```
model{                      # *** PROGRAM STARTS

for(i in 1:ns2) {           # LOOP THROUGH 2-ARM STUDIES

   y[i,2] ~ dnorm(delta[i,2],prec[i,2]) # normal likelihood for 2-arm trials

#Deviance contribution for trial i

   resdev[i] <- (y[i,2]-delta[i,2])*(y[i,2]-delta[i,2])*prec[i,2]

 }



for(i in 1:(ns2)){          #   LOOP THROUGH ALL STUDIES

   for (k in 2:na[i]) {     #  LOOP THROUGH ARMS

     var[i,k] <- pow(se[i,k],2)   # calculate variances

     prec[i,k] <- 1/var[i,k]     # set precisions

     delta[i,k] <-  d[t[i,k]] - d[t[i,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) }

for (c in 1:nt-1){

       for (k in 2:nt) {

               IC[c,k] <- d[k] - d[c]

               exp_IC[c,k] <-exp(IC[c,k])

       }
```

```
        }

# ranking

for (k in 1:nt) {

#    rk[k] <- rank(d[],k)

   rk[k] <- nt+1-rank(d[],k)                # assumes events are 'good'

   rank1[k] <- equals(rk[k],1)

   rank2[k] <- equals(rk[k],2)

   rank3[k] <- equals(rk[k],3)

   rank4[k] <- equals(rk[k],4)


        }


}
```