**Exercise 1 - Running a basic JAGS model in R**

1. Open a new session in R-studio
2. Set a working directory wherever you wish to save the material from the workshop
3. Open a new .txt file in the R session (File -> New File -> Text File)
4. Write the model in new text file:

model{

# Likelihood part:

Positives ~ dbinom(prevalence, TotalTests)

# Prior part:

prevalence ~ dbeta(2, 2)

# Hooks for automatic integration with R:

#data# Positives, TotalTests

#monitor# prevalence

#inits# prevalence

}

1. Save this file as “basic\_model.bug”
2. Open a new R script – (if one is not already open)
3. Attach the “runjags” package

library(runjags)

1. Define the required input data:

Positives <- 20

TotalTests <- 100

1. Define the initial data for the MCMC chains:

prevalence <- list(chain1=0.05, chain2=0.95)

1. Run the model

results <- run.jags('basic\_model.bug', adapt = 0, n.chains=2, burnin=0, sample=100)

1. Plot and view the results

plot(results)

results

1. Increase the adapt iterations (to 1000) burn in (to 5000) and samples (to 10000) look at how these impact on the outputs

results <- run.jags('basic\_model.bug', adapt = 1000, n.chains=2, burnin=5000, sample=10000)

plot(results)

results