# MPT solution

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# One-High Threshold Model ~ results

```r
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) ,
  fas     = c( 4, 4,  0,  1,  2,  0,  3,  1,  3, 0,  0,  1,  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)
  }
"
writeLines( modelString , con = "mpt.txt")
jagsModel = jags.model( file      = "mpt.txt",
                        data      =      data ,
                        n.chains =         3 ,
                        n.adapt  =       500 )
set.seed(0)
samples = coda.samples( jagsModel,
                        variable.names = c("gamma", "rho"),
                        n.iter         = 1000 )
```
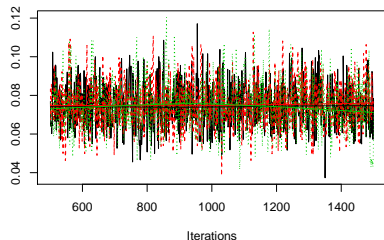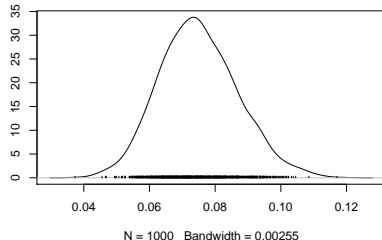
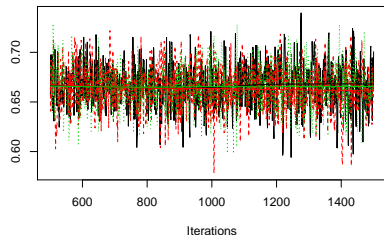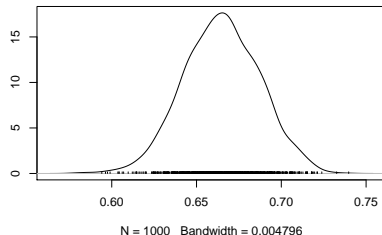# One-High Threshold Model ~ figures

```
plot(samples)
```

## One-High Threshold Model ~ summary statistics

```r
summary(samples)$statistics
```

```
##              Mean         SD    Naive SE Time-series SE
## gamma 0.07494799 0.01192946 0.0002178011   0.0003070961
## rho   0.66475407 0.02244098 0.0004097144   0.0005341563
```

```r
summary(samples)$quantiles
```

```
##               2.5%        25%        50%        75%        97
## gamma 0.05340915 0.06662704 0.07431282 0.08270218 0.1001
## rho   0.62039043 0.64934865 0.66485056 0.68041932 0.7083
```

# One-High Threshold Model ~ convergence

```
effectiveSize(samples)

##    gamma      rho
## 1580.826 1787.262

gelman.diag(samples)

## Potential scale reduction factors:
##
##       Point est. Upper C.I.
## gamma      1.01       1.01
## rho        1.00       1.01
##
## Multivariate psrf
##
## 1
```