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) {                             # indexes studies
  mu[i] ~ dnorm(0, .0001)                            # 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
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
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.nicedsu.org.uk

model {
for(i in 1:NumStudies) {                              # indexes studies
  w[i,1]       <- 0                                   # multi-arm adjustment = 0 for control
  delta[i,1]   <- 0                                   # treatment effect is 0 for control
  mu[i]        ~  dnorm(0, .0001)                     # 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 Dichotomous data; binomial likelihood; logit link

K.1.1 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) {                             # 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 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) {
  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 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) {                             # 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
    logit(p[i,j]) <- 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
  }                                                  # 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
  }                                                  # 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.1.4 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
    }                                                # 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

```
# 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) {                             # 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.13.5 Mixed dichotomous and rate data; binomial likelihood with cloglog link and Poisson likelihood with log link

K.13.5.1 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) {                            # indexes studies with dichotomous data
  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

for(i in 1:NumStudiesC) {                            # indexes studies with count data
  mu[i + NumStudiesD] ~ dnorm(0, .0001)              # vague priors for all trial baselines
  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] + 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) {                            # 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
    }                                                # 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]]
                                + 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
  }                                                  # 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) {                      # indexes studies
  se[i]       <- SD[i] / sqrt(N[i])           # calculate SEs
  prec[i]     <- pow(se[i], -2)               # set precisions
  MC[i]       ~  dnorm(m, prec[i])            # normal likelihood
  }                                           # close study loop
m            ~  dnorm(0, .0001)               # vague prior for mean (baseline)
prob         <- m                             # 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) {                      # indexes studies
  se[i]       <- SD[i] / sqrt(N[i])           # calculate SEs
  prec[i]     <- pow(se[i], -2)               # set precisions
  MC[i]       ~  dnorm(p[i], prec[i])         # normal likelihood
  p[i]        <- mu[i]                        # identity link
  mu[i]       ~  dnorm(m, tau.m)              # 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)
prob         <- m                             # posterior mean
mu.new       ~  dnorm(m, tau.m)               # pred. dist. for baseline
pred         <- mu.new                        # 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) {                    # indexes studies
  k[i]          ~  dbin(p[i], N[i])         # binomial likelihood
  cloglog(p[i]) <- log(Yrs[i]) + m          # model for linear predictor
  }                                         # close study loop
m ~  dnorm(0, 0.0001)                       # vague prior for baseline
cloglog(prob) <- log(1) + m                 # 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) {                     # indexes studies
  k[i]          ~  dbin(p[i], N[i])          # binomial likelihood
  cloglog(p[i]) <- log(Yrs[i]) + mu[i]       # model for linear predictor
  mu[i]         ~  dnorm(m, tau.m)           # 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)
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.2.4 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) {                    # 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 baseline
cloglog(prob) <- log(1) + m                 # 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) {                    # 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
}
```

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.nicedsu.org.uk

model {
for(i in 1:NumStudies) {                     # indexes studies
  se[i]      <- SD[i] / sqrt(N[i])           # calculate SEs
  prec[i]    <- pow(se[i], -2)               # set precisions
  mu[i]      <- m + (Base[i]-xbar) * beta    # identity link with coefficient
  MC[i]      ~  dnorm(mu[i], prec[i])        # 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.nicedsu.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.nicedsu.org.uk

model {
for(i in 1:NumStudies) {                     # indexes studies
  se[i]      <- SD[i] / sqrt(N[i])           # calculate SEs
  prec[i]    <- pow(se[i], -2)               # set precisions
  MC[i]      ~  dnorm(p[i], prec[i])         # normal likelihood
  p[i]       <- mu[i] + (Base[i]-xbar)*beta  # identity link with coefficient
  mu[i]      ~  dnorm(m, tau.m)              # 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
}
```