Appendix M: WinBUGS code

All WinBUGS code used in this guideline was based on specimens given in the NICE Decision Support Unit’s series of Technical Support Documents (TSDs) on evidence synthesis, especially TSD2 and TSD5.

M.1 Relative effects syntheses

M.1.1 Dichotomous data; binomial likelihood; logit link

M.1.1.1 Fixed effects

```
model {
  for (i in 1:NumStudies) {
    # indexes studies
    mu[i] ~ dnorm(0, .0001)                           # vague priors for all trial baselines
    for (j in 1:NumArms[i]) {                         # indexes arms
      k[i,j] ~ dbin(p[i,j], N[i,j])                   # binomial likelihood
      logit(p[i,j]) <- mu[i] + d[Rx[i,j]] - d[Rx[i,1]] # model for linear predictor
      rhat[i,j] <- p[i,j] * N[i,j]                   # expected value of the numerators
      dev[i,j] <- 2 * (k[i,j] * (log(k[i,j]) - log(rhat[i,j])) + (N[i,j] - k[i,j]) * (log(N[i,j] - k[i,j]) - log(N[i,j] - rhat[i,j]))) # deviance contribution
    }
    # close arm loop
    resdev[i] <- sum(dev[i,1:NumArms[i]])            # summed deviance contribution
  }                                                  # close study loop
  totresdev <- sum(resdev[])                         # total deviance
  d[1] <- 0                                          # effect is 0 for reference treatment
  for (j in 2:NumRx) {                               # indexes treatments
    d[j] ~ dnorm(0, .0001)                           # vague priors for treatment effects
  }                                                  # close treatment loop

  # Provide estimates of treatment effects T[j] on the natural (probability) scale
  # Given a Mean Effect, meanA, for 'standard' treatment A,
  # with precision (1/variance) precA
  AMean ~ dnorm(meanA, precA)
  APred ~ dnorm(predA, predPrecA)
  for (j in 1:NumRx) {
    logit(Tmean[j]) <- AMean + d[j]
    logit(Tpred[j]) <- APred + d[j]
  }

  # pairwise ORs and LORs for all possible pair-wise comparisons
  for (c in 1:(NumRx-1)) {
    for (j in (c+1):NumRx) {
      lOR[c,j] <- (d[j] - d[c])
      OR[c,j] <- exp(lOR[c,j])
    }
  }

  # ranking on relative scale
  for (j in 1:NumRx) {
    rk[j] <- blnHiGood*(NumRx+1-rank(d[j])) + (1-blnHiGood)*rank(d[j],j)
    best[j] <- equals(rk[j],1)                          # probability that treat j is best
  }
  for (h in 1:NumRx) {
    pRk[h,j] <- equals(rk[j],h)                       # probability that treat j is hth best
  }
}
```
M.1.1.2 Random effects

# Binomial likelihood, logit link
# Random effects model for multi-arm trials
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
# for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
# http://www.nicedsu.org.uk

model {
  for(i in 1:NumStudies) {  
    mu[i] ~ dnorm(0, .0001)  
    delta[i,1] <- 0  
    w[i,1] <- 0  
    for(j in 1:NumArms[i]) {  
      k[i,j] ~ dbin(p[i,j], N[i,j])  
      logit(p[i,j]) <- mu[i] + delta[i,j]  
      rhat[i,j] <- p[i,j] * N[i,j]  
      dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])) + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j])-log(N[i,j]-rhat[i,j])))  
    }  
    for (j in 2:NumArms[i]) {  
      delta[i,j] ~ dnorm(md[i,j],taud[i,j])  
      md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j]  
      taud[i,j] <- tau *2*(j-1)/j  
      multi-arm trial correction)  
      multi-arm trial correction)  
      w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]])  
      sw[i,j] <- sum(w[i,1:j-1])/(j-1)  
    }  
  }  
  resdev[i] <- sum(dev[i,1:NumArms[i]])  
  totresdev <- sum(resdev[])  
  d[1]<-0  
  for(j in 2:NumRx) {  
    d[j] ~ dnorm(0, .0001)  
  }  
  sdu ~ dunif(RFXpriorParam1, RFXpriorParam2)  
  sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2)  
  sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2)  
  sd  <- sdu * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)  
  tau <- pow(sd,-2)  
  # Provide estimates of treatment effects T[k] on the natural (probability) scale  
  Tmean ~ dnorm(meanA, precA)  
  Tpred ~ dnorm(predA, predPrecA)  
  for (j in 1:NumRx) {  
    logit(Tmean[j]) <- AMean + d[j]  
    logit(Tpred[j]) <- APred + d[j]  
  }  
  # pairwise ORs and LORs for all possible pair-wise comparisons  
  for(c in 1:(NumRx-1)) {  
    for (j in (c+1):NumRx) {  
      LOR[c,j] <- [d[j]-d[c]]  
      OR[c,j] <- exp(d[j]-d[c])  
    }  
  }  
  # ranking on relative scale  
  for(j in 1:NumRx) {  
    rk[j] <- blnHiGood*(NumRx+1-rank(d[],j)) + (1-blnHiGood)*rank(d[],j))  
    best[j] <- equals(rk[j],1)  
    for (h in 1:NumRx) {  
      pRk[h,j] <- equals(rk[j],h)  
    }  
  }  
}
M.1.2 Dichotomous data; binomial likelihood; cloglog link

M.1.2.1 Fixed effects

# Binomial likelihood, cloglog link
# Fixed effects model for multi-arm trials
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
# for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
# http://www.nicedsu.org.uk

model {
  for(i in 1:NumStudies) {  # indexes studies
    mu[i] ~ dnorm(0, .0001)  # vague priors for all trial baselines
    for(j in 1:NumArms[i]) {  # indexes arms
      k[i,j] ~ dbin(p[i,j],N[i,j])  # binomial likelihood
      cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + d[Rx[i,j]] - d[Rx[i,1]]  # model for linear predictor
      rhat[i,j] <- p[i,j] * N[i,j]  # expected value of the numerators
      dev[i,j] <- 2 * (log(k[i,j]) * (log(k[i,j]) - log(rhat[i,j]))
                      + (N[i,j] - k[i,j]) * (log(N[i,j] - k[i,j]) - log(N[i,j] - rhat[i,j])))
                      # deviance contribution
    }
  }
  resdev[i] <- sum(dev[i,1:NumArms[i]])  # summed deviance contribution
  totresdev <- sum(resdev[])  # total residual deviance
}

d[1]<-0  # effect is 0 for reference treatment
for(j in 2:NumRx) {  # indexes treatments
  d[j] ~ dnorm(0, .0001)  # vague priors for treatment effects
}

totresdev <- sum(resdev[])  # close study loop

totresdev <- sum(resdev[])  # close study loop

d[1]<-0  # effect is 0 for reference treatment
for(j in 2:NumRx) {  # indexes treatments
  d[j] ~ dnorm(0, .0001)  # vague priors for treatment effects
}

totresdev <- sum(resdev[])  # close study loop

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

AMean ~ dnorm(meanA, precA)
APred ~ dnorm(predA, predPrecA)
for (j in 1:NumRx) {
  cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
  cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
}

# pairwise HRs and LHRs for all possible pair-wise comparisons
for (c in 1:(NumRx-1)) {
  for (j in (c+1):NumRx) {
    lHR[c,j] <- d[j] - d[c]
    log(HR[c,j]) <- lHR[c,j]
  }
}

# ranking on relative scale
for (j in 1:NumRx) {
  rX[j] <- 1blnHiGood*(NumRx+1.rank(d[,j])) + (1-blHiGood)*rank(d[,j])
  best[j] <- equals(rX[j],1)  # probability that treat j is best
  for (h in 1:NumRx) {
    pRk[h,j] <- equals(rX[j],h)  # probability that treat j is hth best
  }
}

M.1.2.2 Random effects

# Binomial likelihood, cloglog link
# Random effects model for multi-arm trials
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
# for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
# http://www.nicedsu.org.uk

model {
  for(i in 1:NumStudies) {  # indexes studies
    mu[i] ~ dnorm(0, .0001)  # vague priors for all trial baselines
    delta[i,1] <- 0  # effect is zero for control arm
    for(j in 1:NumArms[i]) {  # indexes arms
      k[i,j] ~ dbin(p[i,j],N[i,j])  # binomial likelihood
      cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + d[Rx[i,j]] - d[Rx[i,1]]  # model for linear predictor
      rhat[i,j] <- p[i,j] * N[i,j]  # expected value of the numerators
      dev[i,j] <- 2 * (log(k[i,j]) * (log(k[i,j]) - log(rhat[i,j]))
                      + (N[i,j] - k[i,j]) * (log(N[i,j] - k[i,j]) - log(N[i,j] - rhat[i,j])))
                      # deviance contribution
    }
  }
  resdev[i] <- sum(dev[i,1:NumArms[i]])  # summed deviance contribution
  totresdev <- sum(resdev[])  # total residual deviance
}

d[1]<-0  # effect is 0 for reference treatment
for(j in 2:NumRx) {  # indexes treatments
  d[j] ~ dnorm(0, .0001)  # vague priors for treatment effects
}

totresdev <- sum(resdev[])  # close study loop

d[1]<-0  # effect is 0 for reference treatment
for(j in 2:NumRx) {  # indexes treatments
  d[j] ~ dnorm(0, .0001)  # vague priors for treatment effects
}

totresdev <- sum(resdev[])  # close study loop

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

AMean ~ dnorm(meanA, precA)
APred ~ dnorm(predA, predPrecA)
for (j in 1:NumRx) {
  cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
  cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
}

# pairwise HRs and LHRs for all possible pair-wise comparisons
for (c in 1:(NumRx-1)) {
  for (j in (c+1):NumRx) {
    lHR[c,j] <- d[j] - d[c]
    log(HR[c,j]) <- lHR[c,j]
  }
}

# ranking on relative scale
for (j in 1:NumRx) {
  rX[j] <- 1blnHiGood*(NumRx+1.rank(d[,j])) + (1-blHiGood)*rank(d[,j])
  best[j] <- equals(rX[j],1)  # probability that treat j is best
  for (h in 1:NumRx) {
    pRk[h,j] <- equals(rX[j],h)  # probability that treat j is hth best
  }
}
w[i,1] < 0 # multi-arm adjustment = zero for ctrl
for (j in 1:NumArms[i]) { # indexes arms
  k[i,j] ~ dbin(p[i,j],N[i,j]) # binomial likelihood
cloglog(p[i,j]) <- log(Yrs[i] / 1) + mu[i] + delta[i,j] # model for linear predictor
  rhat[i,j] <- 2 * (k[i,j] / log(Yrs[i] / 1) + N[i,j]) # expected value of the numerators
  dev[i,j] <- 2 * (k[i,j] * (log(k[i,j]) - log(rhat[i,j]) + N[i,j] - k[i,j]) * (log(N[i,j] - k[i,j]) - log(N[i,j] - rhat[i,j]))) # deviance contribution
}
for (j in 2:NumArms[i]) { # indexes arms
  delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific LOR distributions
  md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of LOR distributions (with multi-arm trial correction)
  taud[i,j] <- tau * 2 * (j - 1) / j # precision of LOR distributions (with multi-arm trial correction)
  w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]]) # adjustment for multi-arm RCTs
  sw[i,j] <- sum(w[i,1:j-1]) / (j - 1) # cumulative adjustment for multi-arm trials
}
resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
}
totresdev <- sum(resdev[]) # total residual deviance
d[1] <- 0 # effect is 0 for reference treatment
for (j in 2:NumRx) { # indexes treatments
  d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
}
sdu ~ dunif(RFXpriorParam1, RFXpriorParam2) # uniform between-trial prior
sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2) # normal between-trial prior
sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2) # lognormal between-trial prior
sd <- sdu * equals(RFXpriorD, 1) + sdn * equals(RFXpriorD, 2) + sdl * equals(RFXpriorD, 3) # select correct between-trial prior
tau <- pow(sd, -2) # between-trial precision
# Provide estimates of treatment effects T[j] on the natural (probability) scale
# Given a Mean Effect, meanA, for 'standard' treatment A,
# with precision (1/variance) precA, over a time period timeA
AMean ~ dnorm(meanA, precA)
APred ~ dnorm(predA, predPrecA)
for (j in 1:NumRx) {
cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
}
# pairwise HRs and LHRs for all possible pair-wise comparisons
for (c in 1:(NumRx - 1)) {
  for (j in (c + 1):NumRx) {
    lHR[c,j] <- d[j] - d[c]
    log(HR[c,j]) <- lHR[c,j]
  }
}
# ranking on relative scale
for (j in 1:NumRx) {
  rk[j] <- b1nHiGood * (NumRx + 1 - rank(d[], j)) + (1 - b1nHiGood) * rank(d[], j) # probability that treat j is best
  best[j] <- equals(rk[j], 1)
  for (h in 1:NumRx) {
    pRk[h,j] <- equals(rk[j], h) # probability that treat j is hth best
  }
}

M.1.3 Rate data; Poisson likelihood; log link

M.1.3.1 Fixed effects

# Poisson likelihood, log link
# Fixed effects model for multi-arm trials
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
# for Pairwise and Network Meta-Analysis of Randomized Controlled Trials. 2011.
# http://www.nicedsu.org.uk
model {

National Institute for Health and Care Excellence, 2015
for(i in 1:NumStudies) {  
  mu[i] ~ dnorm(0, .0001)  # indexes studies
  for (j in 1:NumArms[i]) {  # indexes arms
    r[i,j] ~ dpois(theta[i,j])  # Poisson likelihood
    log(lambda[i,j]) <- lambda[i,j] * E[i,j]  # failure rate * exposure
    dev[i,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))  # deviance contribution
    # model for linear predictor
    resdev[i] <- sum(dev[i,1:NumArms[i]])  # summed deviance contribution
  }
  totresdev <- sum(resdev[])  # total residual deviance
}

d[i]<-0  # effect is 0 for reference treatment
for (j in 2:NumRx) {  
  d[j] ~ dnorm(0, .0001)  # vague priors for treatment effects
  }  # close treatment loop

# Provide estimates of treatment effects T[j] on the natural (probability) scale
# Given a Mean Effect, meanA, for ’standard’ treatment A,
# with precision (1/variance) precA, over a time period timeA
AMean ~ dnorm(meanA, precA)
APred ~ dnorm(predA, predPrecA)
for (j in 1:NumRx) {  
  cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
  cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
  }  # pairwise HRs and LHRs for all possible pair-wise comparisons
for (c in 1:(NumRx-1)) {  # based on
  for (j in (c+1):NumRx) {  # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
    lHR[c,j] <- d[j] - d[c]  # mean of LOR distributions
    log(HR[c,j]) <- lHR[c,j]
  }
  }  # ranking on relative scale
for (j in 1:NumRx) {  # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
  rk[j] <- blnHiGood*(NumRx+1-rank(d[],j)) + (1-blnHiGood)*rank(d[],j)  # probability that treat j is best
  best[j] <- equals(rk[j],1)  
  for (h in 1:NumRx) {  
    pRk[h,j] <- equals(rk[j],h)  # probability that treat j is hth best
  }
  }  # Random effects

# Poisson likelihood, log link
# Random effects model for multi-arm trials
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
# for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
# http://www.nicedsu.org.uk
model {  
  for(i in 1:NumStudies) {  
    mu[i] ~ dnorm(0, .0001)  # indexes studies
    delta[i,1] ~ dnorm(0, .0001)  # effect is zero for control arm
    w[i,1] ~ dnorm(0, .0001)  # multi-arm adjustment = zero for ctrl
    for (j in 1:NumArms[i]) {  # indexes arms
      r[i,j] ~ dpois(theta[i,j])  # Poisson likelihood
      log(lambda[i,j]) <- lambda[i,j] * E[i,j]  # failure rate * exposure
      dev[i,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))  # deviance contribution
      # model for linear predictor
      for (h in 1:NumRx) {  
        md[i,j] ~ dnorm(md[i,j],taud[i,j])  # mean of LOR distributions (with multi-arm trial correction)
        md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j]
      }
    }
  }  
  }
```plaintext
# precision of LOR distributions (with multi-arm trial correction)
taud[i,j] <- tau *2*(j-1)/j

# adjustment for multi-arm RCTs
w[i,j] <- (delta[i,j] - d[Rx[i,j]]) + d[Rx[i,1]]

# cumulative adjustment for multi-arm trials
sw[i,j] <- sum(w[i,1:j-1])/(j-1)

resdev[i] <- sum(dev[i,1:NumArms[i]])  # summed deviance contribution

totresdev <- sum(resdev[])  # total residual deviance

d[1]<-0  # effect is 0 for reference treatment
for (j in 2:NumRx) {
  d[j] ~ dnorm(0,.0001)  # indexes treatments
}

dsu ~ dunif(RFXpriorParam1, RFXpriorParam2)  # uniform between-trial prior
sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2)  # normal between-trial prior
sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2)  # lognormal between-trial prior
sd <- sd u * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)  # select correct between-trial prior

tau <- pow(sd, -2)  # between-trial precision

# Provide estimates of treatment effects T[j] on the natural (probability) scale
# Given a Mean Effect, meanA, for 'standard' treatment A,
# with precision (1/variance) precA, over a time period timeA
AMean ~ dnorm(meanA, precA)
APred ~ dnorm(predA, predPrecA)
for (j in 1:NumRx) {
  cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
  cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
}

# pairwise HRs and LHRs for all possible pair-wise comparisons
for (c in 1:(NumRx-1)) {
  for (j in (c+1):NumRx) {
    lHR[c,j]     <- d[j] - d[c]
    log(HR[c,j]) <- lHR[c,j]
  }
}

# ranking on relative scale
for (j in 1:NumRx) {
  rk[j]       <- blnHiGood*(NumRx+1-rank(d[])) + (1-blnHiGood)*rank(d[],j)
}

totresdev <- sum(resdev[])

d[1]<-0  # effect is 0 for reference treatment
for (j in 2:NumRx) {
  d[j] ~ dnorm(0,.0001)  # indexes treatments
}

dsu ~ dunif(RFXpriorParam1, RFXpriorParam2)  # uniform between-trial prior
sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2)  # normal between-trial prior
sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2)  # lognormal between-trial prior
sd <- sd u * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)  # select correct between-trial prior

tau <- pow(sd, -2)  # between-trial precision
```

**M.1.4 Mixed dichotomous and rate data; binomial likelihood with cloglog link and Poisson likelihood with log link**

**M.1.4.1 Fixed effects**

```plaintext
# Effectiveness model for mixed dichotomous and count data
# Binomial likelihood, cloglog link / Poisson likelihood, log link
# Fixed effects
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
# for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
# http://www.nicedsu.org.uk

model {
  for(i in 1:NumStudiesD) {
    mu[i] ~ dnorm(0,.0001)  # indexes studies with dichotomous data
    # vague priors for all trial baselines
    for (j in 1:NumArms[i]) {
      k[i,j] ~ dbin(p[i,j],N[i,j])  # binomial likelihood
      cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + d[Rx[i,j]] - d[Rx[i,1]]  # model for linear predictor
      rhat[i,j] <- p[i,j] * N[i,j]  # expected value of the numerators
      dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])) + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j]))) - log(N[i,j]-rhat[i,j]))  # deviance contribution
    }
  }

  # Provide estimates of treatment effects T[j] on the natural (probability) scale
  # Given a Mean Effect, meanA, for 'standard' treatment A,
  # with precision (1/variance) precA, over a time period timeA
  AMean ~ dnorm(meanA, precA)
  APred ~ dnorm(predA, predPrecA)
  for (j in 1:NumRx) {
    cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
    cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
  }

  # pairwise HRs and LHRs for all possible pair-wise comparisons
  for (c in 1:(NumRx-1)) {
    for (j in (c+1):NumRx) {
      lHR[c,j]     <- d[j] - d[c]
      log(HR[c,j]) <- lHR[c,j]
    }
  }

  # ranking on relative scale
  for (j in 1:NumRx) {
    rk[j]       <- blnHiGood*(NumRx+1-rank(d[])) + (1-blnHiGood)*rank(d[],j)
  }
  # probability that treat j is best
  for (h in 1:NumRx) {
    pRk[h,j]  <- equals(rk[j],h)  # probability that treat j is hth best
  }
```
WinBUGS code

for (i in 1:NumStudiesC) {
  resdev[i] <- sum(dev[i,1:NumArms[i]])
}

for (i in 1:NumStudiesD) {
  mu[i] ~ dnorm(0, .0001)
  w[i] <- 0
  for (j in 1:NumArms[i]) {
    k[i,j] ~ dbin(p[i,j],N[i,j])
    cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + delta[i,j]
    rhat[i,j] <- p[i,j] * N[i,j]
    dev[i,j] <- 2 * (k[i,j] - log(k[i,j]) + log(N[i,j]/1) + mu[i] + delta[i,j])
  }
}

for (i in 1:NumStudiesC) {
  mu[i + NumStudiesD] ~ dnorm(0, .0001)
  for (j in 1:NumArms[i]) {
    r[i,j] ~ dpois(theta[i,j])
    theta[i,j] <- lambda[i,j] * E[i,j]
    log(lambda[i,j]) <- mu[i + NumStudiesD] + d[RxC[i,j]] - d[RxC[i,1]]
    dev[i + NumStudiesD,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))
  }
  resdev[i + NumStudiesD] <- sum(dev[i + NumStudiesD,1:NumArmsC[i]])
}

totresdev <- sum(resdev[])

d[1]<-0

for (j in 2:NumRx) {
  d[j] ~ dnorm(0, .0001)
}

# Provide estimates of
treatment effects T[j] on the natural (probability) scale
# Given a Mean Effect, meanA, for 'standard' treatment A,
# with precision (1/variance) precA, over a time period timeA
AMean ~ dnorm(meanA, precA)
APred ~ dnorm(predA, predPrecA)
for (j in 1:NumRx) {
  cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
  cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
}

# pairwise HRs and LHRs for all possible pairwise comparisons
for (c in 1:(NumRx-1)) {
  for (j in (c+1):NumRx) {
    lHR[c,j] <- d[j] - d[c]
    log(HR[c,j]) <- -lHR[c,j]
  }
}

# ranking on relative scale
for (j in 1:NumRx) {
  rk[j] <- blnHiGood*(NumRx+1-rank(d[],j)) + (1-blnHiGood)*rank(d[],j)
  best[j] <- equals(rk[j],1)
  for (h in 1:NumRx) {
    pRk[h,j] <- equals(rk[j],h)
  }
}

M.1.4.2 Random effects

model {
  for (i in 1:NumStudiesD) {
    mu[i] ~ dnorm(0, .01)
    delta[i,1] <- 0
    w[i,1] <- 0
  }
  for (j in 1:NumArms[i]) {
    k[i,j] ~ dbin(p[i,j],N[i,j])
    cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + delta[i,j]
    rhat[i,j] <- p[i,j] * N[i,j]
    dev[i,j] <- 2 * (k[i,j] - log(k[i,j]) - log(rhat[i,j]))
                         + (N[i,j]-k[i,j]) * log(N[i,j]-k[i,j])
                         - log(N[i,j]-rhat[i,j]))
    dev[i,j] <- dev[i,j] / dev[i,1]
  }
  for (i in 1:NumStudiesC) {
    mu[i + NumStudiesD] ~ dnorm(0, .0001)
    for (j in 1:NumArms[i]) {
      r[i,j] ~ dpois(theta[i,j])
      theta[i,j] <- lambda[i,j] * E[i,j]
      log(lambda[i,j]) <- mu[i + NumStudiesD] + d[RxC[i,j]] - d[RxC[i,1]]
      dev[i + NumStudiesD,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))
    }
  }
  resdev[i + NumStudiesD] <- sum(dev[i + NumStudiesD,1:NumArmsC[i]])
  totresdev <- sum(resdev[])
  for (j in 1:NumRx) {
    d[j] ~ dnorm(0, .0001)
  }
  # Effectiveness model for mixed dichotomous and count data
  # Binomial likelihood, cloglog link / Poisson likelihood, log link
  # Random effects
  # based on
  # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
  # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
  # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
  # http://www.nicedsu.org.uk
  mu[i] ~ dnorm(0, .01)
  delta[i,1] <- 0
  w[i,1] <- 0
  for (j in 1:NumArms[i]) {
    k[i,j] ~ dbin(p[i,j],N[i,j])
    cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + delta[i,j]
    rhat[i,j] <- p[i,j] * N[i,j]
    dev[i,j] <- 2 * (k[i,j] - log(k[i,j]) - log(rhat[i,j]))
                         + (N[i,j]-k[i,j]) * log(N[i,j]-k[i,j])
                         - log(N[i,j]-rhat[i,j]))
    dev[i,j] <- dev[i,j] / dev[i,1]
  }
  for (i in 1:NumStudiesC) {
    mu[i + NumStudiesD] ~ dnorm(0, .0001)
    for (j in 1:NumArms[i]) {
      r[i,j] ~ dpois(theta[i,j])
      theta[i,j] <- lambda[i,j] * E[i,j]
      log(lambda[i,j]) <- mu[i + NumStudiesD] + d[RxC[i,j]] - d[RxC[i,1]]
      dev[i + NumStudiesD,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))
    }
  }
  resdev[i + NumStudiesD] <- sum(dev[i + NumStudiesD,1:NumArmsC[i]])
  totresdev <- sum(resdev[])
  for (j in 1:NumRx) {
    d[j] ~ dnorm(0, .0001)
  }
  # Provide estimates of
treatment effects T[j] on the natural (probability) scale
  # Given a Mean Effect, meanA, for 'standard' treatment A,
  # with precision (1/variance) precA, over a time period timeA
  AMean ~ dnorm(meanA, precA)
  APred ~ dnorm(p, predPrecA)
  for (j in 1:NumRx) {
    cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
    cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
  }
  # pairwise HRs and LHRs for all possible pairwise comparisons
  for (c in 1:(NumRx-1)) {
    for (j in (c+1):NumRx) {
      lHR[c,j] <- d[j] - d[c]
      log(HR[c,j]) <- -lHR[c,j]
    }
  }
  # ranking on relative scale
  for (j in 1:NumRx) {
    rk[j] <- blnHiGood*(NumRx+1-rank(d[],j)) + (1-blnHiGood)*rank(d[],j)
    best[j] <- equals(rk[j],1)
    for (h in 1:NumRx) {
      pRk[h,j] <- equals(rk[j],h)
    }
  }
WinBUGS code

# close arm loop
for (j in 2:NumArms[i]) {
  delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific LHR distributions
  md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of LHR distributions (with multi-arm trial correction)
  taud[i,j] <- tau *2*(j-1)/j # precision of LOR distributions (with multi-arm trial correction)
  w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]]) # adjustment for multi-arm RCTs
  sw[i,j] <- sum(w[i,1:j-1])/(j-1) # cumulative adjustment for multi-arm trials
}
resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
}

for(i in 1:NumStudiesC) { # indexes studies with count data
  mu[i + NumStudiesD] ~ dnorm(0, .01) # vague priors for all trial baselines
  delta[i + NumStudiesD,1] ~ 0 # effect is zero for control arm
  w[i + NumStudiesD,1] ~ 0 # multi-arm adjustment = zero for ctrl
  for (j in 1:NumArmsC[i]) { # indexes arms
    r[i,j] ~ dpois(theta[i,j]) # Poisson likelihood
    theta[i,j] <- lambda[i,j] * E[i,j] # failure rate * exposure
    log(lambda[i,j]) <- mu[i + NumStudiesD] + delta[i + NumStudiesD,j] # model for linear predictor
    dev[i + NumStudiesD,j] <- 2 * ((theta[i,j] - r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j])) # deviance contribution
  }
  for (j in 2:NumArmsC[i]) { # indexes arms
    delta[i + NumStudiesD,j] ~ dnorm(md[i + NumStudiesD,j],taud[i + NumStudiesD,j]) # trial-specific LHR distributions
    md[i + NumStudiesD,j] <- d[RxC[i,j]] - d[RxC[i,1]] + sw[i + NumStudiesD,j] # mean of LHR distributions (with multi-arm trial correction)
    taud[i + NumStudiesD,j] <- tau *2*(j-1)/j # precision of LOR distributions (with multi-arm trial correction)
    w[i + NumStudiesD,j] <- (delta[i + NumStudiesD,j] - d[RxC[i,j]] + d[RxC[i,1]]) # adjustment for multi-arm RCTs
    sw[i + NumStudiesD,j] <- sum(w[i + NumStudiesD,1:j-1])/(j-1) # cumulative adjustment for multi-arm trials
  }
  resdev[i + NumStudiesD] <- sum(dev[i + NumStudiesD,1:NumArmsC[i]]) # summed deviance contribution
}
totresdev <- sum(resdev[]) # total residual deviance

d[1]<-0 # effect is 0 for reference treatment
for (j in 2:NumRx) { # indexes treatments
  d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
  sdu ~ dunif(RFXpriorParam1, RFXpriorParam2) # uniform between-trial prior
  sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2) # normal between-trial prior
  sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2) # lognormal between-trial prior
  sd <- sdu * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3) # select correct between-trial prior
  tau <- pow(sd,-2) # between-trial precision

  # Provide estimates of treatment effects T[j] on the natural (probability) scale
  # Given a Mean Effect, meanA, for 'standard' treatment A,
  # with precision 1/variance precA, over a time period timeA
  #AMean ~ dnorm(meanA, precA)
  #APred ~ dnorm(predA, predPrecA)
  for (j in 1:NumRx) {
    cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
    cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
  }

  # pairwise HRs and LHRs for all possible pair-wise comparisons
  for (c in 1:(NumRx-1)) {
    for (j in (c+1):NumRx) {
      lHR[c,j] <- d[j] - d[c] # log(1HR[c,j]) <- lHR[c,j]
    }
  }
}
# ranking on relative scale
for (j in 1:NumRx) {
  rk[j] <- blnHiGood*(NumRx+1-rank(d[])) + (1-blnHiGood)*rank(d[],j)
  best[j] <- equals(rk[j],1) # probability that treat j is best
  for (h in 1:NumRx) {
    pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
  }
}

M.2 Baseline effects syntheses

M.2.1 Dichotomous data; binomial likelihood; logit link
Not used

M.2.2 Dichotomous data; binomial likelihood; cloglog link
Not used

M.2.3 Rate data; Poisson likelihood; log link

M.2.3.1 Fixed effects

# Baseline model for rate data
# Poisson likelihood, log link
# Fixed-effects model
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
# natural history model. 2011.
# http://www.nicedsu.org.uk

model {
  for(i in 1:NumStudies) { # indexes studies with count data
    r[i] ~ dpois(theta[i]) # Poisson likelihood
    theta[i] <- exp(m) * (E[i] / 365.24) # event rate * exposure
  } # close study loop
  m ~ dnorm(0, 0.0001) # vague prior for base line
cloglog(prob) <- log(1) + m # posterior mean yearly response rate
}

M.2.3.2 Random effects

# Baseline model for rate data
# Poisson likelihood, log link
# Random-effects model
# based on
# Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
# NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
# natural history model. 2011.
# http://www.nicedsu.org.uk

model {
  for(i in 1:NumStudies) { # indexes studies
    mu[i] ~ dnorm(m, tau.m) # trial-specific baseline with random effects
    r[i] ~ dpois(theta[i]) # Poisson likelihood
    theta[i] <- exp(mu[i]) * (E[i] / 365.24) # event rate * exposure
  } # close study loop
  sd.m ~ dunif(0, 5) # vague prior for SD (baseline)
tau.m ~ pow(sd.m, -2) # between-trial precision (baseline)
m ~ dnorm(0, .0001) # vague prior for mean (baseline)
cloglog(prob) <- log(1) + m # posterior mean yearly response rate
  mu.new ~ dnorm(m, tau.m) # pred. dist. for baseline (log-HR)
cloglog(pred) <- log(1) + mu.new # predictive mean yearly response rate
}
M.2.4 Mixed dichotomous and rate data; binomial likelihood with cloglog link and Poisson likelihood with log link

### M.2.4.1 Fixed effects

```winbugs
model {
  for(i in 1:NumStudiesD) {                   # indexes studies with dichotomous data
    k[i]          ~  dbin(p[i], N[i])         # binomial likelihood
    cloglog(p[i]) <- log(Yrs[i]) + m          # model for linear predictor
  }                                         # close study loop
  for(i in 1:NumStudiesC) {                   # indexes studies with count data
    r[i]          ~  dpois(theta[i])          # Poisson likelihood
    theta[i]      <- exp(m) * (E[i] / 365.24) # event rate * exposure
    dummy[i]      <- YrsC[i]                  # not used in this model
  }                                         # close study loop
  m ~  dnorm(0, 0.0001)                       # vague prior for baseline
  cloglog(prob) <- log(1) + m                 # posterior mean yearly response rate
}
```

### M.2.4.2 Random effects

```winbugs
model {
  for(i in 1:NumStudiesC + NumStudiesD) {       # indexes studies
    mu[i]         ~  dnorm(m, tau.m)          # trial-specific baseline with random effects
  }                                         # close study loop
  for(i in 1:NumStudiesD) {                   # indexes studies with dichotomous data
    k[i]          ~  dbin(p[i], N[i])         # binomial likelihood
    cloglog(p[i]) <- log(Yrs[i]) / 1 + mu[i]  # model for linear predictor
  }                                         # close study loop
  for(i in 1:NumStudiesC) {                   # indexes studies with count data
    r[i]          ~  dpois(theta[i])          # Poisson likelihood
    theta[i]      <- exp(mu[NumStudiesD+i]) * (E[i] / 365.24) # event rate * exposure
    dummy[i]      <- YrsC[i]                  # not used in this model
  }                                         # close study loop
  sd.m          ~  dunif(0, 5)                # vague prior for SD (baseline)
  tau.m         <-  pow(sd.m, -2)             # between-trial precision (baseline)
  m             ~  dnorm(0, .0001)            # vague prior for mean (baseline)
  cloglog(prob) <- log(1) + m                 # posterior mean yearly response rate
  mu.new        ~  dnorm(m, tau.m)            # pred. dist. for baseline (log-HR)
  cloglog(pred) <- log(1) + mu.new            # predictive mean yearly response rate
}
```