

Contents

1	Problem and data	3
1.1	About	3
1.2	Fixed and random effects ANOVA	3
2	Fixed effects ANOVA	5
2.1	Maximum likelihood analysis	5
2.2	MCMC analysis	5
3	Random effects ANOVA	7
3.1	Maximum likelihood analysis	7
3.2	MCMC analysis	8
4	Reproducibility	10

1 Problem and data

1.1 About

This is an example from Marc Kery's book "Introduction to WinBUGS for ecologists" [1]. Here we explore fixed and random effects models with ANOVA (a t-test applied more than two groups). First we generate the data— with a number of populations of snakes (**ngroups**) each with an equal number of **nsample** and a single measured co-variate **svl**. From within the function [generateData.R](#) the following snippets show the parameters used to create the fixed-effects and random effects data sets.

```
### generate data for fixed effects ###
ngroups <- 5
nsample <- 10
popMeans <- c(50,40,45,55,60)
sigma <- 3

n <- ngroups * nsample
resid <- rnorm(n,0,sigma)

### generate data for random effects ###
npop <- 10
nsample <- 12
n <- npop * nsample
popGrandMean <- 50
popSd <- 5
popMeans <- rnorm(n=npop,mean=popGrandMean,sd=popSd)
sigma <- 3
```

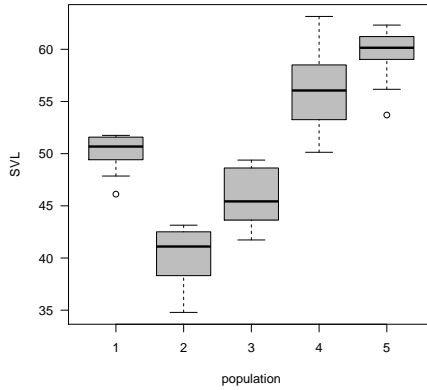


Figure 1.1: The distributions of the five populations of snakes with respect to snout-vent-length

1.2 Fixed and random effects ANOVA

The means parameterization for the one-way ANOVA:

$$y_i = \alpha_{j(i)} + \epsilon_i \quad (1.1)$$

$$\epsilon_i \sim \mathcal{N}(0, \sigma^2) \quad (1.2)$$

$$\alpha_{j(i)} \sim \mathcal{N}(\mu, \tau^2) \quad (1.3)$$

y_i refers to the `svl` of snake i in population j . Eqn 1.3 is the key assumption that moves this from a fixed-effects to a random effects ANOVA. It is not always clear whether we should be using a fixed-effect or random-effects ANOVA, in fact statisticians have differing opinions. Random effects are often used for things like `year`, `month`, or `location`. The decision has to do with whether we want to generalize our conclusions to the larger (unsampled) population as well.

2 Fixed effects ANOVA

2.1 Maximum likelihood analysis

```
data = read.csv("fe-svl.csv")
print(anova(lm(data$y~as.factor(data$x))))
cat("\n")
print(summary(lm(data$y~as.factor(data$x)))$coeff,dig=3)
cat("Sigma:", summary(lm(data$y~as.factor(data$x)))$sigma, "\n")
```

```
[1] "...
Analysis of Variance Table

Response: data$y
          Df Sum Sq Mean Sq F value Pr(>F)
as.factor(data$x) 4 2422.57  605.64  68.109 < 2.2e-16 ***
Residuals  45  400.15    8.89
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  50.11    0.943    53.14  2.99e-42
as.factor(data$x)2  -9.87    1.334   -7.40  2.57e-09
as.factor(data$x)3  -4.36    1.334   -3.27  2.05e-03
as.factor(data$x)4   6.10    1.334    4.57  3.77e-05
as.factor(data$x)5   9.43    1.334    7.07  8.06e-09
Sigma: 2.981976
```

Be reminded that R fits and effects parameterization of ANOVA.

2.2 MCMC analysis

With BUGS we generally fit a mean parameterization and calculate the differences between populations (effects) using derived quantities. See the script [fixedEffectAnova.R](#) for more details. Here is the output.

```
Compiling model graph
  Resolving undeclared variables
  Allocating nodes
  Graph Size: 122

Initializing model

$BUGSoutput
Inference for Bugs model at "fe-anova.txt", fit using jags,
  3 chains, each with 5000 iterations (first 200 discarded), n.thin = 2
  n.sims = 7200 iterations saved
      mean  sd  2.5%  25%   50%  75% 97.5% Rhat n.eff
alpha[1] 50.1 1.0  48.1  49.4  50.1  50.7  52.0   1 7200
alpha[2] 40.2 1.0  38.3  39.5  40.2  40.8  42.1   1 7200
alpha[3] 45.7 1.0  43.8  45.0  45.7  46.4  47.6   1 5300
alpha[4] 56.2 1.0  54.2  55.5  56.2  56.8  58.0   1 2700
alpha[5] 59.5 1.0  57.5  58.8  59.5  60.1  61.4   1 7200
deviance 252.5 3.8 247.3 249.7 251.8 254.6 261.8   1 2100
effe2    -9.9 1.4 -12.6 -10.8  -9.9  -9.0  -7.2   1 7200
effe3    -4.3 1.4  -7.1  -5.3  -4.3  -3.4  -1.6   1 7200
effe4     6.1 1.4   3.4   5.2   6.1   7.0   8.8   1 7200
effe5     9.4 1.4   6.7   8.5   9.5  10.4  12.2   1 7200
sigma     3.1 0.3   2.5   2.8   3.0   3.3   3.8   1 7200
test1   -29.7 2.0 -33.6 -31.1 -29.7 -28.4 -25.8   1 2600
test2    -2.8 2.4  -7.5  -4.4  -2.8  -1.2   2.0   1 4400

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 = var(deviance)/2)
pD = 7.3 and DIC = 259.8
DIC is an estimate of expected predictive error (lower deviance is better).
```

We see that the results are essentially the same. Here are common plots used to examine the posterior.

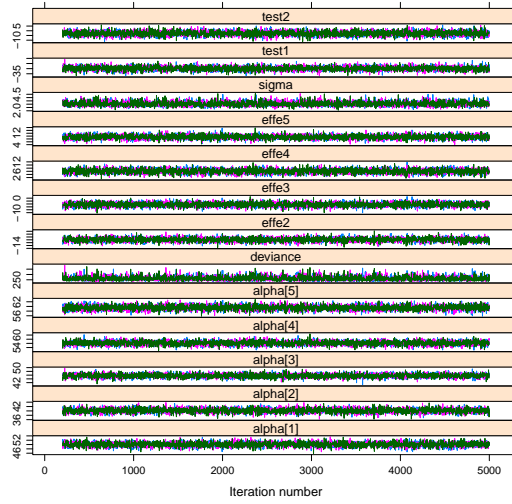


Figure 2.1: The MCMC chains

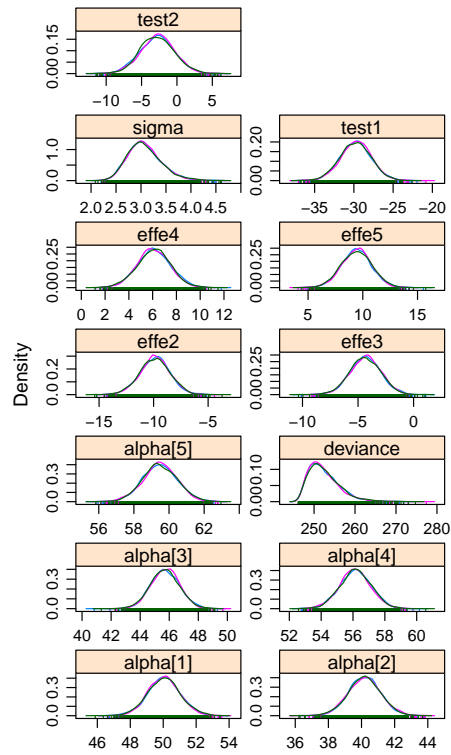


Figure 2.2: MCMC densities

3 Random effects ANOVA

The difference here is the we assume that population means come from a Gaussian distribution.

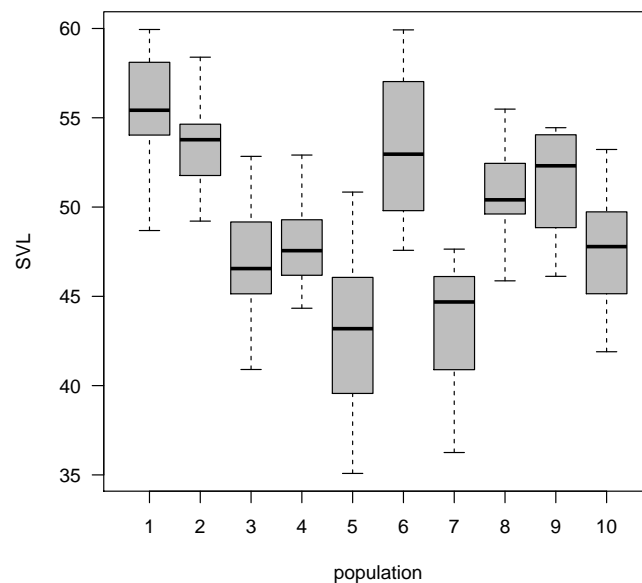


Figure 3.1: The distributions of the 10 populations of snakes with respect to snout-vent-length

3.1 Maximum likelihood analysis

```
library("lme4")
data = read.csv("re-svl.csv")
pop <- as.factor(data$x)
lme.fit <- lmer(data$y~1+1 | pop, REML=TRUE)
print(lme.fit)
print(ranef(lme.fit))
```

```
[1] "...
Linear mixed model fit by REML ['lmerMod']
Formula: data$y ~ 1 + 1 | pop
REML criterion at convergence: 655.1261
Random effects:
Groups Name Std.Dev.
pop (Intercept) 4.105
Residual 3.326
Number of obs: 120, groups: pop, 10
Fixed Effects:
(Intercept)
49.36
$pop
```

```

(Intercept)
1 5.728721
2 3.894882
3 -2.228275
4 -1.460284
5 -5.998548
6 3.706515
7 -5.559655
8 1.302983
9 2.067522
10 -1.453860

```

3.2 MCMC analysis

```

Compiling model graph
Resolving undeclared variables
Allocating nodes
Graph Size: 273

```

Initializing model

\$BUGSoutput

Inference for Bugs model at "re-anova.txt", fit using jags,
3 chains, each with 5000 iterations (first 200 discarded), n.thin = 2
n.sims = 7200 iterations saved

	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
deviance	630.2	5.0	622.6	626.5	629.5	633.0	642.0	1	7200
effe[1]	5.9	1.8	2.5	4.7	5.9	7.1	9.5	1	7200
effe[2]	4.1	1.8	0.5	2.9	4.0	5.2	7.8	1	7200
effe[3]	-2.1	1.8	-5.6	-3.3	-2.1	-0.9	1.5	1	7200
effe[4]	-1.3	1.8	-4.9	-2.5	-1.3	-0.2	2.2	1	7200
effe[5]	-5.9	1.8	-9.5	-7.0	-5.9	-4.7	-2.3	1	7200
effe[6]	3.9	1.8	0.4	2.7	3.8	5.0	7.5	1	7200
effe[7]	-5.4	1.8	-9.0	-6.6	-5.4	-4.3	-1.9	1	7200
effe[8]	1.4	1.8	-2.1	0.3	1.4	2.6	5.0	1	7200
effe[9]	2.2	1.8	-1.4	1.1	2.2	3.3	5.8	1	7200
effe[10]	-1.4	1.8	-4.9	-2.5	-1.4	-0.2	2.2	1	7200
mu	49.2	1.6	46.0	48.2	49.3	50.2	52.4	1	7200
pop.mean[1]	55.1	1.0	53.2	54.5	55.1	55.8	57.0	1	6200
pop.mean[2]	53.3	1.0	51.4	52.7	53.3	53.9	55.1	1	7200
pop.mean[3]	47.1	0.9	45.3	46.5	47.1	47.8	49.0	1	7200
pop.mean[4]	47.9	0.9	46.0	47.3	47.9	48.5	49.8	1	7200
pop.mean[5]	43.3	1.0	41.5	42.7	43.3	44.0	45.2	1	1700
pop.mean[6]	53.1	0.9	51.2	52.5	53.1	53.7	55.0	1	7200
pop.mean[7]	43.8	1.0	41.9	43.1	43.8	44.4	45.7	1	7200
pop.mean[8]	50.7	0.9	48.8	50.0	50.6	51.3	52.5	1	7200
pop.mean[9]	51.4	1.0	49.6	50.8	51.4	52.1	53.3	1	7200
pop.mean[10]	47.9	1.0	46.0	47.2	47.9	48.5	49.8	1	7200
sigma.group	4.8	1.3	2.9	3.8	4.5	5.5	8.0	1	2100
sigma.res	3.4	0.2	3.0	3.2	3.4	3.5	3.8	1	7200

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, $pD = \text{var}(\text{deviance})/2$)
 $pD = 12.5$ and $DIC = 642.7$

DIC is an estimate of expected predictive error (lower deviance is better).

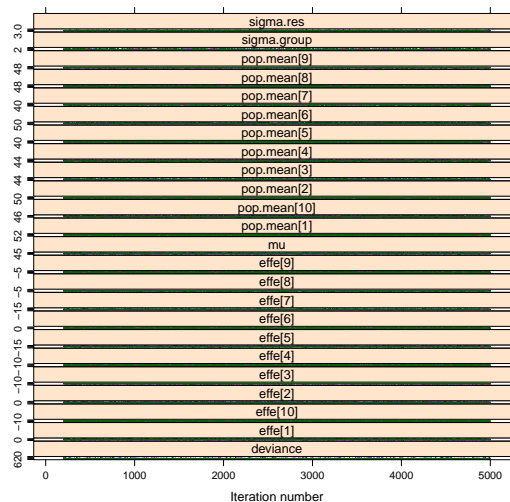


Figure 3.2: The MCMC chains

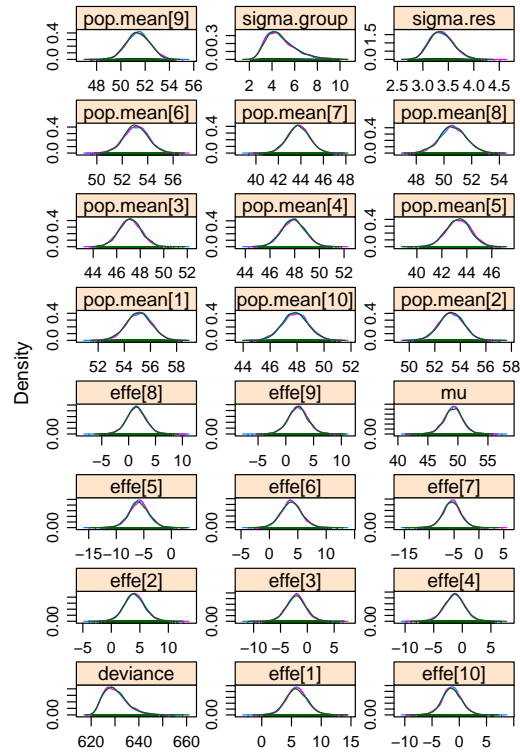


Figure 3.3: MCMC densities

4 Reproducibility

To reproduce this document.

- `$ Rscript generateData.R`
- `$ Rscript fixedEffectAnova.R > fe-anova-out.txt`
- `$ Rscript randomEffectAnova.R > re-anova-out.txt`
- `$ python run.py`

Bibliography

- [1] M. Kery. *Introduction to WinBUGS for Ecologists*, Elsevier Academic Press, 2010.