Appendix 7: Technical appendix

Open Bugs code: random effects consistency model

(http://www.nicedsu.org.uk/Evidence-Synthesis-TSD-series(2391675).htm)

```
model{
for(i in 1:ns){
    w[i,1] <- 0    # adjustment for multi-arm trials is zero for control
arm
    delta[i,1] <- 0           # treatment effect is zero for control arm
    mu[i] ~ dnorm(0,.0001)    # vague priors for all trial baselines

  for (k in 1:na[i]) {
        r[i,k] ~ dbin(p[i,k],n[i,k])      #binomial likelihood
        logit(p[i,k]) <- mu[i] + delta[i,k]     # model for linear
predictor
        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]])

for (k in 2:na[i]) {
# trial-specific LOR distributions
        delta[i,k] ~ dnorm(md[i,k],taud[i,k])
# mean of LOR distributions (with multi-arm trial correction)
        md[i,k] <-  d[t[i,k]] - d[t[i,1]] + sw[i,k]
# precision of LOR distributions (with multi-arm trial correction)
        taud[i,k] <- tau *2*(k-1)/k
# adjustment for multi-arm RCTs
 w[i,k] <- (delta[i,k] - d[t[i,k]] + d[t[i,1]])
# cumulative adjustment for multi-arm trials
sw[i,k] <- sum(w[i,1:k-1])/(k-1)    }   }

totresdev <- sum(resdev[])           # Total Residual Deviance
d[1]<-0       # treatment effect is zero for reference treatment

# vague priors for treatment effects
for (k in 2:nt){  d[k] ~ dnorm(0,.0001) }

sd ~ dunif(0,5)      # vague prior for between-trial SD
tau <- pow(sd,-2)    # between-trial precision = (1/between-trial variance)

# ranking on relative scale
for (k in 1:nt) { rk[k] <- rank(d[],k)     # assumes events are "bad"
best[k] <- equals(rk[k],1)     #calculate probability that treat k is best
# calculates probability that treat k is h-th best
for (h in 1:nt){ prob[h,k] <- equals(rk[k],h) }       }

# pairwise ORs and LORs for all possible pair-wise comparisons
for (c in 1:(nt-1)) {
for (k in (c+1):nt) {
or[c,k] <- exp(d[k] - d[c])
lor[c,k] <- (d[k]-d[c])
}}}
```

2. Prior distributions used in the network meta-analyses of three outcomes reported in the paper

Vaginal delivery
All prior distributions in the vaginal delivery random effects consistency model were vague.

Trial baseline parameter: mu~dnorm(0,10000)
Treatment effect parameter: d~dnorm(0,10000)
Heterogeneity parameter: sd~dunif (0,5)

Caesarean section
All prior distributions in the caesarean section random effects consistency model were vague.

Trial baseline parameter: mu~dnorm(0,10000)
Treatment effect parameter: d~dnorm(0,10000)
Heterogeneity parameter: sd~dunif (0,5)

Hyperstimulation
All prior distributions in the hyperstimulation random effects consistency model were vague.

Trial baseline parameter: mu~dnorm(0,10000)
Treatment effect parameter: d~dnorm(0,10000)
Heterogeneity parameter: sd~dunif (0,5)

3. Details of convergence for all three outcomes reported in the paper for random effects consistency models.

Vaginal delivery
Convergence was assessed using two chains using the Brooks-Gelman-Rubin tool in OpenBUGS and was achieved by 35,000 simulations for vaginal delivery (random effects consistency model). Estimates are based on a further 70,000 updates.

Caesarean section
Convergence was assessed using two chains using the Brooks-Gelman-Rubin tool in OpenBUGS and was achieved by 90,000 simulations for cesarean section (RE consistency model). Estimates are based on a further 180,000 updates.

Hyperstimulation
Convergence was assessed using two chains using the Brooks-Gelman-Rubin tool in OpenBUGS and was achieved by 21,000 simulations (RE consistency model). Estimates are based on a further 60,000 updates.