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# Fixed effects over both studies and reps
model.DTA.meta.analysis.noType2.fixed<-function(){
#Loop over studies reporting 2x2 tables. i=rep no., k=test no. in
study j
for (j in 1:N1){
  for (k in 1:ntests[j]){
    for (i in 1:nreps[j,k]){
      tp[i,j,k]~dbin(pi1[i,j,k],pos[i,j,k])
#Likelihood
      fp[i,j,k]~dbin(pi2[i,j,k],neg[i,j,k])
      tphat[i,j,k]<-pi1[i,j,k]*pos[i,j,k]
#Fitted values
      fphat[i,j,k]<-pi2[i,j,k]*neg[i,j,k]
      dev.tp[i,j,k]<-(2*(tp[i,j,k]*(log(tp[i,j,k])-
log(tphat[i,j,k])))      #Deviance contibution tp
      + (pos[i,j,k]-tp[i,j,k])*(log(pos[i,j,k]-tp[i,j,k]) -
log(pos[i,j,k]-tphat[i,j,k]))))
      dev.fp[i,j,k]<-(2*(fp[i,j,k]*(log(fp[i,j,k])-
log(fphat[i,j,k])))      #Deviance contibution fp
      + (neg[i,j,k]-fp[i,j,k])*(log(neg[i,j,k]-fp[i,j,k]) -
log(neg[i,j,k]-fphat[i,j,k]))))
    }
    dev[j,k]<-sum(dev.tp[1:nreps[j,k],j,k]) +
sum(dev.fp[1:nreps[j,k],j,k])
  }
  sumdev[j]<-sum(dev[j,1:ntests[j]])
}

totresdev<- sum(sumdev[])

#Loop over all studies
for (j in 1:(N1)){
  for (k in 1:ntests[j]){
    for (i in 1:nreps[j,k]){
      logit(pi1[i,j,k])<- beta[t[j,k]]*Q[t[j,k]] +
A[t[j,k]]/2      #Model for sensitivity
      logit(pi2[i,j,k])<- Q[t[j,k]] - A[t[j,k]]/2
      #Model for (1-specificity)
    }
  }
}
}

```

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#PRIORS
for (k in 1:NTests){ #Loop over tests
  Q[k]~dnorm(0,.0001)
  A[k]~dnorm(0,.0001)
  log(beta.true[k])<-l.beta.true
  beta[k]<- include.slope[k]*beta.true[k] + (1-include.slope[k])
}
l.beta.true~dnorm(0,.0001)

for (m in 1:2){
  p.stud[m]<-pow(sd.stud[m],-2)
  p.reps[m]<-pow(sd.reps[m],-2)
  sd.stud[m]~dunif(0,5)
  sd.reps[m]~dunif(0,5)

  # Save the prior distributions
  sd.stud.prior[m]~dunif(0,5)
  sd.reps.prior[m]~dunif(0,5)
}

# Posterior and posterior predictive distribtutions
for(k in 1:NTests){
  theta.pred[k]~dnorm(Q[k],p.stud[1])
  alpha.pred[k]~dnorm(A[k],p.stud[2])
  logit(sens.pred[k])<-
beta[k]*theta.pred[k]+0.5*alpha.pred[k]
  logit(fpr.pred[k])<-theta.pred[k]-0.5*alpha.pred[k]
  spec.pred[k]<- 1 - fpr.pred[k]

  logit(TPR[k])<-(beta[k]*Q[k]+A[k]/2)
  logit(FPR[k])<-(Q[k]-A[k]/2)
  sensitivity[k]<-TPR[k]
  specificity[k]<-1-FPR[k]

  # Diagnostic odds ratio
  dor[k]<-(sensitivity[k]*specificity[k])/((1-
sensitivity[k])*(1-specificity[k]))
  #DOR[k] <- exp(A[k])
}
}

```