

## Inference Tutorial 9

[https://people.maths.bris.ac.uk/~sw15190/TOI/jags\\_user\\_manual.pdf](https://people.maths.bris.ac.uk/~sw15190/TOI/jags_user_manual.pdf) is a link to the JAGS manual. The `str` function in R is useful for examining the structure of an R object that you are unsure of. To use JAGS you have to produce a text file containing your model specification. On the university windows computers the editors ‘notepad’ or ‘wordpad’ can be used for this (‘word’ tends to create problems with hidden characters). It is probably best to create the file wherever you usually store your R script files, for example on the network drive accessed by opening the file manager (3rd icon from lower left in windows), and clicking on ‘Computer’ followed by ‘MyFiles’. If you use this location then `setwd("O:")` (that’s the letter, not zero) within R will cause R to look for jags (and other) files in this location (If you stored your files in a directory called, e.g., ‘foo’ within ‘Myfiles’ then use `setwd("O:/foo")`). Don’t forget `library(rjags)`.

1. As a simple example of the use of JAGS, consider the grasshopper survival data and model from tutorials 7 and 8, one more time, but this time allowing the  $\alpha$  parameter to take any positive value. Recall that the data are observations of  $x$ , the length of time in excess of 14 days that it took for a random sample of 10 grasshoppers infected with a fungal disease to die, where the times are measured from infection.

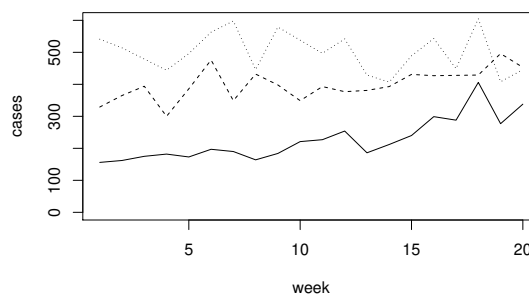
1.6 12.1 5.2 6.2 6.8 9.6 17.8 24.4 4.1 7.8

A gamma distribution may be a good model here, so that the p.d.f. of  $x$  is

$$f(x) = \frac{\beta^\alpha}{(\alpha - 1)!} x^{\alpha-1} e^{-x\beta} \quad x > 0$$

in JAGS the gamma distribution (`dgamma`) is parameterized in terms of  $\alpha$  and  $\beta$ , in that order. Use a gamma prior for  $\beta$  (`dgamma(1, .01)`) and a log normal prior for  $\alpha$  (`dlnorm(1, 1)`).

- (a) Use JAGS to sample 10000 values from the posterior density of  $\alpha, \beta$ .
  - (b) Produce trace plots and ACFs for  $\alpha$  and  $\beta$  to check the chain mixing, convergence and correlation.
  - (c) Compute the correlation lengths and effective sample sizes for the two chains.
  - (d) Produce histograms illustrating the marginal posterior distributions of  $\alpha$  and  $\beta$  and a scatter plot illustrating the posterior correlation.
  - (e) Find 95% credible intervals for  $\alpha$  and  $\beta$ .
2. 20 weeks of new case data for an emergent disease are observed for three neighbouring towns in a remote region. The data are shown here (towns 1, 2 and 3 are shown solid, dashed and dotted, respectively).



The public health department trying to control the disease needs to establish whether the underlying case rate is increasing or decreasing in each town, using the JAGS model specification and R code given at the end of this question. The case data for the 3 towns are stored in vectors `Y1`, `Y2` and `Y3` of list `dat`. Study the code and answer the following questions as concisely as possible.

- (a) Briefly describe the key principles of Gibbs sampling.
- (b) What is the key feature of a directed acyclic graph (DAG), and why is the DAG of a model useful in the automatic construction of Gibbs samplers?
- (c) Write out the model specified in the JAGS code, mathematically.
- (d) What do the `r` parameters and the `alpha` parameters mean in terms of the disease?

- (e) Comment on the final plots from the point of view of chain convergence, and describe two further diagnostics that might be examined.
- (f) Comment on the implications of the results in terms of the disease outbreak, and suggest a further quantitative summary that might be useful to compute.

```

model { ## JAGS model specification
  for (i in 1:M) {
    Y1[i] ~ dpois(mu1[i]+alpha[1]*mu2[i]+alpha[2]*mu3[i])
    d1[i] ~ dnorm(0,tau1)
    mu1[i] <- N1*exp(r1*i+d1[i])
    Y2[i] ~ dpois(mu2[i]+alpha[3]*mu1[i]+alpha[4]*mu3[i])
    d2[i] ~ dnorm(0,tau2)
    mu2[i] <- N2*exp(r2*i+d2[i])
    Y3[i] ~ dpois(mu3[i]+alpha[5]*mu1[i]+alpha[6]*mu2[i])
    d3[i] ~ dnorm(0,tau3)
    mu3[i] <- N3*exp(r3*i+d3[i])
  }
  for (i in 1:6) {
    alpha[i] ~ dunif(0,0.1)
  }
  tau1 ~ dgamma(1.0,0.1)
  r1 ~ dnorm(0,.1)
  N1 ~ dnorm(100,0.01)
  tau2 ~ dgamma(1.0,0.1)
  r2 ~ dnorm(0,.1)
  N2 ~ dnorm(300,0.01)
  tau3 ~ dgamma(1.0,0.1)
  r3 ~ dnorm(0,.1)
  N3 ~ dnorm(500,0.01)
} ## end of JAGS code

## R code...
library(rjags)
load("disease.rda") ## load 'dat' list
dat$M <- length(dat$Y1) ## include number of time points for JAGS
mod <- jags.model("jags.jags",data=dat)
um <- jags.samples(mod,c("r1","r2","r3"),n.iter=50000,thin=10)

par(mfrow=c(2,2),mar=c(4,4,1,1))
plot(um$r1,type="l",ylab="r1")
plot(um$r2,type="l",ylab="r2")
plot(um$r3,type="l",ylab="r3")

```

