NLST-cohort.jags

```
var A[15,15], B[15,9], C[15,8], D[15,15], Q[15,15,NX,NS], Y.T0[9,NC],
Y.T1[9,NC], Y.T2[9,NC], Y.T01[8,NC], Y.T12[8,NC], Y.T23[8,NC], Y.T34[8,NC],
Y.T45[8,NC], Y.T56[8,NC], Y.T67[8,NC], N.T0[NC], N.T1[NC], N.T2[NC],
N.T01[NC], N.T12[NC], N.T23[NC], N.T34[NC], N.T45[NC], N.T56[NC], N.T67[NC];

model {

  ########################################
  # A = State evolution matrix on screening #
  ########################################

  A[1,1] <- 1
  A[1,2:15] <- rep(0,14)
  A[2:15,1] <- rep(0,14)

  for (i in 2:8) {
    for (j in 2:8) {
      A[i,j] <- (1 - sensitivity) * (i == j)
      A[i,j+7] <- sensitivity * (i == j)
    }
  }

  for (i in 9:15) {
    for (j in 2:8) {
      A[i,j] <- 0
    }
    for (j in 9:15) {
      A[i,j] <- 1 * (i == j)
    }
  }

  ################################
  # B = Screening output matrix #
  ################################

  B[1,1] <- specificity
  B[1,2] <- (1-specificity)
  B[1,3:9] <- rep(0,7)
  B[2:8,1] <- rep(1-sensitivity,7)
  B[2:15,2] <- rep(0,14)
  B[9:15,1] <- rep(0,7)

  for (i in 2:15) {
    for (j in 3:9) {
      B[i,j] <- sensitivity * ((i + 1) == j)
    }
  }

  ####################################
  # C = Interval cancer output matrix #
  ####################################

  C[1,1] <- 1
  C[1,2:8] <- rep(0,7)

  for (i in 2:8) {
    C[i,1] <- 1
```

```
    C[i,2:8] <- rep(0,7)
  }
  for (i in 9:15) {
    for (j in 1:8) {
      C[i,j] <- 1 * ((i-7) == j)
    }
  }

  ########################################
  # D = BLANK OUT PEOPLE ALREADY PRESENTED #
  ########################################

  for (i in 1:8) {
    for (j in 1:15) {
      D[i,j] <- 1 * (i == j)
    }
  }

  for (i in 9:15) {
    D[i,1:15] <- rep(0,15)
  }

  # Quantiles of progression heterogeneity parameter
  for (s in 1:NS) {
    re.lnlambda.p[s] <- qnorm((s-0.5)/NS, 0, pow(sigma.lnlambda.p, -2))
    re.lambda.p[s] <- exp(re.lnlambda.p[s])
  }

  # State evolution matrix for each age year
  for (x in 1:NX) {

    h[x] <- log(1-plnorm(X[x], mu.p0_pIA, tau.p0_pIA)) - log(1-plnorm(X[x]+1,
mu.p0_pIA, tau.p0_pIA))

    for (s in 1:NS) {

      ###############################
      # Q = Transition rate matrix #
      ###############################


      Q[1,1,x,s] <- - h[x]
      Q[1,2,x,s] <- h[x]
      Q[1,3:15,x,s] <- rep(0, 13)

      Q[2,1,x,s] <- 0
      Q[2,2,x,s] <- - lambda.pIA_pIB*re.lambda.p[s] - lambda.pIA_cIA
      Q[2,3,x,s] <- lambda.pIA_pIB*re.lambda.p[s]
      Q[2,4:8,x,s] <- rep(0, 5)
      Q[2,9,x,s] <- lambda.pIA_cIA
      Q[2,10:15,x,s] <- rep(0, 6)

      Q[3,1:2,x,s] <- rep(0,2)
      Q[3,3,x,s] <- - lambda.pIB_pIIA*re.lambda.p[s] - lambda.pIB_cIB
      Q[3,4,x,s] <- lambda.pIB_pIIA*re.lambda.p[s]
      Q[3,5:9,x,s] <- rep(0, 5)
      Q[3,10,x,s] <- lambda.pIB_cIB
      Q[3,11:15,x,s] <- rep(0, 5)
```

```
    Q[4,1:3,x,s] <- rep(0,3)
    Q[4,4,x,s] <- - lambda.pIIA_pIIB*re.lambda.p[s] - lambda.pIIA_cIIA
    Q[4,5,x,s] <- lambda.pIIA_pIIB*re.lambda.p[s]
    Q[4,6:10,x,s] <- rep(0, 5)
    Q[4,11,x,s] <- lambda.pIIA_cIIA
    Q[4,12:15,x,s] <- rep(0, 4)

    Q[5,1:4,x,s] <- rep(0,4)
    Q[5,5,x,s] <- - lambda.pIIB_pIIIA*re.lambda.p[s] - lambda.pIIB_cIIB
    Q[5,6,x,s] <- lambda.pIIB_pIIIA*re.lambda.p[s]
    Q[5,7:11,x,s] <- rep(0, 5)
    Q[5,12,x,s] <- lambda.pIIB_cIIB
    Q[5,13:15,x,s] <- rep(0, 3)

    Q[6,1:5,x,s] <- rep(0,5)
    Q[6,6,x,s] <- - lambda.pIIIA_pIIIB*re.lambda.p[s] - lambda.pIIIA_cIIIA
    Q[6,7,x,s] <- lambda.pIIIA_pIIIB*re.lambda.p[s]
    Q[6,8:12,x,s] <- rep(0, 5)
    Q[6,13,x,s] <- lambda.pIIIA_cIIIA
    Q[6,14:15,x,s] <- rep(0, 2)

    Q[7,1:6,x,s] <- rep(0,6)
    Q[7,7,x,s] <- - lambda.pIIIB_pIV*re.lambda.p[s] - lambda.pIIIB_cIIIB
    Q[7,8,x,s] <- lambda.pIIIB_pIV*re.lambda.p[s]
    Q[7,9:13,x,s] <- rep(0, 5)
    Q[7,14,x,s] <- lambda.pIIIB_cIIIB
    Q[7,15,x,s] <- 0

    Q[8,1:7,x,s] <- rep(0,7)
    Q[8,8,x,s] <- - lambda.pIV_cIV
    Q[8,9:14,x,s] <- rep(0, 6)
    Q[8,15,x,s] <- lambda.pIV_cIV

    Q[9,1:15,x,s] <- rep(0, 15)
    Q[10,1:15,x,s] <- rep(0, 15)
    Q[11,1:15,x,s] <- rep(0, 15)
    Q[12,1:15,x,s] <- rep(0, 15)
    Q[13,1:15,x,s] <- rep(0, 15)
    Q[14,1:15,x,s] <- rep(0, 15)
    Q[15,1:15,x,s] <- rep(0, 15)

    expQ[1:15,1:15,x,s] <- mexp(Q[1:15,1:15,x,s])
  }
}

# Loop over (age-defined) cohorts
for (c in 1:NC) {

  INITIAL[1:15,c] ~ ddirch(ALPHA_INITIAL)

  for (s in 1:NS) {
    ############################################
    # PRODUCE X (HIDDEN STATE) AND Y (OUTPUTS) #
    ############################################

    X.T0.s[1:15,c,s]  <- t(INITIAL[1:15,c]) %*% A
    X.T01.s[1:15,c,s] <- X.T0.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c,s]
    X.T1.s[1:15,c,s]  <- X.T01.s[1:15,c,s] %*% D %*% A
    X.T12.s[1:15,c,s] <- X.T1.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c+1,s]
```

```
    X.T2.s[1:15,c,s]  <- X.T12.s[1:15,c,s] %*% D %*% A
    X.T23.s[1:15,c,s] <- X.T2.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c+2,s]
    X.T34.s[1:15,c,s] <- X.T23.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c+3,s]
    X.T45.s[1:15,c,s] <- X.T34.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c+4,s]
    X.T56.s[1:15,c,s] <- X.T45.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c+5,s]
    X.T67.s[1:15,c,s] <- X.T56.s[1:15,c,s] %*% D %*% expQ[1:15,1:15,c+6,s]

    Y.T0.s[1:9,c,s]  <- INITIAL[1:15,c] %*% B
    Y.T1.s[1:9,c,s]  <- X.T01.s[1:15,c,s] %*% B
    Y.T2.s[1:9,c,s]  <- X.T12.s[1:15,c,s] %*% B
    Y.T01.s[1:8,c,s] <- X.T01.s[1:15,c,s] %*% C
    Y.T12.s[1:8,c,s] <- X.T12.s[1:15,c,s] %*% C
    Y.T23.s[1:8,c,s] <- X.T23.s[1:15,c,s] %*% C
    Y.T34.s[1:8,c,s] <- X.T34.s[1:15,c,s] %*% C
    Y.T45.s[1:8,c,s] <- X.T45.s[1:15,c,s] %*% C
    Y.T56.s[1:8,c,s] <- X.T56.s[1:15,c,s] %*% C
    Y.T67.s[1:8,c,s] <- X.T67.s[1:15,c,s] %*% C
  }

  # Average outputs
  for (i in 1:9) {
    Y.T0[i,c] <- mean(Y.T0.s[i,c,1:NS])
    Y.T1[i,c] <- mean(Y.T1.s[i,c,1:NS])
    Y.T2[i,c] <- mean(Y.T2.s[i,c,1:NS])
  }
  for (i in 1:8) {
    Y.T01[i,c] <- mean(Y.T01.s[i,c,1:NS])
    Y.T12[i,c] <- mean(Y.T12.s[i,c,1:NS])
    Y.T23[i,c] <- mean(Y.T23.s[i,c,1:NS])
    Y.T34[i,c] <- mean(Y.T34.s[i,c,1:NS])
    Y.T45[i,c] <- mean(Y.T45.s[i,c,1:NS])
    Y.T56[i,c] <- mean(Y.T56.s[i,c,1:NS])
    Y.T67[i,c] <- mean(Y.T67.s[i,c,1:NS])
  }

  ######################################
  # LIKELIHOOD CONTRIBUTION FROM DATA #
  ######################################

  K.T0[1:9,c]  ~ dmulti(Y.T0[1:9,c],  N.T0[c])
  K.T1[1:9,c]  ~ dmulti(Y.T1[1:9,c],  N.T1[c])
  K.T2[1:9,c]  ~ dmulti(Y.T2[1:9,c],  N.T2[c])
  K.T01[1:8,c] ~ dmulti(Y.T01[1:8,c], N.T01[c])
  K.T12[1:8,c] ~ dmulti(Y.T12[1:8,c], N.T12[c])
  K.T23[1:8,c] ~ dmulti(Y.T23[1:8,c], N.T23[c])
  K.T34[1:8,c] ~ dmulti(Y.T34[1:8,c], N.T34[c])
  K.T45[1:8,c] ~ dmulti(Y.T45[1:8,c], N.T45[c])
  K.T56[1:8,c] ~ dmulti(Y.T56[1:8,c], N.T56[c])
  K.T67[1:8,c] ~ dmulti(Y.T67[1:8,c], N.T67[c])
}



# Priors
mu.p0_pIA ~ dnorm(3, 0.1)
sigma.p0_pIA ~ dunif(0.001, 5)

sigma.lnlambda.p ~ dexp(1)
```

```
  lnlambda.pIA_pIB ~ dnorm(0, 0.1)
  lnlambda.pIB_pIIA ~ dnorm(0, 0.1)
  lnlambda.pIIA_pIIB ~ dnorm(0, 0.1)
  lnlambda.pIIB_pIIIA ~ dnorm(0, 0.1)
  lnlambda.pIIIA_pIIIB ~ dnorm(0, 0.1)
  lnlambda.pIIIB_pIV ~ dnorm(0, 0.1)

  lnlambda.pIA_cIA ~ dnorm(0, 0.1)
  lnlambda.pIB_cIB ~ dnorm(0, 0.1)
  lnlambda.pIIA_cIIA ~ dnorm(0, 0.1)
  lnlambda.pIIB_cIIB ~ dnorm(0, 0.1)
  lnlambda.pIIIA_cIIIA ~ dnorm(0, 0.1)
  lnlambda.pIIIB_cIIIB ~ dnorm(0, 0.1)
  lnlambda.pIV_cIV ~ dnorm(0, 0.1)

  sensitivity ~ dunif(0, 1)
  specificity ~ dunif(0, 1)

  # Transformations
  tau.p0_pIA <- pow(sigma.p0_pIA, -2)

  lambda.pIA_pIB <- exp(lnlambda.pIA_pIB)
  lambda.pIB_pIIA <- exp(lnlambda.pIB_pIIA)
  lambda.pIIA_pIIB <- exp(lnlambda.pIIA_pIIB)
  lambda.pIIB_pIIIA <- exp(lnlambda.pIIB_pIIIA)
  lambda.pIIIA_pIIIB <- exp(lnlambda.pIIIA_pIIIB)
  lambda.pIIIB_pIV <- exp(lnlambda.pIIIB_pIV)

  lambda.pIA_cIA <- exp(lnlambda.pIA_cIA)
  lambda.pIB_cIB <- exp(lnlambda.pIB_cIB)
  lambda.pIIA_cIIA <- exp(lnlambda.pIIA_cIIA)
  lambda.pIIB_cIIB <- exp(lnlambda.pIIB_cIIB)
  lambda.pIIIA_cIIIA <- exp(lnlambda.pIIIA_cIIIA)
  lambda.pIIIB_cIIIB <- exp(lnlambda.pIIIB_cIIIB)
  lambda.pIV_cIV <- exp(lnlambda.pIV_cIV)
}
```