**WinBUGS Codes**

1. **Continuous data model**

model **{**

for (i in 1:**ns**) *#ns=numer of studies*

{*# Likelihood for each arm*

for (k in 1:**na**[i]) *#na[i] = numer of arms in i-th study*

{

**m**[i, k] ~ dnorm(theta[i, k], prec[i, k])

theta[i, k] <- mu[i] + delta[i, k]

prec[i, k] <- pow(**e**[i, k], -2)

}

*# Study-level relative effects*

w[i, 1] <- 0

delta[i, 1] <- 0

for (k in 2:na[i])

{ *# parameterize multi-arm trials using a trick to avoid multidimensional normal distribution*

delta[i, k] ~ dnorm(md[i, k], taud[i, k])

md[i, k] <- d[**t**[i, 1], **t**[i, k]] + sw[i, k]

taud[i, k] <- tau.d \* 2 \* (k - 1) / k

w[i, k] <- delta[i, k] - d[**t**[i, 1], **t**[i, k]]

sw[i, k] <- sum(w[i, 1:k-1]) / (k - 1)

}

}

*# Drug (placebo related) effect priors*

for(i in 2:19){

d.pl[i]~dnorm(0,0.0001)

}

d.pl[1]~dnorm(0,1000000)

*# Study baseline priors*

for (i in 1:**ns**) {

mu[i] ~ dnorm(0,0.001)}

sd.d ~ dunif(0,1.1)

tau.d <- pow(sd.d, -2)

for(i in 1:19)

{ for(j in 2:19 )

{ d[i,j]<-d.pl[i]-d.pl[j] *#effect of j-th drug – effect of i-th drug*

}

}

*# SUCRA*

for(i in 1:19)

{

ranks[i]<-rank(d.pl[],i)

rank.distr[i,1]<-0

cumul[i,1]<-0

for(j in 1:19)

{

antirank[i,j]<-step(j-ranks[i])

rank.distr[i,j+1]<-(rank.distr[i,j]+antirank[i,j])

}

}

*#new numeration – implemented after obtaining results of the SUCRA*

d.pl.n[1]<-d.pl[13]

d.pl.n[2]<-d.pl[7]

d.pl.n[3]<-d.pl[9]

d.pl.n[4]<-d.pl[4]

d.pl.n[5]<-d.pl[3]

d.pl.n[6]<-d.pl[11]

d.pl.n[7]<-d.pl[10]

d.pl.n[8]<-d.pl[5]

d.pl.n[9]<-d.pl[18]

d.pl.n[10]<-d.pl[2]

d.pl.n[11]<-d.pl[6]

d.pl.n[12]<-d.pl[19]

d.pl.n[13]<-d.pl[8]

d.pl.n[14]<-d.pl[12]

d.pl.n[15]<-d.pl[17]

d.pl.n[16]<-d.pl[14]

d.pl.n[17]<-d.pl[15]

d.pl.n[18]<-d.pl[1]

d.pl.n[19]<-d.pl[16]

for(i in 1:19)

{ for(j in 2:19 )

{d.n[i,j]<-d.pl.n[i]-d.pl.n[j]

}

}

#residual deviance

for(i in 1:ns)

{

for(k in 1:na[i])

{

#Deviance contribution

dev[i,k] <- (m[i,k]-theta[i,k])\*(m[i,k]-theta[i,k])\*prec[i,k]

}

# summed residual deviance contribution for this trial

resdev[i] <- sum(dev[i,1:na[i]])

}

totresdev <- sum(resdev[])

**}**

#INPUT DATA:

*list(****t****=structure(.Data=c(1,18,NA,1,18,NA,1,18,NA,1,18,11,1,18,9,1,2,4,1,2,4,1,3,NA,1,4,NA,1,4,NA,1,4,12,1,4,9,1,5,6,1,5,NA,1,6,11,1,6,9,1,6,NA,1,7,NA,1,7,NA,1,7,9,1,8,NA,1,8,NA,1,8,9,1,10,NA,1,10,NA,1,11,12,1,11,14,1,11,16,1,11,16,1,12,NA,1,12,NA,1,12,NA,1,13,NA,1,13,NA,1,15,NA,1,16,NA,1,16,NA,1,17,NA,1,3,NA,1,3,NA,1,14,11,11,4,14,11,12,NA,12,19,NA,12,9,NA,11,4,NA,4,7,NA,7,9,11,11,10,NA,12,4,NA,4,9,NA,18,9,NA,12,4,NA,11,4,NA,12,10,NA), .Dim=c(55,3)),*

***m****=structure(.Data=c(0.292,0.706,NA,0.678,1.178,NA,0.918,0.944,NA,0.869,1.219,1.160,0.948,1.170,1.254,0.706,1.041,1.322,0.665,1.178,1.250,0.603,1.115,NA,0.387,0.814,NA,0.644,1.172,NA,0.882,1.121,0.978,0.564,1.046,1.188,0.788,1.406,1.246,0.994,1.117,NA,0.432,0.943,0.980,0.621,0.918,1.174,0.945,1.288,NA,0.505,1.115,NA,0.729,1.577,NA,0.892,1.434,1.320,0.633,1.007,NA,0.515,1.019,NA,0.571,0.975,1.493,0.514,0.865,NA,0.756,1.604,NA,0.322,0.739,0.736,0.875,0.986,0.857,0.709,1.166,0.692,0.648,1.086,0.505,0.017,1.131,NA,0.825,1.091,NA,0.753,0.895,NA,-1.11,4.371,NA,-0.45,1.563,NA,0.845,0.937,NA,0.737,0.771,NA,0.636,0.507,NA,0.106,0.089,NA,1.017,1.544,NA,1.070,1.446,NA,0.869,0.885,NA,1.677,1.960,1.832,-0.62,-1.66,NA,1.707,1.690,NA,1.415,1.185,NA,1.779,2.167,NA,1.372,1.519,NA,1.137,0.935,1.440,0.887,0.777,NA,1.080,1.391,NA,1.971,2.175,NA,1.437,1.437,NA,1.355,1.575,NA,-5.83,-6.80,NA,2.390,1.516,NA),.Dim=c(55,3)),*

***e****=structure(.Data=c(0.091,0.090,1000,0.087,0.085,1000,0.087,0.062,1000,0.078,0.081,0.080,0.081,0.078,0.078,0.099,0.072,0.072,0.102,0.073,0.070,0.092,0.092,1000,0.113,0.127,1000,0.134,0.134,1000,0.095,0.071,0.074,0.118,0.081,0.211,0.112,0.067,0.071,0.093,0.055,1000,0.101,0.098,0.100,0.099,0.100,0.100,0.079,0.081,1000,0.091,0.088,1000,0.090,0.076,1000,0.088,0.079,0.081,0.129,0.085,1000,0.109,0.089,1000,0.099,0.078,0.076,0.094,0.109,1000,0.091,0.093,1000,0.105,0.212,0.117,0.099,0.178,0.109,0.094,0.094,0.092,0.091,0.093,0.069,0.224,0.247,1000,0.075,0.073,1000,0.120,0.080,1000,0.344,0.362,1000,0.168,0.194,1000,0.075,0.084,1000,0.099,0.069,1000,0.096,0.097,1000,0.306,0.317,1000,0.083,0.053,1000,0.079,0.081,1000,0.106,0.124,100000000,0.254,0.260,0.260,0.150,0.343,1000,0.205,0.155,1000000,0.220,0.253,1000,0.119,0.119,1000,0.077,0.078,1000,0.255,0.262,0.255,0.201,0.206,1000,0.097,0.081,1000,0.066,0.067,1000,0.075,0.078,1000,0.127,0.136,1000,0.230,0.216,1000,0.214,0.295,1000),.Dim=c(55,3)),****na****=c(2,2,2,3,3,3,3,2,2,2,3,3,3,2,3,3,2,2,2,3,2,2,3,2,2,3,3,3,3,2,2,2,2,2,2,2,2,2,2,2,3,3,2,2,2,2,2,3,2,2,2,2,2,2,2),****ns****=55)*

SUCRA -results

**node mean sd MC error 2.5% median 97.5% start sample**

rank.distr[1,20] 2.973 0.9889 0.01908 1.0 3.0 5.0 20101 9900

rank.distr[2,20] 9.862 3.643 0.06082 4.0 10.0 17.0 20101 9900

rank.distr[3,20] 13.06 3.461 0.06098 6.0 14.0 18.0 20101 9900

rank.distr[4,20] 13.77 2.152 0.04557 9.0 14.0 17.0 20101 9900

rank.distr[5,20] 10.33 3.794 0.07036 4.0 10.0 18.0 20101 9900

rank.distr[6,20] 9.516 3.038 0.05328 5.0 9.0 16.0 20101 9900

rank.distr[7,20] 17.01 1.561 0.02905 12.0 18.0 18.0 20101 9900

rank.distr[8,20] 9.216 3.444 0.05943 4.0 9.0 17.0 20101 9900

rank.distr[9,20] 15.24 2.047 0.04096 10.0 16.0 18.0 20101 9900

rank.distr[10,20] 12.0 3.803 0.07795 5.0 12.0 18.0 20101 9900

rank.distr[11,20] 12.63 2.479 0.05225 8.0 13.0 17.0 20101 9900

rank.distr[12,20] 8.574 2.501 0.05699 5.0 8.0 14.0 20101 9900

rank.distr[13,20] 19.0 0.0 1.005E-1219.0 19.0 19.0 20101 9900

rank.distr[14,20] 5.105 2.598 0.04794 1.0 5.0 12.0 20101 9900

rank.distr[15,20] 4.847 3.504 0.05386 1.0 4.0 15.0 20101 9900

rank.distr[16,20] 2.275 1.231 0.02621 1.0 2.0 5.0 20101 9900

rank.distr[17,20] 5.216 5.567 0.1967 1.0 3.0 18.0 20101 9900

rank.distr[18,20] 10.05 2.782 0.04159 5.0 10.0 16.0 20101 9900

rank.distr[19,20] 9.328 5.743 0.1469 1.0 8.0 18.0 20101 9900

1. **Model for binary data (on example of responders)**

model {

for (i in 1:ns) {

# Likelihood for each arm

for (k in 1:na[i]) {

r[i, k] ~ dbin(p[i, k], n[i, k])

logit(p[i, k]) <- mu[i] + delta[i, k]

}

# Study-level relative effects

w[i, 1] <- 0

delta[i, 1] <- 0

for (k in 2:na[i]) { # parameterize multi-arm trials using a trick to avoid dmnorm

delta[i, k] ~ dnorm(md[i, k], taud[i, k])

md[i, k] <- d[t[i, 1], t[i, k]] + sw[i, k]

taud[i, k] <- tau.d \* 2 \* (k - 1) / k

w[i, k] <- delta[i, k] - d[t[i, 1], t[i, k]]

sw[i, k] <- sum(w[i, 1:k-1]) / (k - 1)

}

}

# Study baseline priors

for (i in 1:ns) {

mu[i] ~ dnorm(0,0.0001)

}

for(i in 1:19)

{

for(j in 1:19)

{

d[i,j]<-d.pl[i]-d.pl[j] #effect "j" - effect "i"

}

}

for(i in 2:19){

d.pl[i]~dnorm(0,0.001)

}

d.pl[1]<-0

# d.pl[1]~dnorm(0,1000000)

#absoulte effect (rate), original ordering

for (k in 1:ns.l) # calculated first for Lithium

{

r.l[k]~dbin(p.l[k],n.l[k])

logit(p.l[k])<-mu.l[k]

mu.l[k]~dnorm(mu0.l,tau.l)

}

mu0.l~dnorm(0,0.001)

rate.l<-exp(mu0.l)/(1+exp(mu0.l))

SE.l~dunif(0,2)

tau.l<-1/(SE.l\*SE.l)

for(i in 1:nd)

{

mu0[i]<-mu0.l-d.n[i,9] #’9’ is the origanl ID for Lithium

rate[i]<-exp(mu0[i])/(1+exp(mu0[i]))

}

for(i in 1:nd)

{

for(j in 2:nd)

{

RD[i,j]<-(rate[i]-rate[j]) #NNT = 1/RD was not estimaed here: to avoid division by zero which may occur.

}

}

# *SUCRA*

for(i in 1:19)

{

ranks[i]<-rank(rate[],i)

rank.distr[i,1]<-0

cumul[i,1]<-0

for(j in 1:19)

{

antirank[i,j]<-step(j-ranks[i])

rank.distr[i,j+1]<-(rank.distr[i,j]+antirank[i,j])

#cumul[i,j+1]<-cumul[i,j]+rank.distr[i,j+1]

}

}

# Variance prior

sd.d ~ dunif(0,2)

tau.d <- pow(sd.d, -2)

#new numeration *– implemented after obtaining results of the SUCRA*

d.pl.n[1]<-d.pl[13]

d.pl.n[2]<-d.pl[7]

d.pl.n[3]<-d.pl[9]

d.pl.n[4]<-d.pl[4]

d.pl.n[5]<-d.pl[3]

d.pl.n[6]<-d.pl[11]

d.pl.n[7]<-d.pl[10]

d.pl.n[8]<-d.pl[5]

d.pl.n[9]<-d.pl[18]

d.pl.n[10]<-d.pl[2]

d.pl.n[11]<-d.pl[6]

d.pl.n[12]<-d.pl[19]

d.pl.n[13]<-d.pl[8]

d.pl.n[14]<-d.pl[12]

d.pl.n[15]<-d.pl[17]

d.pl.n[16]<-d.pl[14]

d.pl.n[17]<-d.pl[15]

d.pl.n[18]<-d.pl[1]

d.pl.n[19]<-d.pl[16]

for(i in 1:19)

{ for(j in 2:19 )

{d.n[i,j]<-d.pl.n[i]-d.pl.n[j]

OR[i,j]<-exp(d.n[i,j])

}

}

#residual deviance

for(i in 1:ns)

{

for(k in 1:na[i])

{

rhat[i,k] <- p[i,k] \* n[i,k] # expected value of the numerators

#Deviance contribution

dev[i,k] <- 2 \* (r[i,k] \* (log(r[i,k])-log(rhat[i,k]))

+ (n[i,k]-r[i,k]) \* (log(n[i,k]-r[i,k]) - log(n[i,k]-rhat[i,k]))) }

# summed residual deviance contribution for this trial

resdev[i] <- sum(dev[i,1:na[i]])

}

totresdev <- sum(resdev[])

}

# INPUT DATA

list(ns=53,t=structure(.Data=c(1,2,NA,1,2,NA,1,2,NA,1,2,9,1,2,6,1,3,10,1,3,10,1,5,NA,1,5,NA,1,5,NA,1,10,NA,1,10,NA,1,10,16,1,10,6,1,11,12,1,11,NA,1,12,9,1,12,6,1,12,NA,1,13,NA,1,13,NA,1,13,6,1,18,NA,1,18,NA,1,18,6,1,4,NA,1,4,NA,1,9,16,1,9,7,1,9,7,1,16,NA,1,16,NA,1,14,NA,1,14,NA,1,8,NA,1,9,15,1,9,15,1,15,NA,1,15,NA,1,17,NA,9,7,NA,9,16,NA,16,19,NA,9,10,NA,16,4,NA,9,12,NA,16,6,NA,9,10,NA,9,4,NA,16,10,NA,10,6,NA,2,6,NA,10,13,NA),.Dim=c(53,3)),na=c(2,2,2,3,3,3,3,2,2,2,2,2,3,3,3,2,3,3,2,2,2,3,2,2,3,2,2,3,3,3,2,2,2,2,2,3,3,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2),

r=structure(.Data=c(23,49,NA,43,72,NA,49,110,NA,56,72,71,58,78,80,32,78,111,26,78,94,29,57,NA,60,199,NA,67,93,NA,16,34,NA,24,35,NA,31,82,75,43,53,13,36,106,94,50,143,NA,26,57,52,35,43,55,53,82,NA,29,55,NA,52,107,NA,46,73,68,23,66,NA,19,64,NA,18,65,93,21,38,NA,33,73,NA,18,17,32,30,48,41,44,15,37,2,9,NA,60,90,NA,1,5,NA,1,14,NA,55,55,NA,30,52,31,30,52,58,27,56,NA,29,29,NA,2,3,NA,9,8,NA,12,9,NA,27,24,NA,5,3,NA,11,8,NA,46,60,NA,10,5,NA,52,60,NA,8,8,NA,52,68,NA,127,132,NA,88,70,NA,102,98,NA),.Dim=c(53,3)),

n=structure(.Data=c(120,123,NA,132,136,NA,130,256,NA,163,154,155,152,166,161,94,183,203,103,189,188,117,118,NA,160,332,NA,152,158,NA,66,70,NA,56,54,NA,99,201,186,97,104,20,104,190,192,115,328,NA,95,107,98,100,101,98,159,149,NA,119,127,NA,142,144,NA,138,153,144,66,131,NA,65,137,NA,88,176,170,98,94,NA,115,120,NA,72,35,67,77,77,74,95,36,84,19,17,NA,177,187,NA,8,8,NA,26,32,NA,158,155,NA,112,114,115,111,113,215,99,209,NA,106,107,NA,12,8,NA,15,15,NA,13,14,NA,30,30,NA,20,20,NA,15,15,NA,77,77,NA,21,15,NA,71,69,NA,24,24,NA,123,125,NA,231,213,NA,173,164,NA,164,164,NA),.Dim=c(53,3)),n.l=c(155,98,35,77,36,114,113,15,13,20,77,71,24),r.l=c(71,52,17,48,15,52,52,9,12,5,46,52,8),ns.l=13,nd=19

)

# INITIALS

list(sd.d=1,mu=c(0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),d.pl=c(NA,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0),

,delta=structure(.Data=c(NA,0,NA,NA,0,NA,NA,0,NA,NA,0,0,NA,0,0,NA,0,0,NA,0,0,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,0,NA,0,0,NA,0,0,NA,0,NA,NA,0,0,NA,0,0,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,0,NA,0,NA,NA,0,NA,NA,0,0,NA,0,NA,NA,0,NA,NA,0,0,NA,0,0,NA,0,0,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,0,NA,0,0,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA,NA,0,NA),.Dim=c(53,3)))

**3. Multiple Treatment meta-regression** (the meta-regression parts in **bold**)

model **{**

for (i in 1:**ns**) *#ns=numer of studies*

{*# Likelihood for each arm*

for (k in 1:**na**[i]) *#na[i] = numer of arms in i-th study*

{

**m**[i, k] ~ dnorm(theta[i, k], prec[i, k])

theta[i, k] <- mu[i] + delta[i, k] **+ (beta[t[i,k]]-beta[t[i,1]]) \* (x[i]-mx)**

**#x[i] – value of considered covariate of i-th study**

**#mx – mean value of covariates over all studies**

prec[i, k] <- pow(**e**[i, k], -2)

}

*# Study-level relative effects*

w[i, 1] <- 0

delta[i, 1] <- 0

for (k in 2:na[i])

{ *# parameterize multi-arm trials using a trick to avoid multidimensional normal distribution*

delta[i, k] ~ dnorm(md[i, k], taud[i, k])

md[i, k] <- d[**t**[i, 1], **t**[i, k]] + sw[i, k]

taud[i, k] <- tau.d \* 2 \* (k - 1) / k

w[i, k] <- delta[i, k] - d[**t**[i, 1], **t**[i, k]]

sw[i, k] <- sum(w[i, 1:k-1]) / (k - 1)

}

}

**beta[1]<-0**

**for(i in 2:19){**

**d.pl[i]~dnorm(0,000.1)**

**beta[i]~dnorm(b,tau.b)**

**}**

**tau.b~dnorm(0,0.01)I(0,)**

**b~dnorm(0,0.001)**

*# Drug (placebo related) effect priors*

for(i in 2:19){

d.pl[i]~dnorm(0,0.0001)

}

d.pl[1]~dnorm(0,1000000)

*# Study baseline priors*

for (i in 1:**ns**) {

mu[i] ~ dnorm(0,0.001)}

sd.d ~ dunif(0,1.1)

tau.d <- pow(sd.d, -2)

for(i in 1:19)

{ for(j in 2:19 )

{ d[i,j]<-d.pl[i]-d.pl[j] *#effect of j-th drug – effect of i-th drug*

}

}

for(i in 1:19)

{ for(j in 2:19 )

{d.n[i,j]<-d.pl.n[i]-d.pl.n[j]

}

}

}

**Table 1.** Potential effect modifiers examined by various multiple treatments meta-regression models.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| ***Model*** | ***mean*** | ***Lower 95% CrI*** | ***Upper***  ***95% CrI*** | ***SD*** | ***Z*** | ***p-value*** |
| %Psychotics considering all candidate antimanic drugs | -0.021 | -0.123 | 0.082 | 0.052 | 0.396 | 0.692 |
| %Psychotics considering all effective antimanic drugs | -0.033 | -0.160 | 0.094 | 0.127 | 0.256 | 0.798 |
| %Psychotics considering only Antipsychotics | -0.017 | -0.153 | 0.118 | 0.136 | 0.124 | 0.901 |
| %Psychotics considering only Mood Stabilizers | -0.004 | -0.248 | 0.236 | 0.242 | 0.018 | 0.986 |
| %Psychotics considering Mood Stabilizers and Tamoxifen | -0.027 | -0.230 | 0.178 | 0.204 | 0.134 | 0.894 |
| %Mixed state considering all candidate antimanic drugs | 0.014 | -0.089 | 0.117 | 0.053 | 0.270 | 0.787 |
| %Mixed state considering all effective antimanic drugs | 0,018 | -0,106 | 0,142 | 0,124 | 0,141 | 0,888 |
| Discontinuation rates considering all candidate antimanic drugs | 0.014 | -0.087 | 0.116 | 0.101 | 0.136 | 0.892 |
| Discontinuation rates considering all effective antimanic drugs | 0.019 | -0.100 | 0.139 | 0.120 | 0.158 | 0.874 |
| Publication year considering all candidate antimanic drugs | -0.051 | -0.187 | 0.074 | 0.067 | 0.768 | 0.443 |
| Publication year considering all candidate antimanic drugs without tamoxifen | -0.024 | -0.145 | 0.095 | 0.120 | 0.202 | 0.840 |
| Publication year considering all effective antimanic drugs | -0.054 | -0.207 | 0.084 | 0.145 | 0.369 | 0.712 |
| Publication year considering all effective antimanic drugs without tamoxifen | -0.014 | -0.149 | 0.121 | 0.135 | 0.104 | 0.917 |
| Sponsorship considering all candidate antimanic drugs | -0.501 | -1.240 | 0.312 | 0.396 | 1.265 | 0.206 |
| Sponsorship all effective antimanic drugs | -0.444 | -1.228 | 0.417 | 0.823 | 0.540 | 0.589 |

**4. Model for continouos data: pairwise meta-analysis and loop-consistency testing**

model **{**

for (i in 1:ns)

{# Likelihood for each arm

for (k in 1:na[i])

{

m[i, k] ~ dnorm(theta[i, k], prec[i, k])

theta[i, k] <- mu[i] + delta[i, k]

prec[i, k] <- pow(e[i, k], -2)

}

# Study-level relative effects

w[i, 1] <- 0

delta[i, 1] <- 0

for (k in 2:na[i])

{ # parameterize multi-arm trials using a trick to avoid dmnorm

delta[i, k] ~ dnorm(md[i, k], taud[i, k])

md[i, k] <- d[t[i, 1], t[i, k]] + sw[i, k]

taud[i, k] <- tau.d \* 2 \* (k - 1) / k

w[i, k] <- delta[i, k] - d[t[i, 1], t[i, k]]

sw[i, k] <- sum(w[i, 1:k-1]) / (k - 1)

}

}# no transitivity of effect assumed here,

#arms 2 and 3 from 3-arm studies duplicated as a separate input data (as a extra study) – if not only comparison between arms 1 vs 2 and 1 vs 3 would be considered

for(i in 1:nd){

for(j in (i+1):nd){

d[i,j]~dnorm(0,0.0001)

}

for(j in 1:(i-1))

{d[i,j]<--d[j,i]}

d[i,i]<-0

}

d.pl[1]~dnorm(0,1000000)

# Study baseline priors

for (i in 1:ns) {

mu[i] ~ dnorm(0,0.0001)}

sd.d~dunif(0,1.1)

tau.d<-1/(sd.d\*sd.d)

#new numeration accordingly to SUCRA

for(j in 1:19)

{

for(k in 1:19)

{

d.n[j,k]<-d[nid[j],nid[k]]

}}

nid[1]<-13

nid[2]<-7

nid[3]<-9

nid[4]<-4

nid[5]<-3

nid[6]<-11

nid[7]<-10

nid[8]<-5

nid[9]<-18

nid[10]<-2

nid[11]<-6

nid[12]<-8

nid[13]<-12

nid[14]<-19

nid[15]<-14

nid[16]<-15

nid[17]<-1

nid[18]<-17

nid[19]<-16

#loops for inconsistency testing

for(i in 1:17)

{

for(j in (i+1):18)

{

for(k in (j+1):19)

{

loop[i,j,k]<-d.n[i,j]+d.n[j,k]+d.n[k,i]

}

}

}

**}**

#INPUT DATA: duplicated arms 2 and 3 of three arm-studies included as a separate studies: list(nd=19,t=structure(.Data=c(1,18,NA,1,18,NA,1,18,NA,1,18,11,1,18,9,1,2,4,1,2,4,1,3,NA,1,4,NA,1,4,NA,1,4,12,1,4,9,1,5,6,1,5,NA,1,6,11,1,6,9,1,6,NA,1,7,NA,1,7,NA,1,7,9,1,8,NA,1,8,NA,1,8,9,1,10,NA,1,10,NA,1,11,12,1,11,14,1,11,16,1,11,16,1,12,NA,1,12,NA,1,12,NA,1,13,NA,1,13,NA,1,15,NA,1,16,NA,1,16,NA,1,17,NA,1,3,NA,1,3,NA,1,14,11,11,4,14,11,12,NA,12,19,NA,12,9,NA,11,4,NA,4,7,NA,7,9,11,11,10,NA,12,4,NA,4,9,NA,18,9,NA,12,4,NA,11,4,NA,12,10,NA,18,11,NA,18,9,NA,2,4,NA,2,4,NA,4,12,NA,4,9,NA,5,6,NA,6,11,NA,6,9,NA,7,9,NA,8,9,NA,11,12,NA,11,14,NA,11,16,NA,11,16,NA,14,11,NA,4,14,NA,9,11,NA), .Dim=c(73,3)),

m=structure(.Data=c(0.292,0.706,NA,0.678,1.178,NA,0.918,0.944,NA,0.869,1.219,1.160,0.948,1.170,1.254,0.706,1.041,1.322,0.665,1.178,1.250,0.603,1.115,NA,0.387,0.814,NA,0.644,1.172,NA,0.882,1.121,0.978,0.564,1.046,1.188,0.788,1.406,1.246,0.994,1.117,NA,0.432,0.943,0.980,0.621,0.918,1.174,0.945,1.288,NA,0.505,1.115,NA,0.729,1.577,NA,0.892,1.434,1.320,0.633,1.007,NA,0.515,1.019,NA,0.571,0.975,1.493,0.514,0.865,NA,0.756,1.604,NA,0.322,0.739,0.736,0.875,0.986,0.857,0.709,1.166,0.692,0.648,1.086,0.505,0.017,1.131,NA,0.825,1.091,NA,0.753,0.895,NA,-1.11,4.371,NA,-0.45,1.563,NA,0.845,0.937,NA,0.737,0.771,NA,0.636,0.507,NA,0.106,0.089,NA,1.017,1.544,NA,1.070,1.446,NA,0.869,0.885,1.190,1.677,1.960,1.832,-0.62,-1.66,NA,1.707,1.690,NA,1.415,1.185,NA,1.779,2.167,NA,1.372,1.519,NA,1.137,0.935,1.440,0.887,0.777,NA,1.080,1.391,NA,1.971,2.175,NA,1.437,1.437,NA,1.355,1.575,NA,-5.83,-6.80,NA,2.390,1.516,NA,1.219,1.160,NA,1.170,1.254,NA,1.041,1.322,NA,1.178,1.250,NA,1.121,0.978,NA,1.046,1.188,NA,1.406,1.246,NA,0.943,0.980,NA,0.918,1.174,NA,1.434,1.320,NA,0.975,1.493,NA,0.739,0.736,NA,0.986,0.857,NA,1.166,0.692,NA,1.086,0.505,NA,0.885,1.190,NA,1.960,1.832,NA,0.935,1.440,NA),.Dim=c(73,3)),

e=structure(.Data=c(0.091,0.090,NA,0.087,0.085,NA,0.087,0.062,NA,0.078,0.081,0.080,0.081,0.078,0.078,0.099,0.072,0.072,0.102,0.073,0.070,0.092,0.092,NA,0.113,0.127,NA,0.134,0.134,NA,0.095,0.071,0.074,0.118,0.081,0.211,0.112,0.067,0.071,0.093,0.055,NA,0.101,0.098,0.100,0.099,0.100,0.100,0.079,0.081,NA,0.091,0.088,NA,0.090,0.076,NA,0.088,0.079,0.081,0.129,0.085,NA,0.109,0.089,NA,0.099,0.078,0.076,0.094,0.109,NA,0.091,0.093,NA,0.105,0.212,0.117,0.099,0.178,0.109,0.094,0.094,0.092,0.091,0.093,0.069,0.224,0.247,NA,0.075,0.073,NA,0.120,0.080,NA,0.344,0.362,NA,0.168,0.194,NA,0.075,0.084,NA,0.099,0.069,NA,0.096,0.097,NA,0.306,0.317,NA,0.083,0.053,NA,0.079,0.081,NA,0.106,0.124,0.113,0.254,0.260,0.260,0.150,0.343,NA,0.205,0.155,NA,0.220,0.253,NA,0.119,0.119,NA,0.077,0.078,NA,0.255,0.262,0.255,0.201,0.206,NA,0.097,0.081,NA,0.066,0.067,NA,0.075,0.078,NA,0.127,0.136,NA,0.230,0.216,NA,0.214,0.295,NA,0.081,0.080,NA,0.078,0.078,NA,0.072,0.072,NA,0.073,0.070,NA,0.071,0.074,NA,0.081,0.211,NA,0.067,0.071,NA,0.098,0.100,NA,0.100,0.100,NA,0.079,0.081,NA,0.078,0.076,NA,0.212,0.117,NA,0.178,0.109,NA,0.094,0.092,NA,0.093,0.069,NA,0.124,0.113,NA,0.260,0.260,NA,0.262,0.255,NA), .Dim=c(73,3)),na=c(2,2,2,3,3,3,3,2,2,2,3,3,3,2,3,3,2,2,2,3,2,2,3,2,2,3,3,3,3,2,2,2,2,2,2,2,2,2,2,2,3,3,2,2,2,2,2,3,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2),ns=73)

**Table 2.** *Deviance information criterion* (DIC) and *residual deviance* (Dres) for all the networks, examined.

|  |  |  |  |
| --- | --- | --- | --- |
| **Network** | ***No data points*** | ***Residual deviance*** | ***DIC*** |
| SMD, all treatments | 128 | 162.2 | -59.4 |
| SMD, no Haloperidol | 116 | 154 | -48.5 |
| SMD, no placebo | 62 | 72.5 | -26.6 |
| SMD, no outliers | 118 | 132.2 | -80.5 |
| OR, responders | 122 | 125.8 | 797.8 |
| OR, discontinuations | 129 | 128 | 816.3 |