

# Appendix K: 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, TSD3 and TSD5.

## K.1 Relative effects syntheses

### K.1.1 Continuous data; normal likelihood; identity link

#### K.1.1.1 Fixed effects

```
# Normal likelihood, identity 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) {
    mu[i] ~ dnorm(0, .0001) # indexes studies
    # vague priors for all trial baselines
    for (j in 1:NumArms[i]) { # indexes arms
      se[i,j] <- SD[i,j] / sqrt(N[i,j])
      var[i,j] <- pow(se[i,j],2) # calculate variances
      prec[i,j] <- 1/var[i,j] # set precisions
      MC[i,j] ~ dnorm(theta[i,j],prec[i,j]) # normal likelihood
      theta[i,j] <- mu[i] + d[Rx[i,j]] - d[Rx[i,1]] # model for linear predictor
      dev[i,j] <- (MC[i,j] - theta[i,j]) * (MC[i,j]
        - theta[i,j]) * prec[i,j] # deviance contribution
    } # close arm loop
    resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
  } # close study loop
  totesdev <- 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
  } # 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) {
    Tmean[j] <- AMean + d[j]
    Tpred[j] <- APred + d[j]
  }

  # pairwise MDs for all possible pair-wise comparisons
  for (c in 1:(NumRx-1)) {
    for (j in (c+1):NumRx) {
      MD[c,j] <- (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) # 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
    }
  }
}
```

## K.1.1.2 Random effects

```

# Normal likelihood, identity 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.nicesdsu.org.uk

model {
for(i in 1:NumStudies) {
  w[i,1] <- 0 # indexes studies
  delta[i,1] <- 0 # multi-arm adjustment = 0 for control
  mu[i] ~ dnorm(0, .0001) # treatment effect is 0 for control
  # vague priors for all trial baselines
  for (j in 1:NumArms[i]) { # indexes arms
    se[i,j] <- SD[i,j] / sqrt(N[i,j])
    var[i,j] <- pow(se[i,j],2) # calculate variances
    prec[i,j] <- 1/var[i,j] # set precisions
    MC[i,j] ~ dnorm(theta[i,j], prec[i,j]) # normal likelihood
    theta[i,j] <- mu[i] + delta[i,j] # model for linear predictor
    dev[i,j] <- (MC[i,j] - theta[i,j]) * (MC[i,j]
      - theta[i,j]) * prec[i,j] # deviance contribution
  } # close arm loop
  for (j in 2:NumArms[i]) { # indexes arms
    delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific MD distributions
    md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of MD dists, with multiarm
    taud[i,j] <- tau * 2*(j-1)/j # precision of MD dists, with multiarm
    w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]]) # adjustment, multi-arm RCTs
    sw[i,j] <- sum(w[i,1:j-1])/(j-1) # cumulative adjustment for multi-arm
  }
  resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
} # close study loop
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
} # close treatment loop
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)
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

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

# pairwise MDs for all possible pair-wise comparisons
for (c in 1:(NumRx-1)) {
  for (j in (c+1):NumRx) {
    MD[c,j] <- (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) # 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
  }
}
}

```

## K.1.2 Dichotomous data; binomial likelihood; logit link

### K.1.2.1 Fixed effects

```

# Binomial likelihood, logit 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) {
    mu[i] ~ dnorm(0, .0001) # indexes studies
    # vague priors for all trial baselines
    for (j in 1:NumArms[i]) {
      k[i,j] ~ dbin(p[i,j],N[i,j]) # indexes arms
      # 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 residual deviance

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

```

### K.1.2.2 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) # indexes studies
    # vague priors for all trial baselines
    delta[i,1] <- 0 # effect is zero for control arm
    w[i,1] <- 0 # multi-arm adjustment = zero for ctrl
  }
}

```

```

for (j in 1:NumArms[i]) {
  k[i,j] ~ dbin(p[i,j],N[i,j]) # indexes arms
  logit(p[i,j]) <- mu[i] + delta[i,j] # binomial likelihood
  rhat[i,j] <- p[i,j] * N[i,j] # model for linear predictor
  dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j]))) # expected value of the numerators
  + (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
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]])
  sw[i,j] <- sum(w[i,1:j-1])/(j-1) # adjustment for multi-arm RCTs
} # cumulative adjustment for multi-arm
resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
} # close study loop
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
} # close treatment loop
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[k] on the natural (probability) scale
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(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) # 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
  }
}
}

```

## K.1.3 Dichotomous data; binomial likelihood; cloglog link

### K.1.3.1 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 * (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 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
} # 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)) {
  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) # 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
  }
}
}

```

### K.1.3.2 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
  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] <- 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
  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]          <- blnHiGood*(NumRx+1-rank(d[,j])) + (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
  }
}
}

```

## K.1.4 Rate data; Poisson likelihood; log link

### K.1.4.1 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 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
      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] + d[Rx[i,j]] - d[Rx[i,1]]
                                                    # model for linear predictor
      dev[i,j]          <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[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
} # 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)) {
  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) # 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
  }
}
}

```

#### K.1.4.2 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.nicesdsu.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
  w[i,1] <- 0 # multi-arm adjustment = zero for ctrl
  for (j in 1:NumArms[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] + delta[i,j] # model for linear predictor
    dev[i,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j])) # deviance contribution
  } # close arm loop
  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
} # close study loop
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
} # close treatment loop
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] <- blnHiGood*(NumRx+1-rank(d[,j])) + (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
  }
}
}

```

## K.1.5 Mixed dichotomous and rate data; binomial likelihood with cloglog link and Poisson likelihood with log link

### K.1.5.1 Fixed effects

```

# 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]) # indexes arms
      # binomial likelihood
      cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + d[RxC[i,j]] - d[RxC[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

  for(i in 1:NumStudiesC) {
    mu[i + NumStudiesD] ~ dnorm(0, .0001) # indexes studies with count data
    # vague priors for all trial baselines
    for (j in 1:NumArmsC[i]) {
      r[i,j] ~ dpois(theta[i,j]) # indexes arms
      # Poisson likelihood
      theta[i,j] <- lambda[i,j] * E[i,j] # failure rate * exposure
      log(lambda[i,j]) <- mu[i + NumStudiesD] + d[RxC[i,j]] - d[RxC[i,1]]
      # 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
    } # close arm loop
    resdev[i + NumStudiesD] <- sum(dev[i + NumStudiesD,1:NumArmsC[i]]) # summed deviance contribution
  }
}

```



```

    } # close study loop

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
} # 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 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) # 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
  }
}
}

```

### K.1.5.2 Random effects

```

# 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

model {
  for(i in 1:NumStudiesD) { # indexes studies with dichotomous data
    mu[i] ~ dnorm(0, .01) # vague priors for all trial baselines
    delta[i,1] <- 0 # effect is zero for control arm
    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] <- 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
    for (j in 2:NumArms[i]) { # indexes arms
      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
  } # close study loop
}

```

```

for(i in 1:NumStudiesC) {
  mu[i + NumStudiesD] ~ dnorm(0, .01) # indexes studies with count data
  delta[i + NumStudiesD,1] <- 0 # vague priors for all trial baselines
  w[i + NumStudiesD,1] <- 0 # effect is zero for control arm
  for (j in 1:NumArmsC[i]) { # multi-arm adjustment = zero for ctrl
    r[i,j] ~ dpois(theta[i,j]) # indexes arms
    theta[i,j] <- lambda[i,j] * E[i,j] # Poisson likelihood
    log(lambda[i,j]) <- mu[i + NumStudiesD] # failure rate * exposure
    + 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
  } # close arm loop
  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]] # mean of LHR distributions (with
    + sw[i + NumStudiesD,j] # 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
} # close study loop

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
} # close treatment loop
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] <- blnHiGood*(NumRx+1-rank(d[,j])) + (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
  }
}
}

```

## K.2 Baseline effects syntheses

### K.2.1 Continuous data; normal likelihood; identity link

#### K.2.1.1 Fixed effects

```
# Baseline model for continuous data
# Normal likelihood, identity 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) {
    se[i]      <- SD[i] / sqrt(N[i])      # indexes studies
    prec[i]    <- pow(se[i], -2)          # calculate SEs
    MC[i]      ~ dnorm(m, prec[i])        # set precisions
  }                                         # normal likelihood
  m            ~ dnorm(0, .0001)         # close study loop
  prob        <- m                       # vague prior for mean (baseline)
}                                             # posterior mean
```

#### K.2.1.2 Random effects

```
# Baseline model for continuous data
# Normal likelihood, identity 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) {
    se[i]      <- SD[i] / sqrt(N[i])      # indexes studies
    prec[i]    <- pow(se[i], -2)          # calculate SEs
    MC[i]      ~ dnorm(p[i], prec[i])    # set precisions
    p[i]       <- mu[i]                  # normal likelihood
    mu[i]      ~ dnorm(m, tau.m)         # identity link
  }                                         # trial-specific baseline with random effects
  sd.m        ~ dunif(0, 5)             # close study loop
  tau.m       <- pow(sd.m, -2)          # vague prior for SD (baseline)
  m           ~ dnorm(0, .0001)        # between-trial precision (baseline)
  prob        <- m                       # vague prior for mean (baseline)
  mu.new      ~ dnorm(m, tau.m)        # posterior mean
  pred        <- mu.new                 # pred. dist. for baseline
}                                             # predictive mean for a new observation
```

### K.2.2 Dichotomous data; binomial likelihood; logit link

Not used

### K.2.3 Dichotomous data; binomial likelihood; cloglog link

#### K.2.3.1 Fixed effects

```
# Baseline model for dichotomous data
# Binomial likelihood, cloglog 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) {
  k[i] ~ dbin(p[i], N[i])
  cloglog(p[i]) <- log(Yrs[i]) + m
}
m ~ dnorm(0, 0.0001)
cloglog(prob) <- log(1) + m
}
# indexes studies
# binomial likelihood
# model for linear predictor
# close study loop
# vague prior for baseline
# posterior mean yearly response rate

```

### K.2.3.2 Random effects

```

# Baseline model for dichotomous data
# Binomial likelihood, cloglog 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) {
  k[i] ~ dbin(p[i], N[i])
  cloglog(p[i]) <- log(Yrs[i]) + mu[i]
  mu[i] ~ dnorm(m, tau.m)
}
sd.m ~ dunif(0, 5)
tau.m <- pow(sd.m, -2)
m ~ dnorm(0, .0001)
cloglog(prob) <- log(1) + m
mu.new ~ dnorm(m, tau.m)
cloglog(pred) <- log(1) + mu.new
}
# indexes studies
# binomial likelihood
# model for linear predictor
# trial-specific baseline with random effects
# close study loop
# vague prior for SD (baseline)
# between-trial precision (baseline)
# vague prior for mean (baseline)
# posterior mean yearly response rate
# pred. dist. for baseline (log-HR)
# predictive mean yearly response rate

```

## K.2.4 Rate data; Poisson likelihood; log link

### K.2.4.1 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) {
  r[i] ~ dpois(theta[i])
  theta[i] <- exp(m) * (E[i] / 365.24)
}
m ~ dnorm(0, 0.0001)
cloglog(prob) <- log(1) + m
}
# indexes studies with count data
# Poisson likelihood
# event rate * exposure
# close study loop
# vague prior for baseline
# posterior mean yearly response rate

```

### K.2.4.2 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) {
  mu[i] ~ dnorm(m, tau.m)
  r[i] ~ dpois(theta[i])
  theta[i] <- exp(mu[i]) * (E[i] / 365.24)
}
sd.m ~ dunif(0, 5)
}
# indexes studies
# trial-specific baseline with random effects
# Poisson likelihood
# event rate * exposure
# close study loop
# 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
}

```

## K.2.5 Mixed dichotomous and rate data; binomial likelihood with cloglog link and Poisson likelihood with log link

### K.2.5.1 Fixed effects

```

# Baseline model for mixed dichotomous and count data
# Binomial likelihood, cloglog link / 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: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
}

```

### K.2.5.2 Random effects

```

# Baseline model for mixed dichotomous and count data
# Binomial likelihood, cloglog link / 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: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
}

```

## K.3 Adjusted baseline effects syntheses

### K.3.1 Continuous data; normal likelihood; identity link

#### K.3.1.1 Fixed effects

```
# Baseline model for continuous data
# Normal likelihood, identity link
# Fixed-effects model with meta-regression
# 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.
# and
# Dias, S., Sutton, A.J., Welton, N.J., Ades, A.E.
# NICE DSU Technical Support Document 3: Heterogeneity: subgroups,
# meta-regression, bias and bias-adjustment. 2011
# http://www.nicesdsu.org.uk

model {
for(i in 1:NumStudies) {
  se[i]      <- SD[i] / sqrt(N[i])          # indexes studies
  prec[i]    <- pow(se[i], -2)              # calculate SEs
  mu[i]      <- m + (Base[i]-xbar) * beta   # set precisions
  MC[i]      ~ dnorm(mu[i], prec[i])        # identity link with coefficient
}                                              # normal likelihood
}                                              # close study loop
m          ~ dnorm(0, .0001)                # vague prior for mean (baseline)
beta       ~ dnorm(0, .0001)                # vague prior for coefficient
prob      <- m                             # posterior mean
}
```

#### K.3.1.2 Random effects

```
# Baseline model for continuous data
# Normal likelihood, identity link
# Random-effects model with meta-regression
# 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.nicesdsu.org.uk
# and
# Dias, S., Sutton, A.J., Welton, N.J., Ades, A.E.
# NICE DSU Technical Support Document 3: Heterogeneity: subgroups,
# meta-regression, bias and bias-adjustment. 2011
# http://www.nicesdsu.org.uk

model {
for(i in 1:NumStudies) {
  se[i]      <- SD[i] / sqrt(N[i])          # indexes studies
  prec[i]    <- pow(se[i], -2)              # calculate SEs
  MC[i]      ~ dnorm(p[i], prec[i])        # set precisions
  p[i]       <- mu[i] + (Base[i]-xbar)*beta # normal likelihood
  mu[i]      ~ dnorm(m, tau.m)              # identity link with coefficient
}                                              # trial-specific baseline with random effects
}                                              # 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)
beta        ~ dnorm(0, .0001)                # vague prior for coefficient
prob        <- m                             # posterior mean
mu.new      ~ dnorm(m, tau.m)                # pred. dist. for baseline
pred        <- mu.new                         # predictive mean for a new observation
}
```