```
model{ # *** PROGRAM STARTS

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

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 1:2) { # LOOP THROUGH ARMS

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
dev[i,k] <- 2 * (r[i,k] * (log(r[i,k])-log(rhat[i,k]))) #Deviance contribution
+ (n[i,k]-r[i,k]) * (log(n[i,k]-r[i,k]) - log(n[i,k]-rhat[i,k])))

}

resdev[i] <- sum(dev[i,]) # summed residual deviance contribution for this trial
delta[i,2] ~ dnorm(md[i,2],prec[t[i,2],t[i,1]]) # trial-specific LOR distributions
md[i,2]<-d[t[i,2]] - d[t[i,1]]
}

totresdev <- sum(resdev[]) #Total Residual Deviance
d[1]<- 0 # treatment effect is zero for reference treatment
for (k in 2:nt){ d[k] ~ dnorm(0,.0001) }
#sd ~ dunif(0,5) # vague prior for between-trial SD

priorprec1<-pow(1.54,-2)
priorprec2<-pow(1.73,-2)
priorprec4<-pow(1.27,-2)
priorprec5<-pow(1.47,-2)

tau1~dlnorm(-2.54,priorprec1)
tau4~dlnorm(-1.51,priorprec4)
tau5~dlnorm(-2.1,priorprec5)
tau2~dlnorm(-2.77,priorprec2)

tau[2,1]<-tau1
tau[3,1]<-tau1
tau[4,3]<-tau4
tau[5,4]<-tau5
tau[6,1]<-tau2
tau[7,1]<-tau2

prec[2,1]<-1/tau[2,1]
prec[3,1]<-1/tau[3,1]
prec[4,3]<-1/tau[4,3]
prec[5,4]<-1/tau[5,4]
prec[6,1]<-1/tau[6,1]
prec[7,1]<-1/tau[7,1]


# pairwise ORs and LORs for all possible pair-wise comparisons, if nt>2

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])
}
}

# ranking on relative scale

for (k in 1:nt) {
rk[k] <- nt+1-rank(d[],k) # assumes events are "good"
# rk[k] <- rank(d[],k) # assumes events are "bad"
best[k] <- equals(rk[k],1) #calculate probability that treat k is best
}

# Provide estimates of treatment effects T[k] on the natural (probability) scale
# Given a Mean Effect, meanA, for 'standard' treatment 1, with precision (1/variance) precA

#A ~ dnorm(meanA,precA)
```

```
#for (k in 1:nt) { logit(T[k]) <- A + d[k] }

# Provide estimates of number needed to treat NNT[k], Risk Difference RD[k],
# and Relative Risk RR[k], for each treatment, relative to treatment 1

#for (k in 2:nt) {

#NNT[k] <- 1/(T[k] - T[1]) # assumes events are "good"
# NNT[k] <- 1/(T[1]- T[k]) # assumes events are "bad"
#RD[k] <- T[k] - T[1]
#RR[k] <- T[k]/T[1]
#}
}


list(
d=c( NA,-0.5,-0.5,-0.5,-0.5,-0.5,-0.5),
tau1=0.1,
tau2=0.1,
tau4=0.1,
tau5=0.1,
)

list(
d=c( NA,0.5,0.5,0.5,0.5,0.5,0.5),
tau1=0.5,
tau2=0.5,
tau4=0.5,
tau5=0.5,
)


list(nt=7, ns=9)
```

r[,1]	n[,1]	r[,2]	n[,2]	t[,1]	t[,2]
1	14	10	24	1	2
1	129	4	140	1	2
8	25	10	25	4	5
4	20	1	20	3	4
5	39	54	81	1	6
10	74	45	78	1	3
1	26	7	26	1	7
27	108	161	214	1	3
21	75	7	23	3	4

```
END
```