

# 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),
  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, 0, 2),
  nPeople = 31,
  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)
}
"

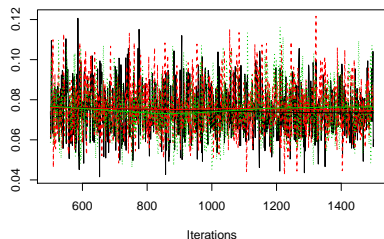
writeLines( modelString , con = "mpt.txt")
jagsModel = jags.model( file = "mpt.txt",
                        data = data ,
                        n.chains = 3 ,
                        n.adapt = 500 )

set.seed(0)
samples = coda.samples( jagsModel,
                        variable.names = c("gamma", "rho"),
                        n.iter = 1000 )
```

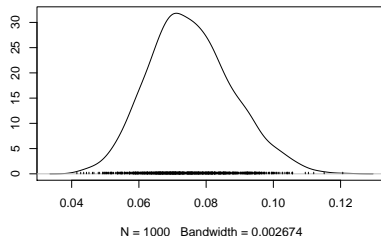
# One-High Threshold Model ~ figures

```
plot(samples)
```

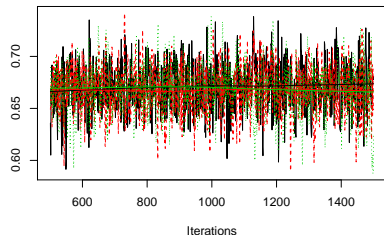
Trace of gamma



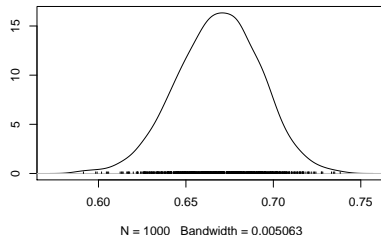
Density of gamma



Trace of rho



Density of rho



## One-High Threshold Model ~ summary statistics

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

##		Mean	SD	Naive SE	Time-series SE
##	gamma	0.07546168	0.01250949	0.0002283909	0.0003014291
##	rho	0.66872167	0.02369004	0.0004325191	0.0005786662

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

##		2.5%	25%	50%	75%	97.5%
##	gamma	0.05320048	0.06666018	0.07458541	0.08350925	0.10220048
##	rho	0.62132143	0.65307971	0.66945952	0.68518871	0.71380048

## One-High Threshold Model ~ convergence

```
effectiveSize(samples)
```

```
##      gamma      rho  
## 1745.486 1730.501
```

```
gelman.diag(samples)
```

```
## Potential scale reduction factors:
```

```
##
```

```
##      Point est. Upper C.I.
```

```
## gamma      1.00      1.01
```

```
## rho        1.01      1.02
```

```
##
```

```
## Multivariate psrf
```

```
##
```

```
## 1.01
```