

This code is part of Dias, Ades, Welton, Jansen and Sutton (2018) Network Meta-Analysis for Decision Making. This work should be cited whenever the code is used whether in its standard form or adapted.

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# Normal likelihood, identity link
# Trial-level data given as treatment differences
# Random effects model for multi-arm trials
model{
    # *** PROGRAM STARTS
    for(i in 1:ns2) {
        # LOOP THROUGH 2-ARM STUDIES
        y[i,2] ~ dnorm(delta[i,2],prec[i,2]) # normal likelihood for 2-arm
        trials
        #Deviance contribution for trial i
        resdev[i] <- (y[i,2]-delta[i,2])*(y[i,2]-delta[i,2])*prec[i,2]
    }
    for(i in (ns2+1):(ns2+ns3)) {
        # LOOP THROUGH THREE-ARM STUDIES
        for (k in 1:(na[i]-1)) {
            # set variance-covariance matrix
            for (j in 1:(na[i]-1)) {
                Sigma[i,j,k] <- V[i]*(1>equals(j,k)) + var[i,k+1]*equals(j,k)
            }
        }
        Omega[i,1:(na[i]-1),1:(na[i]-1)] <- inverse(Sigma[i,,]) #Precision
        matrix
        # multivariate normal likelihood for 3-arm trials
        y[i,2:na[i]] ~ dmnorm(delta[i,2:na[i]],Omega[i,1:(na[i]-1),1:(na[i]-
        1)]))
        #Deviance contribution for trial i
        for (k in 1:(na[i]-1)){
            # multiply vector & matrix
            ydiff[i,k]<- y[i,(k+1)] - delta[i,(k+1)]
            z[i,k]<- inprod2(Omega[i,k,1:(na[i]-1)], ydiff[i,1:(na[i]-1)])
        }
        resdev[i]<- inprod2(ydiff[i,1:(na[i]-1)], z[i,1:(na[i]-1)])
    }
    for(i in 1:(ns2+ns3)){
        # LOOP THROUGH ALL STUDIES
        w[i,1] <- 0 # adjustment for multi-arm trials is zero for control
        arm
        delta[i,1] <- 0 # treatment effect is zero for control arm
        for (k in 2:na[i]) {
            # LOOP THROUGH ARMS
            var[i,k] <- pow(se[i,k],2) # calculate variances
            prec[i,k] <- 1/var[i,k] # set precisions
        }
        for (k in 2:na[i]) {
            # LOOP THROUGH ARMS
            # trial-specific RE distributions
            delta[i,k] ~ dnorm(md[i,k],taud[i,k])
            # mean of random effects distributions, with multi-arm trial correction
            md[i,k] <- d[t[i,k]] - d[t[i,1]] + sw[i,k]
            # precision of random effects distributions (with multi-arm trial
            correction)
            taud[i,k] <- tau *2*(k-1)/k
            # adjustment, multi-arm RCTs
            w[i,k] <- (delta[i,k] - d[t[i,k]] + d[t[i,1]])
            # cumulative adjustment for multi-arm trials
            sw[i,k] <- sum(w[i,1:k-1])/(k-1)
        }
    }
    totresdev <- sum(resdev[]) #Total Residual Deviance
    d[1]<-0 # treatment effect is zero for reference treatment
    # vague priors for treatment effects
    for (k in 2:nt){ d[k] ~ dnorm(0,.0001) }
    sd ~ dunif(0,5) # vague prior for between-trial SD
    tau <- pow(sd,-2) # between-trial precision = (1/between-trial variance)
    # pairwise mean differences for all possible pair-wise comparisons
    for (c in 1:(nt-1)) {
        for (k in (c+1):nt) { diff[c,k] <- d[k]-d[c] }
    }
}

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}
# ranking on relative scale
for (k in 1:nt) {
# rk[k] <- nt+1-rank(d[,k) # assumes higher values are "good"
rk[k] <- rank(d[,k) # assumes higher values are "bad"
best[k] <- equals(rk[k],1) #calculate probability that treat k is best
# calculates probability that treat k is h-th best
for (h in 1:nt){ prob[h,k] <- equals(rk[k],h) }
}
# Provide estimates of treatment effects T[k] on the natural scale
# Given a Mean Effect, meanA, for 'standard' treatment A,
# with precision (1/variance) precA
A ~ dnorm(meanA,precA)
for (k in 1:nt) { T[k] <- A + d[k] }
} # *** PROGRAM ENDS

```