

```

model {

sw[1]<- 0

for(i in 1:n.subjects) {
#likelihood
      y[i] ~ dnorm(theta[i], prec[study[i]])
      theta[i] <- mu[study[i]] + delta[index[i]] * (1 - equals(treat[i],baseline[i])) +
      b_basey * bl_y[i] +
      b_treat_pain1[index[i]] * (1 - equals(treat[i],baseline[i])) * pain1[i] +
      b_treat_pain2[index[i]] * (1 - equals(treat[i],baseline[i])) * pain2[i]
#residual deviance
      dev[i]<-(y[i] - theta[i]) * (y[i] - theta[i])
    }

for(l in 1:n.arms) {
#consistency model for treatment effects and pain type interactions
      delta[l]~dnorm(md[l], precd[l])
      md[l]<- d[treat1[l]] - d[baseline1[l]] + equals(m[l],3) * sw[l]
      precd[l]<- pre * (1 + equals(m[l],3) / 3)
      b_treat_pain1[l] <- btp1[treat1[l]] - btp1[baseline1[l]]
      b_treat_pain2[l] <- btp2[treat1[l]] - btp2[baseline1[l]]
    }

#correction for multi-arm trials
for(k in 2:n.arms) {
      sw[k]<- (delta[k-1] - d[treat1[k-1]] + d[baseline1[k-1]]) / 2
    }

for(j in 1:n.trials) {
#priors on study-specific baseline outcome and precision parameter
      mu[j]~dnorm(0,1.0E-6)
      prec[j] ~ dgamma(0.001, 0.001)
# summed residual deviance contribution for each trial
      resdev[j]<- sum(dev[start[j]:end[j]]) * prec[j]
    }

#total Residual Deviance

```

```
totresdev <- sum(resdev[])
```

```
for (k in 2:NT) {
```

```
  #random effect on pain interaction effects
```

```
    btp1[k] ~ dnorm(m.btp1,prec.btp1)
```

```
    btp2[k] ~ dnorm(m.btp2,prec.btp2)
```

```
  #prior on treatment effects
```

```
    d[k] ~ dnorm(0,1.0E-6)
```

```
  }
```

```
  #prior on random treatment effect variance
```

```
    tau ~ dunif(0,10)
```

```
    tau.sq <- tau * tau
```

```
    pre <- 1 / (tau.sq)
```

```
  #priors on mean and random effect variance for pain type interaction
```

```
    m.btp1 ~ dnorm(0,1.0E-6)
```

```
    tau.btp1 ~ dunif(0,2)
```

```
    tau.sq.btp1 <- tau.btp1 * tau.btp1
```

```
    prec.btp1 <- 1 / (tau.sq.btp1)
```

```
    m.btp2 ~ dnorm(0,1.0E-6)
```

```
    tau.btp2 ~ dunif(0,2)
```

```
    tau.sq.btp2 <- tau.btp2 * tau.btp2
```

```
    prec.btp2 <- 1 / (tau.sq.btp2)
```

```
  #prior on impact of baseline outcome on final outcome
```

```
    b_basey ~ dnorm(0,1.0E-6)
```

```
    d[1] <- 0
```

```
    btp1[1] <- 0
```

```
    btp2[1] <- 0
```

```
  }
```