# **MPT** solution

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#### One-High Threshold Model ~ results

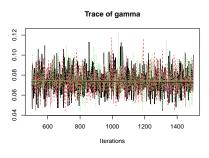
```
library(rjags)
data <- list(
 hits = c(8, 9, 14, 14, 13, 8, 13, 12, 11,
              4, 8, 13, 15, 12, 11, 9, 5, 5,
              6, 15, 11, 14, 12, 12, 11, 1, 14,
              13, 7, 11, 12, 8, 11),
        = c(4, 4, 0, 1, 2, 0, 3, 1, 3, 0, 0, 1,
 fas
             0, 0, 0, 0, 1, 0, 3, 0, 0, 1,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

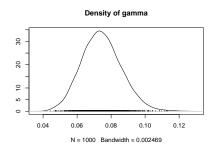
```
modelString = "
  # MPT single high threshold
 model{
    for (i in 1:nPeople){
      hits[i] ~ dbin(thetaHit, nOld)
      fas[i] ~ dbin(thetaFA , nNew)
    thetaHit = rho + (1-rho)*gamma
    thetaFA = gamma
    rho ~ dunif(0, 1)
    gamma ~ dunif(0, 1)
11
modelFile <- "mpt_solution.jags"</pre>
writeLines( modelString , con = modelFile)
```

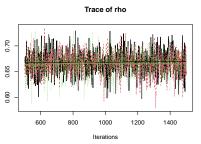
```
jagsModel = jags.model( file = modelFile,
                       data =
                                       data,
                                        3,
                       n.chains =
                                      500)
                       n.adapt =
set.seed(0)
samples = coda.samples(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

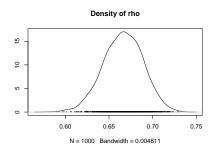
plot(samples)

## One-High Threshold Model $\sim$ figures









### One-High Threshold Model ~ summary statistics

```
summary(samples)$statistics
                         SD
##
             Mean
                               Naive SE Time-series SE
## gamma 0.0743824 0.01159926 0.0002117725 0.0002753438
        0.6660643 0.02250931 0.0004109619 0.0005245267
## rho
summary(samples)$quantiles
##
              2.5%
                         25% 50%
                                              75%
                                                      97.5%
## gamma 0.05333377 0.06620266 0.07376768 0.08168157 0.09842377
## rho
        0.62125677 0.65089322 0.66648069 0.68176974 0.70834532
```

### One-High Threshold Model ~ convergence

```
effectiveSize(samples)
##
                rho
     gamma
## 1856.831 1836.440
gelman.diag(samples)
## Potential scale reduction factors:
##
##
        Point est. Upper C.I.
## gamma
                   1.01
## rho
                     1.02
##
## Multivariate psrf
##
## 1.01
```