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Link to published version (if available):
10.1002/sim.7491
10.1002/sim.7491

Link to publication record in Explore Bristol Research
PDF-document

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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:
- \( N_{\text{study}} = \text{no. of studies} \)
- \( N = \text{no. of studies} \times 2 \text{ arms} \)
- \( N_{\text{ma}} = \text{no. of meta-analyses} \)

Study-level:
- \( \text{treat} = 1 \) if treatment arm, 0 if control
- \( r = \text{no. of events} \)
- \( n = \text{no. of participants} \)
- \( C1[i] = 1 \) if the \( i \)th study has the characteristic of interest, 0 otherwise
- \( ma[i] \) <- meta-analysis index
- \( s[i] \) <- study index

Meta-analysis level:
- \( \kappa_{\text{ok}}[m] = 1 \) 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

```winbugs
model {
  for (i in 1:N) {
    r[i] ~ dbin(p[i],n[i]) # likelihood (binary data \( r/n = \text{no. of events/ no. of participants} \))
    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]])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]])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(0,0.001)}           # priors for study baseline effects - unrelated

  for (m in 1:N_ma) {
    mean[m] <- d[m] + b[m]
    d[m] ~ dnorm(0,0.001)                            # 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))
  }
  b0 ~ dnorm(0,0.001)            # vague prior for overall average difference in effect associated with characteristic
  lambda ~ dlnorm(0,0.1)        # vague prior for change in between-study variation associated with characteristic
}
```

# Prior for unknown parameters
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 ith study has the jth 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 jth characteristic in the mth meta-analysis, 0 otherwise
  clambda[m,j] = 1 if there are 1, K-1 or K studies with or without the jth characteristic in the mth 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 mth meta-analysis with the jth 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] + # with characteristic 1 but don't inform
C1[i,1] * C0[ma[i],1] * C0[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] + # with characteristic 2 but don't inform
C1[i,2] * C0[ma[i],2] * C0[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] + # with characteristic 3 but don't inform
C1[i,3] * C0[ma[i],3] * C0[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(r in 1:3){b[ma[m],r] ~ dnorm(b0[r], p.phi[r])} # 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
  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)
}