

1 Appendix K: WinBUGS code

2 All WinBUGS code used in this guideline was based on specimens given in the NICE
3 Decision Support Unit's series of Technical Support Documents (TSDs) on evidence
4 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

```

8
9 # Normal likelihood, identity link
10 # Fixed effects model for multi-arm trials
11 # based on
12 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
13 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
14 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
15 # http://www.nicedsu.org.uk
16
17 model {
18   for(i in 1:NumStudies) {
19     mu[i] ~ dnorm(0, .0001) # indexes studies
20     for (j in 1:NumArms[i]) { # vague priors for all trial baselines
21       se[i,j] <- SD[i,j] / sqrt(N[i,j]) # indexes arms
22       var[i,j] <- pow(se[i,j],2) # calculate variances
23       prec[i,j] <- 1/var[i,j] # set precisions
24       MC[i,j] ~ dnorm(theta[i,j],prec[i,j]) # normal likelihood
25       theta[i,j] <- mu[i] + d[Rx[i,j]] - d[Rx[i,1]] # model for linear predictor
26       dev[i,j] <- (MC[i,j] - theta[i,j]) * (MC[i,j]
27         - theta[i,j]) * prec[i,j] # deviance contribution
28     } # close arm loop
29     resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
30   } # close study loop
31   totresdev <- sum(resdev[]) # total residual deviance
32
33   d[1]<-0 # effect is 0 for reference treatment
34   for (j in 2:NumRx) { # indexes treatments
35     d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
36   } # close treatment loop
37
38   # Provide estimates of treatment effects T[j] on the natural (probability) scale
39   # Given a Mean Effect, meanA, for 'standard' treatment A,
40   # with precision (1/variance) precA
41   AMean ~ dnorm(meanA, precA)
42   APred ~ dnorm(predA, predPrecA)
43   for (j in 1:NumRx) {
44     Tmean[j] <- AMean + d[j]
45     Tpred[j] <- APred + d[j]
46   }
47
48   # pairwise MDs for all possible pair-wise comparisons
49   for (c in 1:(NumRx-1)) {
50     for (j in (c+1):NumRx) {
51       MD[c,j] <- (d[j] - d[c])
52     }
53   }
54
55   # ranking on relative scale
56   for (j in 1:NumRx) {
57     rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
58     best[j] <- equals(rk[j],1) # probability that treat j is best
59     for (h in 1:NumRx) {
60       pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
61     }
62   }
63 }

```

K.1.12

Random effects

```

2
3
4 # Normal likelihood, identity link
5 # Random effects model for multi-arm trials
6 # based on
7 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
8 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
9 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
10 # http://www.nicesdsu.org.uk
11
12 model {
13   for(i in 1:NumStudies) {
14     w[i,1] <- 0 # indexes studies
15     delta[i,1] <- 0 # multi-arm adjustment = 0 for control
16     mu[i] ~ dnorm(0, .0001) # treatment effect is 0 for control
17     for (j in 1:NumArms[i]) { # vague priors for all trial baselines
18       se[i,j] <- SD[i,j] / sqrt(N[i,j]) # indexes arms
19       var[i,j] <- pow(se[i,j],2) # calculate variances
20       prec[i,j] <- 1/var[i,j] # set precisions
21       MC[i,j] ~ dnorm(theta[i,j], prec[i,j]) # normal likelihood
22       theta[i,j] <- mu[i] + delta[i,j] # model for linear predictor
23       dev[i,j] <- (MC[i,j] - theta[i,j]) * (MC[i,j]
24         - theta[i,j]) * prec[i,j] # deviance contribution
25     } # close arm loop
26     for (j in 2:NumArms[i]) { # indexes arms
27       delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific MD distributions
28       md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of MD dists, with multiarm
29       tau[i,j] <- tau * 2*(j-1)/j # precision of MD dists, with multiarm
30       w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]]) # adjustment, multi-arm RCTs
31       sw[i,j] <- sum(w[i,1:j-1])/(j-1) # cumulative adjustment for multi-arm
32     }
33     resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
34   } # close study loop
35   totresdev <- sum(resdev[]) # total residual deviance
36
37   d[1]<-0 # effect is 0 for reference treatment
38   for (j in 2:NumRx) { # indexes treatments
39     d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
40   } # close treatment loop
41   sdu ~ dunif(RFXpriorParam1, RFXpriorParam2) # uniform between-trial prior
42   sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2) # normal between-trial prior
43   sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2) # lognormal between-trial prior
44   sd <- sdu * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)
45   tau <- pow(sd,-2) # between-trial precision
46
47   # Provide estimates of treatment effects T[j] on the natural (probability) scale
48   # Given a Mean Effect, meanA, for 'standard' treatment A,
49   # with precision (1/variance) precA
50
51   AMean ~ dnorm(meanA, precA)
52   APred ~ dnorm(predA, predPrecA)
53   for (j in 1:NumRx) {
54     Tmean[j] <- AMean + d[j]
55     Tpred[j] <- APred + d[j]
56   }
57
58   # pairwise MDs for all possible pair-wise comparisons
59   for (c in 1:(NumRx-1)) {
60     for (j in (c+1):NumRx) {
61       MD[c,j] <- (d[j] - d[c])
62     }
63   }
64
65   # ranking on relative scale
66   for (j in 1:NumRx) {
67     rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
68     best[j] <- equals(rk[j],1) # probability that treat j is best
69     for (h in 1:NumRx) {
70       pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
71     }
72   }
73 }

```

K.1.12 Dichotomous data; binomial likelihood; logit link**K.1.21 Fixed effects**

```

3
4 # Binomial likelihood, logit link
5 # Fixed effects model for multi-arm trials
6 # based on
7 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
8 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
9 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
10 # http://www.nicedsu.org.uk
11
12 model {
13   for(i in 1:NumStudies) { # indexes studies
14     mu[i] ~ dnorm(0, .0001) # vague priors for all trial baselines
15     for (j in 1:NumArms[i]) { # indexes arms
16       k[i,j] ~ dbin(p[i,j],N[i,j]) # binomial likelihood
17       logit(p[i,j]) <- mu[i] + d[Rx[i,j]] - d[Rx[i,1]] # model for linear predictor
18       rhat[i,j] <- p[i,j] * N[i,j] # expected value of the numerators
19       dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])))
20         + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j]) - log(N[i,j]-rhat[i,j])))
21     } # deviance contribution
22   } # close arm loop
23   resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
24 } # close study loop
25 totresdev <- sum(resdev[]) # total residual deviance
26
27 d[1]<-0 # effect is 0 for reference treatment
28 for (j in 2:NumRx) { # indexes treatments
29   d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
30 } # close treatment loop
31
32 # Provide estimates of treatment effects T[j] on the natural (probability) scale
33 # Given a Mean Effect, meanA, for 'standard' treatment A,
34 # with precision (1/variance) precA
35
36 AMean ~ dnorm(meanA, precA)
37 APred ~ dnorm(predA, predPrecA)
38 for (j in 1:NumRx) {
39   logit(Tmean[j]) <- AMean + d[j]
40   logit(Tpred[j]) <- APred + d[j]
41 }
42
43 # pairwise ORs and LORs for all possible pair-wise comparisons
44 for (c in 1:(NumRx-1)) {
45   for (j in (c+1):NumRx) {
46     lOR[c,j] <- (d[j]-d[c])
47     OR[c,j] <- exp(lOR[c,j])
48   }
49 }
50
51 # ranking on relative scale
52 for (j in 1:NumRx) {
53   rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blNHiGood)*rank(d[,j])
54   best[j] <- equals(rk[j],1) # probability that treat j is best
55   for (h in 1:NumRx) {
56     pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
57   }
58 }
59 }

```

K.1.22 Random effects

```

61
62 # Binomial likelihood, logit link
63 # Random effects model for multi-arm trials
64 # based on
65 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
66 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
67 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
68 # http://www.nicedsu.org.uk
69
70 model {
71   for(i in 1:NumStudies) { # indexes studies
72     mu[i] ~ dnorm(0, .0001) # vague priors for all trial baselines
73     delta[i,1] <- 0 # effect is zero for control arm
74     w[i,1] <- 0 # multi-arm adjustment = zero for ctrl

```

```

1   for (j in 1:NumArms[i]) {
2       k[i,j] ~ dbin(p[i,j],N[i,j]) # indexes arms
3       logit(p[i,j]) <- mu[i] + delta[i,j] # binomial likelihood
4       rhat[i,j] <- p[i,j] * N[i,j] # model for linear predictor
5       dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])))
6           + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j]) - log(N[i,j]-rhat[i,j]))) # expected value of the numerators
7       # deviance contribution
8   } # close arm loop
9   for (j in 2:NumArms[i]) { # indexes arms
10      delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific LOR distributions
11      md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of LOR distributions (with
12      multi-arm trial correction)
13      taud[i,j] <- tau *2*(j-1)/j # precision of LOR distributions (with
14      multi-arm trial correction)
15      w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]])
16          # adjustment for multi-arm RCTs
17      sw[i,j] <- sum(w[i,1:j-1])/(j-1) # cumulative adjustment for multi-arm
18      trials
19  }
20  resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
21  } # close study loop
22  totresdev <- sum(resdev[]) # total residual deviance
23
24  d[1]<-0 # effect is 0 for reference treatment
25  for (j in 2:NumRx) { # indexes treatments
26      d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
27  } # close treatment loop
28  sdu ~ dunif(RFXpriorParam1, RFXpriorParam2) # uniform between-trial prior
29  sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2) # normal between-trial prior
30  sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2) # lognormal between-trial prior
31  sd <- sdu * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)
32      # select correct between-trial prior
33  tau <- pow(sd,-2) # between-trial precision
34
35  # Provide estimates of treatment effects T[k] on the natural (probability) scale
36  AMean ~ dnorm(meanA, precA)
37  APred ~ dnorm(predA, predPrecA)
38  for (j in 1:NumRx) {
39      logit(Tmean[j]) <- AMean + d[j]
40      logit(Tpred[j]) <- APred + d[j]
41  }
42
43  # pairwise ORs and LORs for all possible pair-wise comparisons
44  for (c in 1:(NumRx-1)) {
45      for (j in (c+1):NumRx) {
46          lOR[c,j] <- (d[j]-d[c])
47          OR[c,j] <- exp(d[j]-d[c])
48      }
49  }
50
51  # ranking on relative scale
52  for (j in 1:NumRx) {
53      rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
54      best[j] <- equals(rk[j],1) # probability that treat j is best
55      for (h in 1:NumRx) {
56          pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
57      }
58  }
59  }
60  }
61

```

K.62 Dichotomous data; binomial likelihood; cloglog link

K.163 Fixed effects

```

64 # Binomial likelihood, cloglog link
65 # Fixed effects model for multi-arm trials
66 # based on
67 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
68 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
69 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
70 # http://www.nicedsu.org.uk
71
72 model {
73   for(i in 1:NumStudies) { # indexes studies
74

```

```

1 mu[i] ~ dnorm(0, .0001) # vague priors for all trial baselines
2 for (j in 1:NumArms[i]) { # indexes arms
3   k[i,j] ~ dbin(p[i,j],N[i,j]) # binomial likelihood
4   cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + d[Rx[i,j]] - d[Rx[i,1]] # model for linear predictor
5   # expected value of the numerators
6   rhat[i,j] <- p[i,j] * N[i,j]
7   dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])))
8     + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j]) - log(N[i,j]-rhat[i,j]))) # deviance contribution
9   } # close arm loop
10 resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
11 } # close study loop
12 totresdev <- sum(resdev[]) # total residual deviance
13
14
15 d[1]<-0 # effect is 0 for reference treatment
16 for (j in 2:NumRx) { # indexes treatments
17   d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
18 } # close treatment loop
19
20 # Provide estimates of treatment effects T[j] on the natural (probability) scale
21 # Given a Mean Effect, meanA, for 'standard' treatment A,
22 # with precision (1/variance) precA, over a time period timeA
23
24 AMean ~ dnorm(meanA, precA)
25 APred ~ dnorm(predA, predPrecA)
26 for (j in 1:NumRx) {
27   cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
28   cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
29 }
30
31 # pairwise HRs and LHRs for all possible pair-wise comparisons
32 for (c in 1:(NumRx-1)) {
33   for (j in (c+1):NumRx) {
34     lHR[c,j] <- d[j] - d[c]
35     log(HR[c,j]) <- lHR[c,j]
36   }
37 }
38
39 # ranking on relative scale
40 for (j in 1:NumRx) {
41   rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
42   best[j] <- equals(rk[j],1) # probability that treat j is best
43   for (h in 1:NumRx) {
44     pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
45   }
46 }
47 }

```

K.1.48 Random effects

```

48 # Binomial likelihood, cloglog link
49 # Random effects model for multi-arm trials
50 # based on
51 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
52 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
53 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
54 # http://www.nicedsu.org.uk
55
56 model {
57   for(i in 1:NumStudies) { # indexes studies
58     mu[i] ~ dnorm(0, .0001) # vague priors for all trial baselines
59     delta[i,1] <- 0 # effect is zero for control arm
60     w[i,1] <- 0 # multi-arm adjustment = zero for ctrl
61     for (j in 1:NumArms[i]) { # indexes arms
62       k[i,j] ~ dbin(p[i,j],N[i,j]) # binomial likelihood
63       cloglog(p[i,j]) <- log(Yrs[i] / 1) + mu[i] + delta[i,j] # model for linear predictor
64       rhat[i,j] <- p[i,j] * N[i,j] # expected value of the numerators
65       dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])))
66         + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j]) - log(N[i,j]-rhat[i,j]))) # deviance contribution
67     } # close arm loop
68     for (j in 2:NumArms[i]) { # indexes arms
69       delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific LOR distributions
70       md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of LOR distributions (with
71         # multi-arm trial correction)
72       taud[i,j] <- tau *2*(j-1)/j # precision of LOR distributions (with
73         # multi-arm trial correction)
74     }
75   }
76 }

```

```

1      w[i,j]      <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]]) # adjustment for multi-arm RCTs
2      sw[i,j]     <- sum(w[i,1:j-1])/(j-1)                # cumulative adjustment for multi-arm
3                                                         # trials
4    }
5    resdev[i]    <- sum(dev[i,1:NumArms[i]])              # summed deviance contribution
6  }
7  totresdev    <- sum(resdev[])                          # total residual deviance
8
9  d[1]<-0                                               # effect is 0 for reference treatment
10 for (j in 2:NumRx) {                                  # indexes treatments
11   d[j] ~ dnorm(0, .0001)                              # vague priors for treatment effects
12 }
13 sdu ~ dunif(RFXpriorParam1, RFXpriorParam2)          # uniform between-trial prior
14 sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2)          # normal between-trial prior
15 sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2)         # lognormal between-trial prior
16 sd <- sdu * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)
17                                                         # select correct between-trial prior
18 tau <- pow(sd,-2)                                     # between-trial precision
19
20 # Provide estimates of treatment effects T[j] on the natural (probability) scale
21 # Given a Mean Effect, meanA, for 'standard' treatment A,
22 # with precision (1/variance) precA, over a time period timeA
23
24 AMean ~ dnorm(meanA, precA)
25 APred ~ dnorm(predA, predPrecA)
26 for (j in 1:NumRx) {
27   cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
28   cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
29 }
30
31 # pairwise HRs and LHRs for all possible pair-wise comparisons
32 for (c in 1:(NumRx-1)) {
33   for (j in (c+1):NumRx) {
34     lHR[c,j]      <- d[j] - d[c]
35     log(HR[c,j]) <- lHR[c,j]
36   }
37 }
38
39 # ranking on relative scale
40 for (j in 1:NumRx) {
41   rk[j]          <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
42   best[j]        <- equals(rk[j],1)                    # probability that treat j is best
43   for (h in 1:NumRx) {
44     pRk[h,j]     <- equals(rk[j],h)                    # probability that treat j is hth best
45   }
46 }
47 }

```

K.14 Rate data; Poisson likelihood; log link

K.149 Fixed effects

```

50 # Poisson likelihood, log link
51 # Fixed effects model for multi-arm trials
52 # based on
53 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
54 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
55 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
56 # http://www.nicedsu.org.uk
57
58 model {
59
60   for(i in 1:NumStudies) {
61     mu[i] ~ dnorm(0, .0001) # indexes studies
62     # vague priors for all trial baselines
63     for (j in 1:NumArms[i]) {
64       r[i,j] ~ dpois(theta[i,j]) # indexes arms
65       theta[i,j] <- lambda[i,j] * E[i,j] # Poisson likelihood
66       log(lambda[i,j]) <- mu[i] + d[Rx[i,j]] - d[Rx[i,1]] # failure rate * exposure
67       # model for linear predictor
68       dev[i,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))
69     } # deviance contribution
70   } # close arm loop
71   resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
72 } # close study loop
73 totresdev <- sum(resdev[]) # total residual deviance
74

```

```

1 d[1]<-0 # effect is 0 for reference treatment
2 for (j in 2:NumRx) { # indexes treatments
3   d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
4 } # close treatment loop
5
6 # Provide estimates of treatment effects T[j] on the natural (probability) scale
7 # Given a Mean Effect, meanA, for 'standard' treatment A,
8 # with precision (1/variance) precA, over a time period timeA
9
10 AMean ~ dnorm(meanA, precA)
11 APred ~ dnorm(predA, predPrecA)
12 for (j in 1:NumRx) {
13   cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
14   cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
15 }
16
17 # pairwise HRs and LHRs for all possible pair-wise comparisons
18 for (c in 1:(NumRx-1)) {
19   for (j in (c+1):NumRx) {
20     lHR[c,j] <- d[j] - d[c]
21     log(HR[c,j]) <- lHR[c,j]
22   }
23 }
24
25 # ranking on relative scale
26 for (j in 1:NumRx) {
27   rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
28   best[j] <- equals(rk[j],1) # probability that treat j is best
29   for (h in 1:NumRx) {
30     pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
31   }
32 }
33

```

K.1.1 Random effects

```

34
35 # Poisson likelihood, log link
36 # Random effects model for multi-arm trials
37 # based on
38 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
39 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
40 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
41 # http://www.nicesdsu.org.uk
42
43 model {
44
45   for(i in 1:NumStudies) { # indexes studies
46     mu[i] ~ dnorm(0, .0001) # vague priors for all trial baselines
47     delta[i,1] <- 0 # effect is zero for control arm
48     w[i,1] <- 0 # multi-arm adjustment = zero for ctrl
49     for (j in 1:NumArms[i]) { # indexes arms
50       r[i,j] ~ dpois(theta[i,j]) # Poisson likelihood
51       theta[i,j] <- lambda[i,j] * E[i,j] # failure rate * exposure
52       log(lambda[i,j]) <- mu[i] + delta[i,j] # model for linear predictor
53       dev[i,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))
54         # deviance contribution
55     } # close arm loop
56
57     for (j in 2:NumArms[i]) { # indexes arms
58       delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific LOR distributions
59       md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j] # mean of LOR distributions (with
60         # multi-arm trial correction)
61       taud[i,j] <- tau *2*(j-1)/j # precision of LOR distributions (with
62         # multi-arm trial correction)
63       w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]])
64         # adjustment for multi-arm RCTs
65       sw[i,j] <- sum(w[i,1:j-1])/(j-1) # cumulative adjustment for multi-arm
66         # trials
67     }
68     resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
69   } # close study loop
70   totresdev <- sum(resdev[]) # total residual deviance
71
72   d[1]<-0 # effect is 0 for reference treatment
73   for (j in 2:NumRx) { # indexes treatments
74     d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
75   } # close treatment loop
76   sdu ~ dunif(RFXpriorParam1, RFXpriorParam2) # uniform between-trial prior

```

```

1 sdn ~ dnorm(RFXpriorParam1, RFXpriorParam2) # normal between-trial prior
2 sdl ~ dlnorm(RFXpriorParam1, RFXpriorParam2) # lognormal between-trial prior
3 sd <- sdu * equals(RFXpriorD,1) + sdn * equals(RFXpriorD,2) + sdl * equals(RFXpriorD,3)
4 # select correct between-trial prior
5 tau <- pow(sd,-2) # between-trial precision
6
7 # Provide estimates of treatment effects T[j] on the natural (probability) scale
8 # Given a Mean Effect, meanA, for 'standard' treatment A,
9 # with precision (1/variance) precA, over a time period timeA
10
11 AMean ~ dnorm(meanA, precA)
12 APred ~ dnorm(predA, predPrecA)
13 for (j in 1:NumRx) {
14   cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
15   cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
16 }
17
18 # pairwise HRs and LHRs for all possible pair-wise comparisons
19 for (c in 1:(NumRx-1)) {
20   for (j in (c+1):NumRx) {
21     lHR[c,j] <- d[j] - d[c]
22     log(HR[c,j]) <- lHR[c,j]
23   }
24 }
25
26 # ranking on relative scale
27 for (j in 1:NumRx) {
28   rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
29   best[j] <- equals(rk[j],1) # probability that treat j is best
30   for (h in 1:NumRx) {
31     pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
32   }
33 }
34 }

```

K.15 Mixed dichotomous and rate data; binomial likelihood with cloglog link and Poisson likelihood with log link

K.15.1 Fixed effects

```

38 # Effectiveness model for mixed dichotomous and count data
39 # Binomial likelihood, cloglog link / Poisson likelihood, log link
40 # Fixed effects
41 # based on
42 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
43 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
44 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
45 # http://www.nicedsu.org.uk
46
47 model {
48   for(i in 1:NumStudiesD) {
49     # indexes studies with dichotomous data
50     mu[i] ~ dnorm(0, .0001) # vague priors for all trial baselines
51     for (j in 1:NumArms[i]) {
52       # indexes arms
53       k[i,j] ~ dbin(p[i,j],N[i,j]) # binomial likelihood
54       cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + d[RxC[i,j]] - d[RxC[i,1]]
55       # model for linear predictor
56       rhat[i,j] <- p[i,j] * N[i,j] # expected value of the numerators
57       dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j])))
58         + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j])
59         - log(N[i,j]-rhat[i,j]))) # deviance contribution
60     } # close arm loop
61     resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
62   } # close study loop
63
64   for(i in 1:NumStudiesC) {
65     # indexes studies with count data
66     mu[i + NumStudiesD] ~ dnorm(0, .0001) # vague priors for all trial baselines
67     for (j in 1:NumArmsC[i]) {
68       # indexes arms
69       r[i,j] ~ dpois(theta[i,j]) # Poisson likelihood
70       theta[i,j] <- lambda[i,j] * E[i,j] # failure rate * exposure
71       log(lambda[i,j]) <- mu[i + NumStudiesD] + d[RxC[i,j]] - d[RxC[i,1]]
72       # model for linear predictor
73       dev[i + NumStudiesD,j] <- 2 * ((theta[i,j]-r[i,j]) + r[i,j] * log(r[i,j] / theta[i,j]))
74       # deviance contribution
75     } # close arm loop
76     resdev[i + NumStudiesD] <- sum(dev[i + NumStudiesD,1:NumArmsC[i]]) # summed deviance contribution

```



```

1      } # close study loop
2
3      totresdev <- sum(resdev[]) # total residual deviance
4
5      d[1]<-0 # effect is 0 for reference treatment
6      for (j in 2:NumRx) { # indexes treatments
7          d[j] ~ dnorm(0, .0001) # vague priors for treatment effects
8      } # close treatment loop
9
10     # Provide estimates of treatment effects T[j] on the natural (probability) scale
11     # Given a Mean Effect, meanA, for 'standard' treatment A,
12     # with precision (1/variance) precA, over a time period timeA
13     AMean ~ dnorm(meanA, precA)
14     APred ~ dnorm(predA, predPrecA)
15     for (j in 1:NumRx) {
16         cloglog(Tmean[j]) <- log(YrsA) + AMean + d[j]
17         cloglog(Tpred[j]) <- log(YrsA) + APred + d[j]
18     }
19
20     # pairwise HRs and LHRs for all possible pairwise comparisons
21     for (c in 1:(NumRx-1)) {
22         for (j in (c+1):NumRx) {
23             lHR[c,j] <- d[j] - d[c]
24             log(HR[c,j]) <- lHR[c,j]
25         }
26     }
27
28     # ranking on relative scale
29     for (j in 1:NumRx) {
30         rk[j] <- blnHiGood*(NumRx+1-rank(d[,j])) + (1-blnHiGood)*rank(d[,j])
31         best[j] <- equals(rk[j],1) # probability that treat j is best
32         for (h in 1:NumRx) {
33             pRk[h,j] <- equals(rk[j],h) # probability that treat j is hth best
34         }
35     }
36 }

```

K.1.372 Random effects

```

38
39 # Effectiveness model for mixed dichotomous and count data
40 # Binomial likelihood, cloglog link / Poisson likelihood, log link
41 # Random effects
42 # based on
43 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
44 # NICE DSU Technical Support Document 2: A Generalised Linear Modelling Framework
45 # for Pairwise and Network Meta-Analysis of Randomised Controlled Trials. 2011.
46 # http://www.nicedsu.org.uk
47
48 model {
49     for(i in 1:NumStudiesD) { # indexes studies with dichotomous data
50         mu[i] ~ dnorm(0, .01) # vague priors for all trial baselines
51         delta[i,1] <- 0 # effect is zero for control arm
52         w[i,1] <- 0 # multi-arm adjustment = zero for ctrl
53         for (j in 1:NumArms[i]) { # indexes arms
54             k[i,j] ~ dbin(p[i,j],N[i,j]) # binomial likelihood
55             cloglog(p[i,j]) <- log(Yrs[i]/1) + mu[i] + delta[i,j]
56             # model for linear predictor
57             rhat[i,j] <- p[i,j] * N[i,j] # expected value of the numerators
58             dev[i,j] <- 2 * (k[i,j] * (log(k[i,j])-log(rhat[i,j]))
59                 + (N[i,j]-k[i,j]) * (log(N[i,j]-k[i,j])
60                 - log(N[i,j]-rhat[i,j]))) # deviance contribution
61         } # close arm loop
62         for (j in 2:NumArms[i]) { # indexes arms
63             delta[i,j] ~ dnorm(md[i,j],taud[i,j]) # trial-specific LHR distributions
64             md[i,j] <- d[Rx[i,j]] - d[Rx[i,1]] + sw[i,j]
65             # mean of LHR distributions (with
66             # multi-arm trial correction)
67             taud[i,j] <- tau *2*(j-1)/j # precision of LOR distributions (with
68             # multi-arm trial correction)
69             w[i,j] <- (delta[i,j] - d[Rx[i,j]] + d[Rx[i,1]])
70             # adjustment for multi-arm RCTs
71             sw[i,j] <- sum(w[i,1:j-1])/(j-1)
72             # cumulative adjustment for multi-arm
73             # trials
74         }
75         resdev[i] <- sum(dev[i,1:NumArms[i]]) # summed deviance contribution
76     } # close study loop

```

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71
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

```

4
5 # Baseline model for continuous data
6 # Normal likelihood, identity link
7 # Fixed-effects model
8 # based on
9 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
10 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
11 # natural history model. 2011.
12 # http://www.nicedsu.org.uk
13
14 model {
15   for(i in 1:NumStudies) {
16     se[i]      <- SD[i] / sqrt(N[i])      # indexes studies
17     prec[i]    <- pow(se[i], -2)         # calculate SEs
18     MC[i]      ~ dnorm(m, prec[i])       # set precisions
19   }                                       # normal likelihood
20   m            ~ dnorm(0, .0001)        # close study loop
21   prob         <- m                    # vague prior for mean (baseline)
22 }                                           # posterior mean

```

K.2.1.2 Random effects

```

24
25 # Baseline model for continuous data
26 # Normal likelihood, identity link
27 # Random-effects model
28 # based on
29 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
30 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
31 # natural history model. 2011.
32 # http://www.nicedsu.org.uk
33
34 model {
35   for(i in 1:NumStudies) {
36     se[i]      <- SD[i] / sqrt(N[i])      # indexes studies
37     prec[i]    <- pow(se[i], -2)         # calculate SEs
38     MC[i]      ~ dnorm(p[i], prec[i])    # set precisions
39     p[i]       <- mu[i]                  # normal likelihood
40     mu[i]      ~ dnorm(m, tau.m)        # identity link
41   }                                       # trial-specific baseline with random effects
42   sd.m        ~ dunif(0, 5)            # close study loop
43   tau.m       <- pow(sd.m, -2)          # vague prior for SD (baseline)
44   m           ~ dnorm(0, .0001)        # between-trial precision (baseline)
45   prob        <- m                    # vague prior for mean (baseline)
46   mu.new      ~ dnorm(m, tau.m)        # posterior mean
47   pred        <- mu.new                # pred. dist. for baseline
48 }                                           # predictive mean for a new observation

```

K.2.2 Dichotomous data; binomial likelihood; logit link

50 Not used

K.2.3 Dichotomous data; binomial likelihood; cloglog link

K.2.3.1 Fixed effects

```

53
54 # Baseline model for dichotomous data
55 # Binomial likelihood, cloglog link
56 # Fixed-effects model
57 # based on
58 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
59 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
60 # natural history model. 2011.
61 # http://www.nicedsu.org.uk
62
63 model {

```

```

1 for(i in 1:NumStudies) {
2   k[i] ~ dbin(p[i], N[i]) # indexes studies
3   cloglog(p[i]) <- log(Yrs[i]) + m # binomial likelihood
4 } # model for linear predictor
5 # close study loop
6 m ~ dnorm(0, 0.0001) # vague prior for baseline
7 cloglog(prob) <- log(1) + m # posterior mean yearly response rate

```

K.2.32 Random effects

```

9 # Baseline model for dichotomous data
10 # Binomial likelihood, cloglog link
11 # Random-effects model
12 # based on
13 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
14 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
15 # natural history model. 2011.
16 # http://www.nicedsu.org.uk
17
18
19 model {
20   for(i in 1:NumStudies) {
21     k[i] ~ dbin(p[i], N[i]) # indexes studies
22     cloglog(p[i]) <- log(Yrs[i]) + mu[i] # binomial likelihood
23     mu[i] ~ dnorm(m, tau.m) # model for linear predictor
24   } # trial-specific baseline with random effects
25   # close study loop
26   sd.m ~ dunif(0, 5) # vague prior for SD (baseline)
27   tau.m <- pow(sd.m, -2) # between-trial precision (baseline)
28   m ~ dnorm(0, .0001) # vague prior for mean (baseline)
29   cloglog(prob) <- log(1) + m # posterior mean yearly response rate
30   mu.new ~ dnorm(m, tau.m) # pred. dist. for baseline (log-HR)
31   cloglog(pred) <- log(1) + mu.new # predictive mean yearly response rate

```

K.24 Rate data; Poisson likelihood; log link**K.2.41 Fixed effects**

```

32 # Baseline model for rate data
33 # Poisson likelihood, log link
34 # Fixed-effects model
35 # based on
36 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
37 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
38 # natural history model. 2011.
39 # http://www.nicedsu.org.uk
40
41
42 model {
43   for(i in 1:NumStudies) {
44     r[i] ~ dpois(theta[i]) # indexes studies with count data
45     theta[i] <- exp(m) * (E[i] / 365.24) # Poisson likelihood
46   } # event rate * exposure
47 } # close study loop
48 m ~ dnorm(0, 0.0001) # vague prior for baseline
49 cloglog(prob) <- log(1) + m # posterior mean yearly response rate
50
51

```

K.2.42 Random effects

```

52 # Baseline model for rate data
53 # Poisson likelihood, log link
54 # Random-effects model
55 # based on
56 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
57 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
58 # natural history model. 2011.
59 # http://www.nicedsu.org.uk
60
61
62 model {
63   for(i in 1:NumStudies) {
64     mu[i] ~ dnorm(m, tau.m) # indexes studies
65     r[i] ~ dpois(theta[i]) # trial-specific baseline with random effects
66     theta[i] <- exp(mu[i]) * (E[i] / 365.24) # Poisson likelihood
67   } # event rate * exposure
68 } # close study loop
69 sd.m ~ dunif(0, 5) # vague prior for SD (baseline)
70

```

```

1 tau.m      <- pow(sd.m, -2)           # between-trial precision (baseline)
2 m          ~ dnorm(0, .0001)         # vague prior for mean (baseline)
3 cloglog(prob) <- log(1) + m          # posterior mean yearly response rate
4 mu.new     ~ dnorm(m, tau.m)         # pred. dist. for baseline (log-HR)
5 cloglog(pred) <- log(1) + mu.new     # predictive mean yearly response rate
6 }

```

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

```

10 # Baseline model for mixed dichotomous and count data
11 # Binomial likelihood, cloglog link / Poisson likelihood, log link
12 # Fixed-effects model
13 # Based on
14 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
15 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
16 # natural history model. 2011.
17 # http://www.nicedsu.org.uk
18
19 model {
20   for(i in 1:NumStudiesD) {           # indexes studies with dichotomous data
21     k[i] ~ dbin(p[i], N[i])           # binomial likelihood
22     cloglog(p[i]) <- log(Yrs[i]) + m   # model for linear predictor
23   }                                     # close study loop
24   for(i in 1:NumStudiesC) {           # indexes studies with count data
25     r[i] ~ dpois(theta[i])            # Poisson likelihood
26     theta[i] <- exp(m) * (E[i] / 365.24) # event rate * exposure
27     dummy[i] <- YrsC[i]               # not used in this model
28   }                                     # close study loop
29   m ~ dnorm(0, 0.0001)                # vague prior for baseline
30   cloglog(prob) <- log(1) + m          # posterior mean yearly response rate
31 }
32

```

K.2.5.2 Random effects

```

34 # Baseline model for mixed dichotomous and count data
35 # Binomial likelihood, cloglog link / Poisson likelihood, log link
36 # Random-effects model
37 # Based on
38 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
39 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
40 # natural history model. 2011.
41 # http://www.nicedsu.org.uk
42
43 model {
44   for(i in 1:NumStudiesC+NumStudiesD) { # indexes studies
45     mu[i] ~ dnorm(m, tau.m)             # trial-specific baseline with random effects
46   }                                     # close study loop
47   for(i in 1:NumStudiesD) {           # indexes studies with dichotomous data
48     k[i] ~ dbin(p[i], N[i])           # binomial likelihood
49     cloglog(p[i]) <- log(Yrs[i] / 1) + mu[i] # model for linear predictor
50   }                                     # close study loop
51   for(i in 1:NumStudiesC) {           # indexes studies with count data
52     r[i] ~ dpois(theta[i])            # Poisson likelihood
53     theta[i] <- exp(mu[NumStudiesD+i]) * (E[i] / 365.24) # event rate * exposure
54   }                                     # not used in this model
55   dummy[i] <- YrsC[i]                 # close study loop
56 }
57   sd.m ~ dunif(0, 5)                  # vague prior for SD (baseline)
58   tau.m <- pow(sd.m, -2)              # between-trial precision (baseline)
59   m ~ dnorm(0, .0001)                 # vague prior for mean (baseline)
60   cloglog(prob) <- log(1) + m          # posterior mean yearly response rate
61   mu.new ~ dnorm(m, tau.m)            # pred. dist. for baseline (log-HR)
62   cloglog(pred) <- log(1) + mu.new    # predictive mean yearly response rate
63 }
64

```

K.3 Adjusted baseline effects syntheses

K.3.21 Continuous data; normal likelihood; identity link

K.3.131 Fixed effects

```

4
5 # Baseline model for continuous data
6 # Normal likelihood, identity link
7 # Fixed-effects model with meta-regression
8 # based on
9 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
10 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
11 # natural history model. 2011.
12 # and
13 # Dias, S., Sutton, A.J., Welton, N.J., Ades, A.E.
14 # NICE DSU Technical Support Document 3: Heterogeneity: subgroups,
15 # meta-regression, bias and bias-adjustment. 2011
16 # http://www.nicedsu.org.uk
17
18 model {
19   for(i in 1:NumStudies) {           # indexes studies
20     se[i]      <- SD[i] / sqrt(N[i]) # calculate SEs
21     prec[i]    <- pow(se[i], -2)     # set precisions
22     mu[i]      <- m + (Base[i]-xbar) * beta # identity link with coefficient
23     MC[i]      ~ dnorm(mu[i], prec[i]) # normal likelihood
24   }                                   # close study loop
25   m            ~ dnorm(0, .0001)     # vague prior for mean (baseline)
26   beta         ~ dnorm(0, .0001)     # vague prior for coefficient
27   prob         <- m                  # posterior mean
28 }

```

K.3.132 Random effects

```

30
31 # Baseline model for continuous data
32 # Normal likelihood, identity link
33 # Random-effects model with meta-regression
34 # based on
35 # Dias, S., Welton, N.J., Sutton, A.J. & Ades, A.E.
36 # NICE DSU Technical Support Document 5: Evidence synthesis in the baseline
37 # natural history model. 2011.
38 # http://www.nicedsu.org.uk
39 # and
40 # Dias, S., Sutton, A.J., Welton, N.J., Ades, A.E.
41 # NICE DSU Technical Support Document 3: Heterogeneity: subgroups,
42 # meta-regression, bias and bias-adjustment. 2011
43 # http://www.nicedsu.org.uk
44
45 model {
46   for(i in 1:NumStudies) {           # indexes studies
47     se[i]      <- SD[i] / sqrt(N[i]) # calculate SEs
48     prec[i]    <- pow(se[i], -2)     # set precisions
49     MC[i]      ~ dnorm(p[i], prec[i]) # normal likelihood
50     p[i]       <- mu[i] + (Base[i]-xbar)*beta # identity link with coefficient
51     mu[i]      ~ dnorm(m, tau.m)     # trial-specific baseline with random effects
52   }                                   # close study loop
53   sd.m        ~ dunif(0, 5)         # vague prior for SD (baseline)
54   tau.m       <- pow(sd.m, -2)      # between-trial precision (baseline)
55   m           ~ dnorm(0, .0001)     # vague prior for mean (baseline)
56   beta        ~ dnorm(0, .0001)     # vague prior for coefficient
57   prob        <- m                  # posterior mean
58   mu.new      ~ dnorm(m, tau.m)     # pred. dist. for baseline
59   pred        <- mu.new              # predictive mean for a new observation
60 }

```