

Flat priors

(R = 0 ; G = 0 ;
belief = 0.02)

parametrisation chains (3x)

MCMCglmm

extract

consensus

**Tree
distribution**

one random tree
per mini-chain

**Traits
data**

Model

~ Data + residuals (R) +
+ whole phylogeny (G)
+ phylogeny per clade (G)

mini chains (100x)

MCMCglmm

Priors

(R = median(posterior R)
; G = median(posterior G)
; belief = 0.05)

Burnin

(n iterations to the
median posterior *1.1)

Model results

variance-covariance matrices
for each random terms
and each random tree