```
model{                      # *** PROGRAM STARTS

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

   mu[i] ~ dnorm(0,.0001)      # vague priors for all trial baselines

   for (k in 1:na[i])  {      # LOOP THROUGH ARMS

      r[i,k] ~ dbin(p[i,k],n[i,k])    # binomial likelihood

# model for linear predictor

      logit(p[i,k]) <- mu[i] + d[t[i,k]] - d[t[i,1]]

# expected value of the numerators

      rhat[i,k] <- p[i,k] * n[i,k]

#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]])

   }

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)

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

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

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

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


        }

}
```