

Appendix 4: WINBUGS code for network meta-analysis [posted as supplied by author]

a) Base case analysis

```

# Trial-level data given as treatment differences
# Random effects model for multi-arm trials
model{
  # *** PROGRAM STARTS
  for(i in 1:ns) {
    # LOOP THROUGH STUDIES
    y[i] ~ dnorm(delta[i],prec[i]) # normal likelihood for trials
    var[i] <- pow(se[i],2) # calculate variances
    prec[i] <- 1/var[i] # set precisions

    # Trial-specific meandiff distributions
    delta[i] ~ dnorm(md[i],tau)

    #Mean of random effects distributions,with multi-arm trial correct
    md[i] <- d[t[i,2]] - d[t[i,1]]

    #Deviance contribution
    dev[i] <- (y[i]-delta[i])*(y[i]-delta[i])*prec[i]

    #summed residual deviance contribution for this trial
    resdev[i] <- sum(dev[i])
  }
  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)}
  }
  between.trial.var ~ dunif(0,5)
  tau<- 1/between.trial.var

  test~dnorm(2,4)I(0.1,)

  #Ranking
  for (k in 1:4) {
    rk[k] <- 5-rank(d[],k)
    best[k] <- equals(rk[k],1)}
} # *** PROGRAM ENDS

# ns= number of studies;
# nt=number of treatments;

list(ns=12, nt=4, nc=6)
c[] t[,1] t[,2] y[] se[]
1 1 3 0.4711 0.1647
2 1 4 2.4499 0.1691
3 2 4 0.7974 0.4078
4 4 4 1.0656 0.1131
2 1 4 2.2700 0.3041
1 1 3 5.4996 1.4148
1 1 3 1.9448 0.8245
2 1 4 2.8740 0.1402
1 1 3 1.3230 0.8183
5 3 3 -1.8738 0.6183
6 2 3 0.6408 0.4910
5 3 3 -0.5222 1.2273
END

```

Dbar = post.mean of -2logL; Dhat = -2LogL at post.mean of stochastic nodes

	Dbar	Dhat	pD	DIC
test	0.000	0.000	-0.000	0.000
y	13.467	3.074	10.396	23.860
total	13.467	3.074	10.396	23.860

b) Sensitivity analysis

Code and results for sensitivity analysis excluding studies where interventions were introduced at multiple time points (Helms et al., Kirkland et al., and Al-Tawfiq et al).

```
# Trial-level data given as treatment differences
# Random effects model for multi-arm trials
model{
  for(i in 1:ns) {
    y[i] ~ dnorm(delta[i],prec[i])
    var[i] <- pow(se[i],2)
    prec[i] <- 1/var[i]

    # Trial-specific meandiff distributions
    delta[i] ~ dnorm(md[i],tau)

    #Mean of random effects distributions,with multi-arm trial correct
    md[i] <- d[t[i,2]] - d[t[i,1]]

    #Deviance contribution
    dev[i] <- (y[i]-delta[i])*(y[i]-delta[i])*prec[i]

    #summed residual deviance contribution for this trial
    resdev[i] <- sum(dev[i])
  }
  totresdev <- sum(resdev[])
  d[1]<-0
  for (k in 2:nt){d[k] ~ dnorm(0,.0001)}
  between.trial.var ~ dunif(0,5)
  tau<- 1/between.trial.var

  test~dnorm(2,4)I(0.1,)

  #Ranking
  for (k in 1:4) {
    rk[k] <- 5-rank(d[],k)
    best[k] <- equals(rk[k],1)}
}

# ns= number of studies;
# nt=number of treatments;
```

```
list(ns=9, nt=4, nc=6)
c[] t[,1] t[,2] y[] se[]
1 1 3 0.4711 0.1647
3 2 4 0.7974 0.4078
4 4 4 1.0656 0.1131
2 1 4 2.2700 0.3041
2 1 4 2.8740 0.1402
1 1 3 1.3230 0.8183
5 3 3 -1.8738 0.6183
6 2 3 0.6408 0.4910
5 3 3 -0.5222 1.2273
END
```

Dbar = post.mean of -2logL; Dhat = -2LogL at post.mean of stochastic nodes

	Dbar	Dhat	pD	DIC
test	0.000	0.000	-0.000	0.000
y	6.661	-1.189	7.851	14.512
total	6.661	-1.189	7.851	14.512