# Bayesian statistics with R
# 8. Heterogeneity and multilevel models (aka mixed models)

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# Multilevel (aka mixed-effect) models

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- Random effects are statistical parameters that attempt to **explain noise caused by clusters** of the population you are trying to model.
- A multilevel model assumes that the dataset being analysed consists of **a hierarchy of different populations** whose differences relate to that hierarchy.
- Measurement that come **in clusters** or groups.
- Come up with examples of clusters or groups.

## Clusters might be:

- Classrooms within schools
- Students within classrooms
- Chapters within books
- Individuals within populations
- Populations within species
- Trajectories within individuals
- Fishes within tanks
- Frogs within ponds
- PhD applicants in doctoral schools
- Nations in continents
- Sex or age are not clusters per se (if we were to sample again, we would take the same levels, e.g. male/female and young/old)

# Why do we need multilevel models?

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- Model the clustering itself.
- Interested in variance components (environmental vs. genetic variance).
- Control for bias due to pseudoreplication (time, space, individual).

# McElreath's explanation of multilevel models

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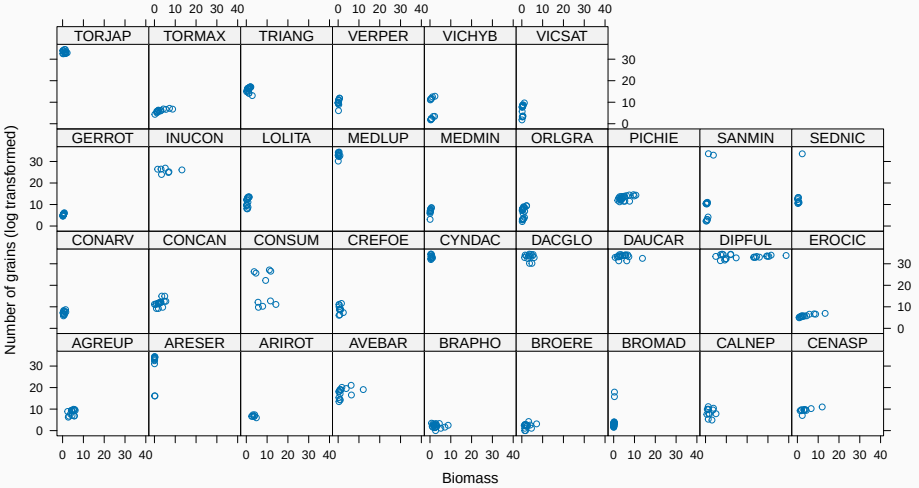
- No information passed among clusters.
- Multilevel models remember and pool information. They have memory.
- Properties of clusters come from a population.
- If previous clusters improve your guess about a new cluster, you want to use pooling.

# Plant experiment in the field at CEFE

Courtesy of Pr Eleni Kazakou

# Number of grains per species (cluster) as a function of biomass



# GLM with complete pooling

$$
\begin{aligned}
\mathrm{Y}_i &\sim \text{Distribution}(\text{mean}_i) && \text{[likelihood]} \\
\text{link}(\text{mean})_i &= \alpha + \beta\, x_i && \text{[linear model]} \\
\alpha &\sim \text{to be determined} && \text{[prior for intercept]} \\
\beta &\sim \text{to be determined} && \text{[prior for slope]}
\end{aligned}
$$

**Model with complete pooling. All clusters the same.**

# GLM with no pooling

$$
\begin{aligned}
\mathrm{Y}_i &\sim \mathrm{Distribution}(\mathrm{mean}_i) && \text{[likelihood]} \\
\mathrm{link}(\mathrm{mean})_i &= \alpha_{\mathrm{CLUSTER}[i]} + \beta\, x_i && \text{[linear model]} \\
\alpha_j &\sim \text{to be determined} && \text{[prior for intercept]} \\
\beta &\sim \text{to be determined} && \text{[prior for slope]}
\end{aligned}
$$

**Model with no pooling. All clusters unrelated (fixed effect).**

# GLMM or GLM with partial pooling

$$
\begin{aligned}
Y_i &\sim \text{Distribution}(\text{mean}_i) && \text{[likelihood]} \\
\text{link}(\text{mean})_i &= \alpha_{\text{CLUSTER}[i]} + \beta\, x_i && \text{[linear model]} \\
\alpha_j &\sim \text{Normal}(\bar{\alpha}, \sigma) && \text{[prior for varying intercepts]} \\
\bar{\alpha} &\sim \text{to be determined} && \text{[prior for population mean]} \\
\sigma &\sim \text{to be determined} && \text{[prior for standard deviation]} \\
\beta &\sim \text{to be determined} && \text{[prior for slope]}
\end{aligned}
$$

**Model with partial pooling. Clusters are somehow related (random effect).**

# Back to the plant example

# Model with complete pooling (all species are the same)

$$\text{nseeds}_i \sim \text{Normal}(\mu_i, \sigma^2) \quad \text{[likelihood]}$$

$$\mu_i = \alpha + \beta\ \text{biomass}_i \quad \text{[linear model]}$$

$$\alpha \sim \text{Normal}(0, 1000) \quad \text{[prior for intercept]}$$

$$\beta \sim \text{Normal}(0, 1000) \quad \text{[prior for slope]}$$

$$\sigma \sim \text{Uniform}(0, 100) \quad \text{[prior for standard deviation]}$$

# Read in and manipulate data

```r
# read in data
VMG <- read_csv2(here::here("slides","dat","VMG.csv")) %>%
  mutate(Sp = as_factor(Sp), Vm = as.numeric(Vm))
# nb of seeds
y <- log(VMG$NGrTotest)
# biomass
x <- VMG$Vm
x <- (x - mean(x))/sd(x)
# species name
Sp <- VMG$Sp
# species label
species <- as.numeric(Sp)
# species name
nbspecies <- length(levels(Sp))
# total nb of measurements
n <- length(y)
```

# Specify the model in Jags

```
model <-
paste("
model{
for(i in 1:n){
    y[i] ~ dnorm(mu[i], tau.y)
    mu[i] <- a + b * x[i]
    }
tau.y <- 1 / (sigma.y * sigma.y)
sigma.y ~ dunif(0,100)
a ~ dnorm(0,0.001)
b ~ dnorm(0,0.001)
}
")
writeLines(model,here::here("slides","code","completepooling.bug"))
```

# Prepare ingredients for running Jags

```
# data
allom.data <- list(y = y, n = n, x = x)

# initial values
init1 <- list(a=rnorm(1), b=rnorm(1),sigma.y=runif(1))
init2 <- list(a=rnorm(1), b=rnorm(1),sigma.y=runif(1))
inits <- list(init1,init2)

# parameters to be estimated
allom.parameters <- c("a", "b", "sigma.y")
```

# Run Jags

```
allom.1 <- jags(allom.data,
                inits,
                allom.parameters,
                n.iter = 2500,
                model.file = here::here("slides","code","completepooling.bug"),
                n.chains = 2,
                n.burn = 1000)
#> Compiling model graph
#>    Resolving undeclared variables
#>    Allocating nodes
#> Graph information:
#>    Observed stochastic nodes: 488
#>    Unobserved stochastic nodes: 3
#>    Total graph size: 1956
#>
#> Initializing model
```

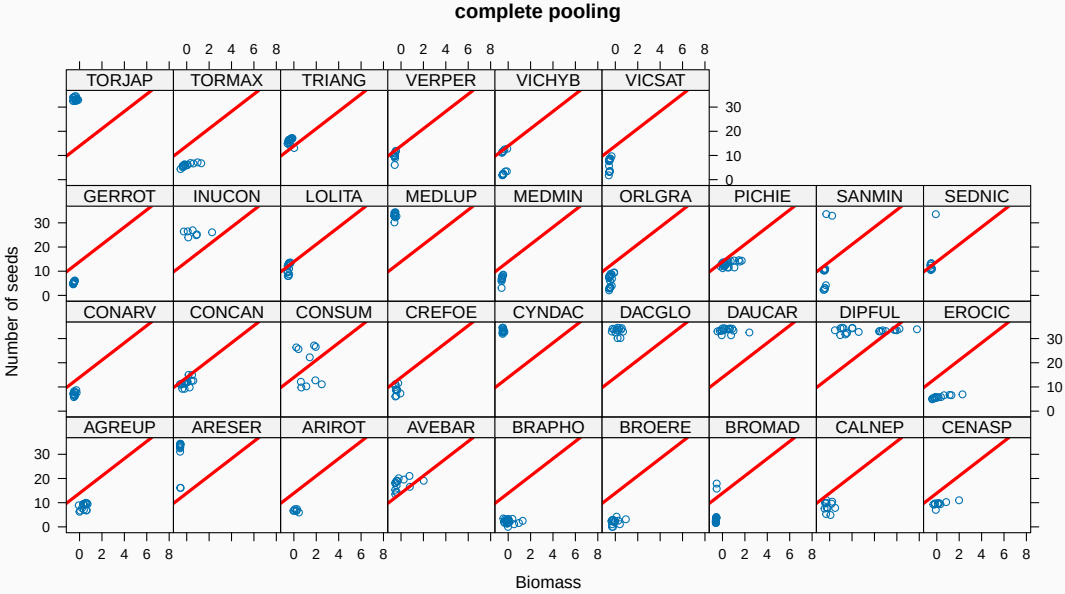
# Display results

```
allom.1
#> Inference for Bugs model at "/Users/oliviergimenez/Dropbox/OG/GITHUB/bayesian-stats-wit
#>  2 chains, each with 2500 iterations (first 1000 discarded)
#>  n.sims = 3000 iterations saved
#>           mu.vect sd.vect     2.5%      25%      50%      75%    97.5%  Rhat
#> a          13.928   0.475   12.963   13.611   13.938   14.250   14.840 1.001
#> b           3.589   0.470    2.686    3.267    3.596    3.897    4.526 1.001
#> sigma.y    10.432   0.331    9.817   10.203   10.416   10.642   11.134 1.004
#> deviance 3671.994   2.434 3669.240 3670.196 3671.342 3673.092 3678.467 1.009
#>          n.eff
#> a         3000
#> b         3000
#> sigma.y    910
#> deviance   760
#>
#> For each parameter, n.eff is a crude measure of effective sample size,
#> and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
```

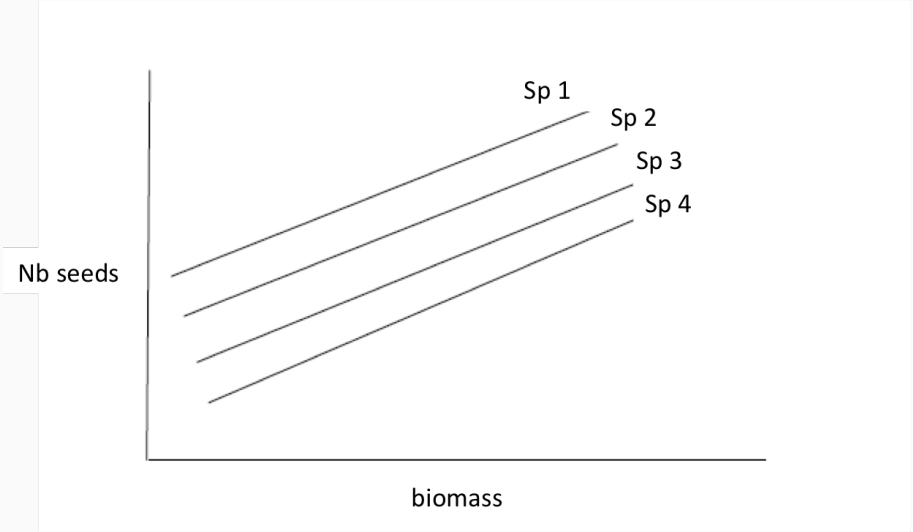
# Compare with Frequentist approach

```
freq_lm <- lm(y ~ x, data = allom.data)
freq_lm
#>
#> Call:
#> lm(formula = y ~ x, data = allom.data)
#>
#> Coefficients:
#> (Intercept)            x
#>      13.927        3.578
```

# Output


complete pooling
TORJAP
TORMAX
TRIANG
VERPER
VICHYB
VICSAT
GERROT
INUCON
LOLITA
MEDLUP
MEDMIN
ORLGRA
PICHIE
SANMIN
SEDNIC
CONARV
CONCAN
CONSUM
CREFOE
CYNDAC
DACGLO
DAUCAR
DIPFUL
EROCIC
AGREUP
ARESER
ARIROT
AVEBAR
BRAPHO
BROERE
BROMAD
CALNEP
CENASP
Number of seeds
Biomass

# Model with partial pooling (species random effect)



# Model with partial pooling (all species related in some way)

$$\text{nseeds}_i \sim \text{Normal}(\mu_i, \sigma^2) \quad \text{[likelihood]}$$

$$\mu_i = \alpha_{\text{species}[i]} + \beta\ \text{biomass}_i \quad \text{[linear model]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma_\alpha) \quad \text{[prior for varying intercepts]}$$

$$\bar{\alpha} \sim \text{Normal}(0, 1000) \quad \text{[prior for population mean]}$$

$$\sigma_\alpha \sim \text{Uniform}(0, 100) \quad \text{[prior for } \sigma_\alpha\text{]}$$

$$\beta \sim \text{Normal}(0, 1000) \quad \text{[prior for slope]}$$

$$\sigma \sim \text{Uniform}(0, 100) \quad \text{[prior for } \sigma\text{]}$$

# Implementation in Jags

```
model <- paste("
model {
  for (i in 1:n){
    y[i] ~ dnorm(mu[i], tau.y)
    mu[i] <- a[species[i]] + b * x[i]
  }
  tau.y <- 1/ (sigma.y * sigma.y)
  sigma.y ~ dunif(0, 100)
  for (j in 1:nbspecies){
    a[j] ~ dnorm(mu.a, tau.a)
  }
  mu.a ~ dnorm(0, 0.001)
  tau.a <- 1/(sigma.a * sigma.a)
  sigma.a ~ dunif(0, 100)
  b ~ dnorm (0, 0.001)
}")
writeLines(model,here::here("slides","code","varint.bug"))
```

## Prepare ingredients for running Jags

```
allom.data <- list(n = n,
                   nbspecies = nbspecies,
                   x = x,
                   y = y,
                   species = species)
init1 <- list(a = rnorm(nbspecies), b = rnorm(1), mu.a = rnorm(1),
              sigma.y = runif(1), sigma.a=runif(1))
init2 <- list(a = rnorm(nbspecies), b = rnorm(1), mu.a = rnorm(1),
              sigma.y = runif(1), sigma.a = runif(1))
inits <- list(init1,init2)
allom.parameters <- c("b", "mu.a","sigma.y", "sigma.a")
```

# Run Jags

```
allom.2 <- jags(allom.data,
                inits,
                allom.parameters,
                n.iter = 2500,
                model.file = here::here("slides","code","varint.bug"),
                n.chains = 2,
                n.burn = 1000)
#> Compiling model graph
#>    Resolving undeclared variables
#>    Allocating nodes
#> Graph information:
#>    Observed stochastic nodes: 488
#>    Unobserved stochastic nodes: 37
#>    Total graph size: 2484
#>
#> Initializing model
```

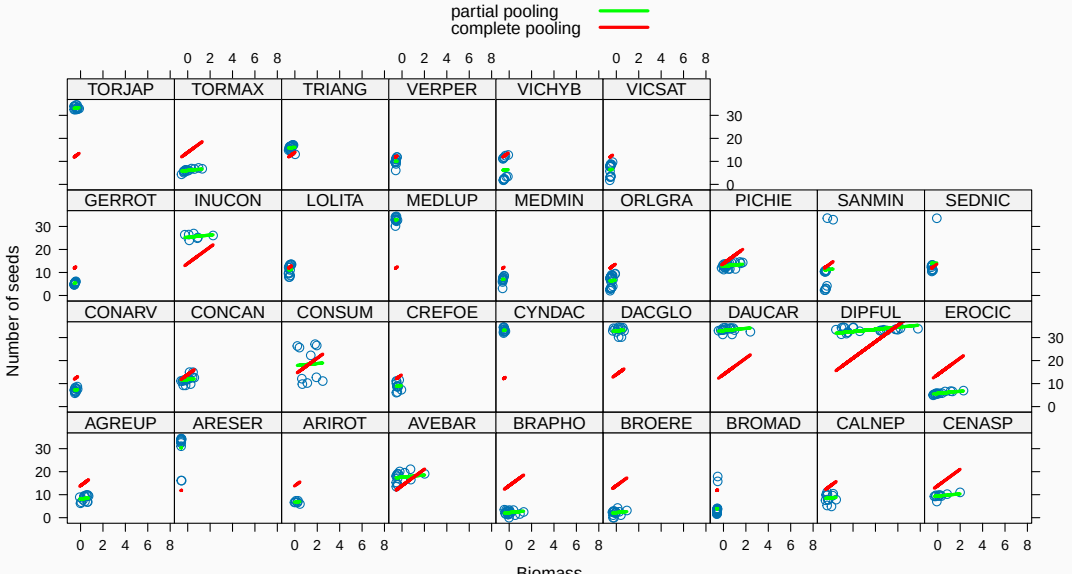
# Display results

```
allom.2
#> Inference for Bugs model at "/Users/oliviergimenez/Dropbox/OG/GITHUB/bayesian-stats-wit
#>  2 chains, each with 2500 iterations (first 1000 discarded)
#>  n.sims = 3000 iterations saved
#>           mu.vect sd.vect     2.5%      25%      50%      75%    97.5%  Rhat
#> b           0.481   0.235    0.003    0.327    0.485    0.641    0.924 1.001
#> mu.a       14.516   1.920   10.674   13.258   14.484   15.800   18.363 1.001
#> sigma.a    10.973   1.438    8.576   10.013   10.837   11.799   14.274 1.003
#> sigma.y     3.070   0.104    2.867    3.001    3.071    3.135    3.280 1.001
#> deviance 2478.052   8.494 2463.382 2471.939 2477.310 2483.364 2496.411 1.001
#>          n.eff
#> b         3000
#> mu.a      3000
#> sigma.a    970
#> sigma.y   2600
#> deviance  3000
#>
```

# Compare with Frequentist approach

```
library(lme4)
freq_lmm <- lmer(y ~ x + (1 | species), allom.data, REML = FALSE)
freq_lmm
#> Linear mixed model fit by maximum likelihood  ['lmerMod']
#> Formula: y ~ x + (1 | species)
#>    Data: allom.data
#>       AIC       BIC    logLik  deviance  df.resid
#>  2652.606  2669.368 -1322.303  2644.606       484
#> Random effects:
#>  Groups   Name        Std.Dev.
#>  species  (Intercept) 10.472
#>  Residual              3.058
#> Number of obs: 488, groups:  species, 33
#> Fixed Effects:
#> (Intercept)            x
#>      14.526        0.479
```

# Compare complete pooling vs partial pooling



# Model with no pooling (all species unrelated)

$$
\begin{aligned}
\text{nseeds}_i &\sim \text{Normal}(\mu_i, \sigma^2) && \text{[likelihood]} \\
\mu_i &= \alpha_{\text{species}[i]} + \beta\ \text{biomass}_i && \text{[linear model]} \\
\alpha_j &\sim \text{Normal}(0, 1000) && \text{[prior for intercepts]} \\
\beta &\sim \text{Normal}(0, 1000) && \text{[prior for slope]} \\
\sigma &\sim \text{Uniform}(0, 100) && \text{[prior for}\sigma\text{]}
\end{aligned}
$$

# Implementation in Jags

```
model <- paste("
model {
  for (i in 1:n){
    y[i] ~ dnorm (mu[i], tau.y)
    mu[i] <- a[species[i]] + b * x[i]
  }
  tau.y <- 1 / (sigma.y * sigma.y)
  sigma.y ~ dunif(0, 100)
  for (j in 1:nbspecies){
    a[j] ~ dnorm(0, 0.001)
  }
  b ~ dnorm(0,0.1)
}")
writeLines(model,here::here("slides","code","nopooling.bug"))
```

# Prepare ingredients

```
allom.data <- list(n = n,
                   nbspecies = nbspecies,
                   x = x,
                   y = y,
                   species = species)
init1 <- list(a = rnorm(nbspecies), b = rnorm(1), sigma.y = runif(1))
init2 <- list(a = rnorm(nbspecies), b = rnorm(1), sigma.y = runif(1))
inits<-list(init1, init2)
allom.parameters <- c("a","b","sigma.y")
```

# Run JAGS

```
allom.3 <- jags(data = allom.data,
                inits = inits,
                parameters.to.save = allom.parameters,
                n.iter = 2500,
                model.file = here::here("slides","code","nopooling.bug"),
                n.chains = 2,
                n.burn = 1000)
#> Compiling model graph
#>    Resolving undeclared variables
#>    Allocating nodes
#> Graph information:
#>    Observed stochastic nodes: 488
#>    Unobserved stochastic nodes: 35
#>    Total graph size: 2481
#>
#> Initializing model
```

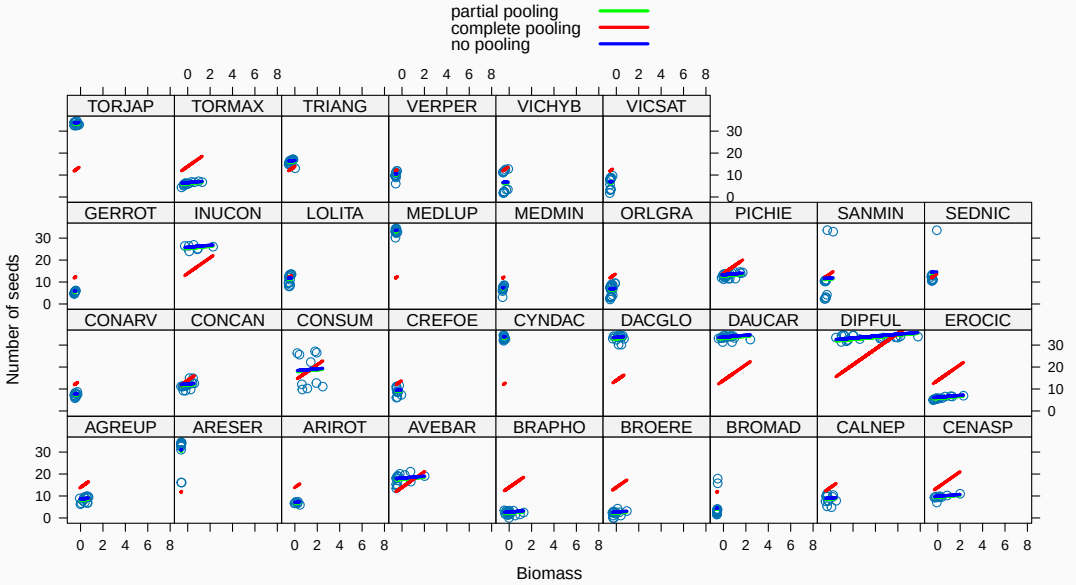
# Display results

```
allom.3$BUGSoutput$summary[c(1:4, 32:33, 34), -c(4,6)]
#>              mean        sd       2.5%        50%      97.5%     Rhat n.eff
#> a[1]    8.1493032 0.8366735  6.5547332  8.1440024  9.8056666 1.001352  2200
#> a[2]   30.7663345 0.9043055 29.0363830 30.7757908 32.5596575 1.000943  3000
#> a[3]    6.6158205 1.1409685  4.3211961  6.6068844  8.8678759 1.000816  3000
#> a[4]   17.6300040 0.8037752 16.0493069 17.6157091 19.2201409 1.000725  3000
#> a[32]   6.3592679 0.7903879  4.7492959  6.3570281  7.9060671 1.000668  3000
#> a[33]   6.6446541 0.8017678  5.1032418  6.6644456  8.1955637 1.002338   900
#> b       0.4387732 0.2397934 -0.0381318  0.4401736  0.9027882 1.001761  1400
```

# Compare with Frequentist approach

```
lm(y ~ -1 + as.factor(species) + x, data = allom.data) %>%
  broom::tidy() %>%
  slice(c(1:4, 32:33, 34))
#> # A tibble: 7 x 5
#>   term                  estimate std.error statistic   p.value
#>   <chr>                    <dbl>     <dbl>     <dbl>     <dbl>
#> 1 as.factor(species)1      8.17      0.824      9.92 3.92e- 21
#> 2 as.factor(species)2     30.8       0.895     34.4  1.67e-128
#> 3 as.factor(species)3      6.67      1.16       5.76 1.56e-  8
#> 4 as.factor(species)4     17.6       0.791     22.3  5.32e- 75
#> 5 as.factor(species)32     6.38      0.797      8.01 9.95e- 15
#> 6 as.factor(species)33     6.63      0.800      8.29 1.33e- 15
#> 7 x                        0.441     0.243      1.81 7.06e-  2
```

# Compare complete pooling vs partial pooling vs no pooling



# Bonus: Model with varying intercept and varying slope

# Code: part 1

```
model <-
paste("
# varying-intercept, varying-slope allometry model
# with Vm as a species predictor

model {
  for (i in 1:n){
    y[i] ~ dnorm (mu[i], tau.y)
    mu[i] <- a[species[i]] + b[species[i]] * x[i]
  }

  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif (0, 100)
```

# Code: part 2

```
  for (j in 1:nbspecies){
    a[j] ~ dnorm (mu.a, tau.a)
    b[j] ~ dnorm (mu.b, tau.b)
  }

  mu.a ~ dnorm (0, .001)
  tau.a <- pow(sigma.a, -2)
  sigma.a ~ dunif (0, 100)
  mu.b ~ dnorm (0, .001)
  tau.b <- pow(sigma.b, -2)
  sigma.b ~ dunif (0, 100)

}
")
```

# Prepare ingredients

```
init1 <- list(a = rnorm(nbspecies), b = rnorm(nbspecies),
              mu.a = rnorm(1), mu.b = rnorm(1),
              sigma.y = runif(1), sigma.a = runif(1), sigma.b = runif(1))
init2 <- list(a = rnorm(nbspecies), b = rnorm(nbspecies),
              mu.a = rnorm(1), mu.b = rnorm(1),
              sigma.y = runif(1), sigma.a = runif(1), sigma.b = runif(1))
inits <- list(init1, init2)
allom.parameters <- c ("a","b","mu.a","mu.b","sigma.y","sigma.a","sigma.b")
```

# Run Jags

```
allom.4 <- jags(data = allom.data,
                inits = inits,
                parameters.to.save = allom.parameters,
                n.iter = 2500,
                model.file = here::here("slides","code","varintvarslope.bug"),
                n.chains = 2,
                n.burn = 1000)
#> Compiling model graph
#>    Resolving undeclared variables
#>    Allocating nodes
#> Graph information:
#>    Observed stochastic nodes: 488
#>    Unobserved stochastic nodes: 71
#>    Total graph size: 2521
#>
#> Initializing model
```

# Display results

```
round(allom.4$BUGSoutput$summary[c(1:2, 32:33, 34:35, 65:66, 68:72), -c(4,6)],2)
#>           mean    sd   2.5%   50% 97.5% Rhat n.eff
#> a[1]      7.77  1.27   5.29  7.77 10.29 1.00  2300
#> a[2]     25.26  6.09  12.40 25.85 35.59 1.47     7
#> a[32]     8.31  1.92   4.67  8.27 11.89 1.03    57
#> a[33]    13.47  3.84   5.92 13.61 21.18 1.07   140
#> b[1]      1.63  2.75  -3.76  1.64  7.01 1.00  1000
#> b[2]     -9.07 10.59 -31.56 -8.02  8.63 1.50     6
#> b[32]     5.07  4.42  -3.27  5.06 13.48 1.04    47
#> b[33]    13.72  7.41  -0.89 14.03 28.46 1.05   720
#> mu.a     16.62  1.95  12.67 16.61 20.39 1.00  3000
#> mu.b      4.97  2.40   0.34  4.90  9.82 1.01   430
#> sigma.a  10.70  1.46   8.25 10.56 13.97 1.00  3000
#> sigma.b  12.21  2.58   8.23 11.81 18.28 1.32     9
#> sigma.y   2.66  0.09   2.49  2.66  2.86 1.01   120
```

# Compare with Frequentist approach

```
freq_lmm2 <- lmer (y ~ x + (1 + x | species), allom.data, REML = FALSE)
freq_lmm2
#> Linear mixed model fit by maximum likelihood  ['lmerMod']
#> Formula: y ~ x + (1 + x | species)
#>    Data: allom.data
#>       AIC       BIC    logLik  deviance  df.resid
#>  2609.941  2635.083 -1298.971  2597.941       482
#> Random effects:
#>  Groups   Name        Std.Dev. Corr
#>  species  (Intercept) 10.409
#>           x           11.325   0.22
#>  Residual              2.652
#> Number of obs: 488, groups:  species, 33
#> Fixed Effects:
#> (Intercept)            x
#>      16.866        5.244
```

# Compare with Frequentist approach - with no correlation

```
freq_lmm_wocorr <- lmer(y ~ x + (1 | species) +
                                    (0 + x | species), allom.data, REML = FALSE)
freq_lmm_wocorr
#> Linear mixed model fit by maximum likelihood  ['lmerMod']
#> Formula: y ~ x + (1 | species) + (0 + x | species)
#>    Data: allom.data
#>       AIC       BIC    logLik  deviance  df.resid
#>  2609.086  2630.037 -1299.543  2599.086       483
#> Random effects:
#>  Groups    Name        Std.Dev.
#>  species   (Intercept) 10.203
#>  species.1 x           10.632
#>  Residual               2.661
#> Number of obs: 488, groups:  species, 33
#> Fixed Effects:
#> (Intercept)            x
#>      16.688        4.929
```

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- Varying effects: adaptive regularization through cluster variance estimation.
- Further from mean, more shrinkage.
- Fewer data in cluster, more shrinkage.

# Multilevel models are awesome!

## Multilevel models in a nutshell

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- We may consider **varying slopes**. We'd need to deal with correlations between intercept and slope random effects. Open a whole new world with spatial (or time) autocorrelation, phylogenetic regressions, quantitative genetics, network models.
- We may **include predictors at the cluster level**. Imagine we know something about functional traits, and wish to determine whether some species-to-species variation in the allometry relationship is explained by these traits.

# Your turn: Practical 8

# Conclusions

# Take-home messages about Bayesian statistics

- Frees the modeler in you (M. Kéry)
  - Uses probability to quantify uncertainty for everything (propagation of uncertainty).
  - Allows use of prior information ('better' estimates).
  - Can fit complex (hierarchical) models with same MCMC algorithms.

# Take-home messages about Bayesian statistics

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  - Uses probability to quantify uncertainty for everything (propagation of uncertainty).
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  - Can fit complex (hierarchical) models with same MCMC algorithms.
- With great tools come great responsabilities
  - Checking convergence is painful.
  - Specifying priors might be tricky.
  - Model adequacy should be checked (posterior predictive checks - not covered).
  - Computational burden can be high (see function `R2jags::jags.parallel()` and package 'jagsUI'.

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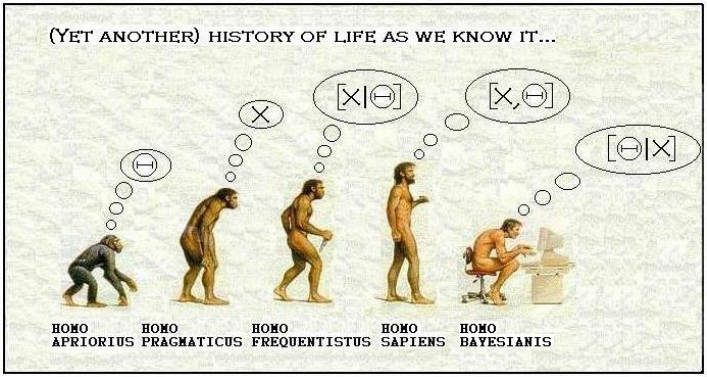
- So what?
  - Make an informed and pragmatic choice.
  - Are you after complexity, speed, uncertainties, etc?
  - Talk to colleagues.


(YET ANOTHER) HISTORY OF LIFE AS WE KNOW IT...
HOMO APRIORIUS
HOMO PRAGMATICUS
HOMO FREQUENTISTUS
HOMO SAPIENS
HOMO BAYESIANIS

# Why become a bayesian? Ask twitter!

# Your turn: Practical 9