

Appendix 1. JAGS code for Bayesian models

```
#####
#### The AB-NMA model (as in tipping point analysis step 1)
####
#####

model{
  for(i in 1:len){
    logit(p[i]) <- mu[t[i]] + vi[s[i], t[i]]
    r[i] ~ dbin(p[i], totaln[i])
    rhat[i] <- p[i]*totaln[i]
    dev[i] <- 2*(r[i]*(log(r[i]) - log(rhat[i]))) +
      (totaln[i] - r[i])*(log(totaln[i] - r[i]) - log(totaln[i] -
        rhat[i])))
  }
  totesdev <- sum(dev[])
  for(j in 1:nstudy){
    vi[j, 1:ntrt] ~ dmnorm(zeros[1:ntrt], T[1:ntrt, 1:ntrt])
  }
  for(j in 1:ntrt){
    AR[j] <- 1/(1 + exp(-mu[j]/sqrt(1 + (16*sqrt(3)
      /(15*3.1415926))^2*pow(sigma[j], 2))))
    mu[j] ~ dnorm(0, 0.001)
    sigma[j] ~ dunif(0.0001, 10)

    # Alternative HHC prior for standard deviation
    #sigma[j] ~ dt(0, a_sd, 1)
  }

  #a_sd ~ dunif(0, 5)

  for(j in 1:ntrt){
    for(k in 1:ntrt){
      T[j,k] <- 1/sigma[j]*1/sigma[k]*ifelse(j == k, diag, offdiag
        )
    }
  }
  diag <- (1 + (ntrt - 2)*rho)/(1 + (ntrt - 2)*rho - (ntrt - 1)*
    rho^2)
  offdiag <- (-rho/(1 + (ntrt - 2)*rho - (ntrt - 1)*rho^2))

#####
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rho ~ dunif(-1/(ntrt - 1), 0.9999)

#####

for(j in 1:ntrt){
  for(k in 1:ntrt){
    LRR[j,k] <- log(RR[j,k])
    LOR[j,k] <- log(OR[j,k])
    LOR.med[j,k] <- mu[j] - mu[k]
    RR[j,k] <- AR[j]/AR[k]
    RD[j,k] <- AR[j]-AR[k]
    OR[j,k] <- AR[j]/(1 - AR[j])/AR[k]*(1 - AR[k])
    OR.med[j,k] <- exp(LOR.med[j,k])
    #####
    # check Prob(RR>1)
    P1[j,k] <- step(RR[j,k]-1)
    #####
  }
}
rk[1:ntrt] <- (ntrt + 1 - rank(AR[]))*ifelse(higher.better, 1,
  0) + (rank(AR[]))*ifelse(higher.better, 0, 1)
rk.med[1:ntrt] <- (ntrt + 1 - rank(mu[]))*ifelse(higher.better
  , 1, 0) + (rank(mu[]))*ifelse(higher.better, 0, 1)
for(i in 1:ntrt){
  rank.prob[1:ntrt, i] <- equals(rk[], i)
  rank.prob.med[1:ntrt, i] <- equals(rk.med[], i)
}

}

#####
#### The AB-NMA model with a fixed value of correlation
parameter rho (as in tipping point analysis step 2) ####
#####

model{
  for(i in 1:len){
    logit(p[i]) <- mu[t[i]] + vi[s[i], t[i]]
    r[i] ~ dbin(p[i], totaln[i])
    rhat[i] <- p[i]*totaln[i]
    dev[i] <- 2*(r[i]*(log(r[i]) - log(rhat[i])) +
      (totaln[i] - r[i])*(log(totaln[i] - r[i]) - log(totaln[i] -
        rhat[i])))
  }
}

```

```

}
totresdev <- sum(dev[])
for(j in 1:nstudy){
  vi[j, 1:ntrt] ~ dmnorm(zeros[1:ntrt], T[1:ntrt, 1:ntrt])
}
for(j in 1:ntrt){
  AR[j] <- 1/(1 + exp(-mu[j]/sqrt(1 + (16*sqrt(3)
    /(15*3.1415926))^2*pow(sigma[j], 2))))
  mu[j] ~ dnorm(0, 0.001)
  sigma[j] ~ dunif(0.0001, 10)

  # Alternative HHC prior for standard deviation
  #sigma[j] ~ dt(0, a_sd, 1)
}

#a_sd ~ dunif(0, 5)

for(j in 1:ntrt){
  for(k in 1:ntrt){
    T[j,k] <- 1/sigma[j]*1/sigma[k]*ifelse(j == k, diag, offdiag
    )
  }
}
diag <- (1 + (ntrt - 2)*rho)/(1 + (ntrt - 2)*rho - (ntrt - 1)*
  rho^2)
offdiag <- (-rho/(1 + (ntrt - 2)*rho - (ntrt - 1)*rho^2))

#####

# rho will be assigned a fixed value

#####

for(j in 1:ntrt){
  for(k in 1:ntrt){
    LRR[j,k] <- log(RR[j,k])
    LOR[j,k] <- log(OR[j,k])
    LOR.med[j,k] <- mu[j] - mu[k]
    RR[j,k] <- AR[j]/AR[k]
    RD[j,k] <- AR[j]-AR[k]
    OR[j,k] <- AR[j]/(1 - AR[j])/AR[k]*(1 - AR[k])
    OR.med[j,k] <- exp(LOR.med[j,k])
    #####
    # check Prob(RR>1)

```

```

P1[j,k] <- step(RR[j,k]-1)
#####
}
}
rk[1:ntrt] <- (ntrt + 1 - rank(AR[]))*ifelse(higher.better, 1,
0) + (rank(AR[]))*ifelse(higher.better, 0, 1)
rk.med[1:ntrt] <- (ntrt + 1 - rank(mu[]))*ifelse(higher.better
, 1, 0) + (rank(mu[]))*ifelse(higher.better, 0, 1)
for(i in 1:ntrt){
  rank.prob[1:ntrt, i] <- equals(rk[], i)
  rank.prob.med[1:ntrt, i] <- equals(rk.med[], i)
}
}

```

Appendix 2. Supplemental results

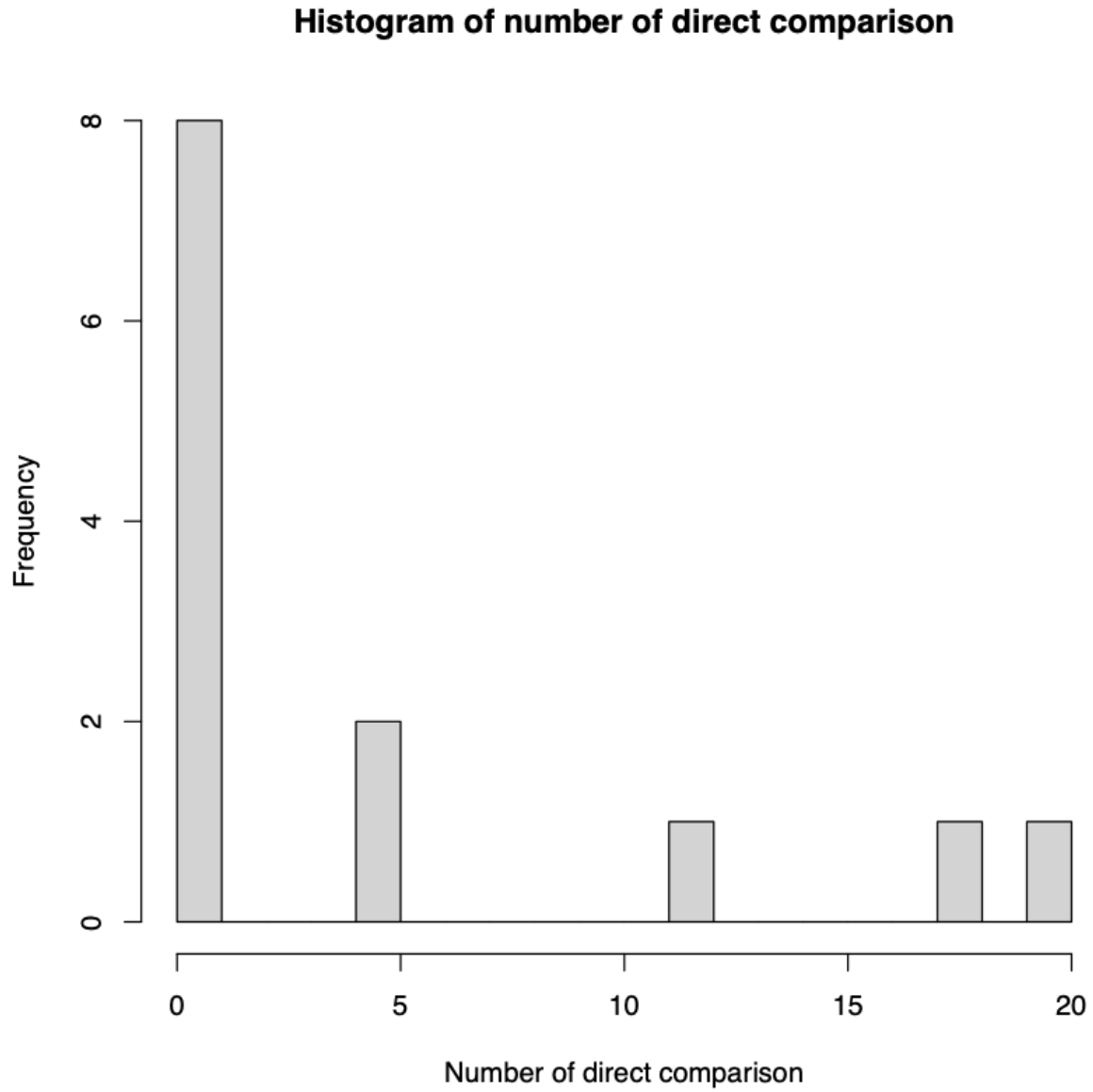


Figure S1: Histogram of the number of direct comparisons among pairs with an *interval conclusion change* tipping point in 14 selected NMA datasets.