

From fixed to random effects

Bayesian statistics 4 – random and mixed effects models

Frédéric Barraquand (CNRS, IMB)

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Some things that we learned the last time(s)

Session 3

- MCMC = Monte Carlo + Markov Chain
- Requires two types of convergence to compute an posterior means or posterior distribution
- JAGS uses the Gibbs sampler, a multicomponent variant of the Metropolis algorithm
- The Gibbs sampler allows to sample parameter-rich models

Session 2

- T-tests, ANOVA and the likes can be framed as the General Linear Model
- The Linear Model $Y = X\beta + E$, $E \sim \mathcal{N}(0, \Sigma)$ is easily fitted with JAGS
- Uncertainties in effects \rightarrow posteriors

Back to Snout-Vent Length (SVL) Snake data

From Kéry (2010) & TD 2

```
### Data generation
```

```
# same as TD2 but number of groups x 2
```

```
npop <- 10 # Number of populations: now choose 10 rather than 5
```

```
nsample <- 12 # Number of snakes in each
```

```
n <- npop * nsample # Total number of data points
```

```
pop.grand.mean <- 50 # Grand mean SVL
```

```
pop.sd <- 5 # sd of population effects about mean
```

```
pop.means <- rnorm(n = npop, mean = pop.grand.mean, sd = pop.sd)
```

```
sigma <- 3 # Residual sd
```

```
eps <- rnorm(n, 0, sigma) # Draw residuals
```

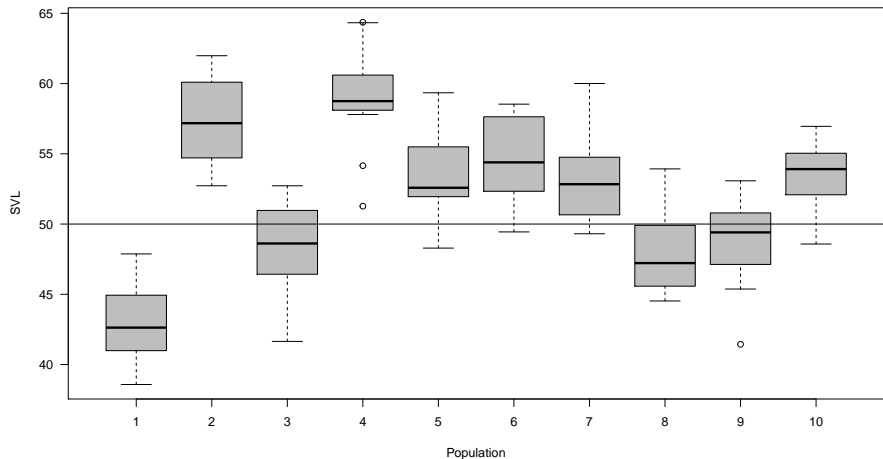
```
x <- rep(1:npop, rep(nsample, npop))
```

```
X <- as.matrix(model.matrix(~ as.factor(x)-1))
```

```
y <- as.numeric(X %*% as.matrix(pop.means) + eps) # as.numeric is E
```

The data: Snout-vent length in snakes

```
boxplot(y ~ x, col = "grey", xlab = "Population", ylab = "SVL", main = "Snout-vent length in snakes")  
abline(h = pop.grand.mean)
```



Questions that we could ask

- Effect of being in population i
- Is there more variation between populations or more residual variation?

The one-way ANOVA: from code to maths

$J = 10$ Groups. Notations

$$Y_{ij} = \alpha_j + \epsilon_{ij}, \epsilon_{ij} \sim \mathcal{N}(0, \sigma^2)$$

Practical if $i = 1, \dots, l$ is the same number of individuals per group.
 $n = l \times J$.

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or again

$$Y_{ij} \sim \mathcal{N}(\mu_{ij}, \sigma^2), \mu_{ij} = \alpha_j$$

By that we mean that $\mathbb{E}(Y_{ij}) = \alpha_j$.

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or again with $i = 1, \dots, n$

$$Y_i \sim \mathcal{N}(\mu_i, \sigma^2), \mu_i = \alpha_{k[i]}$$

where $k[i]$ returns in which group is i . How we coded this JAGS.

Running again the ANOVA

```
## List of 2
## $ y: num [1:120] 40.9 41.6 45.5 43.6 47.9 ...
## $ x: int [1:120] 1 1 1 1 1 1 1 1 1 1 ...

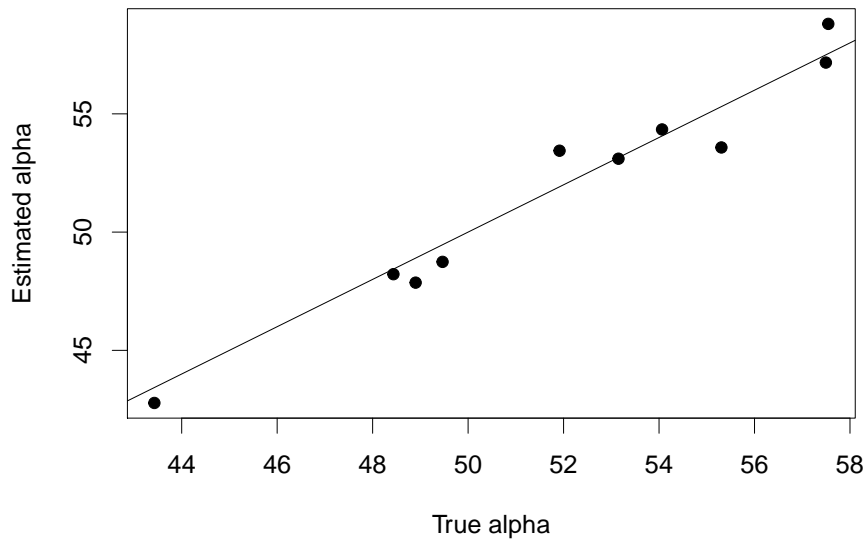
# Specify model in BUGS language
cat(file = "anova.txt", "
    model {

        # Priors
        for (i in 1:10){                # Implicitly define alpha as a vector
            alpha[i] ~ dnorm(0, 0.001) # Beware that a mean at 0 only works because
        }
        sigma ~ dunif(0, 100)

        # Likelihood
        for (i in 1:120) {
            y[i] ~ dnorm(mean[i], tau)
            mean[i] <- alpha[x[i]]
        }

        # Derived quantities
        tau <- 1 / ( sigma * sigma)
    }
```

Estimated effects vs theoretical effects



Classical random effect modelling I

```
### Restricted maximum likelihood (REML) analysis using R
library('lme4')                # Load lme4

pop <- as.factor(x)            # Define x as a factor and call it pop

lme.fit <- lmer(y ~ 1 + 1 | pop, REML = TRUE)
lme.fit                        # Inspect results
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: y ~ 1 + 1 | pop
## REML criterion at convergence: 640.7965
## Random effects:
##   Groups      Name          Std.Dev.
##   pop        (Intercept)  4.774
##   Residual                        3.080
## Number of obs: 120, groups:  pop, 10
## Fixed Effects:
## (Intercept)
```

Classical random effect modelling II

```
##          51.85
```

```
ranef(lme.fit)           # Print random effects
```

```
## $pop
```

```
##      (Intercept)
```

```
## 1      -8.761097
```

```
## 2       5.203301
```

```
## 3      -3.458541
```

```
## 4       6.790861
```

```
## 5       1.567910
```

```
## 6       2.484507
```

```
## 7       1.239695
```

```
## 8      -3.802799
```

```
## 9      -2.967132
```

```
## 10      1.703295
```

```
##
```

```
## with conditional variances for "pop"
```

Classical random effect model - maths

$$Y_i \sim \mathcal{N}(\mu_i, \sigma^2), \mu_i = \alpha_{k[i]}$$

where $k[i]$ returns in which group is i . What's missing?

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i.i.d. observations. And then?

We estimate the variance of the random effects

$$\alpha_j \sim \mathcal{N}(\mu_\alpha, \sigma_\alpha^2)$$

for $j = 1, \dots, J$ (we have to specify a mean μ_α too, we can set it to zero if there is an overall mean μ though)

Random effect model in a Bayesian framework I

```
# Bundle and summarize the data set passed to JAGS  
str(bdata <- list(y = y, x = x, npop = npop, n = n))
```

```
## List of 4  
## $ y : num [1:120] 40.9 41.6 45.5 43.6 47.9 ...  
## $ x : int [1:120] 1 1 1 1 1 1 1 1 1 1 ...  
## $ npop: num 10  
## $ n : num 120
```

Random effect model in a Bayesian framework II

Specify model in BUGS language

```
cat(file = "re.anova.txt", "  
model {
```

```
# Priors and some derived things
```

```
for (i in 1:npop){  
    alpha[i] ~ dnorm(mu, tau.alpha)      # Prior for population means  
    effect[i] <- alpha[i] - mu           # Population effects as derived quantities  
}
```

```
mu ~ dnorm(0,0.001)                     # Hyperprior for grand mean svl  
sigma.alpha ~ dunif(0, 10)              # Hyperprior for sd of population effects  
sigma.res ~ dunif(0, 10)                 # Prior for residual sd
```

```
# Likelihood
```

```
for (i in 1:n) {  
    y[i] ~ dnorm(mean[i], tau.res)  
    mean[i] <- alpha[x[i]]  
}
```

```
# Derived quantities
```

Fitting the model I

Inits function

```
inits <- function(){ list(mu = runif(1, 0, 100), sigma.alpha = rlnor
```

Params to estimate

```
params <- c("mu", "alpha", "effect", "sigma.alpha", "sigma.res")
```

MCMC settings

```
nb <- 1000 ; nc <- 3 ; ni <- 2000 ; nt <- 2
```

Call JAGS, check convergence and summarize posteriors

```
out2 <- jags(bdata, inits, params, "re.anova.txt", n.thin = nt, n.cl  
          n.burnin = nb, n.iter = ni)
```

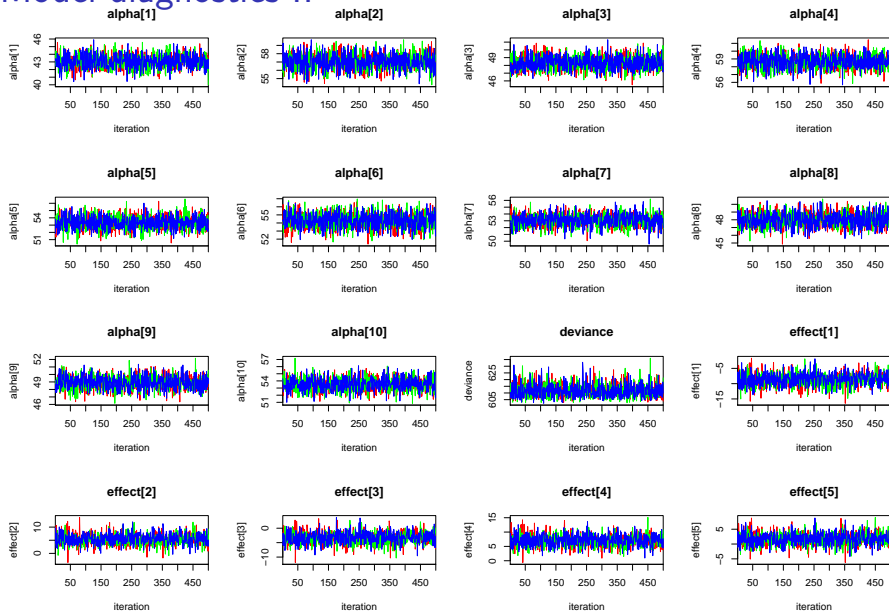
Fitting the model II

```
## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
## Graph information:
##   Observed stochastic nodes: 120
##   Unobserved stochastic nodes: 13
##   Total graph size: 273
##
## Initializing model
```

Model diagnostics I

```
traceplot(out2,mfrow=c(4,4))
```

Model diagnostics II



Model results I

```
print(out2,dig=3)
```

```
## Inference for Bugs model at "re.anova.txt", fit using jags,
## 3 chains, each with 2000 iterations (first 1000 discarded), n.thin = 2
## n.sims = 1500 iterations saved
##
```

	mu.vect	sd.vect	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
## alpha[1]	43.047	0.890	41.401	42.437	43.047	43.647	44.780	1.000	1500
## alpha[2]	57.066	0.903	55.195	56.461	57.108	57.677	58.861	1.001	1500
## alpha[3]	48.325	0.870	46.679	47.713	48.302	48.914	50.051	1.001	1500
## alpha[4]	58.678	0.878	56.883	58.106	58.698	59.260	60.359	1.000	1500
## alpha[5]	53.368	0.881	51.641	52.780	53.374	53.940	55.144	1.002	1500
## alpha[6]	54.304	0.911	52.441	53.698	54.303	54.900	56.124	1.007	300
## alpha[7]	53.088	0.890	51.296	52.518	53.101	53.677	54.738	1.000	1500
## alpha[8]	47.994	0.888	46.290	47.407	47.996	48.592	49.820	1.002	1500
## alpha[9]	48.916	0.865	47.221	48.354	48.925	49.448	50.618	1.000	1500
## alpha[10]	53.537	0.890	51.764	52.939	53.529	54.123	55.242	1.000	1500
## effect[1]	-8.596	2.004	-12.663	-9.829	-8.614	-7.305	-4.545	1.006	490
## effect[2]	5.423	2.019	1.550	4.099	5.380	6.698	9.479	1.004	690
## effect[3]	-3.318	1.983	-7.298	-4.610	-3.321	-2.041	0.472	1.005	460
## effect[4]	7.036	1.992	3.072	5.786	6.980	8.319	11.053	1.006	620
## effect[5]	1.725	1.989	-2.174	0.449	1.692	2.993	5.889	1.004	770
## effect[6]	2.661	2.055	-1.397	1.319	2.603	4.033	6.722	1.005	460
## effect[7]	1.445	2.034	-2.462	0.149	1.412	2.697	5.658	1.005	480

Model results II

```
## effect[8]      -3.648    1.973   -7.470   -4.922   -3.692   -2.372    0.324  1.005    600
## effect[9]      -2.726    1.976   -6.605   -3.948   -2.743   -1.460    1.092  1.004    450
## effect[10]      1.894    1.999   -2.147    0.641    1.858    3.138    5.928  1.004    490
## mu             51.643    1.845   47.984   50.445   51.699   52.809   55.295  1.005    470
## sigma.alpha     5.518    1.381    3.419    4.480    5.335    6.414    8.721  1.003   1500
## sigma.res       3.110    0.220    2.709    2.961    3.103    3.238    3.600  1.000   1500
## deviance       611.719    4.941  604.350  608.042  610.971  614.540  623.296  1.000   1500
##
## 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).
##
## DIC info (using the rule,  $pD = \text{var}(\text{deviance})/2$ )
##  $pD = 12.2$  and  $DIC = 623.9$ 
## DIC is an estimate of expected predictive error (lower deviance is better).
```


Comparison of variance estimates

```
### Well, comparison of sigma's...
```

```
VarCorr(lme.fit)
```

```
## Groups      Name      Std.Dev.  
## pop      (Intercept) 4.7740  
## Residual              3.0801
```

```
out2$BUGSoutput$mean$sigma.res #true value is 3
```

```
## [1] 3.109739
```

```
out2$BUGSoutput$mean$sigma.alpha #true value is 5
```

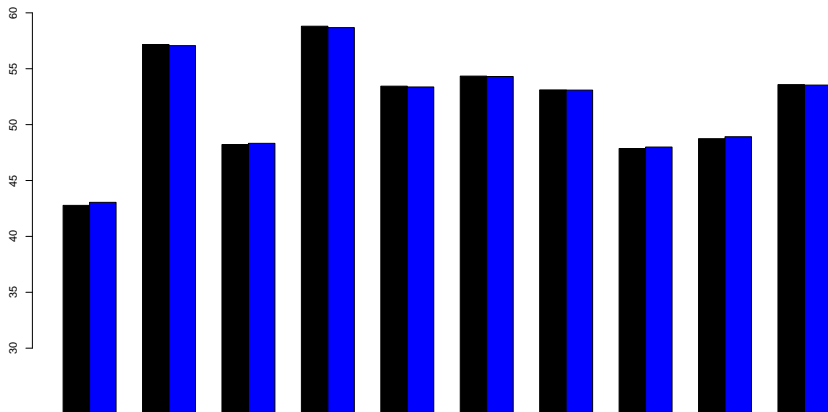
```
## [1] 5.517962
```

Comparison of fixed and random effects

```
## Plotting shrinkage
```

```
alpha_mean2 = out2$BUGSoutput$mean$alpha
```

```
barplot(t(matrix(c(alpha_mean,alpha_mean2),ncol=2,nrow=10)),beside=T)
```



Re-running the analysis with more shrinkage I

Now we assume a prior $\sigma_\alpha \sim \text{Gamma}(100, 50)$.

More details on the [Gamma distribution](#)

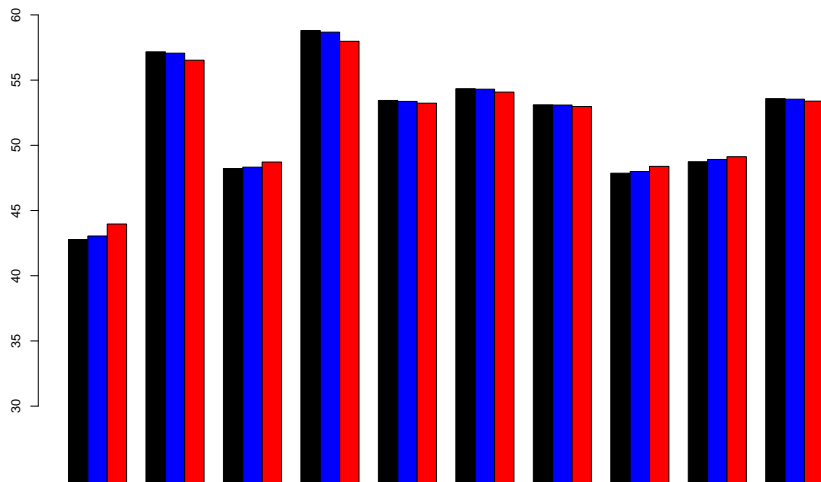
- $X \sim \text{Gamma}(a, b)$ with $a = \text{shape}$, $b = \text{rate} = \frac{1}{\theta}$ where θ is scale.
- Properties: $\mathbb{E}(X) = a\theta = 100/50 = 2$ and $\mathbb{V}(X) = a\theta^2 = \frac{100}{2500} = 0.04$ so that $\text{SD}(X) = 0.2$.

```
alpha_mean3 = out3$BUGSoutput$mean$alpha
out3$BUGSoutput$mean$sigma.alpha
```

```
## [1] 2.408461
```

```
barplot(t(matrix(c(alpha_mean, alpha_mean2, alpha_mean3), ncol=3,
```

Re-running the analysis with more shrinkage II



To wrap up – ANOVA vs REs in a Bayesian setup

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- RE model with more shrinkage $\sigma_\alpha \sim \text{Gamma}(100, 50)$.

More material

- Shrinkage aka partial pooling is a property of mixed models, not Bayesian estimation (though you can top it up using informative priors)
- Kruschke's post on parameterizing the Gamma distribution

Bonus: fun and pretty snakes



Figure 1: *Vipera ursinii* Benny Trapp (CC BY)

Super épisode de La méthode scientifique sur France Culture, 08/11/2021