MPT solution

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One-High Threshold Model ~ results

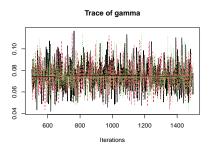
```
library(rjags)
data <- list(
 hits = c(8, 9, 14, 14, 13, 8, 13, 12, 11,
              4, 8, 13, 15, 12, 11, 9, 5, 5,
              6, 15, 11, 14, 12, 12, 11, 1, 14,
              13, 7, 11, 12, 8, 11),
        = c(4, 4, 0, 1, 2, 0, 3, 1, 3, 0, 0, 1,
 fas
             0, 0, 0, 0, 1, 0, 3, 0, 0, 1, 2, 1,
             2, 0, 0, 0, 2, 1, 2, 0, 2),
 nPeople = 33,
 nOld = 15,
 nNew = 15)
```

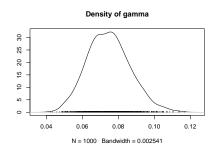
```
modelString = "
  # MPT single high threshold
 model{
    for (i in 1:nPeople){
      hits[i] ~ dbin(thetaHit, nOld)
      fas[i] ~ dbin(thetaFA , nNew)
    thetaHit = rho + (1-rho)*gamma
    thetaFA = gamma
    rho ~ dunif(0, 1)
    gamma ~ dunif(0, 1)
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modelFile <- "mpt_solution.jags"</pre>
writeLines( modelString , con = modelFile)
```

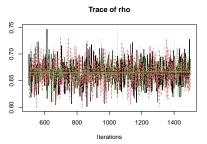
```
jagsModel = jags.model( file = modelFile,
                       data =
                                       data,
                                        3,
                       n.chains =
                                      500)
                       n.adapt =
set.seed(0)
samples = coda.samples( jagsModel,
                       variable.names = c("gamma",
                                          "rho"),
                                      = 1000)
                       n.iter
```

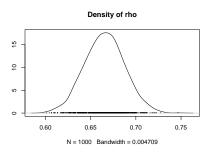
plot(samples)

One-High Threshold Model ~ figures









One-High Threshold Model ~ summary statistics

summary(samples)\$statistics

```
##
              Mean
                          SD
                                Naive SE Time-series SE
  gamma 0.07469895 0.01189014 0.0002170833 0.0002755683
        0.66542650 0.02202969 0.0004022052 0.0005046011
## rho
summary(samples)$quantiles
                         25% 50%
##
              2.5%
                                             75%
                                                      97.5%
## gamma 0.05271075 0.06630381 0.07423132 0.08228381 0.09955606
## rho
        0.62229776 0.65041471 0.66557979 0.68027602 0.70956385
```

One-High Threshold Model ~ convergence

```
effectiveSize(samples)
##
                rho
     gamma
## 1868.057 1913.821
gelman.diag(samples)
## Potential scale reduction factors:
##
##
        Point est. Upper C.I.
## gamma
                   1.00
## rho
                     1.01
##
## Multivariate psrf
##
## 1
```