```
model {
# likelihood
for (i in 1:studnum) {
for (j in 1:studobs[i]) {
 r[i,j] \sim dbin(theta[i,j],n[i,j])
 }
 }
# model
for (i in 1:studnum-2) {
for (j in 1:studobs[i]) {
 theta[i,j] <- ((z[i,j] / n[i,j]) * (1 - exp(-lambda.C[1] * t[i,j]))
+
                       (1 - (z[i,j] / n[i,j])) * (1 - exp(-lambda.C[2]
* t[i,j])))
                / (psi / (1 - ((1-psi) * equals(seind[i,j],0))))
 }
 }
# Left-truncated studies with repeat observations
for (i in 8:9) {
for (j in 1:studobs[i]) {
 temp[i,j,1] <- ((z[i,1] / n[i,1]) * exp(-lambda.C[1] * T[i,j]) /</pre>
                  ((z[j,1] / n[i,1]) * exp(-lambda.C[1] * T[i,j]) +
                  (1 - (z[i,1] / n[i,1])) * exp(-lambda.C[2] *
T[i,j]))) *
                  (1 - \exp(-\text{lambda.C}[1] * t[i,j]))
  temp[i,j,2] <- ((1 - (z[i,j] / n[i,1])) * exp(-lambda.C[2] *
T[i,j]) /
                   (0.00001+(z[i,1] / n[i,1]) * exp(-lambda.C[1] *
T[i,j]) +
                   (1 - (z[i,1] / n[i,1])) * exp(-lambda.C[2] *
T[i,j]))) *
                   (1 - \exp(-\text{lambda.C}[2] * t[i,j]))
  theta[i,j] <- (temp[i,j,1] + temp[i,j,2]) /</pre>
                 (psi / (1 - ((1-psi) * equals(seind[i,j],0))))
  }
}
# priors
p1 \sim dbeta(1,1)
lambda.C[1] <- 120
lambda.C[2] \sim dexp(0.001)
psi ~ dbeta(78,8) #sensitivity of culture given initial positive
# culture
# Class proportions
# t=0 studies
for (i in 1:4) {
for (j in 1:studobs[i]) {
 z[i,j] \sim dbin(p1,n[i,j]) \# start at t=0
 }
 }
# Left-truncated studys
for (i in 5:studnum) {
 for (j in 1:studobs[i]) {
 z[i,j] ~ dbin(w1,n[i,j])
```

}

deviance for (i in 1:studnum) { for (j in 1:studobs[i]) { dev[i,j] <- 2 * (r[i,j] * log(r[i,j] / (theta[i,j] * n[i,j])) +</pre> (n[i,j] - r[i,j]) * log((n[i,j] - r[i,j]) / (n[i,j] - (n[i,j] * theta[i,j])))) } dev.stud[i] <- sum(dev[i,1:studobs[i]])</pre> } sumdev <- sum(dev.stud[])</pre> # left truncation w1 <- (p1 / lambda.C[1]) / (p1 / lambda.C[1] + (1 - p1) / lambda.C[2]) # summary statistics dur <- 1 / lambda.C[2]</pre> # Predicted values for Forest plot for (i in 1:studnum) { for (j in 1:studobs[i]) { stud.lambda.Cexpect[i,j] <- -log(1 - theta[i,j]) / t[i,j]</pre> stud.dur.expect[i,j] <- 1 / stud.lambda.Cexpect[i,j]</pre> } } } # Data list(# duration # study order # 1 Johhanisson # 2 Jovner # 3 Geisler # 4 Paavonen # 5 Rahm # 6 Sorensen # 7 McCormack # 8 Morre # 9 Mollano r = structure(.Data=c(10,7,6,6,NA, 2,7,1,0,3, 23, NA, NA, NA, NA, 3, NA, NA, NA, NA, 17,0,0,NA,NA, 8, NA, NA, NA, NA, 3, NA, NA, NA, NA, 2,2,4,0,2, 44,23,7,2,NA),.Dim=c(9,5)), n = structure(.Data=c(23,14,14,8,NA, 12,28,4,8,6,

}

```
93,1,1,NA,NA,
13, NA, NA, NA, NA,
7, NA, NA, NA, NA,
20,5,15,1,13,
82,37,14,6,NA
),.Dim=c(9,5)),
t=structure(.Data=c(
0.038,0.058,0.077,0.125,NA,
0.012,0.03,0.049,0.088,0.274,
0.045, NA, NA, NA, NA,
0.083, NA, NA, NA, NA,
0.25,0.5,0.75,NA,NA,
1, NA, NA, NA, NA,
1.375, NA, NA, NA, NA,
0.083,0.5,0.417,0.917,0.5,
1,1,1,1,NA
),.Dim=c(9,5)),
seind = structure(.Data=c(
1,1,1,1,NA,
0,0,0,0,0,
0, NA, NA, NA, NA,
1, NA, NA, NA, NA,
1,1,1,NA,NA,
0, NA, NA, NA, NA,
1, NA, NA, NA, NA,
0,0,0,0,0,
0,0,0,0,NA
),.Dim=c(9,5)),
T=structure(.Data=c(
NA, NA, NA, NA, NA,
0,0,0.083,0.083,0.5,
0,1,2,3,NA
),.Dim=c(9,5)),
studnum = 9,
studobs = c(4, 5, 1, 1, 3, 1, 1, 5, 4),
)
# Initial values - 1
list(
psi = 0.9,
lambda.C = c(NA, 0.7),
p1 = 0.2,
)
# Initial values - 2
list(
psi = 0.6,
lambda.C = c(NA, 0.1),
p1 = 0.5
)
```