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Supporting Information: WinBUGS code for label-invariant models

Univariable model for the influence of a single study-level characteristic

Data required:

N_study=no. of studies
N=no. of studies x 2 arms
N_ma=no. of meta-analyses

Study-level:

treat=1 if treatment arm, 0 if control
r=no. of events
n= no. of participants
C1[i] = 1 if the *i*th study has the characteristic of interest, 0 otherwise
ma[i]<- meta-analysis index
s[i]<-study index

Meta-analysis level:

kappa_ok[m] = 1 if there are at least two studies with, and two studies without, the characteristic in the *m*th meta-analysis, 0 otherwise

The WinBUGS model

```
model{
for (i in 1:N) {
  r[i] ~ dbin(p[i],n[i]) # likelihood (binary data r/n=no.of events/no. of participants)
  logit(p[i]) <- alpha[s[i]] + treat[i]*(theta.minus[i]*+ beta[i] *C1[i])
    # model (treat indicator of treatment group; C1 indicator of study characteristic)
  beta[i]~dnorm(mean[ma[i]],p.k2[ma[i]]|(-10,10)
    # between study, within meta-analysis, variation in difference in effect associated
with characteristic
theta.minus[i]~dnorm(d[ma[i]],p.d[ma[i]]|(-10,10) #RE for intervention effect within meta-analysis

  rhat[i] <- p[i] * n[i]      #calculate residual deviance
  dev[i] <- 2 * (r[i] * (log(r[i])-log(rhat[i])) + (n[i]-r[i]) * (log(n[i]-r[i]) - log(n[i]-rhat[i])))
}
resdev <- sum(dev[])

for (j in 1:N_study) {alpha[j] ~ dnorm(0,.001)}      # priors for study baseline effects - unrelated

for (m in 1:N_ma) {
  mean[m] <- d[m] + b[m]
  d[m] ~ dnorm(0,.001)          # priors for true fixed (unrelated) intervention effects
  b[m] ~ dnorm(b0,p.phi)       # between meta-analysis variation in average difference in
effect associated with characteristic
  var_d[m]~dlnorm(mu,p.tau)    # log-normal distribution for between-study variances
  p.d[m] <- 1/var_d[m]
  p.k2[m] <- equals(kappa_ok[m],1)/(var_d[m]*lambda)
    +equals(kappa_ok[m],0)/(var_d[m]*cut(lambda))
}
#Prior for unknown parameters
b0 ~ dnorm(0,.001)      # vague prior for overall average difference in effect associated with
characteristic
lambda ~dlnorm(0,1)    # vague prior for change in between-study variation associated with characteristic
```

```

p.phi1 ~ dgamma(.001,.001) # vague prior for between meta-analysis variation in average
difference in effect associated with characteristic
phi <- pow(p.phi,-0.5)
p.phi <- p.phi1/(1-patom.phi)
patom.phi ~ dbeta(1,1)
mu~dnorm(0,0.001)
p.tau<-1/(sd.tau*sd.tau)
sd.tau~dunif(0,2)

log.tau2.new~dlnorm(mu,p.tau) # predictive distn for heterogeneity among studies without the characteristic
tau2.new<-exp(log.tau2.new)

# Parameters to monitor
q[1] <- b0
q[2] <- exp(b0)
q[3] <- lambda
q[4] <- phi
q[5]<- log.tau2.new
q[6]<-tau2.new

}

```

Multivariable model for the influence of three study-level characteristics

Data required:

N_study=no. of studies
 N=no. of studies x 2 arms
 N_ma=no. of meta-analyses

Study-level:

treat=1 if treatment arm, 0 if control
 r=no. of events
 n= no. of participants
 C1[i,j] = 1 if the *i*th study has the *j*th characteristic, 0 otherwise
 ma[i]<- meta-analysis index
 s[i]<-study index

Meta-analysis level:

kappa_ok[m,j] = 1 if there are at least two studies with, and two studies without, the *j*th characteristic in the *m*th meta-analysis, 0 otherwise
 clambda[m,j] = 1 if there are 1, K-1 or K studies with or without the *j*th characteristic in the *m*th meta-analysis, 0 otherwise, where K is the no. of studies in the meta-analysis.
 C0[m,j]=1 if there are no studies in the *m*th meta-analysis with the *j*th characteristic

The WinBUGS model

```

model {
for (i in 1:N) {
  r[i] ~ dbin(p[i],n[i]) # likelihood (binary data r/n=no.of events/no. of participants)
  logit(p[i]) <- alpha[s[i]] + theta[i]*treat[i]

  theta[i]<-theta.minus[i]* (1-C1[i,1]) *(1-C1[i,2]) *(1-C1[i,3]) #effect in study without any of the
characteristics
  +theta.plus[i]* (1-(1-C1[i,1]) *(1-C1[i,2]) *(1-C1[i,3])) effect in studies with
one or more characteristics

```

```

theta.plus[i] ~ dnorm(mean[i], p.k2[i])|(-10,10)

theta.minus[i]~dnorm(d[ma[i]],p.d[ma[i]])|(-10,10) #RE for treatment effects within meta-analysis

mean[i]<-d[ma[i]]+b[ma[i],1]*C1[i,1]+b[ma[i],2]*C1[i,2]+b[ma[i],3]*C1[i,3]

k2[i]<- ( (1-C1[i,1]) + # without characteristic 1
C1[i,1] * kappa_ok[ma[i],1] * lambda[1] + # with characteristic 1 and inform
C1[i,1] * clambda[ma[i],1] * cut(lambda[1]) + # with characteristic 1 but don't inform
C1[i,1] * CO[ma[i],1] *1) * # no studies have characteristic 1 in the MA
( (1-C1[i,2]) + # without characteristic 2
C1[i,2] * kappa_ok[ma[i],2] * lambda[2] + # with characteristic 2 and inform
C1[i,2] * clambda[ma[i],2] * cut(lambda[2]) + # with characteristic 2 but don't inform
C1[i,2] * CO[ma[i],2] *1) *# no studies have characteristic 2 in the MA
( (1-C1[i,3]) + # without characteristic 3
C1[i,3] * kappa_ok[ma[i],3] * lambda[3] + # with characteristic 3 and inform
C1[i,3] * clambda[ma[i],3] * cut(lambda[3]) + # with characteristic 3 but don't inform
C1[i,3] * CO[ma[i],3] *1)* # no studies have characteristic 1 in the MA
var_d[ma[i]]

p.k2[i]<-1/k2[i]

rhat[i] <- p[i] * n[i] #calculate residual deviance
dev[i] <- 2 * (r[i] * (log(r[i])-log(rhat[i])) + (n[i]-r[i]) * (log(n[i]-r[i]) - log(n[i]-rhat[i])))

}

resdev <- sum(dev[]))

for (j in 1:N_study) {alpha[j] ~ dnorm(0,.01)} # priors for study baseline effects - unrelated

for(m in 1:N_ma){
  d[m] ~ dnorm(0,0.01) # priors for true fixed (unrelated) intervention effects
  for(j in 1:3){b[m,j] ~ dnorm(b0[j], p.phi[j])} # between meta-analysis variation in average
difference in effect associated with characteristic
  var_d[m]~dlnorm(mu,p.tau) # log-normal distribution for between-study variances
  p.d[m] <- 1/var_d[m]
}

#Prior for unknown parameters
for(j in 1:3){
  b0[j] ~dnorm(0,0.001) # vague prior for overall average difference in effect associated with
characteristic
  lambda[j] ~ dlnorm(0,0.1) # vague prior for change in between-study variation associated with characteristic j
  p.phi1[j] ~ dgamma(0.001, 0.001)
  phi[j] <- pow(p.phi[j],-0.5)
  p.phi[j] <-p.phi1[j]/(1-patom.phi[j]) # vague prior for between meta-analysis variation in average
difference in effect associated with characteristic
  patom.phi[j] ~ dbeta(1,1)
}

```

```
exp.b0[j]<-exp(b0[j])
}

mu~dnorm(0,0.01)
p.tau<-1/(sd_tau*sd_tau)
sd_tau~dunif(0,2)

log.tau2.new~dlnorm(mu,p.tau) # predictive distn for heterogeneity among studies without the characteristics
tau2.new<-exp(log.tau2.new)

}
```