**Exercise 1 – True prevalence estimation model**

Before we apply the 2-test 2-population (Hui-Walter model) let’s start with running a basic JAGS model in R. This model is the so called “true prevalence estimation” model, where we estimate the true prevalence of infection adjusting for test imperfection.

*Steps*

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

model {

y ~ dbin(ap,n)

ap <- tp\*Se + (1-tp)\*(1-Sp)

# Uniform (non-informative) prior distribution

tp ~ dbeta(1,1)

# Informative priors for Se and Sp

Se ~ dbeta(25.4, 3.4)

Sp ~ dbeta(95, 5)

#data# n, y

#monitor# tp, Se, Sp

#inits# tp, Se, Sp

}

1. Save this file as “tp\_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:

n = 4072

y = 1210

1. Define the initial values data for the MCMC chains:

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

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

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

1. Run the model

results <- run.jags(“tp\_model.bug”, n.chains=2, burnin=5000, sample=10000)

1. Plot and view the results

plot(results) # Click backwards to view all plots

summary(results)