```
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 A data: 0-30; 30-60; >60
for (i in (ns+1):(ns+nsA)){        # loop through studies with type A data
  for (j in 1:3){                  # loop through all categories
    r[i,j,1:3] ~ dmulti(pA[j,], n[i,j])
    # calculate residual deviance
    for (m in 1:3){                # loop through all reported thresholds
      # predicted number events
      rhat[i,j,m] <-  pA[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,1:3])
   }
  # summed residual deviance contribution for this trial
  resdev[i] <- sum(dev[i,1:3])
 }
# link probabilities
# type A: true < 30
pA[1,1] <- p[1,1]                  # POC <30
pA[1,2] <- p[1,2] + p[1,3]         # 30 < POC < 60
pA[1,3] <- p[1,4]                  # POC >60
# type A: 30 < true < 60
sumA <- T[2]+T[3]
pA[2,1] <- p[2,1]*T[2]/sumA + p[3,1]*T[3]/sumA  # POC <30
pA[2,2] <- (p[2,2]+p[2,3])*T[2]/sumA + (p[3,2]+p[3,3])*T[3]/sumA # 30 < POC < 60
pA[2,3] <- p[2,4]*T[2]/sumA + p[3,4]*T[3]/sumA  # POC >60
# type A: true > 60
pA[3,1] <- p[4,1]                  # POC <30
pA[3,2] <- p[4,2] + p[4,3]         # 30 < POC < 60
pA[3,3] <- p[4,4]                  # POC >60
#
# type C data: 0-30; 30-45; >45
for (i in (ns+nsA+1):(ns+nsA+nsC)){ # loop through studies with type C data
  for (j in 1:3){                  # loop through all categories
    r[i,j,1:3] ~ dmulti(pC[j,], n[i,j])
    # calculate residual deviance
    for (m in 1:3){                # loop through all reported thresholds
      # predicted number events
      rhat[i,j,m] <-  pC[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,1:3])
   }
  # summed residual deviance contribution for this trial
  resdev[i] <- sum(dev[i,1:3])
 }
# link probabilities
# type C: true < 30
pC[1,1] <- p[1,1]                  # POC <30
pC[1,2] <- p[1,2]                  # 30 < POC < 45
pC[1,3] <- p[1,3] + p[1,4]         # POC >45
# type C: 30 < true < 45
pC[2,1] <- p[2,1]                  # POC <30
pC[2,2] <- p[2,2]                  # 30 < POC < 45
pC[2,3] <- p[2,3] + p[2,4]         # POC >45
```

```
# type C: true > 45
sumC <- T[3]+T[4]
pC[3,1] <- p[3,1]*T[3]/sumC + p[4,1]*T[4]/sumC  # POC <30
pC[3,2] <- p[3,2]*T[3]/sumC + p[4,2]*T[4]/sumC  # 30 < POC < 45
pC[3,3] <- (p[3,3]+p[3,4])*T[3]/sumC + (p[4,3]+p[4,4])*T[4]/sumC # POC >45
#
# type E data: 0-60; >60
for (i in (ns+nsA+nsC+1):(ns+nsA+nsC+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)
   }
  # 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 C2 data: TRUE 0-30; 30-45; >45 (extra info of POC categories)
for (i in (ns+nsA+nsC+nsE+1):(ns+nsA+nsC+nsE+nsC2)){# loop through studies w/ type
C2 data
  for (j in 1:2){                   # loop through true eGFR categories 1 and 2
    r[i,j,1:4] ~ dmulti(p[j,], n[i,j]) # all POC categories reported
    # 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,1:4])
   }
  # true eGFR category 3
  r[i,3,1:3] ~ dmulti(pC2[3,], n[i,3]) # 3 POC categories reported
  # calculate residual deviance
  for (m in 1:3){                   # loop through all reported thresholds
    # predicted number events
    rhat[i,3,m] <-  pC2[3,m] * n[i,3]
    r1[i,3,m] <- max(r[i,3,m], 0.1) # correction for zero cell
    rhat1[i,3,m] <- max(rhat[i,3,m], 0.1) # correction for p=0
    # Deviance contribution when non-zero cell (allows p=0)
    dv1[i,3,m] <- 2*r1[i,3,m]*(log(r1[i,3,m])-log(rhat1[i,3,m]))
    # Calculate deviance contribution, when zero cell=zero
```

```
    dv[i,3,m] <- dv1[i,3,m]*(1-equals(r[i,3,m],0))
#    dv[i,3,m] <- 2*r[i,3,m]*(log(r[i,3,m])-log(rhat[i,3,m]))
   }
  dev[i,3] <- sum(dv[i,3,1:3])
  # summed residual deviance contribution for this trial
  resdev[i] <- sum(dev[i,1:3])
 }
# link probabilities
# type C: true > 45
pC2[3,1] <- pC[3,1]                # POC <30
pC2[3,2] <- pC[3,2]                # 30 < POC < 45
pC2[3,3] <- pC[3,3]                # POC >45
}
```