Introductory Bayesian Course

Dr. Joseph L. Thorley

October 20th, 2014

Contents

1 Background

The purpose of these course notes is to introduce participants to Bayesian analysis with R, RStudio and JAGS. It is assumed that participants are familiar with R and RStudio as covered in the Introductory R Course notes at http://www.poissonconsulting.ca/course/2014/09/12/an-introduction-to-r-course.html.

1.1 Licence

1.2 Installation

If you haven't already done so, download the the most recent version of the R base distribution binary for your platform from http://cran.r-project.org/ and install using the default options. Next download and install RStudio from http://www.rstudio.com/products/rstudio/download/ using the default options. Then, download JAGS from http://sourceforge.net/projects/mcmc-jags/files/JAGS/ and install with the default options.

To make sure you have all the required packages installed on your hard drive execute the following code at the command line

```
install.packages("devtools", quiet = TRUE)
library(devtools)

install.packages("dplyr", quiet = TRUE)

install.packages("ggplot2", quiet = TRUE)
```

```
install.packages("scales", quiet = TRUE)

install_github("poissonconsulting/tulip@v0.0.11")
install_github("poissonconsulting/datalist@v0.4")
install_github("poissonconsulting/juggler@v0.1.3")
install_github("poissonconsulting/jaggernaut@v2.1.0")
```

Then start any scripts with

```
library(dplyr)
library(ggplot2)
library(scales)
library(jaggernaut)
```

1.3 Bayesian and Frequentist Statistical Analysis

Statistical analysis uses probability models to provide bounded estimates of parameter values (θ) from the data (y).

There are two primary approaches to statistical analysis: Bayesian and frequentist. As far as a frequentist is concerned the best estimates of θ are those values that maximise the *likelihood* which is the probability of the data given the estimates, i.e., $p(y|\theta)$. A Bayesian on the other hand chooses the values with the highest *posterior* probability - that is to say the probability of the estimates given the data , i.e., $p(\theta|y)$.

1.3.1 Coin Flips

Consider the case where $n = 10$ flips of a coin produce $y = 3$ tails. We can model this using a binomial distribution

$$y \sim dbin(\theta, n)$$

where θ is the probability of throwing a head.

1.3.1.1 Maximum Likelihood

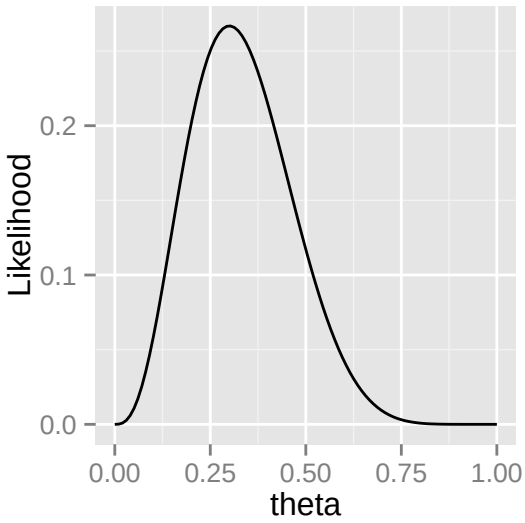
The likelihood for the binomial model is given by the following equation

$$p(y|\theta) = \binom{n}{y} \theta^y (1-\theta)^{n-y}$$

.

The likelihood values for different values of θ are therefore as follows

```
likelihood <- function(theta, n = 10, y = 3) {
    choose(n, y) * theta^y * (1 - theta)^(n - y)
}
theta <- seq(from = 0, to = 1, length.out = 100)

qplot(theta, likelihood(theta), geom = "line", ylab = "Likelihood", xlab = "theta")
```



The estimate ($\hat{\theta}$) is the value of θ with the maximum likelihood (ML) value, which in this case is 0.3.

A 95% confidence interval (CI) can then be calculated using the asymptotic normal approximation

$$\hat{\theta} \pm 1.96 \frac{1}{\sqrt{I(\hat{\theta})}}$$

where $I(\hat{\theta})$ is the expected second derivative of the log-likelihood at the estimate. This calculation is based on the assumption that the sample size is of sufficient size that the likelihood is normally distributed.

In the current case,

$$I(\hat{\theta}) = \frac{n}{\hat{\theta}(1-\hat{\theta})}$$

which gives a point estimate of 0.3 and lower and upper 95% confidence intervals of 0.02 and 0.58 respectively.

1.3.1.2 Posterior Probability

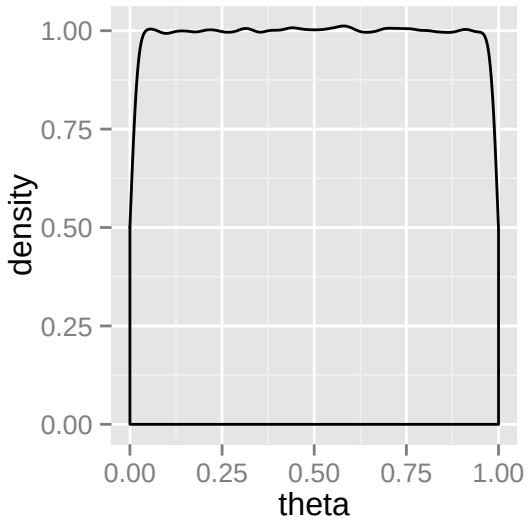
The posterior probability on the other hand is given by Bayes rule which states that

$$p(\theta|y) \propto p(y|\theta)p(\theta)$$

where $p(\theta)$ is the prior probability.

Bayesians consider this an advantage because prior information can be incorporated into an analysis while frequentists consider it subjective. In most cases Bayesians use *low-information* priors which have very small effects on the posteriors. For example a uniform distribution with a lower limit of 0 and an upper limit of 1 ($dunif(0,1)$) is commonly used for probabilities.

```
qplot(runif(10^6, 0, 1), geom = "density", xlab = "theta")
```



As it is generally not possible to calculate the posterior probability, the posterior probability distribution is sampled using Markov Chain Monte Carlo (MCMC) algorithms such as Gibbs Sampling.

1.3.1.2.1 Gibbs Sampling Consider the case where the parameters $\theta = (\theta_1, \theta_2, \ldots, \theta_k)$ then Gibbs Sampling proceed as follows

Step 1 Choose starting *initial* values for $\theta_1^{(0)}$ and $\theta_2^{(0)}$

Step 2 Sample $\theta_1^{(1)}$ from $p(\theta_1|\theta_2^{(0)}, y)$

Sample $\theta_2^{(1)}$ from $p(\theta_2|\theta_1^{(1)}, y)$

Step 3 *Iterate* step 2 thousands (or millions) of times to obtain a sample from $p(\theta|y)$.

Typically this is performed for two or more independent chains.

1.4 JAGS and BUGS

Programming an efficient MCMC algorithm for a particular model is outside the scope of most research projects. Fortunately, JAGS (which stands for Just Another Gibbs Sampler) can take a dataset and a model specified in the simple but flexible BUGS language (which stands for Bayesian Analysis Using Gibbs Sampling) and perform MCMC sampling for us.

In order to do this we will use the `jaggernaut` package to talk to the standalone JAGS program via the `rjags` package.

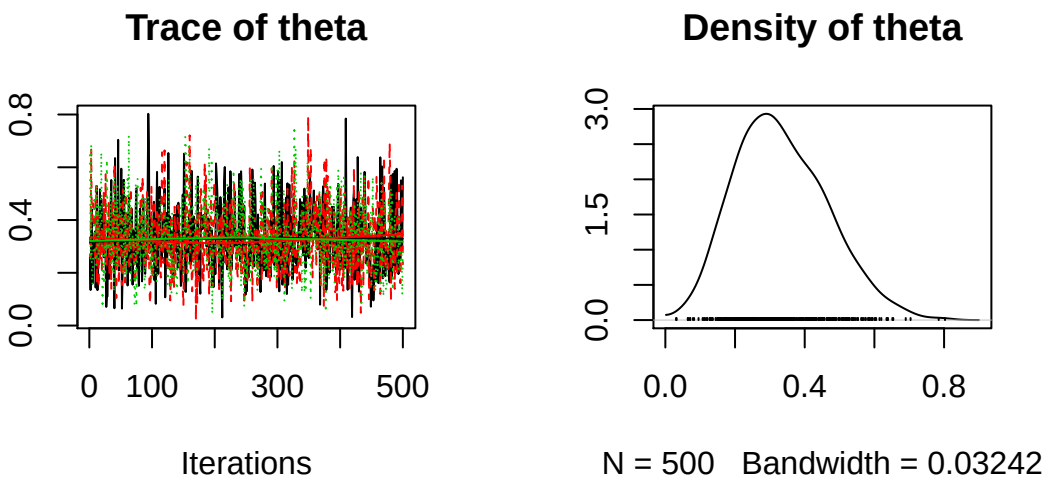
First we need to specify the underlying probability model in the BUGS language and save it as an object of class `jags_model`.

```
model1 <- jags_model("model {
  theta ~ dunif(0, 1)
  y ~ dbin(theta, n)
}")
```

then we call JAGS using `jaggernaut` in the default report mode to generate samples from θ's posterior probability distribution.

```
data <- data.frame(n = 10, y = 3)
analysis1 <- jags_analysis(model1, data = data)
```

```
plot(analysis1)
```




```
coef(analysis1)
```

```
##        estimate     lower     upper      sd error significance
## theta 0.3330172 0.1136778 0.6172016 0.13206    76            0
```

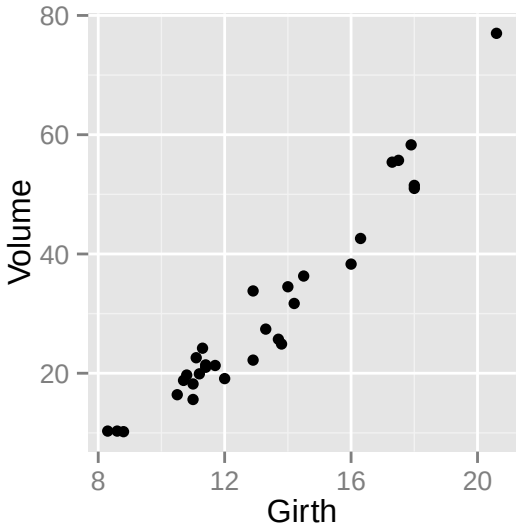
The model output indicates that the point estimate (in this case the mean of the samples) is 0.33 and the 95% credible interval (in this case the 2.25th and 97.75th percentiles) is 0.11 to 0.62. The model output also indicates that the posterior probability distribution has a standard deviation (sd) of 0.13. The significance and error values are discussed later.

Exercise 1 *Previous studies indicate that the coin was definitely biased towards tails. Modify the prior distribution accordingly and rerun the above model. How does the posterior distribution change?*

1.5 Black Cherry Trees

The `trees` data set in the dataset package provides information on the girth and volume of 31 black cherry trees.

```
qplot(x = Girth, y = Volume, data = trees)
```



Algebraically, the linear regression of `Volume` against `Girth` can be defined as follows

$$Volume_i = \alpha + \beta * Girth_i + \epsilon_i$$

where α is the intercept and β is the slope and the error terms (ϵ_i) are drawn from a normal distribution with an standard deviation of σ.

The model can be defined as follows in the BUGS language where `<-` indicates a *deterministic* as opposed to *stochastic* node (which is indicated by `~`).

```
model1 <- jags_model("model {
  alpha ~ dnorm(0, 50^-2)
  beta ~ dnorm(0, 10^-2)
  sigma ~ dunif(0, 10)

  for(i in 1:length(Volume)) {
    eMu[i] <- alpha + beta * Girth[i]
    Volume[i] ~ dnorm(eMu[i], sigma^-2)
  }
}")
```

The standard deviations of the normal distributions are raised to the power of `-2` because (for historical reasons) Bayesians quantify variation in terms of the *precision* (τ) as opposed to the variance (σ^2) or standard deviation (σ) where $\tau = 1/\sigma^2$.

1.5.1 Parallel Chains

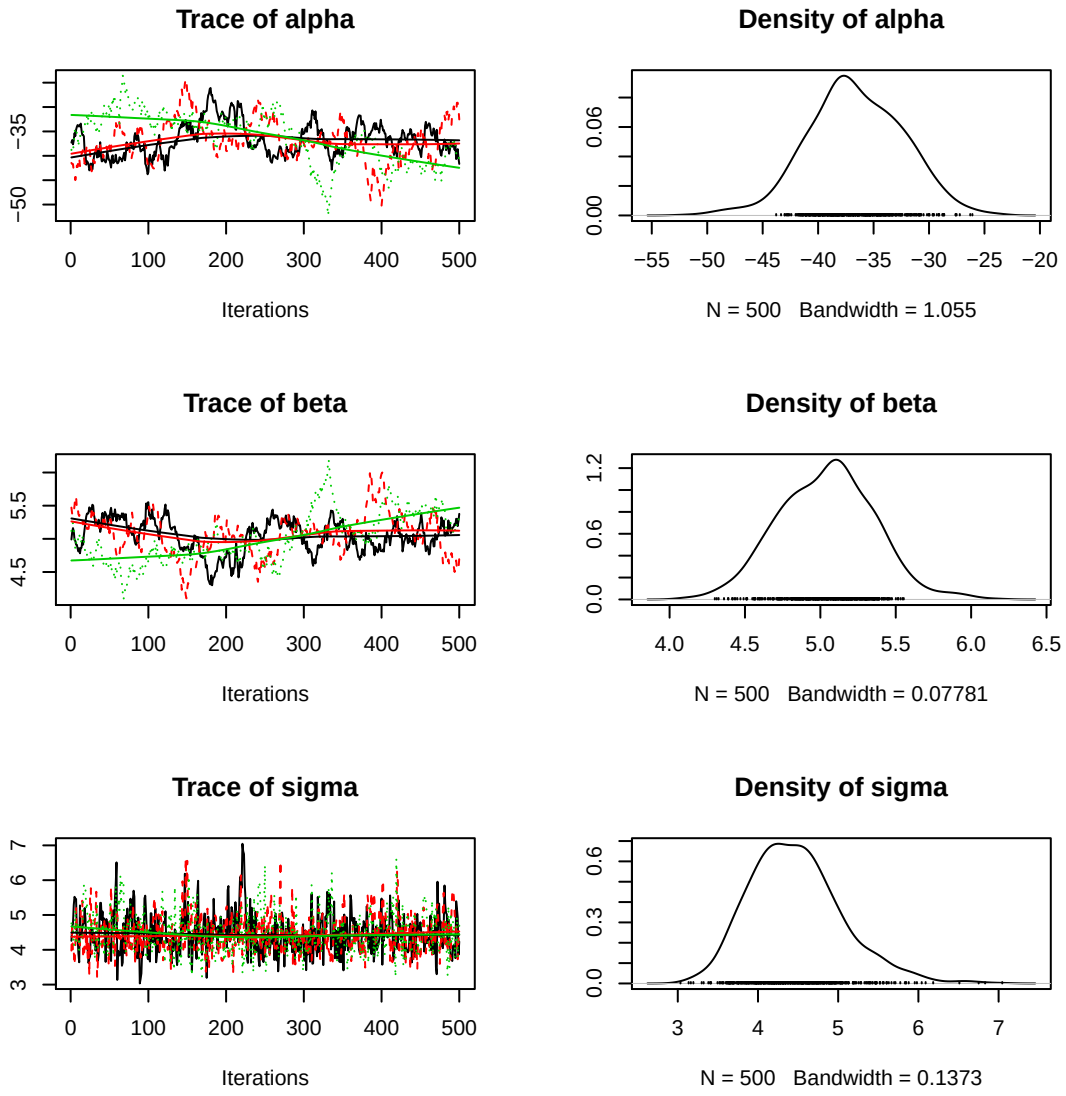
To reduce the analysis time, MCMC chains can be run on parallel processes. In jaggernaut this achieved using the `registerDoParallel` function and by setting the parallel option to be `TRUE`. This only needs to be done once at the start of a session.

```
registerDoParallel()
opts_jagr(parallel = TRUE)
```

The resultant trace plots and coefficients for the `trees` analysis are as follows.

```
data(trees)
analysis1 <- jags_analysis(model1, data = trees)
```

```
plot(analysis1)
```




```
coef(analysis1)
```

```
##         estimate      lower      upper      sd error significance
## alpha -36.604784 -45.143395 -28.581025 4.31380    23            0
## beta    5.041664   4.434013   5.672065 0.31690    12            0
## sigma   4.473256   3.531306   5.807566 0.57913    25            0
```

Exercise 2 *What do you notice about the trace plots? The output of* `auto_corr(analysis1)` *and* `cross_cor(analysis1)` *might give you some clues.*

1.5.2 Chain Mixing

Cross-correlations between parameters, which cause poor chain mixing (i.e., high auto-correlation), can sometimes be eliminated or reduced by reparameterising the model. In the current model, `Girth` can be centered, i.e., `Girth - mean(Girth)`, using the following code `select_data(model1) <- c("Volume", "Girth+")`.

Exercise 3 *What is the effect of centring* `Girth` *on the trace plots?*

Note if you ever want to examine the actual data being passed to JAGS set the modify_data term of your `jags_model` object to be a simple function that prints and returns its one argument

```
modify_data(model1) <- function (data) { print(data); data }
```

1.5.2.1 glm Module In the case of generalized linear mixed models the JAGS `glm` module uses block updating to free the user of the need to centre predictor variables. It currently only works on parameters that have a normal prior distribution. The `glm` module can be loaded using the following code. The `list.models()` function lists the currently loaded modules.

```
library(rjags)
list.modules()
load.module("glm")
list.modules()
unload.module("glm")
list.modules()
```

For further information see the JAGS User Manual.

Exercise 4 *What is the effect of loading the* `glm` *module (without manually centring* `Girth`*) on the trace plots?*

1.5.3 Derived Parameters

Many researchers estimate fitted values, predictions and residuals and perform posterior preditive checks by monitoring additional nodes in their model code.

The disadvantages of this approach are that:

- the model code becomes more complicated.
- the MCMC sampling takes longer.
- adding derived parameters requires a model rerun.
- the table of parameter estimates becomes unwiedly.

`jaggernaut` overcomes these problems by allowing derived parameters to be defined in a separate chunk of BUGS code as demonstrated below.

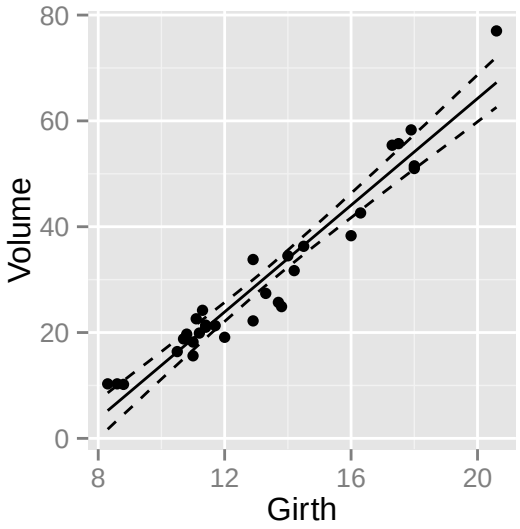
```
dcode <- "data {
  for(i in 1:length(Volume)) {
    prediction[i] <- alpha + beta * Girth[i]

    simulated[i] ~ dnorm(prediction[i], sigma^-2)

    D_observed[i] <- log(dnorm(Volume[i], prediction[i], sigma^-2))
```

```
    D_simulated[i] <- log(dnorm(simulated[i], prediction[i], sigma^-2))
  }
  residual <- (Volume - prediction) / sigma
  discrepancy <- sum(D_observed) - sum(D_simulated)

}"
```

1.5.3.1 Predictions xxx

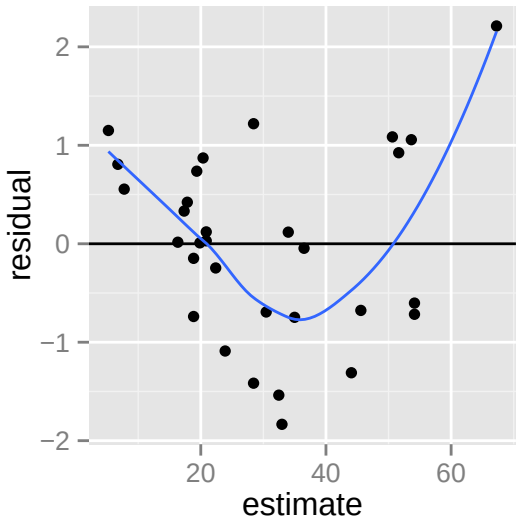
```
prediction <- predict(analysis1, newdata = "Girth", derived_code = dcode)
```

```
gp <- ggplot(data = prediction, aes(x = Girth, y = estimate))
gp <- gp + geom_point(data = dataset(analysis1), aes(y = Volume))
gp <- gp + geom_line()
gp <- gp + geom_line(aes(y = lower), linetype = "dashed")
gp <- gp + geom_line(aes(y = upper), linetype = "dashed")
gp <- gp + scale_y_continuous(name = "Volume")

print(gp)
```



1.5.3.2 Residuals xxx

```
fitted <- fitted(analysis1, derived_code = dcode)
fitted$residual <- residuals(analysis1, derived_code = dcode)$estimate

qplot(estimate, residual, data = fitted) + geom_hline(yintercept = 0) +
    geom_smooth(se = FALSE)
```



1.5.3.3 Posterior Predictive Checks xxx

```
predictive_check(analysis1, derived_code = dcode)
```

```
##     parameter  estimate     lower    upper     sd error significance
## 1 discrepancy 0.5939063 -9.145227 10.62569 5.0694  1664       0.9533
```

1.5.4 Allometry

As discussed in the R course notes the relationship between Volume and Girth is expected to be allometric because the cross-sectional area at an given point scales to the square of the girth (circumference).

Expressed as an allometric relationship the model becomes

$$Volume_i = \alpha * Girth_i^{\beta} * \epsilon_i$$

which can be reparameterised as a linear regression by log transforming `Volume` and `Girth`.

$$log(Volume_i) = \alpha + \beta * log(Girth_i) + \epsilon_i$$

Variables can be log transformed in the model code or in the select_data argument, i.e., `select_data(model1) <- c("log(Volume)", "log(Girth)")`.

Exercise 5 *Fit the above allometric model to the* `trees` *data set. Is the model fit improved?*

Exercise 6 *Is there any support for adding log transformed Height to the model?*

1.5.5 Significance Values

The significance value in the jaggernaut table of coefficients is twice the probability that the posterior distribution spans zero. As such it represents the Bayesian equivalent of a frequentist two-sided p-value (Greenland and Poole 2013). By definition parameters that represent standard deviations, which must be greater than zero, will have a significance value of 0.

1.5.6 Error Values

The error value in the table of coefficients is the *percent relative error*, which is half the credible interval as a percent of the point estimate, i.e.,

$$error = (upper - lower) * 0.5/estimate * 100$$

.

Standard deviations with a uniform prior distribution that is not updated by the data have error values of 0.95. As a general rule, I question the informativeness of parameters representing standard deviations which have an error value ≥ 0.8.

References

Greenland, Sander, and Charles Poole. 2013. "Living with P Values: Resurrecting a Bayesian Perspective on Frequentist Statistics." *Epidemiology* 24 (1): 62–68. doi:10.1097/EDE.0b013e3182785741. http://content.wkhealth.com/linkback/openurl?sid=WKPTLP:landingpage&an=00001648-201301000-00009.