

Worksheet: Chain Binomial models using BUGS

Nathan Green, Imperial College London

5/02/2020

1 Introduction

In this practical we will revisit the chain-binomial model we met for the likelihood practical and implement it in the Bayesian software BUGS via R.

2 Measle example

We will infer the probability of infection p and estimate subpopulation sizes. Open up R or RStudio and start a new session. Make sure to have a BUGS implementation installed, e.g. OpenBUG or jags. We will be using jags but the code is identical unless stated otherwise. The BUGS script is in file `chain-binomial-hh3.txt`.

First load packages

```
library(R2jags)
```

```
## Loading required package: rjags
```

```
## Loading required package: coda
```

```
## Linked to JAGS 4.3.0
```

```
## Loaded modules: basemod,bugs
```

```
##
```

```
## Attaching package: 'R2jags'
```

```
## The following object is masked from 'package:coda':
```

```
##
```

```
##      traceplot
```

```
library(R2WinBUGS)
```

```
## Loading required package: boot
```

Next we define the setting of the MCMC algorithm. Since this is a simple example we won't need many iterations and burn-in and thinning can be small too.

```
n_iter <- 1000
```

```
n_burnin <- 10
```

```
n_thin <- 1
```

We need to tell BUGS which parameters we wish to 'monitor', that is which to save for us to use afterwards. We will choose the vector of probabilities and predicted subpopulation sizes. The BUGS code will make their definition more clear.

```
params <-
  c("prob",
    "X_pred")
```

Importantly, we will now specify the data we are going to fit to. Recall from the lecture that we have a total sample size of 334. This is defined in a `list` object, because it allows us to have different length entries, unlike say a matrix.

```
jags_dat <- list(X = c(34, 25, 36, 239),
                N = 334)
```

I have the BUGS code in the following directory but change it to match where you have saved your file.

```
my_file_location <- "C:/Users/ngreen1/Google Drive/AIMS/my practicals/chain-binomial-hh3.txt"
```

Finally, we are in a position to run the MCMC sampler. If you are using OpenBUGS then use `bugs()` instead of `jags()`.

```
out <- jags(jags_dat,
            parameters.to.save = params,
            model.file = my_file_location,
            n.chains = 2,
            n.iter = n_iter,
            n.burnin = n_burnin,
            n.thin = n_thin,
            DIC = FALSE,
            working.directory = getwd(),
            progress.bar = "text")
```

```
## module glm loaded
```

```
## module dic loaded
```

```
## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
## Graph information:
##   Observed stochastic nodes: 1
##   Unobserved stochastic nodes: 3
##   Total graph size: 19
##
## Initializing model
```

Now we have run the model we can inspect the output. If we `attach` the BUGS output to the workspace then we don't have to keep writing out.

```
R2WinBUGS::attach.bugs(out$BUGSoutput)
```

Using the base R plotting features we can view the posterior distributions of the subsample sizes. We have also indicated the sample value with vertical red lines.

```

par(mfrow = c(2,2))

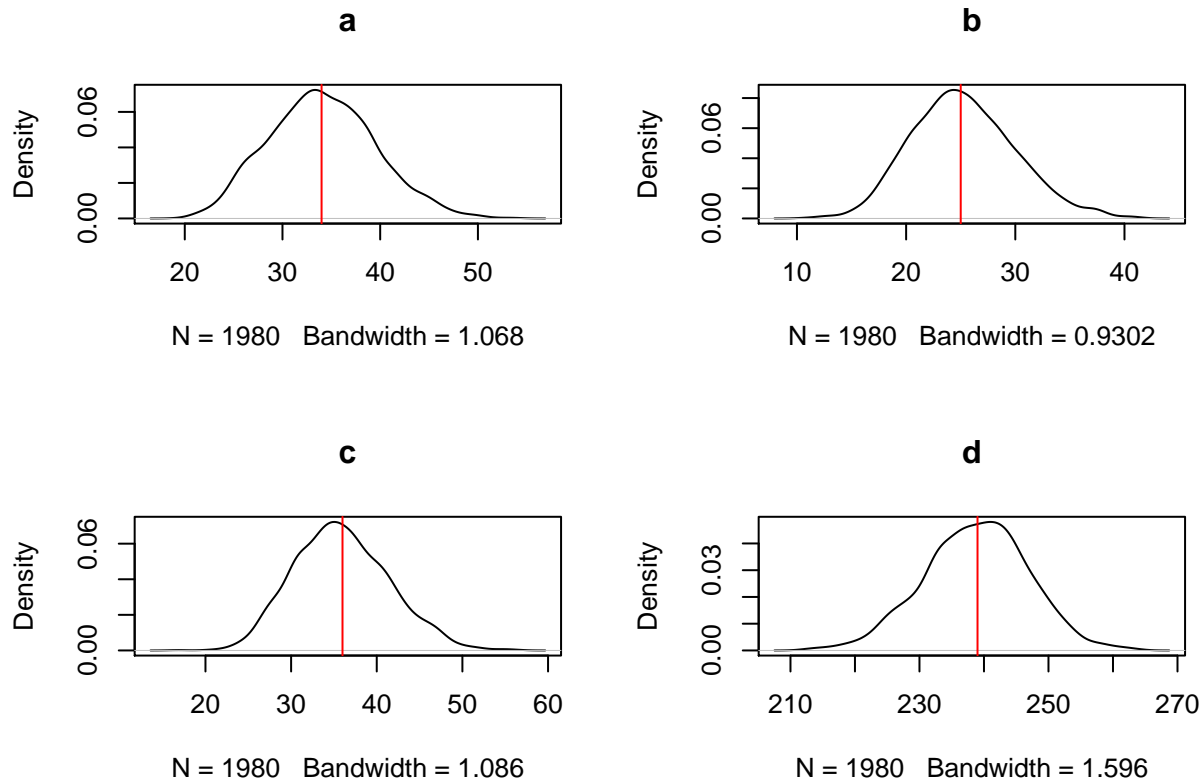
plot(density(X_pred[,1]), main = "a")
abline(v = 34, col = "red")

plot(density(X_pred[,2]), main = "b")
abline(v = 25, col = "red")

plot(density(X_pred[,3]), main = "c")
abline(v = 36, col = "red")

plot(density(X_pred[,4]), main = "d")
abline(v = 239, col = "red")

```



Compare this to the analysis done with the likelihood approach in previous work.

3 Your turn

Can you extend the previous model to households of size 4. For data $n = 500$, and $a = 11, b = 12, c = 14, d = 27, e = 49, f = 63, g = 152, h = 172$.

You will need to

- In the BUGS code, modify the `prob` and `phi` vectors to have length 4.

- Change the loop to go up to 4
- Change `jags_dat`

Compare the output to the different models.