Supplementary Table S3. All network meta-analysis commands used in R

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| Package | Commands |
| gemtcrjags | network <-mtc.network(data)plot(network) |
| model <-mtc.model(network, type = "consistency", factor = 2.5, n.chain=4,likelihood="binom",link="log",linearModel="random")results <-mtc.run(model, n.adapt = 5000, n.iter = 20000, thin = 1,sampler ="rjags") |
| model <-mtc.model(network,type = "consistency",n.chain = 3,likelihood="normal",link="identity",linearModel="random")results <- mtc.run(model, sampler = "rjags", n.adapt = 5000, n.iter = 20000, thin = 1) |
| gelman.plot(results) |
| forest(relative.effect(results, "placebo"),digits=4) |
| windows()plot(results) |
| ranks<- rank.probability(results,preferredDirection=1)print(ranks)plot(ranks, beside=TRUE)write.csv(ranks,"ranks.csv") |
| result.anohe <-mtc.anohe(network, n.adapt=10000, n.iter=15000)summary.anohe <- summary(result.anohe)plot(summary.anohe, xlim=log(c(0.2, 5)),digits=4)dev.off()summary.anohe |
| result<-mtc.nodesplit(network)summary(result)names(result)summary(result$d.A.C)pdf("nodesplit.pdf")summary.ns <- summary(result)print(summary.ns)plot(summary.ns,digits=4) |