library(gemtc)

library(rjags)

library(igraph)

library(dmetar)

library(ggplot2)

library(forcats)

**HR meta-analysis**

network <- mtc.network(data.re = hr)

summary(network)

plot(network, vertex.color=c("#df8f44","#00a1d5","#79af97"), vertex.size=60, vertex.label.color="black", vertex.label.cex=1)

model <- mtc.model(network,

linearModel = "random",

n.chain = 4)

mcmc2 <- mtc.run(model, n.adapt = 5000, n.iter = 100000, thin = 10)

summary(mcmc2)

plot(mcmc2)

gelman.plot(mcmc2)

gelman.diag(mcmc2)$mpsrf

nodesplit <- mtc.nodesplit(network,

linearModel = "random",

n.adapt = 5000,

n.iter = 100000,

thin = 10)

summary(nodesplit)

plot(summary(nodesplit))

rank <- rank.probability(mcmc2, preferredDirection = -1)

plot(rank, beside=TRUE, cex.names=0.5)

rank.probability <- rank.probability(mcmc2)

sucra <- sucra(rank.probability, lower.is.better = TRUE)

plot(sucra)

**IRR network meta-analysis**

network <- mtc.network(data.re = irr)

summary(network)

plot(network, vertex.color=c("#df8f44","#00a1d5","#79af97"), vertex.size=60, vertex.label.color="black", vertex.label.cex=1)

model <- mtc.model(network,

linearModel = "random",

n.chain = 4)

mcmc2 <- mtc.run(model, n.adapt = 5000, n.iter = 100000, thin = 10)

summary(mcmc2)

plot(mcmc2)

gelman.plot(mcmc2)

gelman.diag(mcmc2)$mpsrf

nodesplit <- mtc.nodesplit(network,

linearModel = "random",

n.adapt = 5000,

n.iter = 100000,

thin = 10)

summary(nodesplit)

plot(summary(nodesplit))

rank <- rank.probability(mcmc2, preferredDirection = -1)

plot(rank, beside=TRUE, cex.names=0.5)

rank.probability <- rank.probability(mcmc2)

sucra <- sucra(rank.probability, lower.is.better = TRUE)

plot(sucra)

write.csv(rank, file = "rank.csv")