

Heritability of fertility in mares estimated with the MCMCgIimm package

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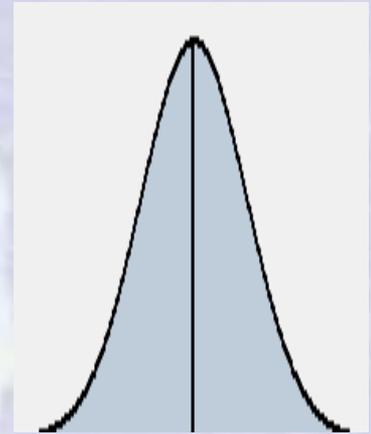
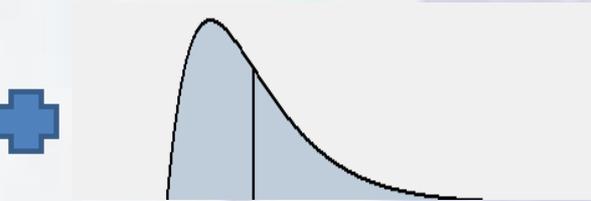
MCMCglmm package

- Author: Jarrod Hadfield
- Analysis of Generalized Linear Mixed Models with Monte Carlo method
- Includes most of the commonly applied distributions (Gaussian, Poisson, exponential, multinomial...)
- Enables analysis of multitrait models with various covariance matrices
- Creates relationship matrix based on pedigree

Bayesian approach



or



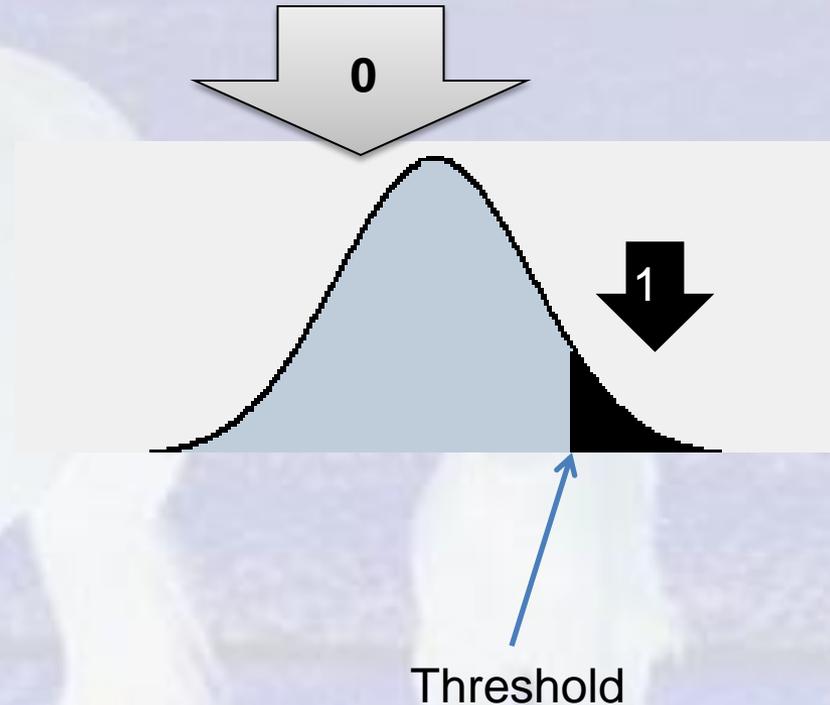
prior

data

posterior

Thershold model

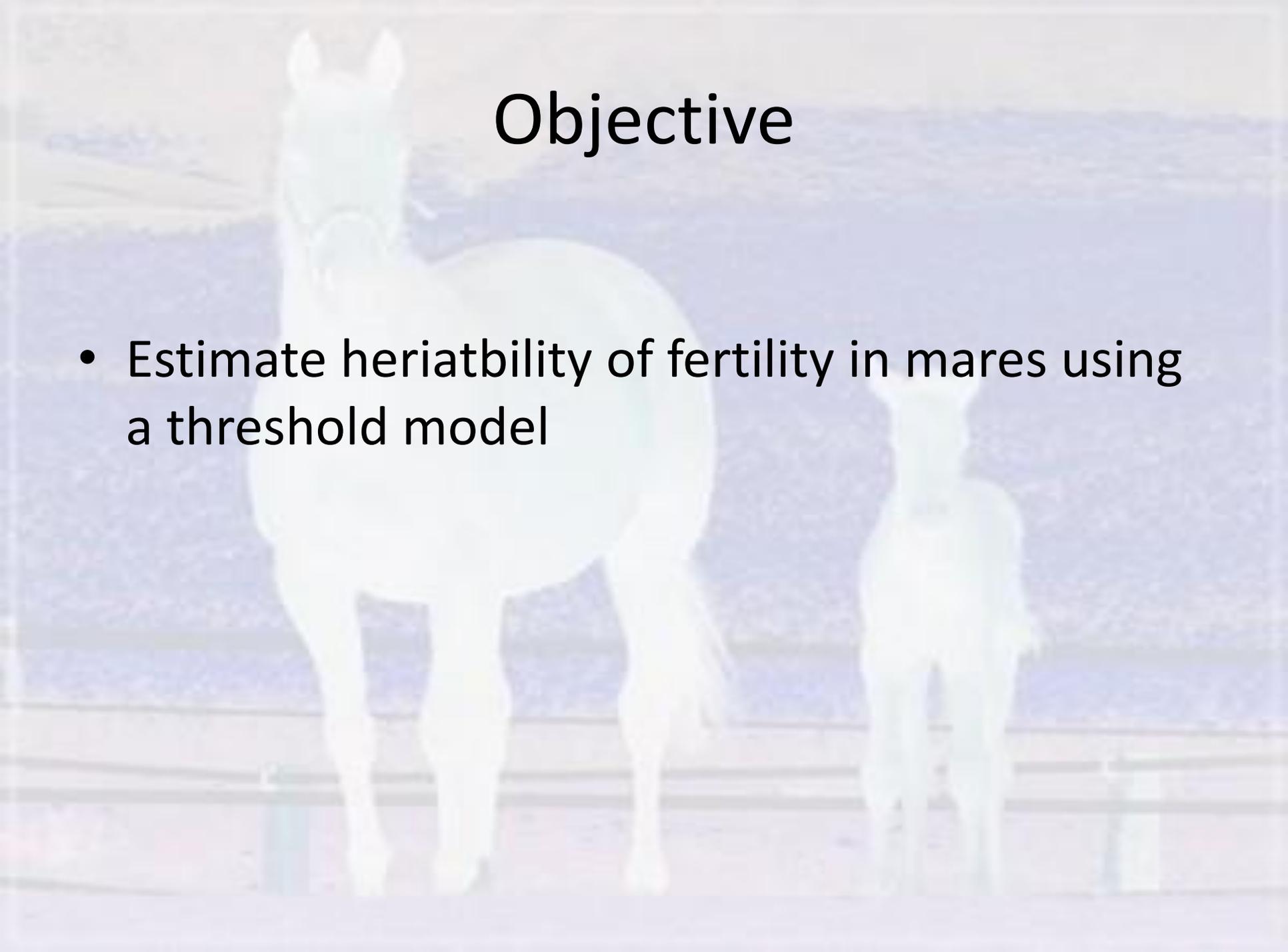
It is assumed that a trait with binary phenotypic expression is continuous on an unobserved scale called liability. If liability exceeds some threshold value the trait has a value of 1 and 0 otherwise. The liability is treated as a polygenic trait (determined by many genes with small effects).



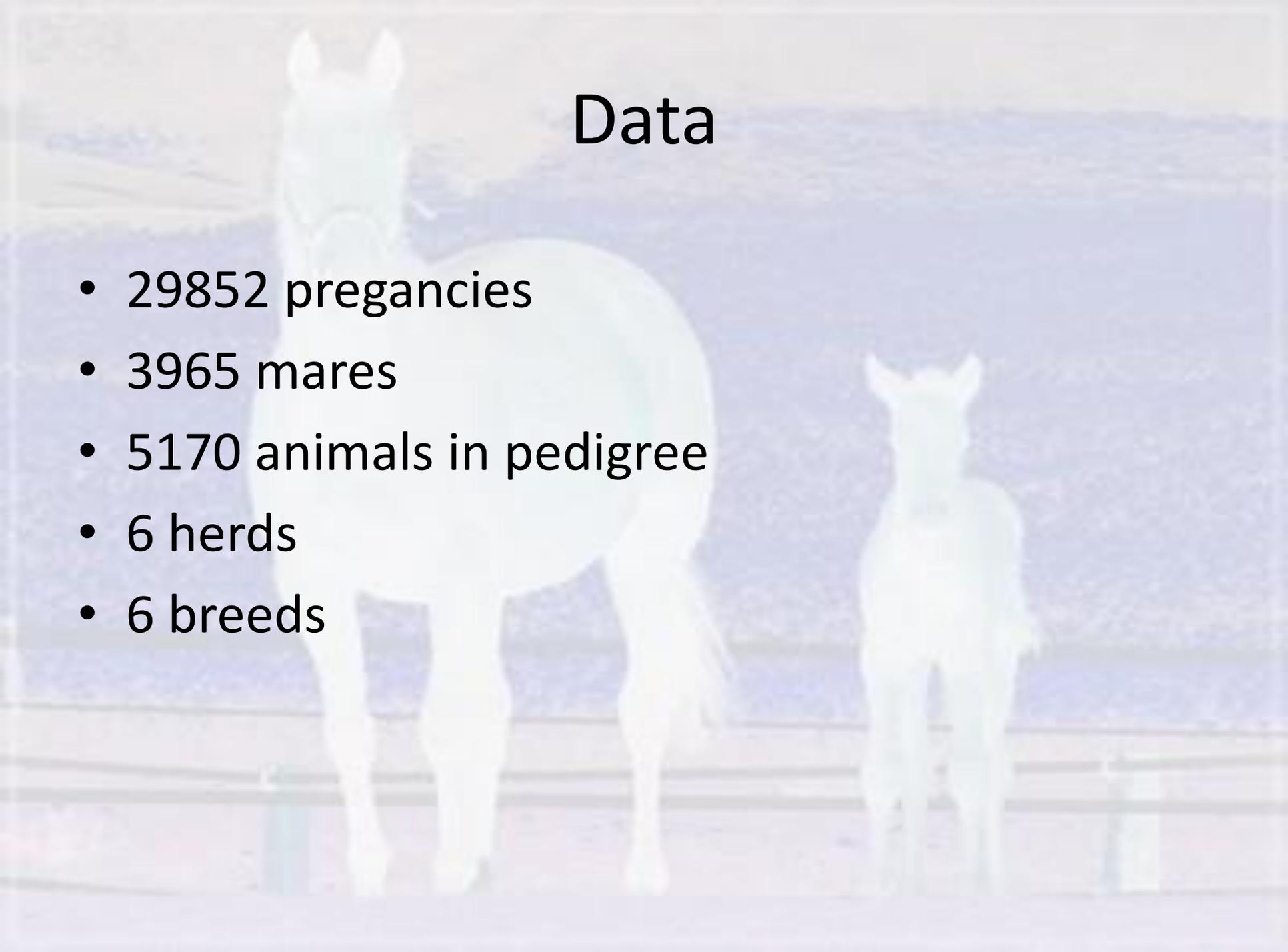
A basic parameter in animal breeding is **heritability** – proportion of genetic variance in total phenotypic variance

Objective

- Estimate heritability of fertility in mares using a threshold model



Data

A photograph of a white mare and her foal in a paddock. The mare is on the left, facing forward, and the foal is on the right, facing away from the camera. They are standing in a grassy area with a wooden fence in the foreground and a blue sky in the background.

- 29852 pregnancies
- 3965 mares
- 5170 animals in pedigree
- 6 herds
- 6 breeds

Model

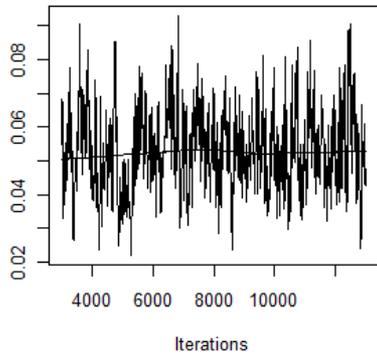
```
model1<- MCMCglmm(cbind(FER, NFER) ~ herd + breed, random =  
  ~sire, family = "multinomial2", data = datafer1, verbose = FALSE)  
prior2 = list(R = list(V = 1, n = 0), G = list(G1=list(V = 0.06,n = 1)))
```

other priors may be more appropriate

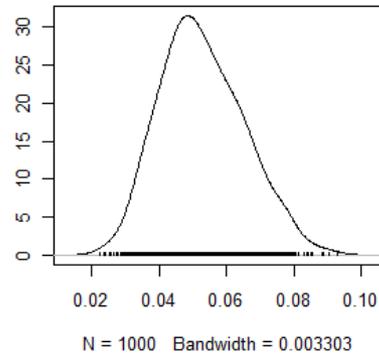
```
model2 <- MCMCglmm(cbind(FER, NFER) ~ herd + breed, random  
  = ~animal, family = "multinomial2", data = datafer1,  
  pedigree=pedhorse, prior = prior2, verbose = FALSE)  
h2AM <- model2$VCV[, 1]/(model2$VCV[, 1] +model2$VCV[, 2]+3.27)  
plot(model2$VCV)  
posterior.mode(model2$VCV)  
mean(model2$VCV[, 1])  
HPDinterval(model2$VCV, 0.95)
```

Results - sire model

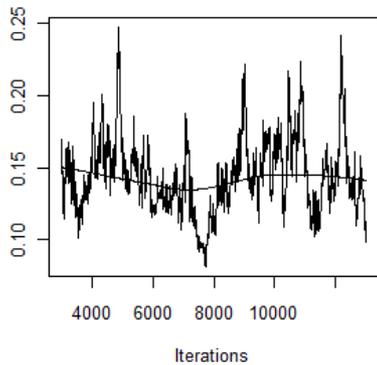
Trace of sire



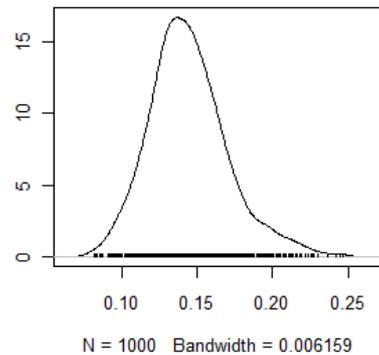
Density of sire



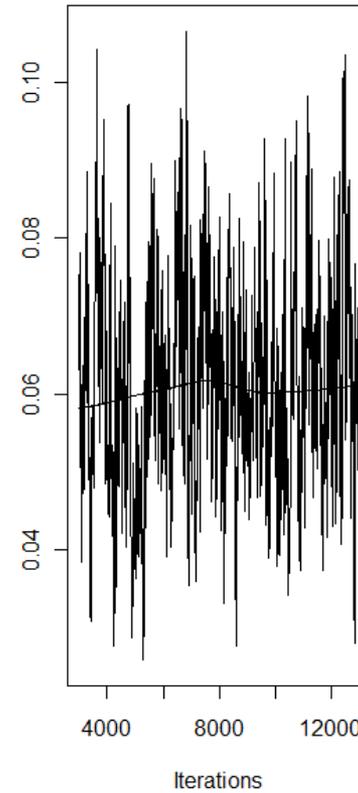
Trace of units



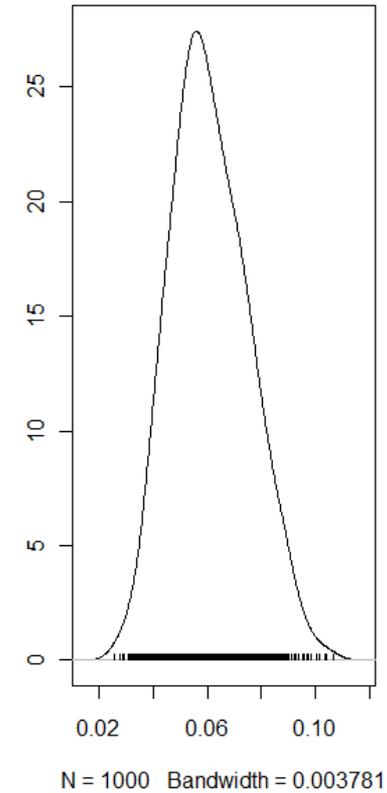
Density of units



Trace of var1



Density of var1



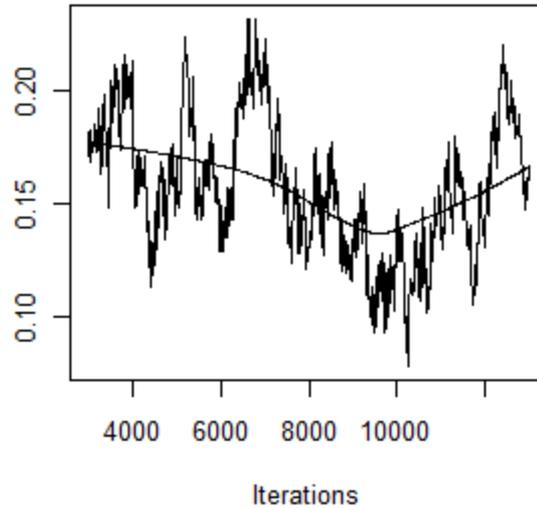
Variance components

Heritability

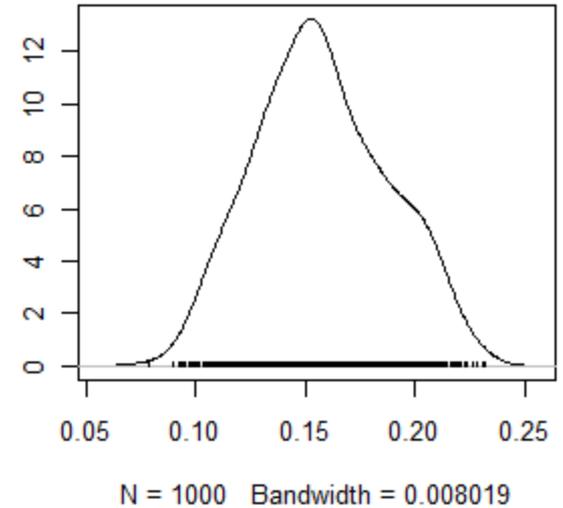
Results AM

The process should be continued until it approaches stationarity

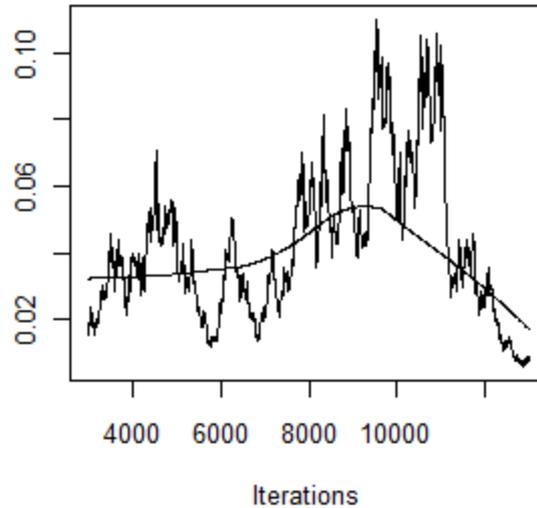
Trace of animal



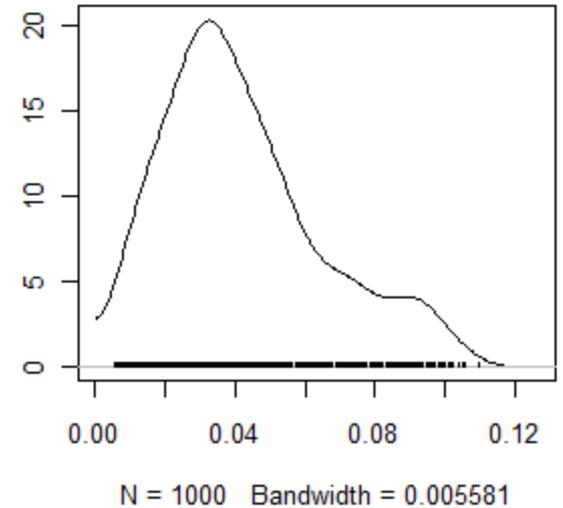
Density of animal



Trace of units



Density of units



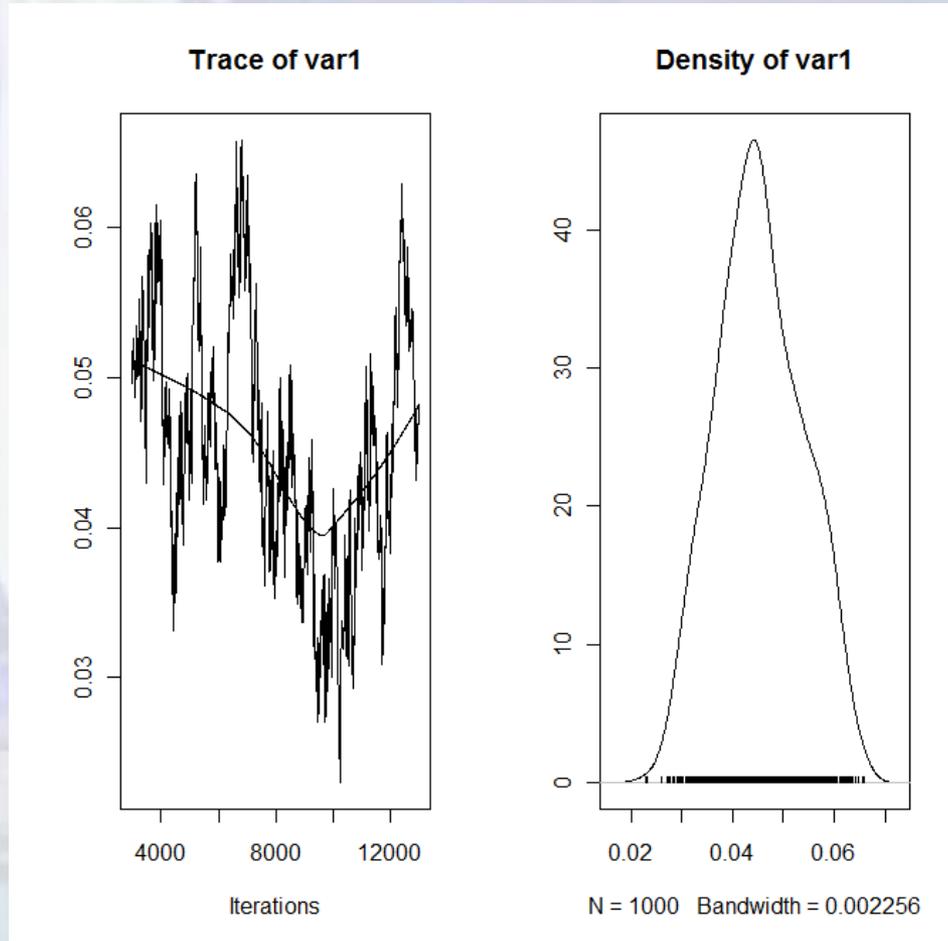
Results AM

animal	mode	median	mean
	0.1532	0.1552	0.1575

HPDinterval

animal	(0.1032, 0.2135)
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Results - heritability



HPDinterval (0.0292 0.0603)

Conclusions

- Heritability of fertility in mares with probability of 95% lies between 0.03 and 0.06
- MCMC proces converges well for sire model, for animal model more iterations would be needed
- MCMCpackage enables an analysis of wide range of Generalized Linear Mixed Models including animal model