```
model {

# Duration
# Duration of asymptomatic infection
dura ~ dnorm(0,0.0001) I(0,)
D ~ dnorm(dura,pr.D)
dev.D <- pr.D*pow((dura-D),2)   # Duration Deviance
lambdaC <- 1/dura               # clearance rate

# Duration of symptomatic infection
durs ~ dunif(0.0767,0.1533)  # symptomatic, 4-8 weeks
#durs ~ dunif(0.0577,0.2308) #symptomatic, 3-12 weeks sensitivity
# analysis
cut.durs <- cut(durs)        # pevents updating of durs
lambdaS <- 1 / cut.durs      # clearance rate

# Probability ct is symptomatic
r.phi ~ dbin(phi,n.phi)   phi ~ dbeta(1,1)
dev.phi <- 2 * (r.phi * log(r.phi / (phi *  n.phi)) +  (n.phi -
r.phi) *
            log((n.phi - r.phi) / (n.phi - (n.phi * phi))))  #
# Deviance

# Mean duration of infection
dur <- phi*cut.durs + (1-phi)*dura




# Incidence model
# Likelihood and model
for (i in 1:2) { # loop over rate, 1=infection, 2=reinfection
 for (s in 1:3) { # loop over setting - GP=1, fP=2, GUM=3
  for (a in 1:3) { # loop over age group:1=16,17;2=18-20, 3=21-24
   lambda[i,s,a] <- equals(i,1)*(gamma[a] * rho[s] * lambda111) +
                    equals(i,2)*(gamma[a] * rho[s] * lambda111 *
eta[s])
   r.inc[i,s,a] ~ dbin(theta.inc[i,s,a],n.inc[i,s,a])
   theta.inc[i,s,a] <- phi * (
                       (1 - (lambdaS + lambda[i,s,a] *
                        exp(-(lambdaS + lambda[i,s,a]) * 0.5)) /
                       (lambdaS + lambda[i,s,a]))
                       ) + (1 - phi) * (
                       (1 - (lambdaC + lambda[i,s,a] *
                       exp(-(lambdaC + lambda[i,s,a]) * 0.5)) /
                       (lambdaC + lambda[i,s,a]))
                                       )
  dev.inc.rat[i,s,a] <- 2 * (r.inc[i,s,a] * log(r.inc[i,s,a] /
                        (theta.inc[i,s,a] * n.inc[i,s,a])) +
(n.inc[i,s,a]-
                        r.inc[i,s,a]) * log((n.inc[i,s,a] -
r.inc[i,s,a]) /
                        (n.inc[i,s,a] - (n.inc[i,s,a] *
theta.inc[i,s,a]))))
   }
  }
 }
sumdev.inc.rat <- sum(dev.inc.rat[ , , ])    # Deviance, # LaMontagne

#priors for log incidence parameters
```

```
loglambda111 ~ dnorm(0,.0001)                          #Age 16-17, GP,
# infection
log(lambda111) <- loglambda111

for (s in 1:3) {
 logeta[s] ~ dnorm(0,.0001)      # GP=1, fP=2, GUM=3
 log(eta[s]) <- logeta[s]
 }
logrho[1] <- 0                   # GPtheta.inc
for (s in 2:4) {
 logrho[s] ~ dnorm(0,.0001) # 2=fp, 3=GUM, 4=pop, rel to GP
 }
for (s in 1:4) {
 log(rho[s]) <- logrho[s]
 }

loggamma[1] <- 0            #1 = 16-17
for (a in 2:5) {
 loggamma[a] ~ dnorm(0,.01) #2=18-19, 3=20-24,4=25-29,5=30-44 rel to
# 16-17
}
for (a in 1:5) {
 log(gamma[a]) <- loggamma[a]
 }

# setting specific Odds ratios from Adams
for (s in 1:3) {                                  #s+1= 2=FP, 3=GUM, 4=pop,
# rel to GP
   r.OR[s] ~ dnorm(logrho[s+1],pr.OR[s])
   dev.OR[s] <- pr.OR[s] * pow((r.OR[s]-logrho[s+1]),2)  # OR
# deviance
}
sumdev.OR <- sum(dev.OR[])

# overall age-specific incidence in population, 1=16-17, 2=18-19,
# 3=20-24,
#                                             4=25-29, 5=30-44
for (a in 1:3) {
 p[a] ~ dbeta(aprior[a],bprior[a])
 cut.p[a] <- cut(p[a])                          # prevents updating p[a]
 lamda.F[a] <- rho[4]*((1-cut.p[a])*lambda[1,1,a] +
               cut.p[a]*lambda[2,1,a])
 lamda.pop[a] <- lamda.F[a] / (1 - lamda.F[a] * dur)
 }
for (a in 4:5) {
 lamda.pop[a] <- lamda.pop[1] * gamma[a]
 }

# Age-specific Prevalence from Adams, 1=18-19, 2=20-24, 3=25-29,
# 4=30-44
for (a in 1:4) {
 Lprev[a]~dnorm(lprev[a+1],pr.Lprev[a])
 dev.prev[a] <- pr.Lprev[a] * pow((Lprev[a]-lprev[a+1]),2)
 }
for (a in 1:5) {
 lprev[a] <- logit(prev[a])
 }

for (a in 1:3) {
 prev[a] <- min(.999,(dur * lamda.pop2[a]))
}
```

```
prev[4] <- prev[3] * gamma[4]/gamma[3]
prev[5] <- prev[3] * gamma[5]/gamma[3]

sumdev.prev <- sum(dev.prev[])

sumdev <- dev.D + sumdev.inc.rat + sumdev.OR + sumdev.prev + dev.phi


# incidence in difference age bands, using population weights N[]
for (a in 16:17) {inc[a] <- lamda.pop[1]}
for (a in 18:20) {inc[a] <- lamda.pop[2]}
for (a in 21:24) {inc[a] <- lamda.pop[3]}
for (a in 25:29) {inc[a] <- lamda.pop[4]}
for (a in 30:44) {inc[a] <- lamda.pop[5]}

lamda.pop2[1] <- lamda.pop[1]  # age 16,17
lamda.pop2[2] <- lamda.pop[2]  # age 18,19.
lamda.pop2[3] <- inprod(inc[20:24],N[20:24])/sum(N[20:24])  # age 20-
# 24

inc1624 <- inprod(inc[16:24],N[16:24])
inc2544 <- inprod(inc[25:44],N[25:44])
inc1644 <- inprod(inc[16:44],N[16:44])

lamda.pop2[4] <- inc1624 / sum(N[16:24]) # age 16-24
lamda.pop2[5] <- inc2544 / sum(N[25:44]) # age 25-44
lamda.pop2[6] <- inc1644 / sum(N[16:44]) # age 16-44

# other population summaries
prop.treat.1624.2002 <- 31510 / inc1624
prop.treat.1624.2003 <- 34660 / inc1624
prop.asymp.clin.1624.2003 <- 1 - (phi / prop.treat.1624.2003)

# prevalence in reconstructed age groups
for (a in 1:6) {
 prev.pop2[a] <- dur * lamda.pop2[a]
 }
} # end of program



Data
list(

# duration
D=1.36, pr.D=59.17,    # from Duration paper 2-Class estimate

# incidence
r.inc=structure(.Data=c(
4,3,4, 9,5,7, 5,16,9,
5,7,10, 13,12,5, 6,15,5
),.Dim=c(2,3,3)),

n.inc=structure(.Data=c(
73,195,188, 194,273,201, 102,235,245,
14,65,79, 95,127,63, 40,139,81
),.Dim=c(2,3,3)),

# priors for infection/reinfection weights, 16-17, 18-20, 21-24
aprior=c(46.5,73.1,106.4), bprior=c(400,634.6,938.4),

# Logit Prevalence
```

```
Lprev=c(-2.987,-3.41,-4.185,-4.82),
pr.Lprev=c(19.3,20.8,18.4,17.2),

# Setting-specific Log Odds Ratios. Fp,GUM, pop
r.OR= c(0.239,0.871, -.511),
pr.OR= c(67.03,35.21, 17.28),

# symptomatic ct - Geisler
r.phi = 26, n.phi = 115,

# Population sizes from census, age =1...44 - 2002
N=c(NA,NA,NA,NA,NA, NA,NA,NA,NA,NA, NA,NA,NA,NA,NA,
305500,306300,296400,291400,294800,
310100,313900,305600,294700,295000,
304100,317000,329600,349600,370300,
380900,376900,387800,390900,399400,
401200,402600,398700,391900,381900, 370900,356200,349000,343800)
)


# Initial values - 1
# Duration
list(dura=1,  durs=.115,

# incidence
loglambda111=-2.5,
logeta=c(1,.5,.5),
logrho=c(NA, 1, 1.5,-.5),
loggamma=c(NA,-.2,-.5,-.7,-.8),

# probability symptomatic
phi = 0.5,

# proportion re-infection
p=c(.1, .1, .1)
)


# Initial values - 2
# Duration
list(dura=.2,  durs=.112,

# incidence
loglambda111=-4,
logeta=c(.5,1,1),
logrho=c(NA, 0, 0,0),
loggamma=c(NA,0,0,0,0),

# probability symptomatic
phi = .1,

# proportion re-infection
p=c(.3, .05, .2)
)
```