```
model{
# T = probability of true eGFR belonging to each category
#
# All categories
for (i in 1:ny){                        # loop through studies with all categories
  y[i,1:4] ~ dmulti(T[], N[i])
  # calculate residual deviance
  for (m in 1:4){                       # loop through all reported thresholds
    yhat[i,m] <-  T[m] * N[i]           # predicted number events
    y1[i,m] <- max(y[i,m], 0.1)         # correction for zero cell
    yhat1[i,m] <- max(yhat[i,m], 0.1)   # correction for p=0
    # Deviance contribution when non-zero cell (allows p=0)
    ydv1[i,m] <- 2*y1[i,m]*(log(y1[i,m])-log(yhat1[i,m]))
    # Calculate deviance contribution, when zero cell=zero
    ydv[i,m] <- ydv1[i,m]*(1-equals(y[i,m],0))
  }
  yresdev[i] <- sum(ydv[i,])            # summed residual deviance contribution for this
study
 }
totresdevT <- sum(yresdev[])            # Total Residual Deviance
T[1:4] ~ ddirch(omega[])                # prior distribution for T (WinBUGS compatible)
for (j in 1:4){                         # loop through all categories
  omega[j] <- 1                         # Dirichlet parameter (non-inf)
 }
# type A data: 0-30; 30-60; >60
for (i in (ny+1):(ny+nyA)){             # loop through studies with type A data
  y[i,1:3] ~ dmulti(TA[], N[i])
  # calculate residual deviance
  for (m in 1:3){                       # loop through all reported thresholds
    yhat[i,m] <-  TA[m] * N[i]          # predicted number events
    y1[i,m] <- max(y[i,m], 0.1)         # correction for zero cell
    yhat1[i,m] <- max(yhat[i,m], 0.1)   # correction for p=0
    # Deviance contribution when non-zero cell (allows p=0)
    ydv1[i,m] <- 2*y1[i,m]*(log(y1[i,m])-log(yhat1[i,m]))
    # Calculate deviance contribution, when zero cell=zero
    ydv[i,m] <- ydv1[i,m]*(1-equals(y[i,m],0))
  }
  yresdev[i] <- sum(ydv[i,1:3])         # summed residual deviance contribution for this
study
 }
# link probabilities
TA[1] <- T[1]                           # type A: true < 30
TA[2] <- T[2] + T[3]                    # type A: 30 < true < 60
TA[3] <- T[4]                           # type A: true > 60
#
# type C data: 0-30; 30-45; >45
for (i in (ny+nyA+1):(ny+nyA+nyC)){ # loop through studies with type C data
  y[i,1:3] ~ dmulti(TC[], N[i])
  # calculate residual deviance
  for (m in 1:3){                       # loop through all reported thresholds
    yhat[i,m] <-  TC[m] * N[i]          # predicted number events
    y1[i,m] <- max(y[i,m], 0.1)         # correction for zero cell
    yhat1[i,m] <- max(yhat[i,m], 0.1) # correction for p=0
    # Deviance contribution when non-zero cell (allows p=0)
    ydv1[i,m] <- 2*y1[i,m]*(log(y1[i,m])-log(yhat1[i,m]))
    # Calculate deviance contribution, when zero cell=zero
    ydv[i,m] <- ydv1[i,m]*(1-equals(y[i,m],0))
  }
  yresdev[i] <- sum(ydv[i,1:3])         # summed residual deviance contribution for this
study
 }
# link probabilities
TC[1] <- T[1]                           # type C: true < 30
TC[2] <- T[2]                           # type C: 30 < true < 45
TC[3] <- T[3] + T[4]                    # type C: true > 45
#
# type E data: 0-60; >60
```

```
for (i in (ny+nyA+nyC+1):(ny+nyA+nyC+nyE)){  # loop through studies with type E
data
   y[i,1] ~ dbin(TE[1], N[i])
   # Deviance contribution
   yhat[i,1] <- TE[1] * N[i]         # expected value of the numerators
   y1[i,1] <- max(y[i,1], 0.1)        # correction for zero cell
   yhat1[i,1] <- max(yhat[i,1], 0.1) # correction for p=0
   # Deviance contribution when non-zero cell (allows p=0)
   ydev1[i,1] <- 2 * (y1[i,1]*(log(y1[i,1])-log(yhat1[i,1]))
             +(N[i]-y1[i,1])*(log(N[i]-y1[i,1])
               - log(N[i]-yhat1[i,1])))
   # Deviance contribution when zero cell (allows p=0)
   ydev0[i,1] <- 2*N[i]*log(N[i]/(N[i]-yhat[i,1]))
   # Calculate deviance contribution
   yresdev[i] <- ydev1[i,1]*(1-equals(y[i,1],0)) + ydev0[i,1]*equals(y[i,1],0)
 }
# link probabilities
TE[1] <- T[1] + T[2] + T[3]        # type E: true < 60
TE[2] <- T[4]                      # type E:  true > 60
#
# type F data: 0-30; >30
for (i in (ny+nyA+nyC+nyE+1):(ny+nyA+nyC+nyE+nyF)){ # loop through studies with
type F data
   y[i,1] ~ dbin(TF[1], N[i])
   # Deviance contribution
   yhat[i,1] <- TF[1] * N[i]         # expected value of the numerators
   y1[i,1] <- max(y[i,1], 0.1)        # correction for zero cell
   yhat1[i,1] <- max(yhat[i,1], 0.1) # correction for p=0
   # Deviance contribution when non-zero cell (allows p=0)
   ydev1[i,1] <- 2 * (y1[i,1]*(log(y1[i,1])-log(yhat1[i,1]))
             +(N[i]-y1[i,1])*(log(N[i]-y1[i,1])
               - log(N[i]-yhat1[i,1])))
   # Deviance contribution when zero cell (allows p=0)
   ydev0[i,1] <- 2*N[i]*log(N[i]/(N[i]-yhat[i,1]))
   # Calculate deviance contribution
   yresdev[i] <- ydev1[i,1]*(1-equals(y[i,1],0)) + ydev0[i,1]*equals(y[i,1],0)
 }
# link probabilities
TF[1] <- T[1]                      # type F: true < 30
TF[2] <- T[2] + T[3] + T[4]        # type F:  true > 30
#
# p[j,m]: probability of being in true category j and POC category m
#
# All categories
for (i in 1:ns){                       # loop through studies with all categories
   for (j in 1:4){                     # loop through all categories
     r[i,j,1:4] ~ dmulti(p[j,], n[i,j])
     # calculate residual deviance
     for (m in 1:4){                   # loop through all reported thresholds
       # predicted number events
       rhat[i,j,m] <-  p[j,m] * n[i,j]
       r1[i,j,m] <- max(r[i,j,m], 0.1) # correction for zero cell
       rhat1[i,j,m] <- max(rhat[i,j,m], 0.1) # correction for p=0
       # Deviance contribution when non-zero cell (allows p=0)
       dv1[i,j,m] <- 2*r1[i,j,m]*(log(r1[i,j,m])-log(rhat1[i,j,m]))
       # Calculate deviance contribution, when zero cell=zero
       dv[i,j,m] <- dv1[i,j,m]*(1-equals(r[i,j,m],0))
#      dv[i,j,m] <- 2*r[i,j,m]*(log(r[i,j,m])-log(rhat[i,j,m]))
     }
     dev[i,j] <- sum(dv[i,j,])
   }
   # summed residual deviance contribution for this trial
   resdev[i] <- sum(dev[i,1:4])
 }
totresdev <- sum(resdev[])        # Total Residual Deviance
for (j in 1:4){                    # loop through all categories
   p[j,1:4] ~ ddirch(alpha[])        # prior distribution for p (WinBUGS compatible)
   alpha[j] <- 1                     # Dirichlet parameter (non-inf)
```

```
  }
#
# type E data: 0-60; >60
for (i in (ns+1):(ns+nsE)){         # loop through studies with type E data
  for (j in 1:2){                   # loop through all categories
    r[i,j,1] ~ dbin(pE[j,1], n[i,j])
    # Deviance contribution
    rhat[i,j,1] <- pE[j,1] * n[i,j] # expected value of the numerators
    r1[i,j,1] <- max(r[i,j,1], 0.1) # correction for zero cell
    rhat1[i,j,1] <- max(rhat[i,j,1], 0.1) # correction for p=0
    # Deviance contribution when non-zero cell (allows p=0)
    dev1[i,j,1] <- 2 * (r1[i,j,1]*(log(r1[i,j,1])-log(rhat1[i,j,1]))
            +(n[i,j]-r1[i,j,1])*(log(n[i,j]-r1[i,j,1])
              - log(n[i,j]-rhat1[i,j,1])))
    # Deviance contribution when zero cell (allows p=0)
    dev0[i,j,1] <- 2*n[i,j]*log(n[i,j]/(n[i,j]-rhat[i,j,1]))
    # Calculate deviance contribution
    dev[i,j] <- dev1[i,j,1]*(1-equals(r[i,j,1],0)) + dev0[i,j,1]*equals(r[i,j,1],0)
#     dev[i,j] <- 2 * (r[i,j,1] * (log(r[i,j,1])-log(rhat[i,j,1]))
#             +  (n[i,j]-r[i,j,1]) * (log(n[i,j]-r[i,j,1]) - log(n[i,j]-
rhat[i,j,1])))
    }
  # summed residual deviance contribution for this study
  resdev[i] <- sum(dev[i,1:2])
 }
for (j in 1:2){                     # loop through all categories
  pE[j,2] <- 1-pE[j,1]
 }
# link probabilities
# type E: true < 60
sumE <- T[1]+T[2]+T[3]
pE[1,1] <- (p[1,1]+p[1,2]+p[1,3])*T[1]/sumE + (p[2,1]+p[2,2]+p[2,3])*T[2]/sumE
+ (p[3,1]+p[3,2]+p[3,3])*T[3]/sumE # POC <60
# type E: true > 60
pE[2,1] <- p[4,1]+p[4,2]+p[4,3]     # POC <60
#
# type F data: 0-30; >30
for (i in (ns+nsE+1):(ns+nsE+nsF)){ # loop through studies with all categories
  for (j in 1:2){                   # loop through all categories
    r[i,j,1] ~ dbin(pF[j,1], n[i,j])
    # Deviance contribution
    rhat[i,j,1] <- pF[j,1] * n[i,j] # expected value of the numerators
    r1[i,j,1] <- max(r[i,j,1], 0.1) # correction for zero cell
    rhat1[i,j,1] <- max(rhat[i,j,1], 0.1) # correction for p=0
    # Deviance contribution when non-zero cell (allows p=0)
    dev1[i,j,1] <- 2 * (r1[i,j,1]*(log(r1[i,j,1])-log(rhat1[i,j,1]))
            +(n[i,j]-r1[i,j,1])*(log(n[i,j]-r1[i,j,1])
              - log(n[i,j]-rhat1[i,j,1])))
    # Deviance contribution when zero cell (allows p=0)
    dev0[i,j,1] <- 2*n[i,j]*log(n[i,j]/(n[i,j]-rhat[i,j,1]))
    # Calculate deviance contribution
    dev[i,j] <- dev1[i,j,1]*(1-equals(r[i,j,1],0)) + dev0[i,j,1]*equals(r[i,j,1],0)
#     dev[i,j] <- 2 * (r[i,j,1] * (log(r[i,j,1])-log(rhat[i,j,1]))
#             +  (n[i,j]-r[i,j,1]) * (log(n[i,j]-r[i,j,1]) - log(n[i,j]-
rhat[i,j,1])))
    }
  # summed residual deviance contribution for this trial
  resdev[i] <- sum(dev[i,1:2])
 }
for (j in 1:2){                     # loop through all categories
  pF[j,2] <- 1-pF[j,1]
 }
# link probabilities
# type F: true < 30
pF[1,1] <- p[1,1]                   # POC <30
# type F: true > 30
sumF <- T[2]+T[3]+T[4]
pF[2,1] <- p[2,1]*T[2]/sumF + p[3,1]*T[3]/sumF + p[4,1]*T[4]/sumF # POC <30

}
```