

```

model{

  for (i in 1:N){      # N - No. of individuals

    y1[i] ~ dnorm(mul[i], tau.y1)      # Normal response

    mul[i] <- beta[1,1] + u[cluster[i],1] +
      beta[2,1]*treat[i] + beta[3,1]*x1[i] + beta[4,1]*x2[i]

    y2[i] ~ dbern(p[i])      # Latent Normal response

    p[i] <- phi(
      beta[1,2] + u[cluster[i],2] +
      beta[2,2]*treat[i] + beta[3,2]*x3[i] + beta[4,2]*x4[i]
      + alpha*(y1[i]-mul[i])      # correlation parameterization
    )
  }

  # Study-level random effects

  for (j in 1:J){      # J - No. of studies

    #u[j, 1:2] ~ dmnorm(zero[1:2], tau.u[1:2,1:2])
    u[j, 1:2] ~ dmnorm(zero, tau.u[1:2,1:2])
  }

  # Wishart prior on random effects
  tau.u[1:2,1:2] ~ dwish(R[1:2,1:2],2)

  # Prior on betas

  beta[1:4,1] ~ dmnorm(b0 , B0[1:4,1:4])
  beta[1:4,2] ~ dmnorm(b0 , B0[1:4,1:4])

  # Priors on covariance matrix

  rho ~ dunif(-1, 1)
  sigma.y1 ~ dunif(0,100)
  sigma.y2<-1      #var(y2)=1

  # Node transformations

  sigma2.y1<-sigma.y1*sigma.y1
  tau.y1<-1/sigma2.y1

  alpha<-rho*(sigma.y2/sigma.y1)

  sigma2.u[1:2,1:2]<-inverse(tau.u[,])

}

```