

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	8

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 a random effects model with ANOVA (a t-test applied more than two groups). First we generate the data—five populations of snakes each with $n = 10$ and a single measured co-variate. See the function `generateData.R`.

```
#!/usr/bin/Rscript

### 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)
means <- rep(popMeans, rep(nsample,ngroups))
x <- rep(1:5,rep(nsample,ngroups))

## create design matrix and target variables
X <- as.matrix(model.matrix(~as.factor(x)-1))
y <- as.numeric(X)%*% as.matrix(popMeans) + resid

## plot the data
pdf("fe-svl-data.pdf",height=6,width=6)
boxplot(y~x,col="grey",xlab="population",ylab="SVL",main="",las=1)
dev.off()

## write to outfile
xyFrame <- data.frame(x,y)
write.csv(xyFrame,file="fe-svl.csv",row.names=FALSE)

### 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
resid <- rnorm(n,0,sigma)
x <- rep(1:npop, rep(nsample, npop))

## create the design matrix and target variables
X <- as.matrix(model.matrix(~ as.factor(x)-1))
y <- as.numeric(X %*% as.matrix(popMeans)+resid)

# Plot of generated data
pdf("re-svl-data.pdf",height=6,width=6)
boxplot(y~x, col="grey", xlab="population", ylab="SVL",main="", las=1)
dev.off()

## write to outfile
xyFrame <- data.frame(x,y)
write.csv(xyFrame,file="re-svl.csv",row.names=FALSE)
print("done.")
```

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

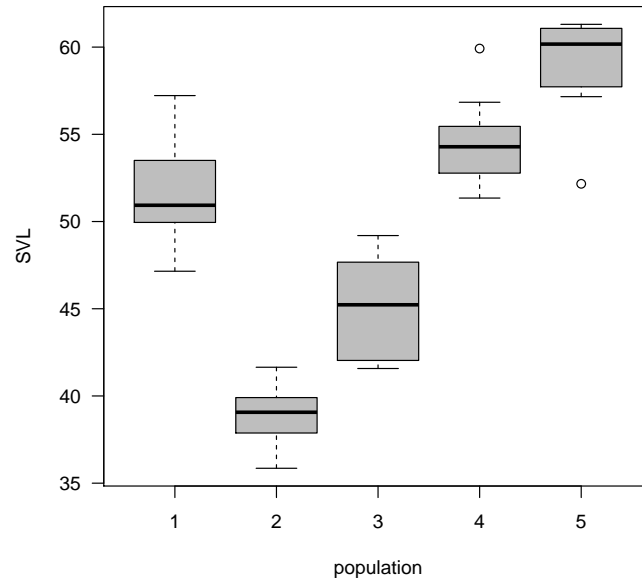


Figure 1.1: The distributions of the five populations of snakes with respect to snout-vent-length

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 2537.15  634.29  91.992 < 2.2e-16 ***
Residuals  45  310.28    6.90
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

              Estimate Std. Error t value Pr(>|t|)
(Intercept)  51.60    0.83  62.15  2.86e-45
as.factor(data$x)2  -12.75    1.17  -10.86  3.74e-14
as.factor(data$x)3   -6.43    1.17   -5.48  1.84e-06
as.factor(data$x)4    2.98    1.17    2.53  1.48e-02
as.factor(data$x)5    7.49    1.17    6.38  8.47e-08
Sigma: 2.625846
```

2.2 MCMC analysis

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

Initializing model

null device
1
null device
1
$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] 50.5 0.8  48.9 50.0 50.5 51.0 52.0  1 7200
alpha[2] 40.2 0.8  38.7 39.7 40.2 40.7 41.7  1 3900
alpha[3] 45.7 0.8  44.1 45.1 45.7 46.2 47.2  1 7200
alpha[4] 54.8 0.8  53.2 54.3 54.8 55.3 56.4  1 7200
alpha[5] 61.3 0.8  59.7 60.7 61.3 61.8 62.8  1 7200
deviance 231.7 3.7 226.5 229.0 231.1 233.7 240.7  1 7200
effe2   -10.3 1.1 -12.5 -11.1 -10.3  -9.6  -8.1  1 2700
effe3    -4.8 1.1  -7.0  -5.6  -4.9  -4.1  -2.6  1 7200
effe4     4.3 1.1   2.0   3.5   4.3   5.0   6.5  1 7200
effe5    10.7 1.1   8.6  10.0  10.7  11.5  13.0  1 7200
sigma     2.5 0.3   2.0   2.3   2.5   2.7   3.1  1 7200
test1   -30.2 1.6 -33.4 -31.3 -30.2 -29.1 -27.0  1 6800
test2     2.2 2.0  -1.7   0.9   2.2   3.5   6.1  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 = var(deviance)/2)
pD = 6.9 and DIC = 238.7
DIC is an estimate of expected predictive error (lower deviance is better).
```

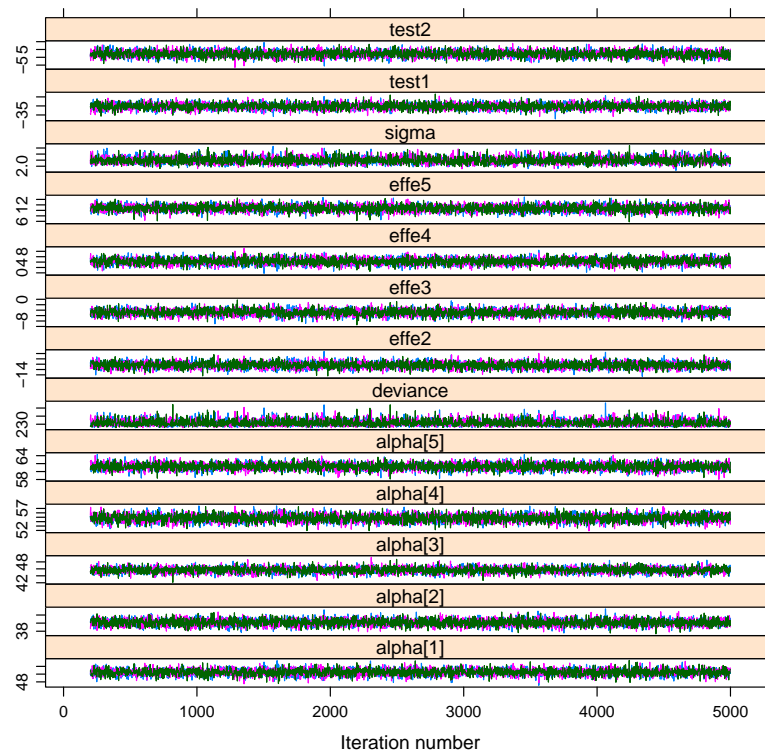


Figure 2.1: The MCMC chains

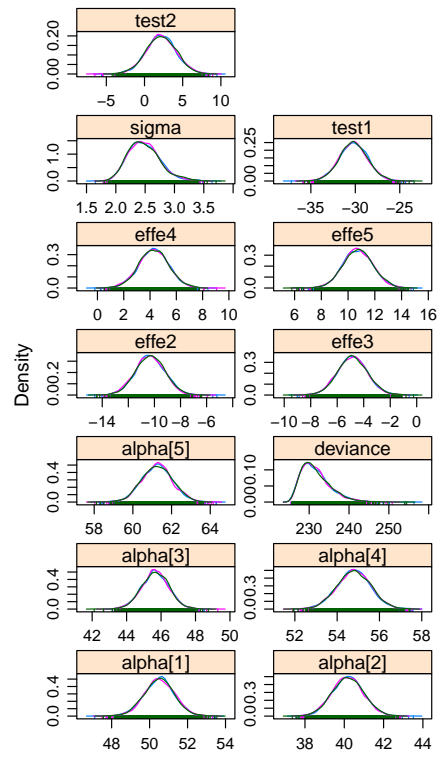


Figure 2.2: MCMC densities

3 Random effects ANOVA

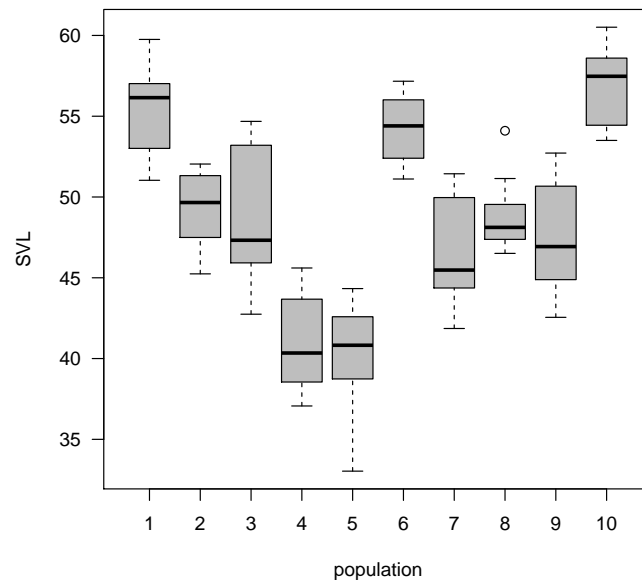


Figure 3.1: The distributions of the five populations of snakes with respect to snout-vent-length

Bibliography

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