**Exercise 3 – Multi-test Multi-populations Hui-Walter models**

Now let’s move to the 2-tests - 5-populations setting.

1. Encode the following table in your R working directory, as a matrix and save it as a variable named Cross\_Classified.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Pop\_1 | Pop\_2 | Pop\_3 | Pop\_4 | Pop\_5 |
| T1- | T2- | 92 | 126 | 54 | 119 | 88 |
| T1+ | T2- | 39 | 20 | 45 | 36 | 34 |
| T1- | T2+ | 15 | 17 | 14 | 20 | 14 |
| T1+ | T2+ | 63 | 24 | 70 | 46 | 64 |

*Solution*

*Download the csv file that has been emailed to you and load into the working directory*

Cross\_Classified = read.csv("ex3.csv", sep=";")

1. Write the 2\_test\_5\_population model and save as “hw2\_blca.bug”.

model{

for(p in 1:Populations){

Cross\_Classified [1:4, p] ~ dmulti(prob[1:4, p], TotalTests[p])

# Test1- Test2-

prob[1,p] <- (prev[p] \* ((1-se[1])\*(1-se[2]))) + ((1-prev[p]) \* ((sp[1])\*(sp[2])))

# Test1+ Test2-

prob[2,p] <- (prev[p] \* ((se[1])\*(1-se[2]))) + ((1-prev[p]) \* ((1-sp[1])\*(sp[2])))

# Test1- Test2+

prob[3,p] <- (prev[p] \* ((1-se[1])\*(se[2]))) + ((1-prev[p]) \* ((sp[1])\*(1-sp[2])))

# Test1+ Test2+

prob[4,p] <- (prev[p] \* ((se[1])\*(se[2]))) + ((1-prev[p]) \* ((1-sp[1])\*(1-sp[2])))

prev[p] ~ dbeta(1, 1)

}

se[1] ~ dbeta(1, 1)T(1-sp[1], )

sp[1] ~ dbeta(1, 1)

se[2] ~ dbeta(1, 1)T(1-sp[2], )

sp[2] ~ dbeta(1, 1)

#data# Cross\_Classified, TotalTests, Populations

#monitor# prev, se, sp

#inits# prev, se, sp

}

1. Attach the “runjags” package

library(runjags)

1. Specify the data in R environment

Populations <- 5

TotalTests <- 2

# Cross\_Classified is already defined in step 1

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

prev <- list(chain1=c(0.1, 0.1, 0.1, 0.9, 0.9), chain2=c(0.9, 0.9, 0.9, 0.1, 0.1))

se <- list(chain1=c(0.5,0.99), chain2=c(0.99,0.5))

sp <- list(chain1=c(0.5,0.99), chain2=c(0.99,0.5))

1. Run the model

results <- run.jags(“hw2\_blca.bug”, n.chains=2, burnin=5000, sample=10000)

1. Plot and view the results

summary(results)

pt <- plot(results)

pt$`prev[1].plot1`

pt$`prev[1].plot3`

print(pt[["prev[1].plot1"]])

print(pt[["se[1].plot1"]])

print(pt[["sp[1].plot1"]])

print(pt[["sp[1].plot3"]])

1. Apply the model to 3 populations instead of 5 and see if there is any change to the results.