0.130583 4012 -3.061687 0.00222
```

MCMCglmm

What's a Markov Chain? A sequence of random variables (or vectors) where the distribution for the next one in the sequence ('chain') depends on the past only through the most recent value of the variable, i.e. the future depends on the past values of the variable (vector) only through the present values of the variable (vector). This is more general than it seems. If the next value depends on today's and yesterday's, we simply redefine the MC so it's a vector of values for two successive days.

What's a Monte Carlo Markov Chain? A Markov Chain generated by a computer.

What's Markov Chain Monte Carlo? The process (and its study) of producing a Monte Carlo Markov Chain. Just say MCMC and you won't have to think about this.

What's so hot about Markov Chain Monte Carlo? It accomplishes the seemingly impossible … but only by going to an awful lot of trouble.

From Andrieu (2003):

> Many papers on Monte Carlo simulation appeared in the physics literature after 1953. From an inference perspective, the most significant contribution was the generalisation of the Metropolis algorithm by Hastings in 1970. Hastings and his student Peskun showed that Metropolis and the more general Metropolis-Hastings algorithms are particular instances of a large family of algorithms, which also includes the Boltzmann algorithm (Hastings, 1970; Peskun, 1973). They studied the optimality of these algorithms and introduced the formulation of the Metropolis-Hastings algorithm that we adopt in this paper. In the 1980's, two important MCMC papers appeared in the fields of computer vision and artificial intelligence (Geman & Geman, 1984; Pearl, 1987). Despite the existence of a few MCMC publications in the statistics literature at this time, it is generally accepted that it was only in 1990 that MCMC made the first significant impact in statistics (Gelfand & Smith, 1990). In the neural networks literature, the publication of Neal (1996) was particularly influential.

Example:

- Let's say you really want to sample a bivariate distribution for (Y_1, Y_2). Note that Y here is generic and the principle works with anything random (vector or variable): Y_{mis}, β, u, ε.
- But you can't: you don't have a way of generating random (Y_1, Y_2).
- But you **do** know something:
  - You know to generate **Y_1 given Y_2** and
    you know how to generate **Y_2 given Y_1**.
    You can do **conditionals** but you can't do the **joint** or the **marginal.**
    You could generate random values, but you can't get started.
    - Note 1: This is not far fetched: This is exactly the problem with Y_{mis} and β in the missing data problem. And in many other problems.
    - Note 2: If you knew how to generate either marginally, say Y_1, then you could easily generate Y_2 given Y_1 and that would give you a sample for (Y_1, Y_2).

- **Solution**:
  - Since you can't generate a random Y_1 to get started, **just make it up**!
  - Then keep going back and forth: Y_2 from Y_1, and then Y_1 from Y_2 and keep going for a very long time. Under the *right conditions*, *eventually*, the starting value that you made up won't matter and the (Y_1, Y_2) you get will be a random observation from the joint distribution. [**burnin time]**
  - If you want more than one random observation, you can keep going but observations are dependent on each other so if you want them nearly independent, you will need to wait a while between the random observations you choose. **[thinning the chain]**
  - The ***right conditions***?
    - No isolated islands of high probability surrounded by seas of low or no probability. Otherwise you'll be stuck on an island for a long time until your MCMC discovers the canoe. You might *never* discover that the world is really a larger place.
    - Also, no single probability peak where you might get stuck.

How to tell if it's working:

- How do you know how long to **burnin** and to **thin**?
- How do you know whether the results make sense?

Example:

- Suppose you want to generate a random sample from the bivariate Normal with mean (5,5), standard deviation 2 and correlation 0.95
- But you haven't yet discovered how to do this. However, you know how to generate a Y_2 given Y_1 and Y_1 given Y_2. Recall the missing data problem as an example:
  - If I knew Y_{mis} I could estimate β and if I knew β I could impute Y_{mis}. Given Y1 , I could estimate beta.
- If only I could get started there'd be no problem because P(A) x P(B|A) = P(A and B).
- The MCMC solution: Start with a guess.

The MCMC hope:

- Eventually the initial choice won't matter [burnin time]
- If you pick random observations far enough from each other, they will be close to independent: [thinning]

A fundamental principle:

- Under some conditions, if you know all the conditional distributions of each variable given the others and *there is* a joint distribution that is consistent with these conditionals, then that joint distribution is unique, i.e. if there is one, there is only one.

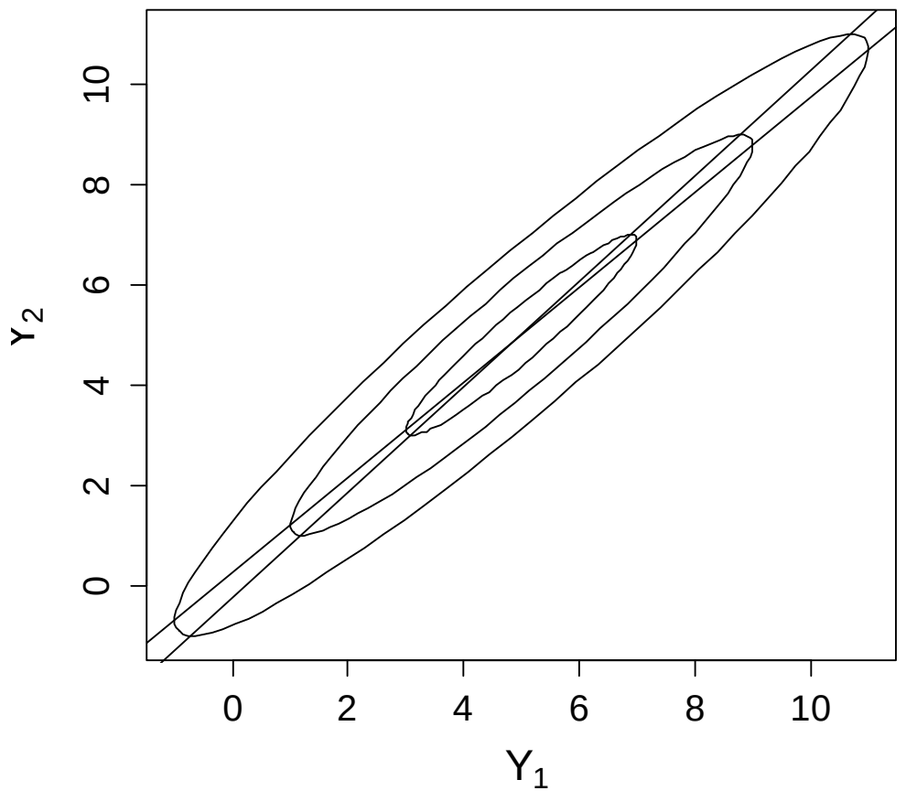
The craft of MCMC:

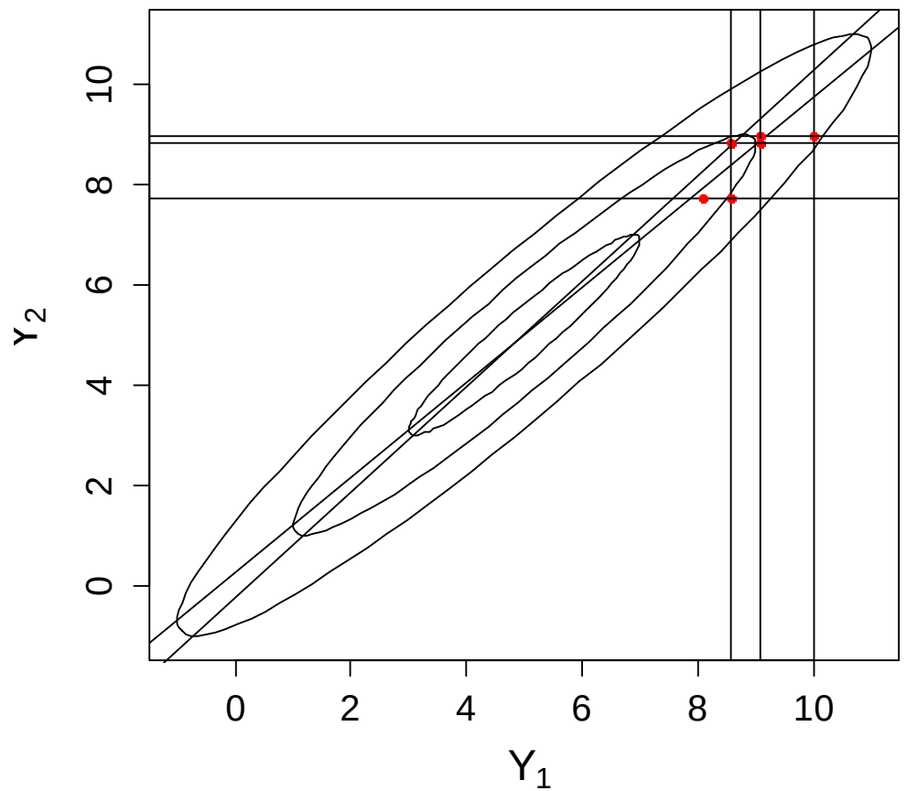
a) **Is it working?**

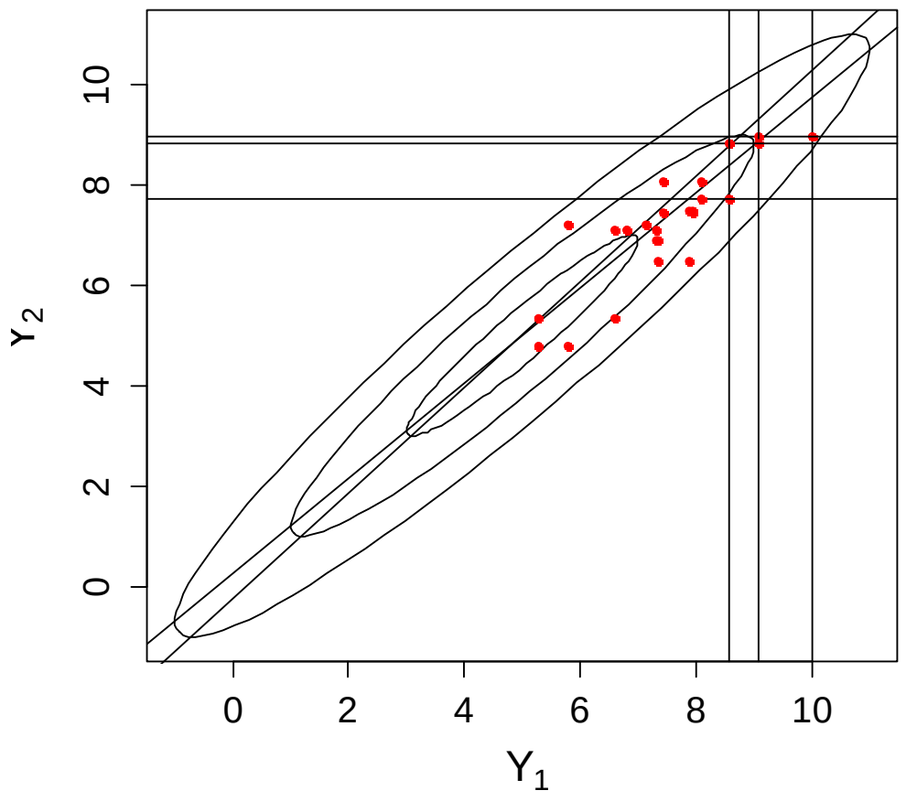
b) **What's the right burnin?** How long do I have to wait?

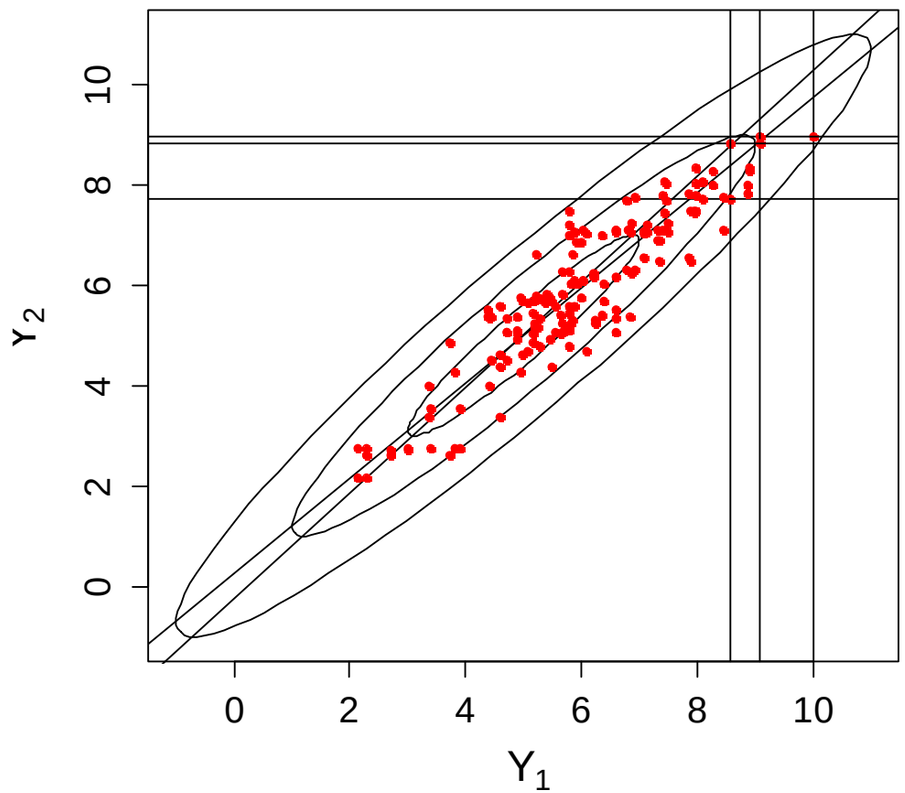
c) **What's the right thinning?** How many do I skip?

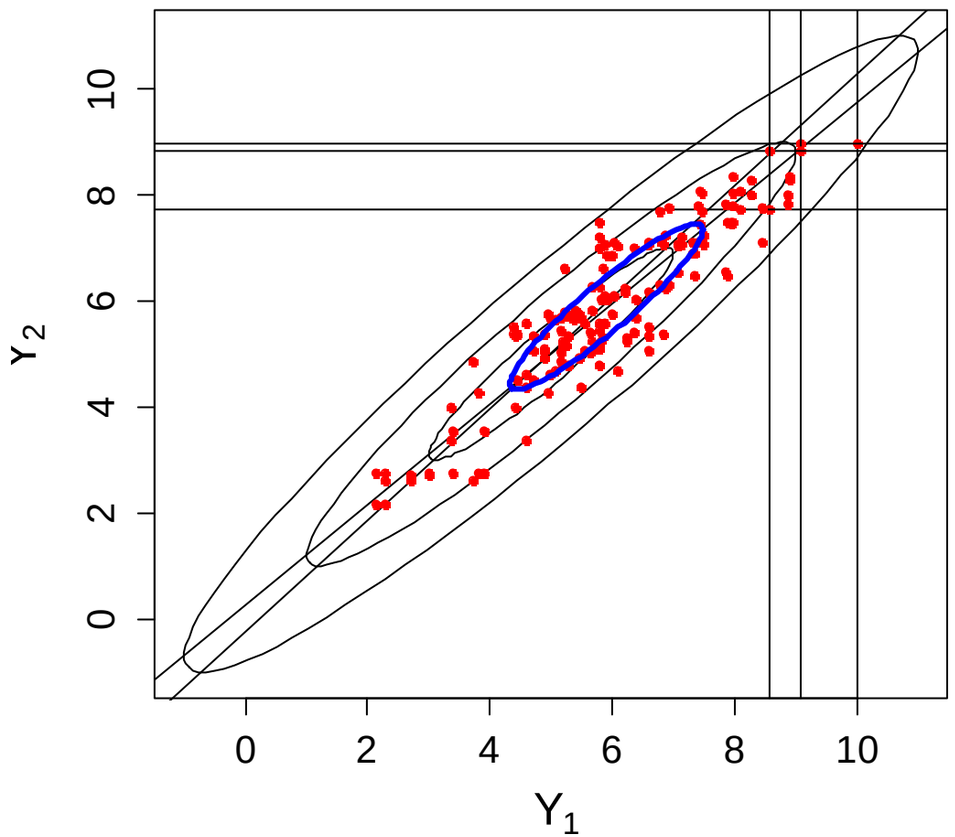
Will depend: mainly on the dependence of Y1 on Y2. If independent, the conditional = marginal and we really knew the marginal all along. We can take burnin = 1, thinning = 1/1.


Y2
0
2
4
6
8
10
Y1
0
2
4
6
8
10


Y2
0
2
4
6
8
10
Y1
0
2
4
6
8
10


Y2
0
2
4
6
8
10
Y1
0
2
4
6
8
10


Y2
0
2
4
6
8
10
Y1
0
2
4
6
8
10



The mean of Y_1 in the sample is 5.902

The SE of the mean is:

$$\frac{\sigma_1}{\sqrt{n}} = \frac{2}{\sqrt{83}} = 0.220$$

So the mean of the sample is

$$\frac{5.902 - 5}{0.220} = 4.1$$

SEs away from the population mean, which is much too large for such a sample.

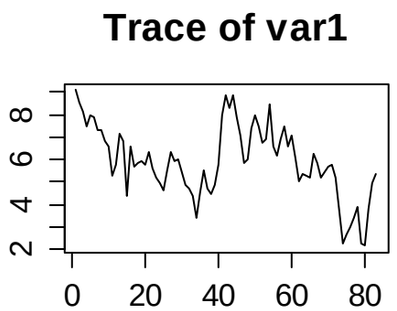
But the points in the sample are not independent. Using autocorrelation the effective sample size is:

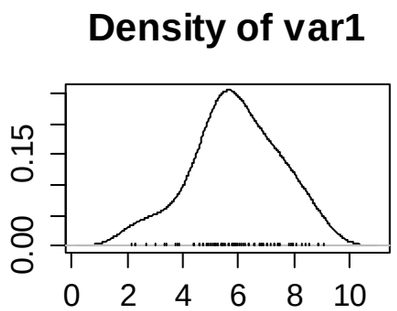
```
>   effectiveSize( Ysample)
     var1     var2
8.109846 9.606072
```

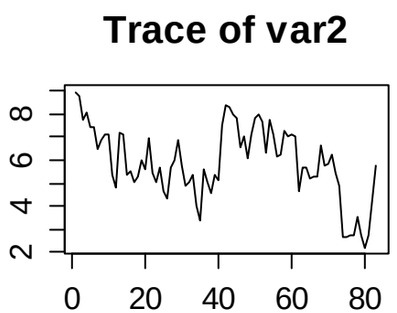
so the mean is only 1.28 SEs away.

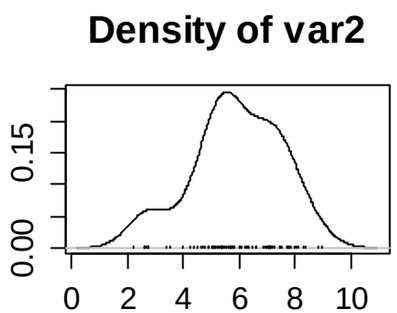
MCMC diagnostics

```
> Ysample <- mcmc(Ysample)
> plot(Ysample)
```

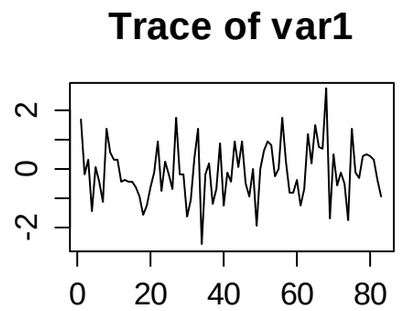


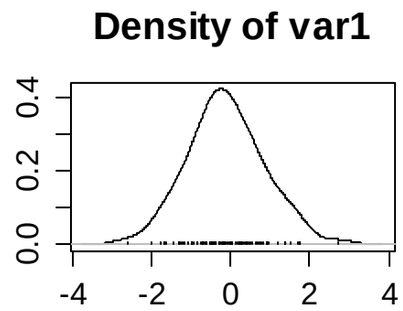


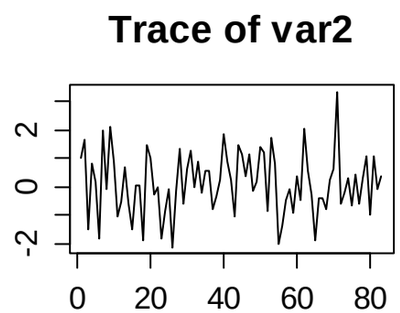


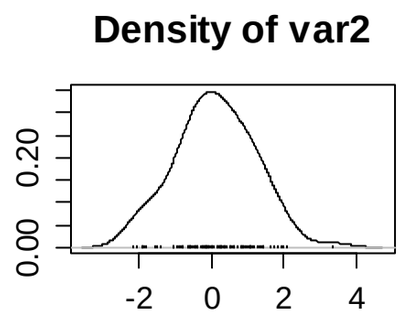



```
> Zsample <- mcmc( matrix( rnorm(2*83),
ncol = 2))
> effectiveSize(Zsample)
var1 var2
  83   83
> plot(Zsample)
```









Using MCMCglmm

Distributions for response:

Base	Modifications
poisson	zipoisson, cenpoisson, zapoisson, ztpoisson, hupoisson
categorical	[binomial logistic or multinomial with factor as response variable]
ordinal	[binomial probit]
exponential	cenexponential
binomial, multinomial*J*	zibinomial [multinomial*J* with *J* columns for category counts]
gaussian	cengaussian
geometric	

Modifications:

cen	**censoring:** some values can be at floor or ceiling, can vary from case to case
zi	**zero-inflated**, e.g. 0's over and above what you would expect from a Poisson as shown by the frequencies of values >0.
za	**zero-altered:** Could be too many or too few zeros
zt	**zero-truncated:** Only observe values >0 and shape of Poisson for Y > 0 gives appropriate probabilities
hu	**hurdle:** binomial to determine 0 or >0, zt if greater

Note 1: No negative binomial: but to the extent that the negative binomial is used to have an extra parameter for overdispersion, MCMCglmm might be better when its model is faithful to dynamics of process.

Note 2: Can handle multivariate with different distributions!!

E.g. one component gaussian, other binomial. ‘family’ distributions can be supplied as variable in data frame.

Note 3: What it won’t do: non-linear models, but maybe we can try to manage with splines

Multivariate Generalised Linear Mixed Models

Description

Markov chain Monte Carlo Sampler for Multivariate Generalised Linear Mixed Models with special emphasis on correlated random effects arising from pedigrees and phylogenies (Hadfield 2010). Please read the course notes: `vignette("CourseNotes", "MCMCglmm")` or the overview`vignette("Overview", "MCMCglmm")`

Usage

```
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=TRUE,
    saveZ=TRUE, saveXL=TRUE, slice=FALSE, ginverse=NULL)
```

Arguments

`fixed`	`formula` for the fixed effects, multiple responses are passed as a matrix using cbind
`random`	`formula` for the random effects. Multiple random terms can be passed using the +operator, and in the most general case each random term has the form `variance.function(formula):random.term`. Currently, the only `variance.functions` available are `idv`, `idh`, `us` and `cor`. `idv` fits a constant variance across all components in `formula`, and `cor` fixes the variances to 1. Both`idh` and `us` fit different variances across each component in `formula`, but `us` will also fit the covariances. The `formula` can contain both factors and numeric terms (i.e. random regression) although it should be noted that the intercept term is suppressed. The (co)variances are the (co)variances of the `random.term` effects. For simple random effects the `variance.function(formula)` can be omitted and the model syntax has the simpler form `~random1+random2+...`. There are two reserved variables: `units` which index rows of the response variable and `trait` which index columns of the response variable
`rcov`	`formula` for residual covariance structure. This has to be set up so that each data point is associated with a unique residual. For example a multi-response model might have the R-structure defined by `~us(trait):units`
`family`	optional character vector of trait distributions.

	Currently, "gaussian", "poisson","categorical", "multinomial", "ordinal", "exponential","geometric", "cengaussian", "cenpoisson", "cenexponential","zipoisson", "zapoisson", "ztpoisson", "hupoisson" and"zibinomial" are supported, where the prefix "cen" means censored, the prefix"zi" means zero inflated, the prefix "za" means zero altered, the prefix "zt"means zero truncated and the prefix "hu" means hurdle. If NULL, data needs to contain a family column.
mev	optional vector of measurement error variances for each data point for random effect meta-analysis.
data	data.frame
start	optional list having 4 possible elements: R (R-structure) G (G-structure) and liab (latent variables or liabilities) should contain the starting values where G itself is also a list with as many elements as random effect components. The fourth element QUASI should be logical: if TRUE starting latent variables are obtained heuristically, if FALSE then they are sampled from a Z-distribution
prior	optional list of prior specifications having 3 possible elements: R (R-structure) G (G-structure) and B (fixed effects). B is a list containing the expected value (mu) and a (co)variance matrix (V) representing the strength of belief: the defaults are B$mu=0 and B$V=I*1e+10, where where I is an identity matrix of appropriate dimension. The priors for the variance structures (R and G) are lists with the expected (co)variances (V) and degree of belief parameter (nu) for the

	inverse-Wishart, and also the mean vector (`alpha.mu`) and covariance matrix (`alpha.V`) for the redundant working parameters. The defaults are `nu=0`, `V=1`, `alpha.mu=0`, and `alpha.V=0`. When `alpha.V` is non-zero, parameter expanded algorithms are used.
`tune`	optional (co)variance matrix defining the proposal distribution for the latent variables. If NULL an adaptive algorithm is used which ceases to adapt once the burn-in phase has finished.
`nitt`	number of MCMC iterations
`thin`	thinning interval
`burnin`	burnin
`pr`	logical: should the posterior distribution of random effects be saved?
`pl`	logical: should the posterior distribution of latent variables be saved?
`verbose`	logical: if `TRUE` MH diagnostics are printed to screen
`DIC`	logical: if `TRUE` deviance and deviance information criterion are calculated
`singular.ok`	logical: if `FALSE` linear dependencies in the fixed effects are removed. if `TRUE` they are left in and estimated, although all information comes from the prior
`saveX`	logical: save fixed effect design matrix
`saveZ`	logical: save random effect design matrix
`saveXL`	logical: save structural parameter design matrix

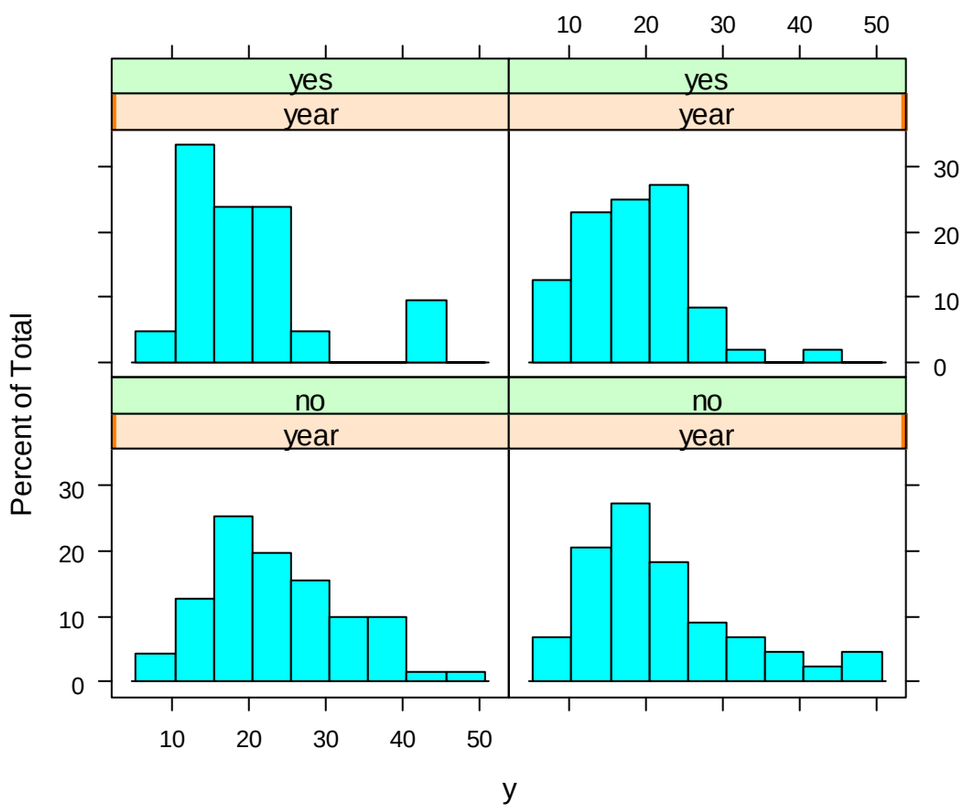
`slice`	logical: should slice sampling be used? Only applicable for binary trials with independent residuals
`ginverse`	a list of sparse inverse matrices (*solve(A)*) that are proportional to the covariance structure of the random effects. The names of the matrices should correspond to columns in `data` that are associated with the random term. All levels of the random term should appear as rownames for the matrices.

Value

`Sol`	Posterior Distribution of MME solutions, including fixed effects
`VCV`	Posterior Distribution of (co)variance matrices
`CP`	Posterior Distribution of cut-points from an ordinal model
`Liab`	Posterior Distribution of latent variables
`Fixed`	list: fixed formula and number of fixed effects
`Random`	list: random formula, dimensions of each covariance matrix, number of levels per covariance matrix, and term in random formula to which each covariance belongs
`Residual`	list: residual formula, dimensions of each covariance matrix, number of levels per covariance matrix, and term in residual formula to which each covariance belongs
`Deviance`	deviance -2*log(p(y|...))
`DIC`	deviance information criterion
`X`	sparse fixed effect design matrix

`Z`	sparse random effect design matrix
`XL`	sparse structural parameter design matrix
`error.term`	residual term for each datum
`family`	distribution of each datum

Non-mixed example: Overdispersed Poisson with a ‘real’ model




```
> library(MCMCglmm)
> ?Traffic
> head(Traffic)
  year day limit  y
1 1961   1    no  9
2 1961   2    no 11
3 1961   3    no  9
4 1961   4    no 20
5 1961   5    no 31
6 1961   6    no 26
> xqplot(Traffic)
> tab( Traffic, ~ year + limit)
        limit
year      no yes Total
  1961    71  21    92
  1962    44  48    92
  Total 115  69   184
> histogram( ~ y|
+     paste(year)*paste('limit =',limit),
+     Traffic)
```

Dataset:

Number of accidents per day in Sweden according to

- Year
- Limit: whether a speed limit was enforced on that day
- Day of the year (only about 80 days per year)

It is natural to model y = number of road accidents in a day as a Poisson random variable. The Poisson would be the correct distribution of the number of accidents if

1) On a given day, everyone has the same probability of an accident
2) Accidents are independent.
3) There is no unexplained heterogeneity: All days that are predicted to have the same number of expected accidents do, in fact, have the same number of expected accidents.

Any violation will tend to make you model fishy -- an 'overdispersed' Poisson.

```
> Traffic$yr <- factor(Traffic$year)
> fit <- glm( y ~ yr + limit + day, Traffic,
+   family = 'poisson')
> summary(fit)

Call:
```

```
glm(formula = y ~ yr + limit + day, family = "poisson",
      data = Traffic)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.0467406  0.0372985  81.685  < 2e-16 ***
yr1962      -0.0605503  0.0334364  -1.811   0.0702 .
limityes    -0.1749337  0.0355784  -4.917 8.79e-07 ***
day          0.0024164  0.0005964   4.052 5.09e-05 ***

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 625.25  on 183  degrees of freedom
Residual deviance: 569.25  on 180  degrees of freedom
AIC: 1467.2
```

Fitting an overdispersed Poisson:

```
> fit.q <- glm( y ~ yr + limit + day, Traffic,
+   family = 'quasipoisson')

> summary(fit.q)

Call:
glm(formula = y ~ yr + limit + day, family = "quasipoisson",
    data = Traffic)
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.046741   0.067843  44.909  < 2e-16 ***
yr1962      -0.060550   0.060818  -0.996  0.32078
```

```
limityes     -0.174934   0.064714  -2.703  0.00753 **
day           0.002416   0.001085   2.227  0.02716 *
```

```
(Dispersion parameter for quasipoisson family taken to be
3.308492)

    Null deviance: 625.25  on 183  degrees of freedom
Residual deviance: 569.25  on 180  degrees of freedom
AIC: NA
```

Using MCMCglmm

$$y \sim Poisson(\mu) \quad \mu = \exp(\eta) \quad \eta = X\beta + \varepsilon$$

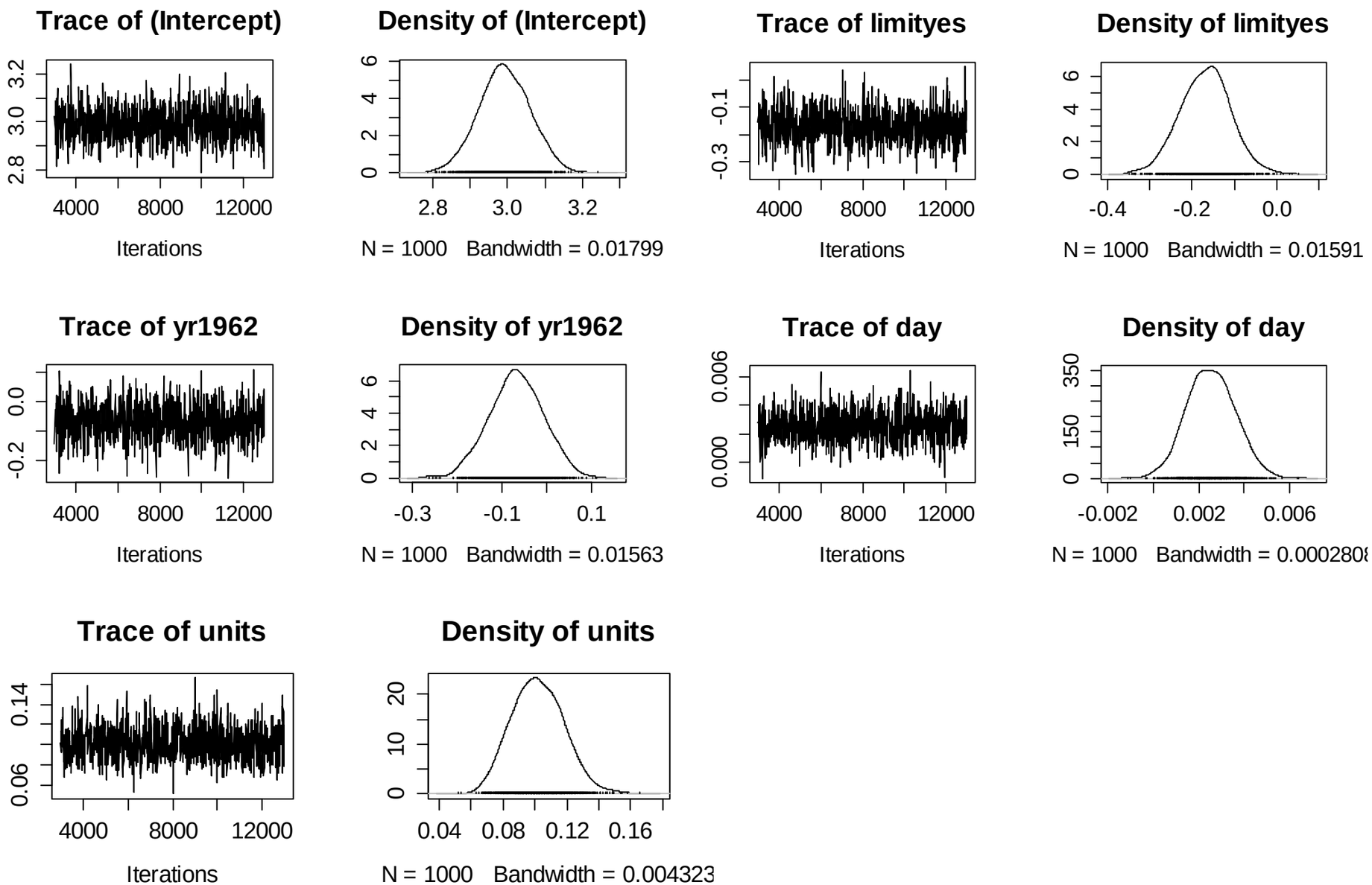
$$\varepsilon \sim N(0, \sigma^2 I)$$

Epsilon is NOT in the glm “poisson” model. Nor in the glm “quasipoisson” model.
It allows for overdispersion due to unmodeled heterogeneity. It fits a Poisson model without assuming no overdispersion but fitting a real model, in contrast with the use of estimating equations with quasipoisson.

```
> fitmc <- MCMCglmm( y ~ yr + limit + day,
+                    data = Traffic,
+                    family = 'poisson')

                     MCMC iteration = 0

  Acceptance ratio for latent scores = 0.000239

                     MCMC iteration = 1000
                         .
                         .
  Acceptance ratio for latent scores = 0.389538

                     MCMC iteration = 13000

  Acceptance ratio for latent scores = 0.388163
```

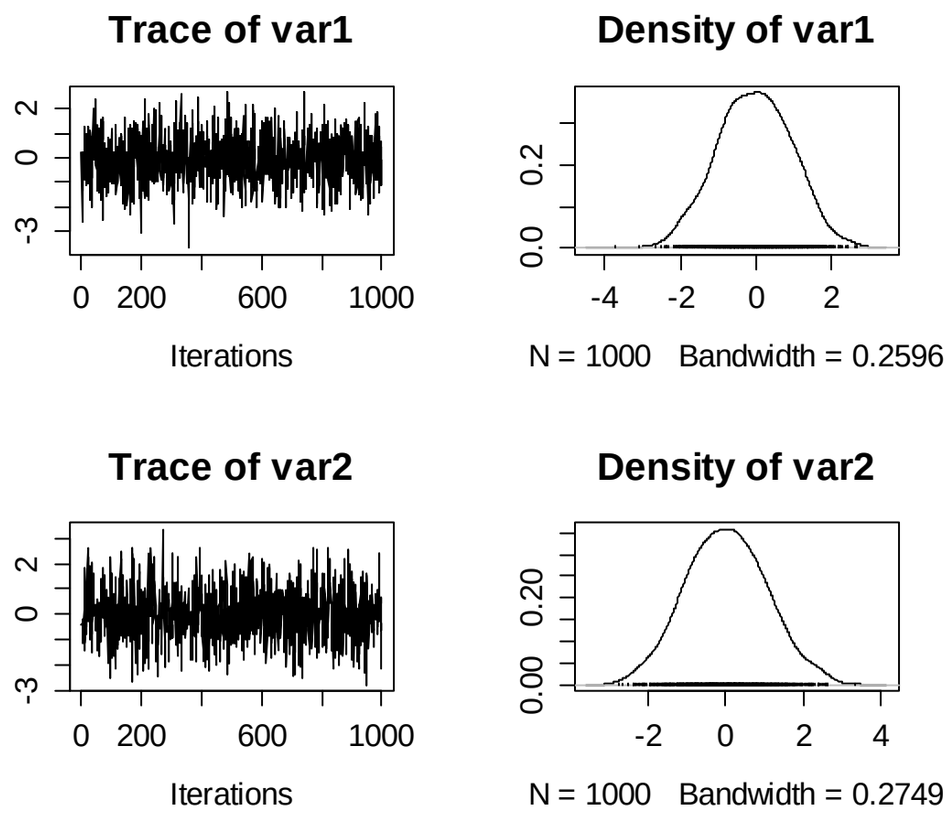
```
>   summary(fitmc)  # much more similar to quasipoisson than to poisson

 Iterations = 3001:12991
 Thinning interval  = 10
 Sample size  = 1000

 DIC: 1197.334

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units    0.1008   0.0704   0.1359    816.6

 Location effects: y ~ yr + limit + day

             post.mean   l-95% CI   u-95% CI eff.samp  pMCMC
(Intercept)  2.9923658  2.8533073  3.1146312   1000.0 <0.001 ***
yr1962      -0.0677055 -0.1909837  0.0391579   1000.0  0.252
limityes    -0.1720560 -0.2787613 -0.0400451   1000.0  0.004 **
day          0.0025657  0.0003546  0.0046178    880.5  0.030 *
```

```
>   plot(fitmc, auto.layout = FALSE)
```



Eyeball training:

```
>   Z <- matrix(rnorm(2000),ncol=2)
>   head(Z)
            [,1]       [,2]
[1,]  0.2087386 -0.3803337
[2,] -2.6537110 -0.3144766
[3,] -1.0373284 -0.2916398
[4,]  0.2288955 -1.1388010
[5,] -1.3748541 -1.1512625
[6,] -0.7583837 -0.2082907
>   plot( mcmc(Z))
```



Increasing the number of iterations to raise effective sample > 1000:

```
>   fitmc.u <- MCMCglmm( y ~ yr + limit + day,
+                        data = Traffic,
+                        family = 'poisson',
+                        nitt = 24000)

                       MCMC iteration = 0

  Acceptance ratio for latent scores = 0.000255
                            .
                            .
                            .
                       MCMC iteration = 24000

  Acceptance ratio for latent scores = 0.378212
>   summary(fitmc.u)

 Iterations = 3001:23991
 Thinning interval  = 10
 Sample size  = 2100

 DIC: 1195.948

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units    0.1003  0.07189   0.1314     1511
```

```
 Location effects: y ~ yr + limit + day

             post.mean   l-95% CI   u-95% CI eff.samp  pMCMC
(Intercept)  2.9901543  2.8535135  3.1127372     1888 <5e-04 ***
yr1962      -0.0655085 -0.1796330  0.0537198     1934 0.2724
limityes    -0.1695618 -0.2992701 -0.0470397     1832 0.0114 *
day          0.0026028  0.0003648  0.0046528     1882 0.0133 *
```

MCMCglmm with a mixed model

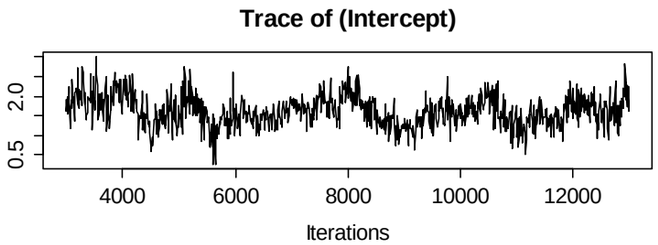
```
>   head(ds)
  id ha time dos hatype female age airq medication treat
1  1  1  -11 753   Aura      1  30    9 Continuing FALSE
2  1  1  -10 754   Aura      1  30    7 Continuing FALSE
3  1  1   -9 755   Aura      1  30   10 Continuing FALSE
4  1  1   -8 756   Aura      1  30   13 Continuing FALSE
5  1  1   -7 757   Aura      1  30   18 Continuing FALSE
6  1  1   -6 758   Aura      1  30   19 Continuing FALSE
>   ds $ treat <- 1*ds$treat
>   ds $ time.eff <- with(ds, exp(-time/13)*treat)
>   prior <- list( R = list(V=.05,nu=0,fix=1),
+                  G = list(G1=list(V=diag(3), nu = .02)))
>   ds $ id <- factor( ds $ id )
>   ds $ treat <- 1*ds$treat
>   ds $ time.eff <- with(ds, exp(-time/13)*treat)
>
```

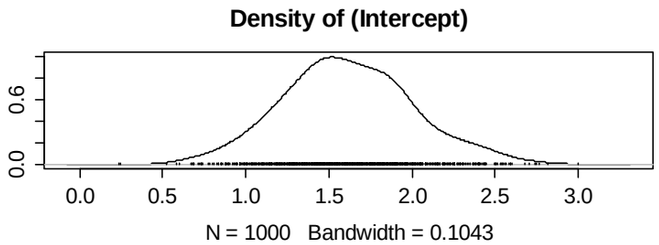
```
>   prior <- list( R = list(V=.05,nu=0,fix=1),
+                  G = list(G1=list(V=diag(3), nu = .02)))
>
>   ds $ id <- factor( ds $ id )
>
>   fit4mc<- MCMCglmm ( ha ~ (treat + I( exp( - time / 13) * treat)) * medication ,
+                    data = ds,
+                    family = "categorical",
+                    random = ~ us( 1 + treat + time.eff):id,
+                    prior = prior)

                      MCMC iteration = 0

  Acceptance ratio for latent scores = 0.000400

                      MCMC iteration = 1000

  Acceptance ratio for latent scores = 0.428833

                     .
                     .
                     .
                      MCMC iteration = 13000

  Acceptance ratio for latent scores = 0.457138
```

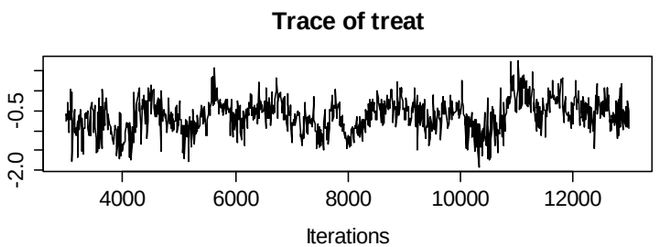
```
> summary(fit4mc)

 Iterations = 3001:12991
 Thinning interval  = 10
 Sample size  = 1000
 DIC: 4155.28
 G-structure:  ~us(1 + treat + time.eff):id

                            post.mean l-95% CI u-95% CI eff.samp
(Intercept):(Intercept).id   1.64437  0.79660  2.53289   31.365
treat:(Intercept).id         0.08521 -0.84724  0.83576    8.879
time.eff:(Intercept).id      0.18009 -0.57144  0.95664   14.401
(Intercept):treat.id         0.08521 -0.84724  0.83576    8.879
treat:treat.id               1.78350  0.56580  3.25219   11.060
time.eff:treat.id           -1.56453 -2.74539 -0.06871    8.787
(Intercept):time.eff.id      0.18009 -0.57144  0.95664   14.401
treat:time.eff.id           -1.56453 -2.74539 -0.06871    8.787
time.eff:time.eff.id         2.25575  0.03524  5.30354    3.345

 R-structure:  ~units

      post.mean l-95% CI u-95% CI eff.samp
units      0.05     0.05     0.05        0
```

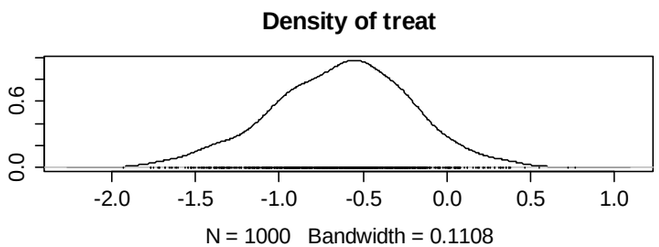
```
 Location effects: ha ~ (treat + I(exp(-time/13) * treat)) * medication

                                                post.mean l-95% CI u-95% CI eff.samp  pMCMC
(Intercept)                                       1.61481  0.87917  2.44988    38.54 <0.001 ***
treat                                            -0.63092 -1.52981  0.08006    45.71  0.130
I(exp(-time/13) * treat)                          2.80017  1.61635  3.73388    15.80 <0.001 ***
medicationContinuing                             -0.80660 -1.74130  0.12437    34.43  0.094 .
medicationNone                                   -1.19420 -2.28772 -0.22304    79.32  0.016 *
treat:medicationContinuing                        0.35670 -0.60453  1.36830    39.08  0.476
treat:medicationNone                             -0.95212 -2.05963  0.14111    66.04  0.102
I(exp(-time/13) * treat):medicationContinuing    -1.43442 -2.67162  0.12373     7.48  0.090 .
I(exp(-time/13) * treat):medicationNone          -1.14386 -2.59092  0.25944    25.79  0.120

>   wald(fit4mc, 'medication')
           numDF denDF F.value p.value
medication     6   Inf 5.48184   1e-05

Coefficients                                      Estimate Std.Error  DF   t-value p-value
  medicationContinuing                           -0.806599  0.485507 Inf -1.661353 0.09664
  medicationNone                                 -1.194200  0.530661 Inf -2.250399 0.02442
  treat:medicationContinuing                      0.356696  0.505269 Inf  0.705952 0.48022
  treat:medicationNone                           -0.952119  0.582397 Inf -1.634828 0.10209
  I(exp(-time/13) * treat):medicationContinuing -1.434419  0.743038 Inf -1.930479 0.05355
  I(exp(-time/13) * treat):medicationNone       -1.143860  0.735718 Inf -1.554754 0.12000

Coefficients                                     Lower 0.95 Upper 0.95
  medicationContinuing                            -1.758176   0.144978
  medicationNone                                  -2.234277  -0.154123
  treat:medicationContinuing                      -0.633613   1.347005
  treat:medicationNone                            -2.093596   0.189358
  I(exp(-time/13) * treat):medicationContinuing   -2.890747   0.021908
  I(exp(-time/13) * treat):medicationNone         -2.585839   0.298120
```

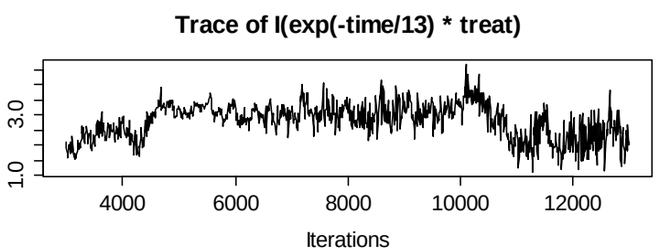
```
#  Note: very small effective sample sizes
> plot(fitmc)
```

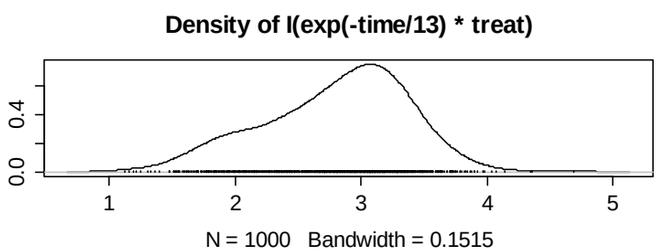


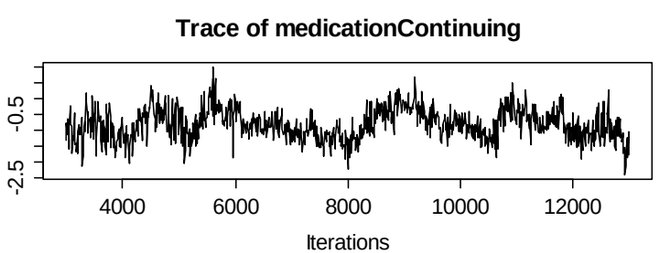


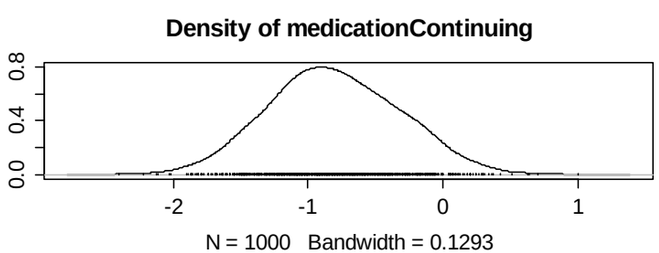


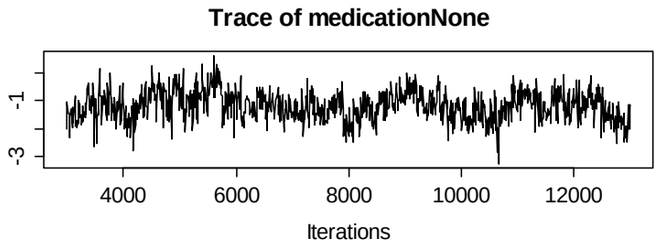


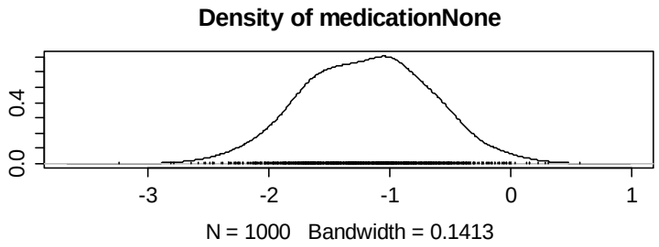


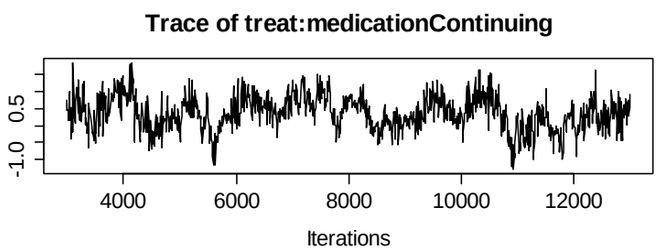


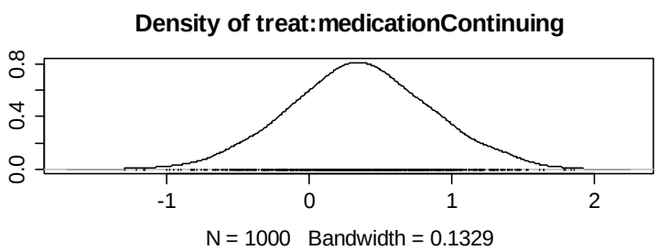


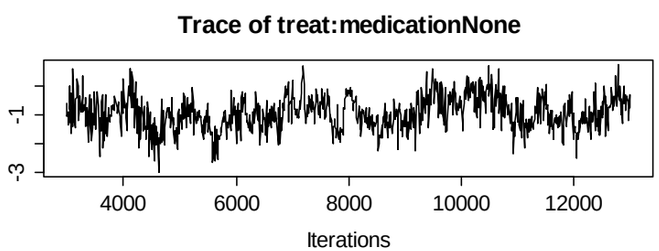


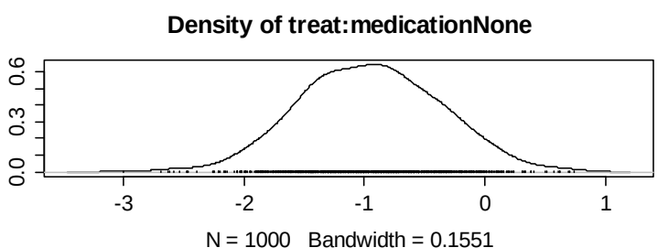

Trace of medicationNone
-3
-1
4000
6000
8000
10000
12000
Iterations

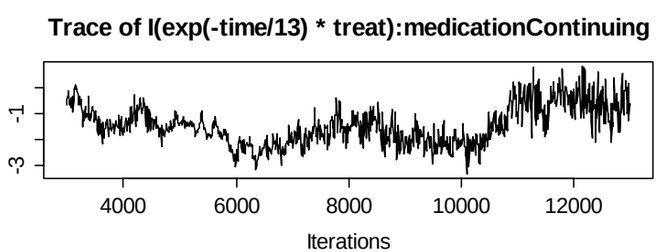

Density of medicationNone
0.0
0.4
-3
-2
-1
0
1
N = 1000 Bandwidth = 0.1413

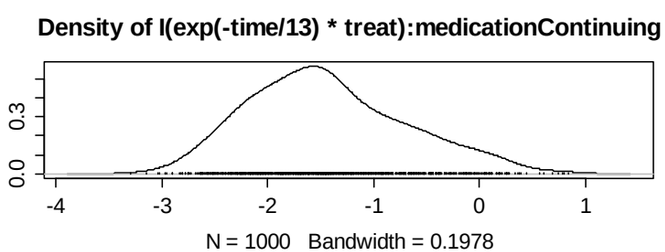

Trace of treat:medicationContinuing
-1.0
0.5
4000
6000
8000
10000
12000
Iterations

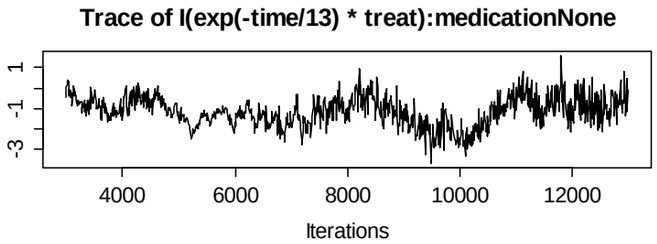

Density of treat:medicationContinuing
0.0
0.4
0.8
-1
0
1
2
N = 1000 Bandwidth = 0.1329

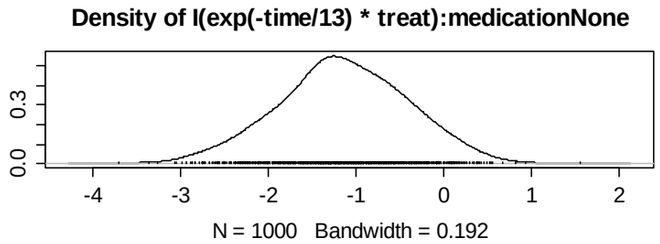

Trace of treat:medicationNone
-3
-1
4000
6000
8000
10000
12000
Iterations

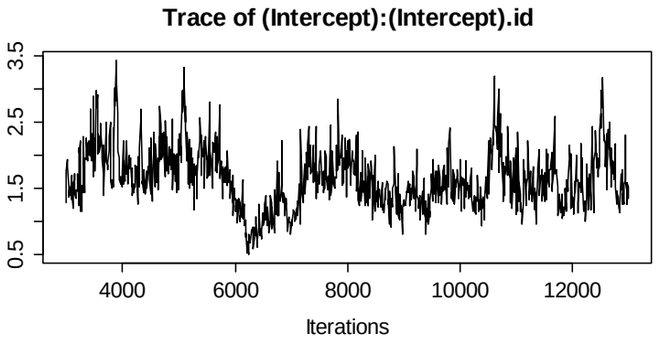

Density of treat:medicationNone
0.0
0.3
0.6
-3
-2
-1
0
1
N = 1000 Bandwidth = 0.1551

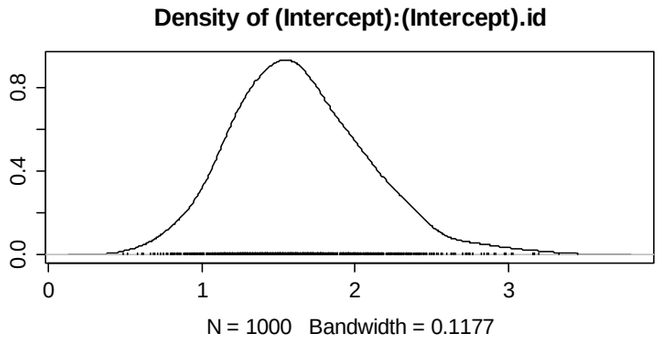

Trace of I(exp(-time/13) * treat):medicationContinuing
-3
-1
4000
6000
8000
10000
12000
Iterations

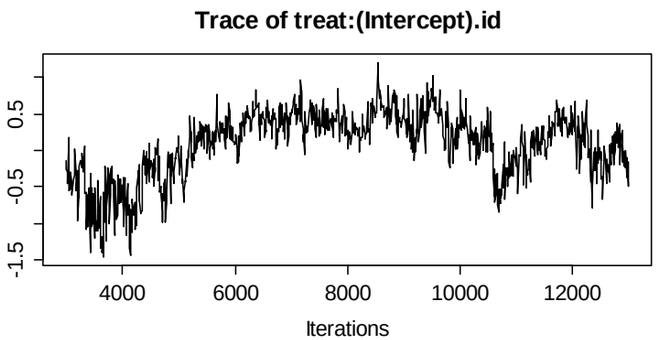

Density of I(exp(-time/13) * treat):medicationContinuing
0.0
0.3
-4
-3
-2
-1
0
1
N = 1000 Bandwidth = 0.1978

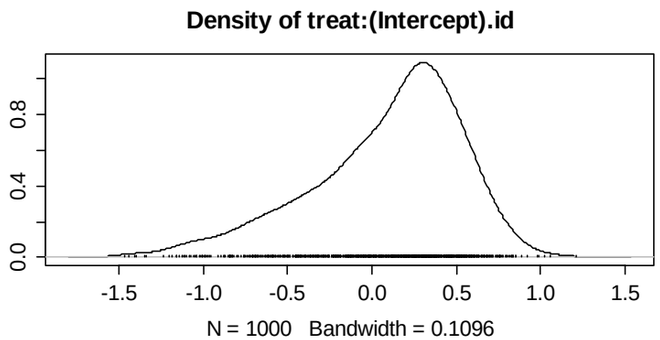

Trace of I(exp(-time/13) * treat):medicationNone
-3
-1
1
4000
6000
8000
10000
12000
Iterations

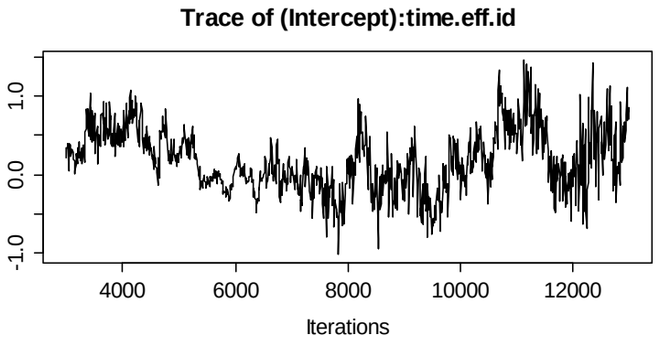

Density of I(exp(-time/13) * treat):medicationNone
0.0
0.3
-4
-3
-2
-1
0
1
2
N = 1000 Bandwidth = 0.192

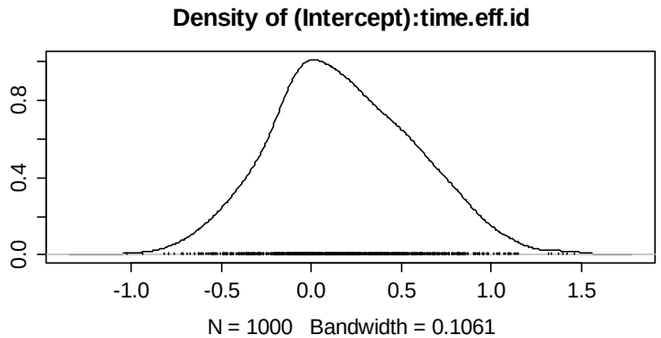

Trace of (Intercept):(Intercept).id
0.5
1.5
2.5
3.5
4000
6000
8000
10000
12000
Iterations

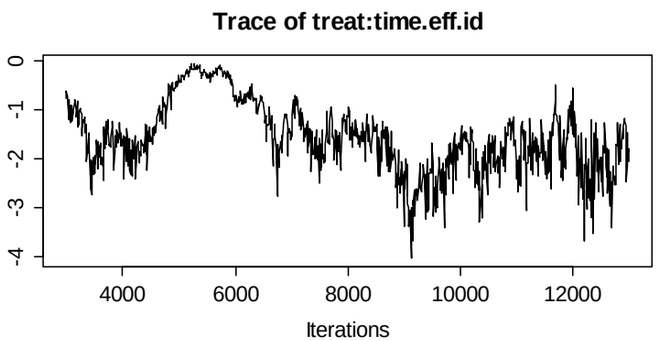

Density of (Intercept):(Intercept).id
0.0
0.4
0.8
0
1
2
3
N = 1000 Bandwidth = 0.1177

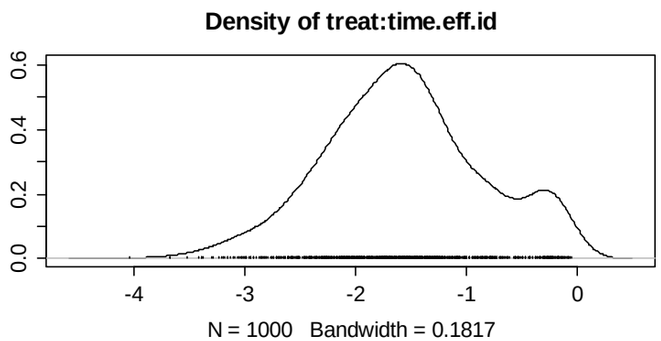

Trace of treat:(Intercept).id
-1.5
-0.5
0.5
4000
6000
8000
10000
12000
Iterations

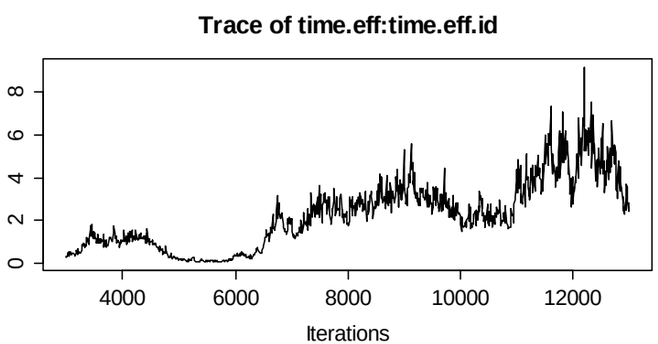

Density of treat:(Intercept).id
0.0
0.4
0.8
-1.5
-1.0
-0.5
0.0
0.5
1.0
1.5
N = 1000 Bandwidth = 0.1096

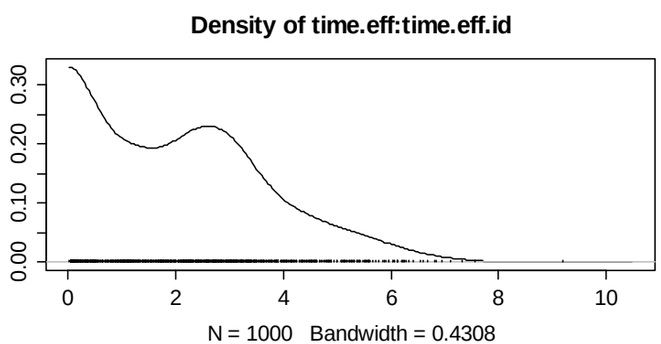

Trace of (Intercept):time.eff.id
1.0
0.0
-1.0
4000
6000
8000
10000
12000
Iterations

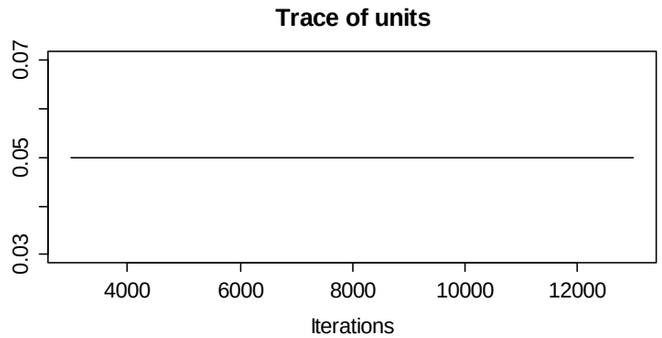

Density of (Intercept):time.eff.id
0.8
0.4
0.0
-1.0
-0.5
0.0
0.5
1.0
1.5
N = 1000 Bandwidth = 0.1061

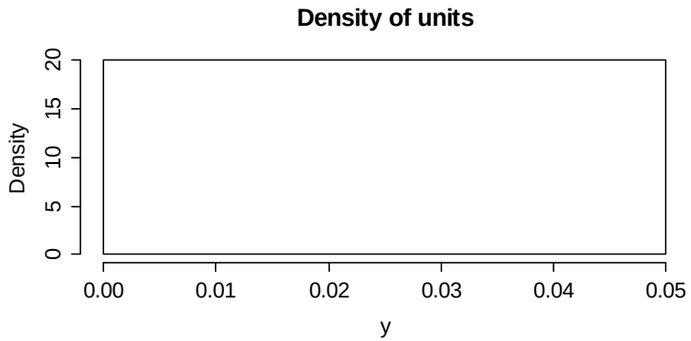

Trace of treat:time.eff.id
0
-1
-2
-3
-4
4000
6000
8000
10000
12000
Iterations


Density of treat:time.eff.id
0.6
0.4
0.2
0.0
-4
-3
-2
-1
0
N = 1000 Bandwidth = 0.1817


Trace of time.eff:time.eff.id
8
6
4
2
0
4000
6000
8000
10000
12000
Iterations


Density of time.eff:time.eff.id
0.30
0.20
0.10
0.00
0
2
4
6
8
10
N = 1000 Bandwidth = 0.4308





Note: This MCMC is far from having converged. We would like an effective sample size of at least 1,000. The last trace would be a sign that the MCMC got stuck, except that this parameter was fixed at 0.05.

Wald test of the ‘medication’ effect: not to be taken too seriously:

```
>   wald(fit4mc, 'medication')
            numDF denDF F.value p.value
medication      6   Inf 5.48184   1e-05

Coefficients                                          Estimate Std.Error  DF   t-value p-value
  medicationContinuing                               -0.806599  0.485507 Inf -1.661353 0.09664
  medicationNone                                     -1.194200  0.530661 Inf -2.250399 0.02442
  treat:medicationContinuing                          0.356696  0.505269 Inf  0.705952 0.48022
  treat:medicationNone                               -0.952119  0.582397 Inf -1.634828 0.10209
  I(exp(-time/13) * treat):medicationContinuing      -1.434419  0.743038 Inf -1.930479 0.05355
  I(exp(-time/13) * treat):medicationNone            -1.143860  0.735718 Inf -1.554754 0.12000
```

Why does R: $\sigma^2 =$ 0.05 work?

With no σ^2 if $\hat{p}$ for a points gets close to 1 or 0, the variance for that point

becomes close to 0 which makes the model stick to the point.

Keeping a minimal variance for each point prevents the model from sticking to them.

What to do next:

1) Consider centering random effects if their variance matrix approaches singularity.
2) Increase nitt, burnin and thin by a factor, perhaps 100, so
   So nitt = 130000, burnin = 30000, thin = 1000
   -- Might take all night
3) Explore the lab on GLMMs.
4) Read Jarrod Hadfields's MCMCglmm Course Notes (2012)