WinBUGS code

Fixed effects binomial likelihood with logit link

```
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 (c+1):nt) {

       or[c,k] <- exp(d[k] - d[c])

       lor[c,k] <- (d[k]-d[c])

      }

}


# ranking

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
}

}
```

Random effects binomial likelihood with logit link

```
model{                              # *** PROGRAM STARTS

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

    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]) {            # 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

#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]) {            # LOOP THROUGH ARMS

# 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)


# 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])
      }
}


# ranking
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
}


}
```

Fixed effects normal likelihood and identify link

```
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
        var[i,k] <- pow(se[i,k],2)      # calculate variances
        prec[i,k] <- 1/var[i,k]         # set precisions
        y[i,k] ~ dnorm(theta[i,k],prec[i,k]) # binomial likelihood
# model for linear predictor
        theta[i,k] <- mu[i] + d[t[i,k]] - d[t[i,1]]
#Deviance contribution
        dev[i,k] <- (y[i,k]-theta[i,k])*(y[i,k]-theta[i,k])*prec[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 control arm
# 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]
       }
       }
# ranking
for (k in 1:nt) {
     rk[k] <- nt + 1- rank(d[],k)
   best[k] <- equals(rk[k],1)
       }
       }
```

Random effects normal likelihood and identify link

```
model{                               # *** PROGRAM STARTS
for(i in 1:ns){                      #   LOOP THROUGH STUDIES
    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]) {             #  LOOP THROUGH ARMS
        var[i,k] <- pow(se[i,k],2)   # calculate variances
        prec[i,k] <- 1/var[i,k]      # set precisions
        y[i,k] ~ dnorm(theta[i,k],prec[i,k]) # binomial likelihood
        theta[i,k] <- mu[i] + delta[i,k]  # model for linear predictor
#Deviance contribution
        dev[i,k] <- (y[i,k]-theta[i,k])*(y[i,k]-theta[i,k])*prec[i,k]
      }
#  summed residual deviance contribution for this trial

    resdev[i] <- sum(dev[i,1:na[i]])

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

# 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, 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 control arm

# 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)

for (c in 1:nt-1){

       for (k in 2:nt) {

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

       }

       }

# ranking

for (k in 1:nt) {

     rk[k] <- nt + 1- rank(d[],k)

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

       }

}
```