HW07

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"I have executed these exercises on my own and written the answers in my own words. Signed: [Shashi Shankar]

1A.

```r
graphics.off()
rm(list=ls())
source("DBDA2E-utilities.R")
```

```
##
## *********************************************************************
## Kruschke, J. K. (2015). Doing Bayesian Data Analysis, Second Edition:
## A Tutorial with R, JAGS, and Stan. Academic Press / Elsevier.
## *********************************************************************
```

```
## Loading required package: coda
```

```
## Linked to JAGS 4.2.0
```

```
## Loaded modules: basemod,bugs
```
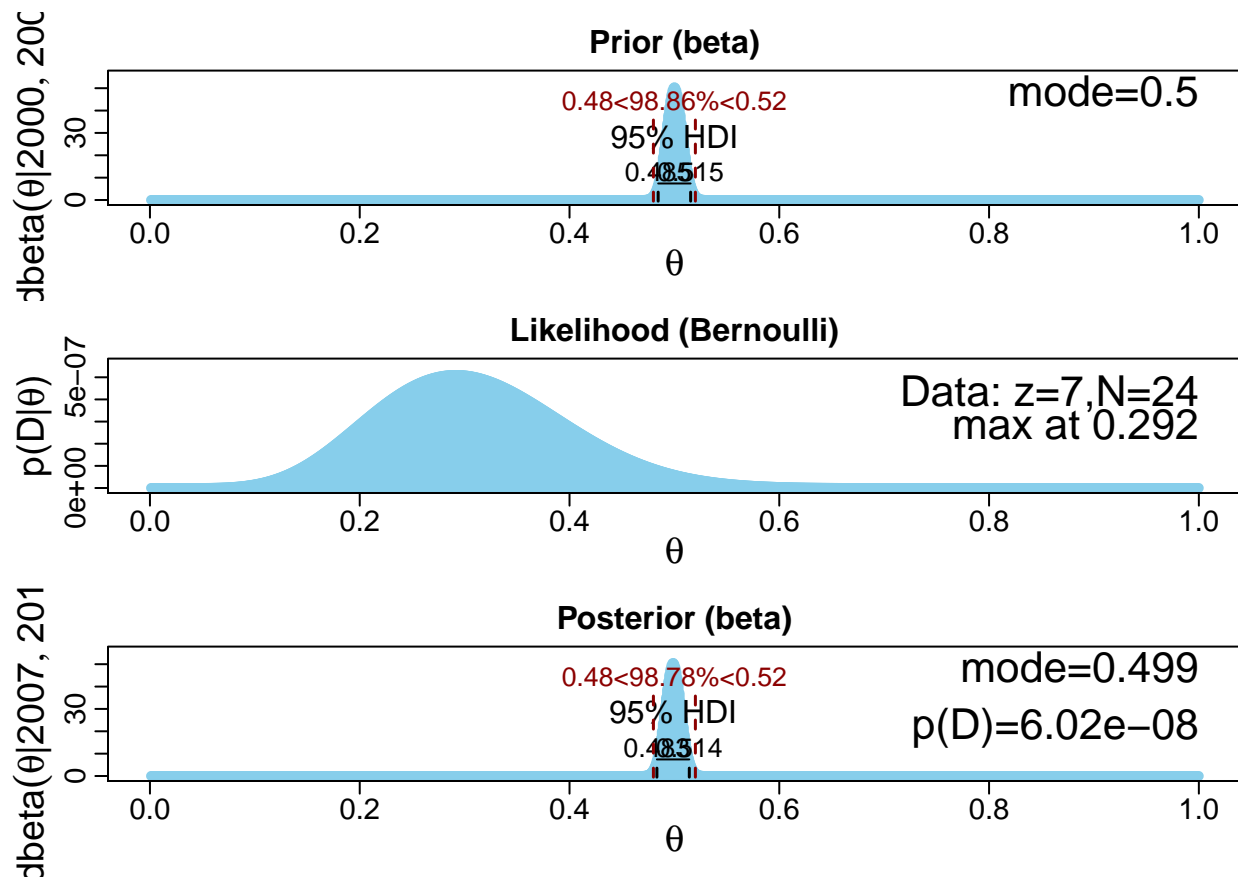
```r
source("BernBeta.R")
z = 7 ; N = 24
theta = 0.5
pDgTheta = theta^z * (1-theta)^(N-z)
show( pDgTheta )
```

```
## [1] 5.960464e-08
```

Probability of data given theta is 5.960464e-08

1B.

```r
source("BernBeta.R")
a = 2000 ; b = 2000
openGraph(width=5,height=7)
BernBeta( c(a,b) , c(rep(0,N-z),rep(1,z)) , ROPE=c(0.48,0.52) ,
plotType="Bars" , showCentTend="Mode" , showHDI=TRUE , showpD=TRUE )
```
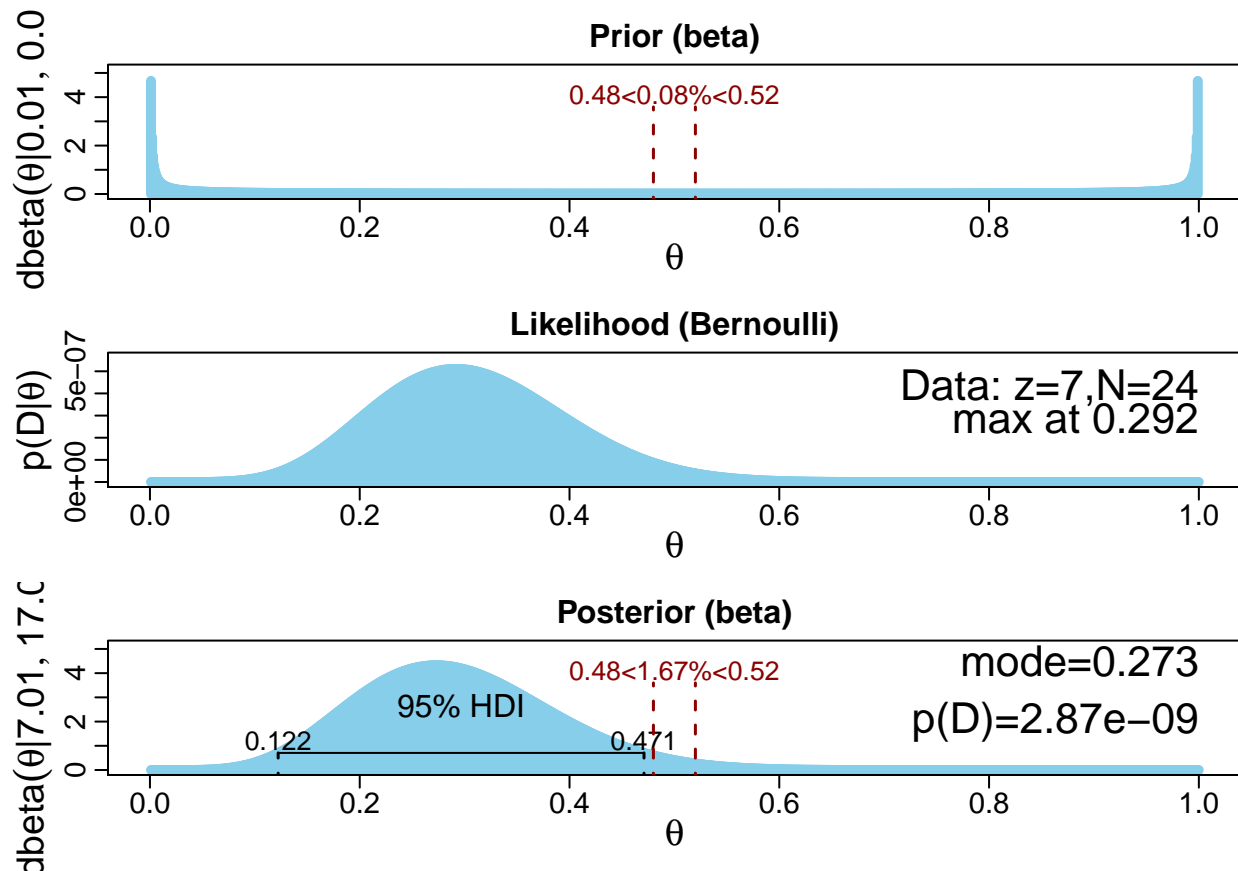
Prior (beta)

0.48<98.86%<0.52
95% HDI
0.485 15
mode=0.5

Likelihood (Bernoulli)

Data: z=7,N=24
max at 0.292

Posterior (beta)

0.48<98.78%<0.52
95% HDI
0.485 14
mode=0.499
p(D)=6.02e−08

```
## [1] 2007 2017
```

p(D)=6.02e-08

1C.

```
a = 0.01 ; b = 0.01
openGraph(width=5,height=7)
BernBeta( c(a,b) , c(rep(0,N-z),rep(1,z)) , ROPE=c(0.48,0.52) ,
plotType="Bars" , showCentTend="Mode" , showHDI=TRUE , showpD=TRUE )
```

```
## [1]  7.01 17.01
# Bayes factor, Haldane/null:
show( 2.87e-09 / 5.96e-08 )
```

```
## [1] 0.04815436
```
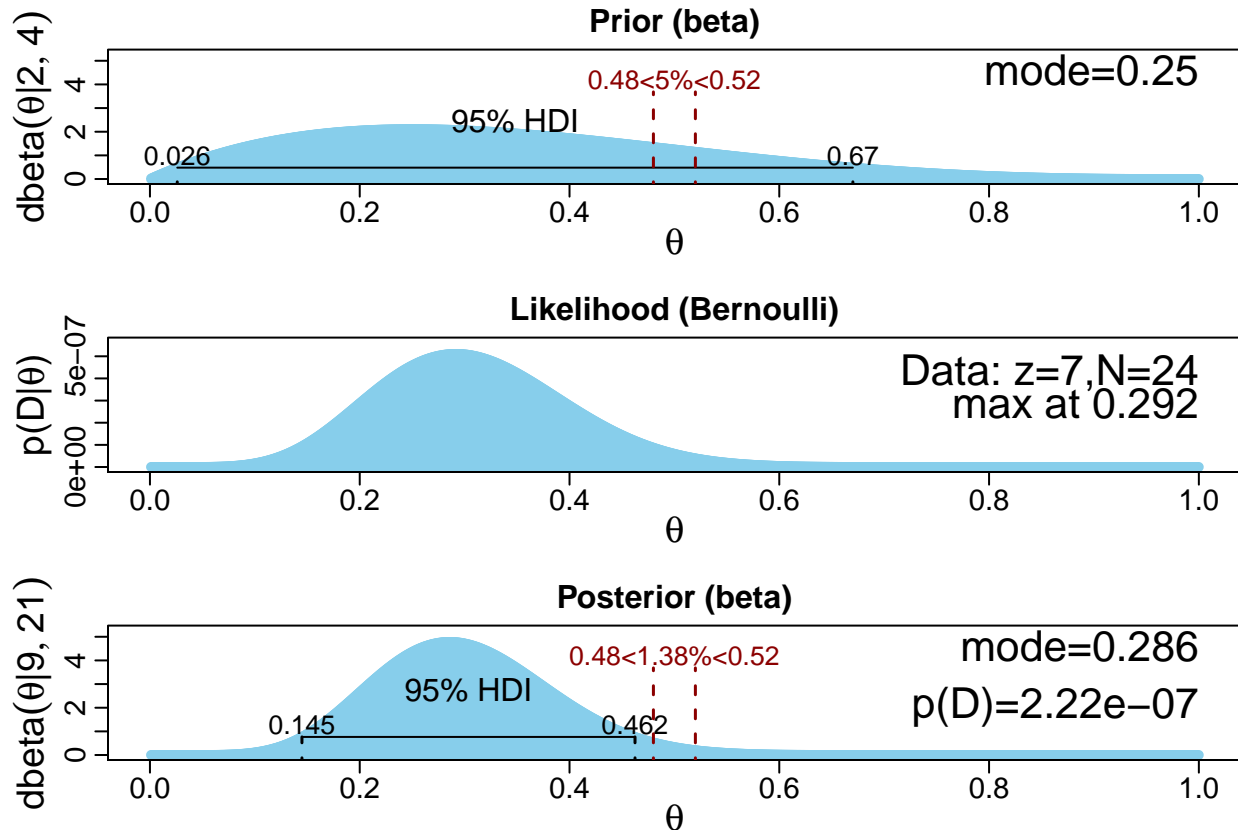
p(D)=2.87e-09 Baye's factor = 0.048

1D.

```
show( 0.08 / 1.67 )
```

```
## [1] 0.04790419
```

Haldane prior, prior p in ROPE is 0.08% and posterior p in ROPE is 1.67%. The ratio is 0.0479.

1E.

```
a = 2 ; b = 4
openGraph(width=5,height=7)
BernBeta( c(a,b) , c(rep(0,N-z),rep(1,z)) , ROPE=c(0.48,0.52) ,
plotType="Bars" , showCentTend="Mode" , showHDI=TRUE , showpD=TRUE )
```

```
## [1]  9 21
```

```
show( 2.22e-07 / 5.96e-08 )
```

```
## [1] 3.724832
```

p(D) is 2.22e-07 Bayes factor, informed/null is 3.72

1F.

```
print( 5.0 / 1.38 )
```

```
## [1] 3.623188
```

Informed prior, prior p in ROPE is 5% and posterior p in ROPE is 1.38%. The ratio is 3.62.

1G.

While using the Haldance prior, the 95% posterior HDI is between 0.122 to 0.471 whereas using the informed prior, the posterior HDI is between 0.145 to 0.462. The posterior HDI's are not very different and they both exclude the ROPE. The Bayes factors are very different and make opposite decisions.
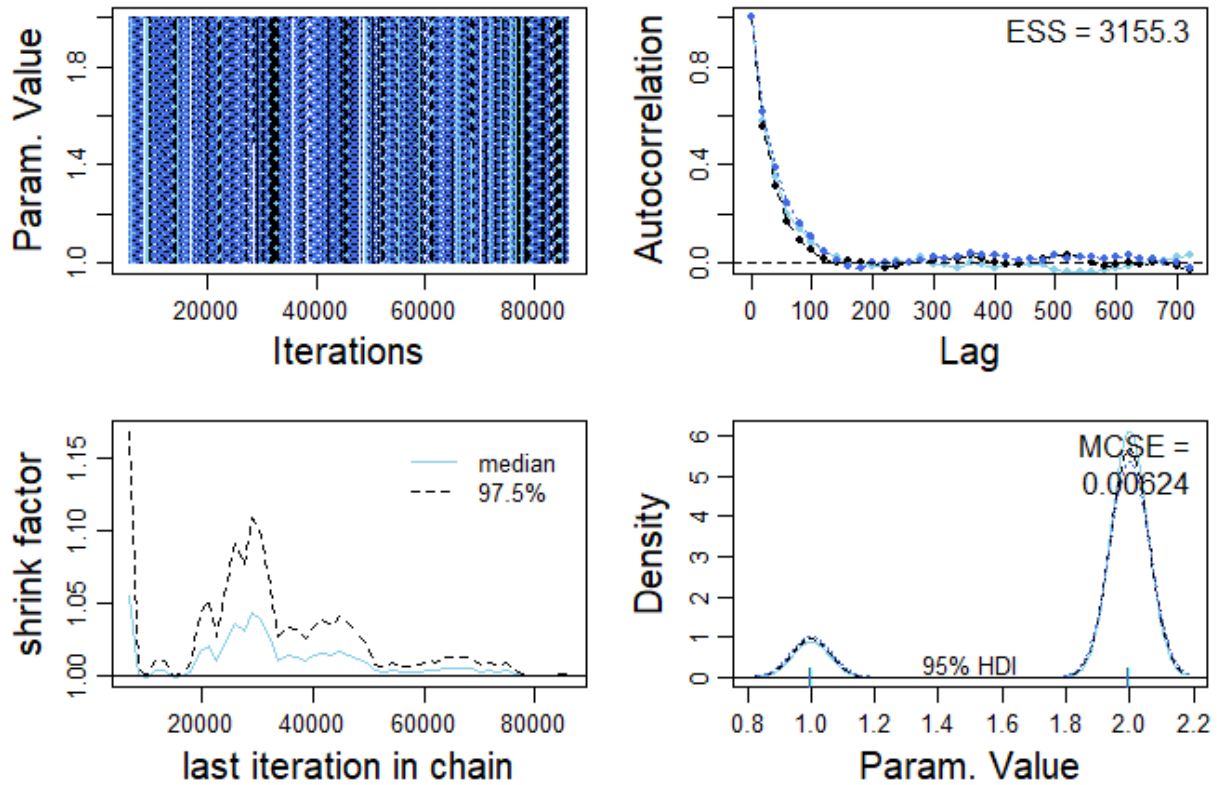
Figure 1:

1H.

According to me Parameter estimation is more informative than model comparison because it gives explicit information about the magnitude of the parameters which describe the data. Bayes Factor only tells which model is more credible without saying anything about the parameter magnitude.

In the model-comparison approach, the mildly informed prior is more meaningful than the Haldane prior as Haldane prior fails to express a theoretically meaningful hypothesis.

2A.

```
#source("OneOddGroupModelComp2E.R")
```

In the plot for model index 2 ESS of model-index chain is about 2879, which is reasonable for our purposes. Model index 2 is preferred, with a posterior probability of about 85%. The single-mode model is preferred over the mutil-modal model.

2B.

The graph of differences of modes are considerably different such as the w1-w4. This conclusion disagrees with the conclusion of model comparison. But the model index and the group modes are all parameters being

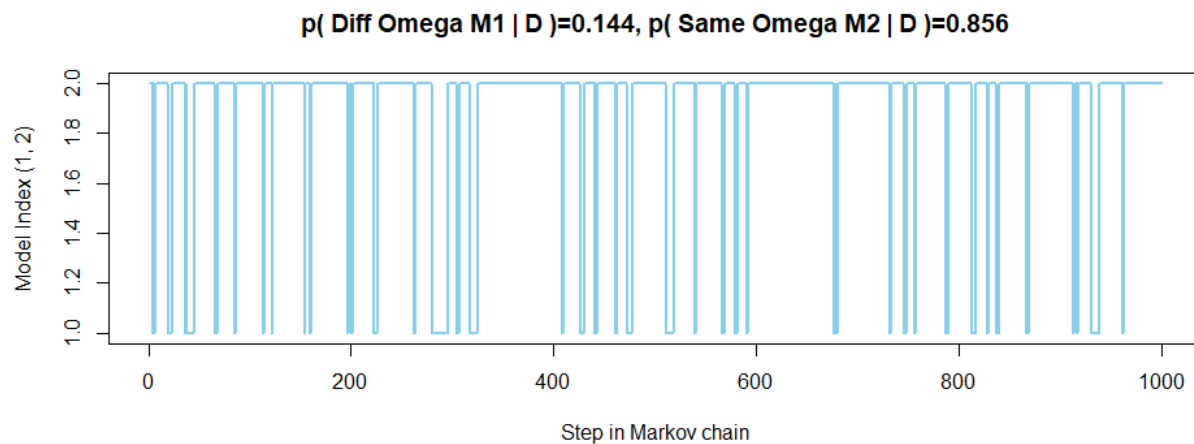**p(Diff Omega M1 | D)=0.144, p(Same Omega M2 | D)=0.856**

Figure 2:

simultaneously updated so there is no real contradiction.

The single mode model can account for the data better than the multi modal model when taking into account the prior distributed over a larger parameter space. The posterior on the model-index tells us that which prior better accounts for the data and the posterior on the four mode parameters addresses the question of what are credible estimates of the group modes.

2C.

```
#source("OneOddGroupModelComp2E.R")
```

After doing the code changes as required in the question only the first two groups have their own priors, and groups 3 and 4 are fixed to match group 2. Model index 1 is the two mode model, and model index 2 is the single-mode model.

Two-mode model is strongly preferred, with a posterior probability of more than 93%.

2D.

The differences of the w2-w3, w2-w4, w3-w4 modes are exactly zero. Even though it seems model 1 is preferred, It's not really meaningful as it seems probable but false.This conclsuion doesn't seem to agree with model comaprison model.

2E.

The most meaningful approach is to estimate the magnitudes and make decisions based on the posterior distribution of the modes Because it is implausible that the group modes are truly and exactly identical.

3.
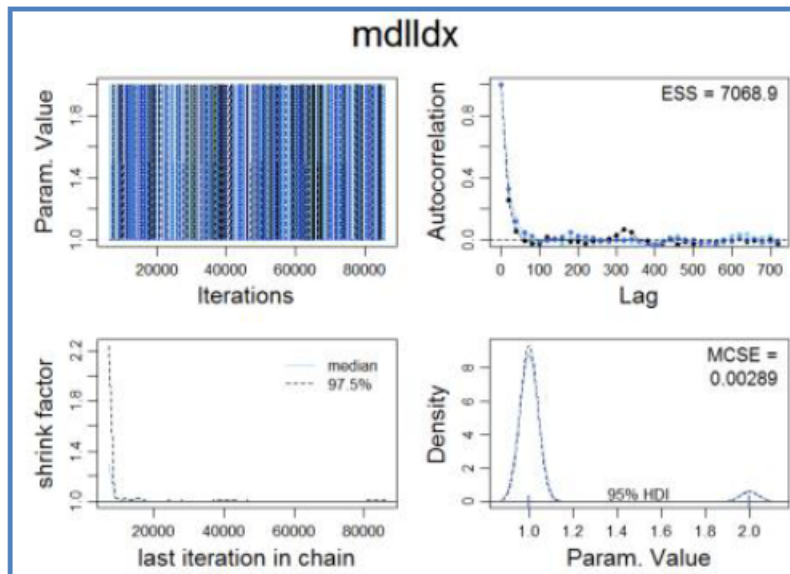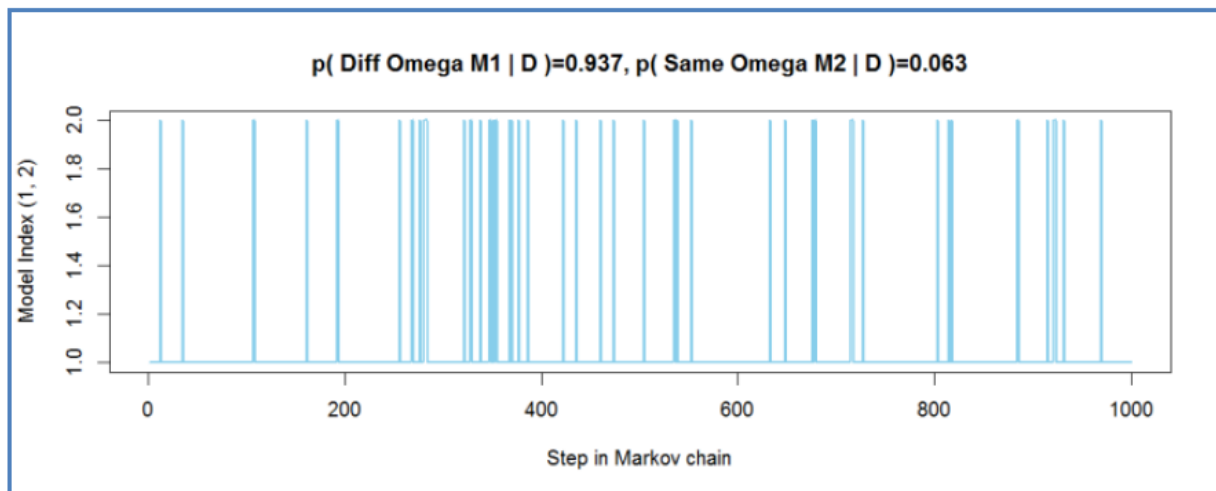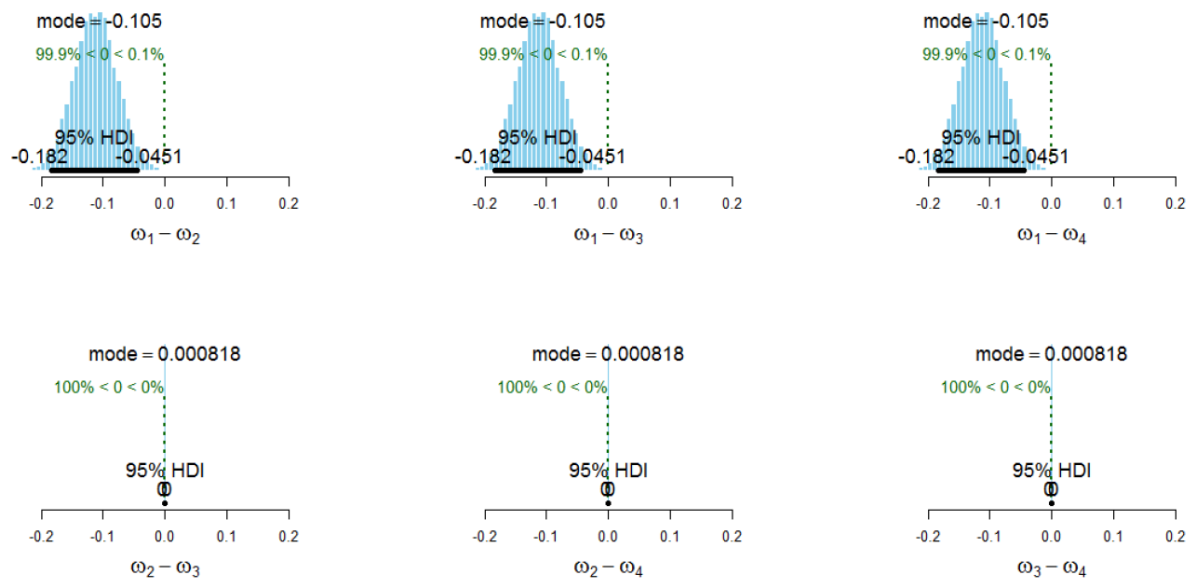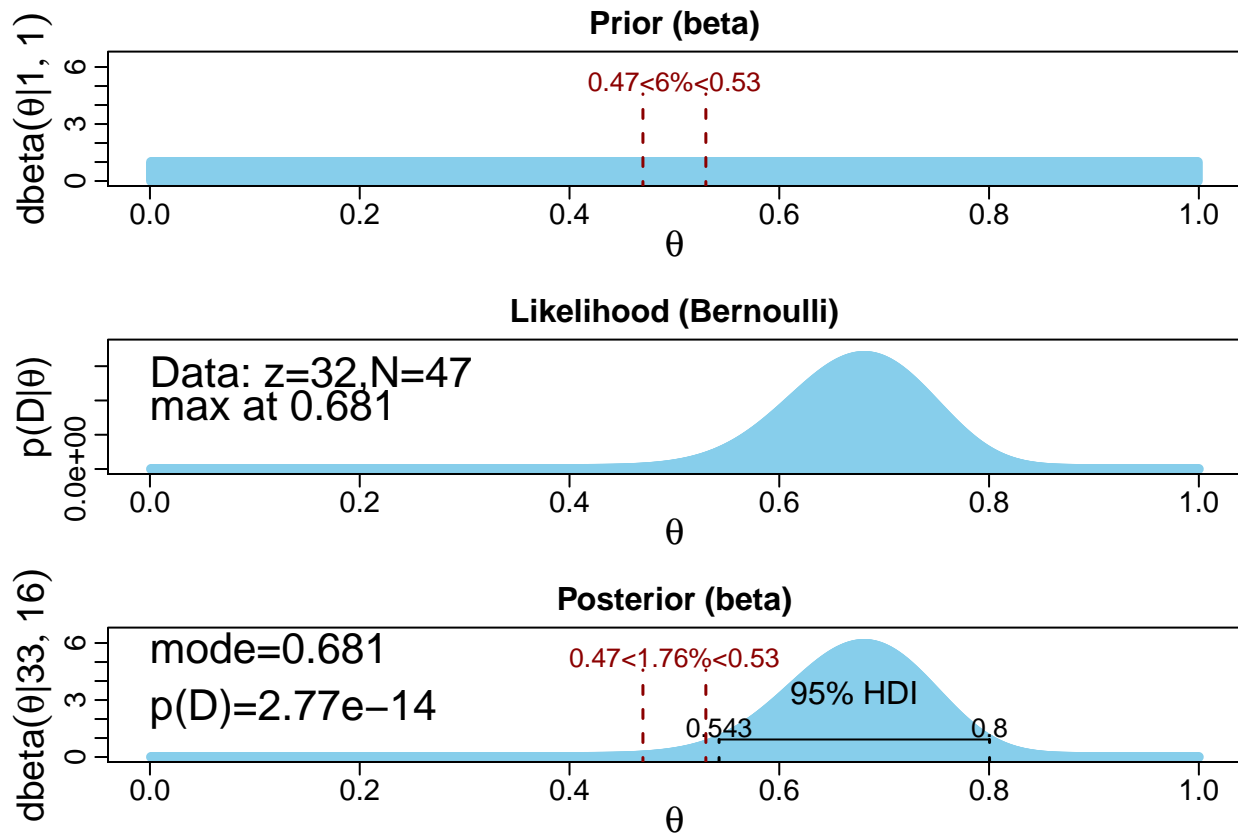
Figure 3:

Figure 4:

7

Figure 5:

```
source("BernBeta.R")
a = 1 ; b = 1
z = 32; N = 47
openGraph(width=5,height=7)
BernBeta( c(a,b) , c(rep(0,N-z),rep(1,z)) , ROPE=c(0.47,0.53) ,
plotType="Bars" , showCentTend="Mode" , showHDI=TRUE , showpD=TRUE )
```

Prior (beta)

0.47<6%<0.53

Likelihood (Bernoulli)

Data: z=32,N=47
max at 0.681

Posterior (beta)

mode=0.681
p(D)=2.77e−14

0.47<1.76%<0.53

95% HDI
0.543   0.8
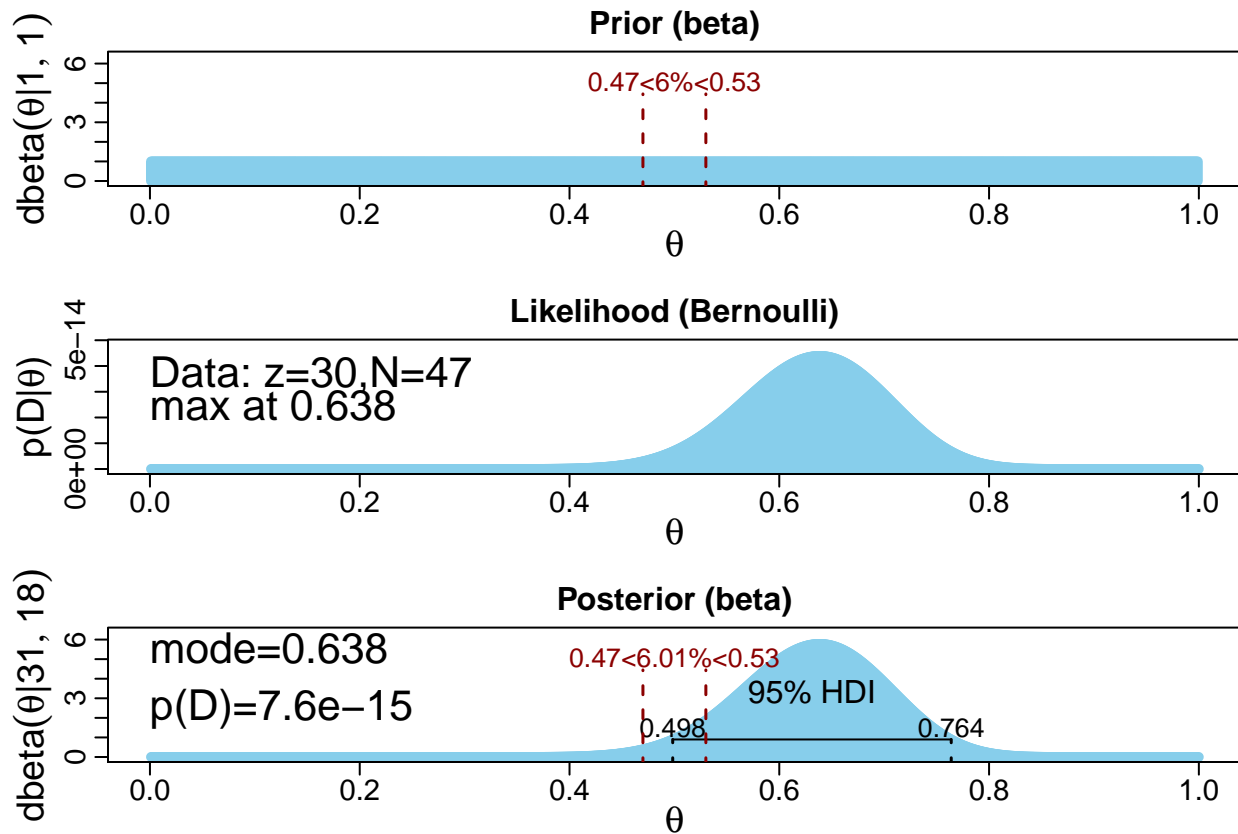
```
## [1] 33 16
```

```r
source("BernBeta.R")
a = 1 ; b = 1
z = 30; N = 47
openGraph(width=5,height=7)
BernBeta( c(a,b) , c(rep(0,N-z),rep(1,z)) , ROPE=c(0.47,0.53) ,
plotType="Bars" , showCentTend="Mode" , showHDI=TRUE , showpD=TRUE )
```

Prior (beta)

0.47<6%<0.53

Likelihood (Bernoulli)

Data: z=30,N=47
max at 0.638

Posterior (beta)

mode=0.638
p(D)=7.6e−15

0.47<6.01%<0.53

95% HDI

0.498   0.764

```
## [1] 31 18
source("BernBeta.R")
a = .1 ; b = .1
z = 330; N = 600
openGraph(width=5,height=7)
BernBeta( c(a,b) , c(rep(0,N-z),rep(1,z)) , ROPE=c(0.47,0.53) ,
plotType="Bars" , showCentTend="Mode" , showHDI=TRUE , showpD=TRUE )
```
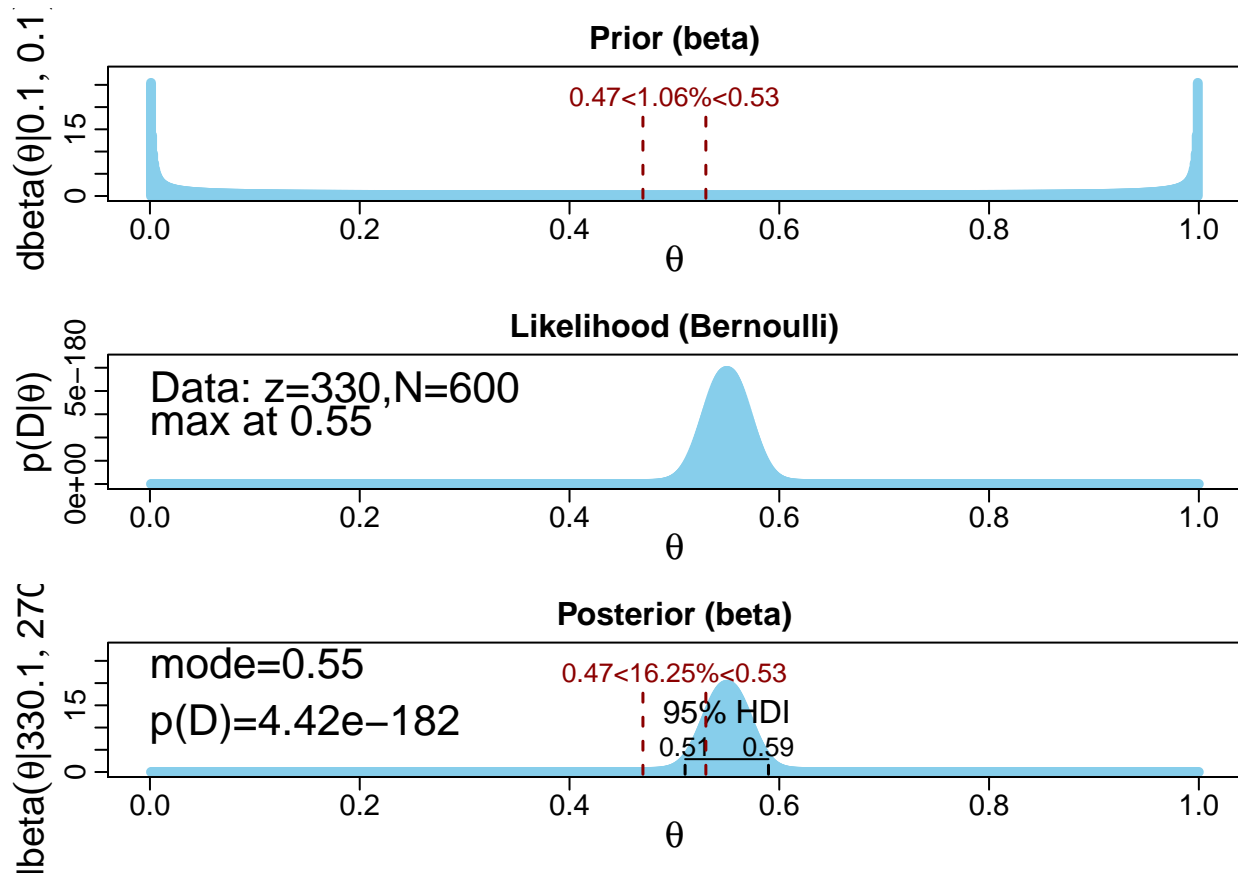
Prior (beta)

dbeta(θ|0.1, 0.1)

0.47<1.06%<0.53

Likelihood (Bernoulli)

p(D|θ)

Data: z=330,N=600
max at 0.55

Posterior (beta)

lbeta(θ|330.1, 270...

mode=0.55
p(D)=4.42e−182

0.47<16.25%<0.53
95% HDI
0.51   0.59

```
## [1] 330.1 270.1
```

```r
#p(D|null) / p(D|Haldane)
show(2.42e-181 / 4.42e-182)
```

```
## [1] 5.475113
```

```r
#p(D|informed) / p(D|null)
show(1.34e-180 / 2.42e-181)
```

```
## [1] 5.53719
```

```r
#BF = p(D|flat) / p(D|null)
show(7.6e-15 / 7.11e-15)
```

```
## [1] 1.068917
```

4A.

The one line code change in order to use the TowelReuse data is given below.

dataSource = c("TowelReuse" , "BetaBlocker")[1]

```r
source("Jags-MetaAnalysis-TwoProportions.R")
```

```
##
## *********************************************************************
## Kruschke, J. K. (2015). Doing Bayesian Data Analysis, Second Edition:
## A Tutorial with R, JAGS, and Stan. Academic Press / Elsevier.
```

```
## *********************************************************************
##
## Calling 3 simulations using the parallel method...
## Following the progress of chain 1 (the program will wait for all
## chains to finish before continuing):
## Welcome to JAGS 4.2.0 on Tue Feb 27 02:09:41 2018
## JAGS is free software and comes with ABSOLUTELY NO WARRANTY
## Loading module: basemod: ok
## Loading module: bugs: ok
## . . Reading data file data.txt
## . Compiling model graph
##    Resolving undeclared variables
##    Allocating nodes
## Graph information:
##    Observed stochastic nodes: 14
##    Unobserved stochastic nodes: 18
##    Total graph size: 150
## . Reading parameter file inits1.txt
## . Initializing model
## . Adapting 1000
## -------------------------------------------------| 1000
## +++++++++++++++++++++++++++++++++++++++++++++++++ 100%
## Adaptation successful
## . Updating 1000
## -------------------------------------------------| 1000
## ************************************************* 100%
## . . . . . . . . . . . . Updating 100000
## -------------------------------------------------| 100000
## ************************************************* 100%
## . . . . Updating 0
## . Deleting model
## .
## All chains have finished
## Simulation complete.  Reading coda files...
## Coda files loaded successfully
## Finished running the simulation

## Calculating summary statistics...
## Calculating the Gelman-Rubin statistic for 34 variables....
```

4B.

4C.

There is conclusive evidence that the treatment increases towel re-use. Although Bayesian evidence synthesis
provided strong support for the effect, The authors think that this conclusion is wrong and Bayesian evidence
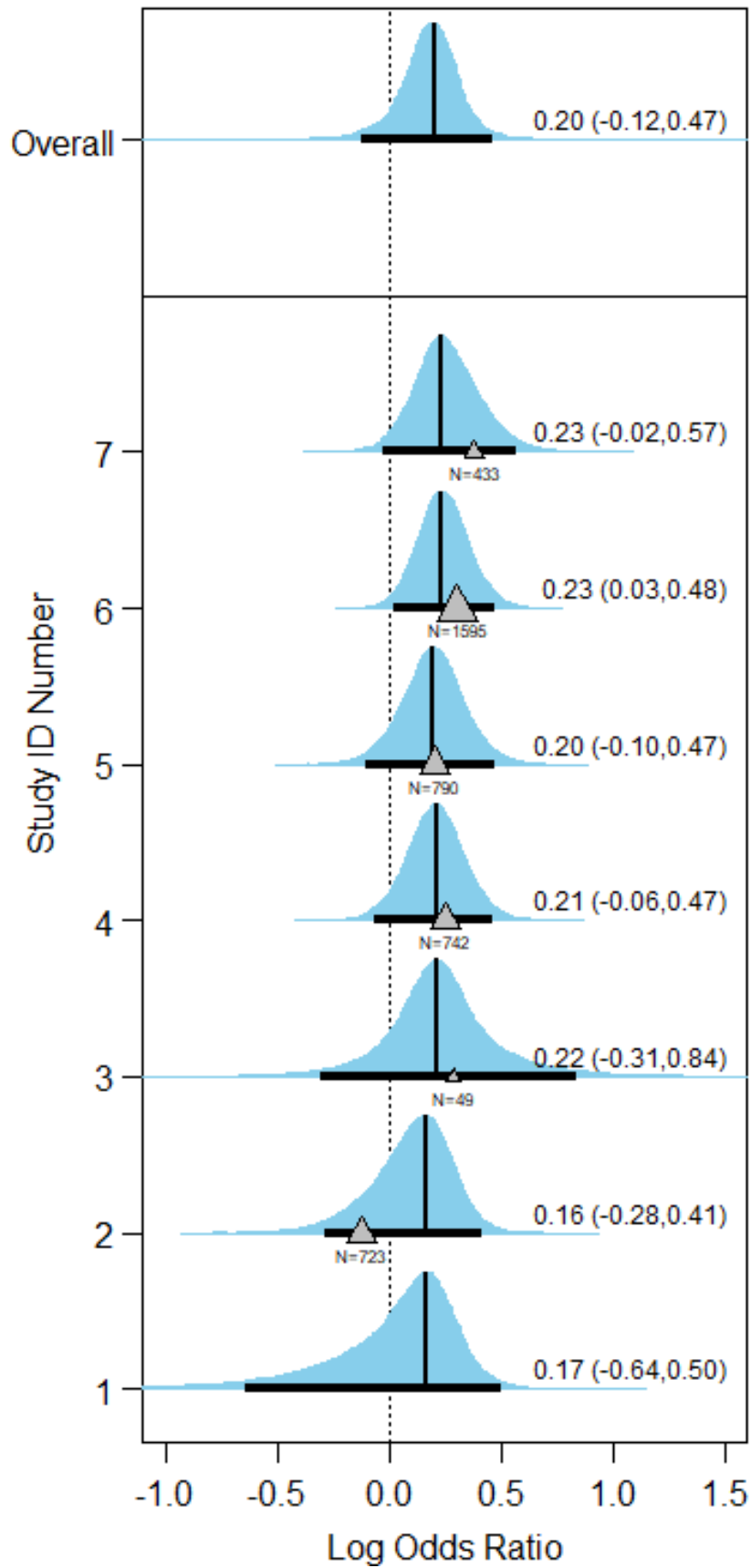synthesis is inherently flawed.

Figure 6:

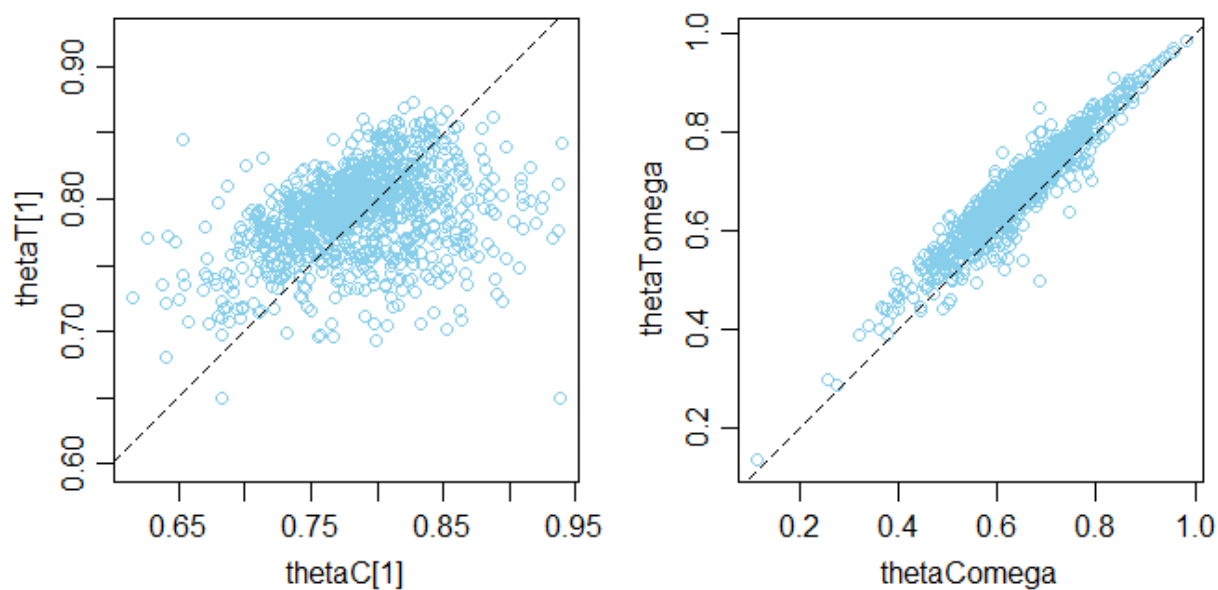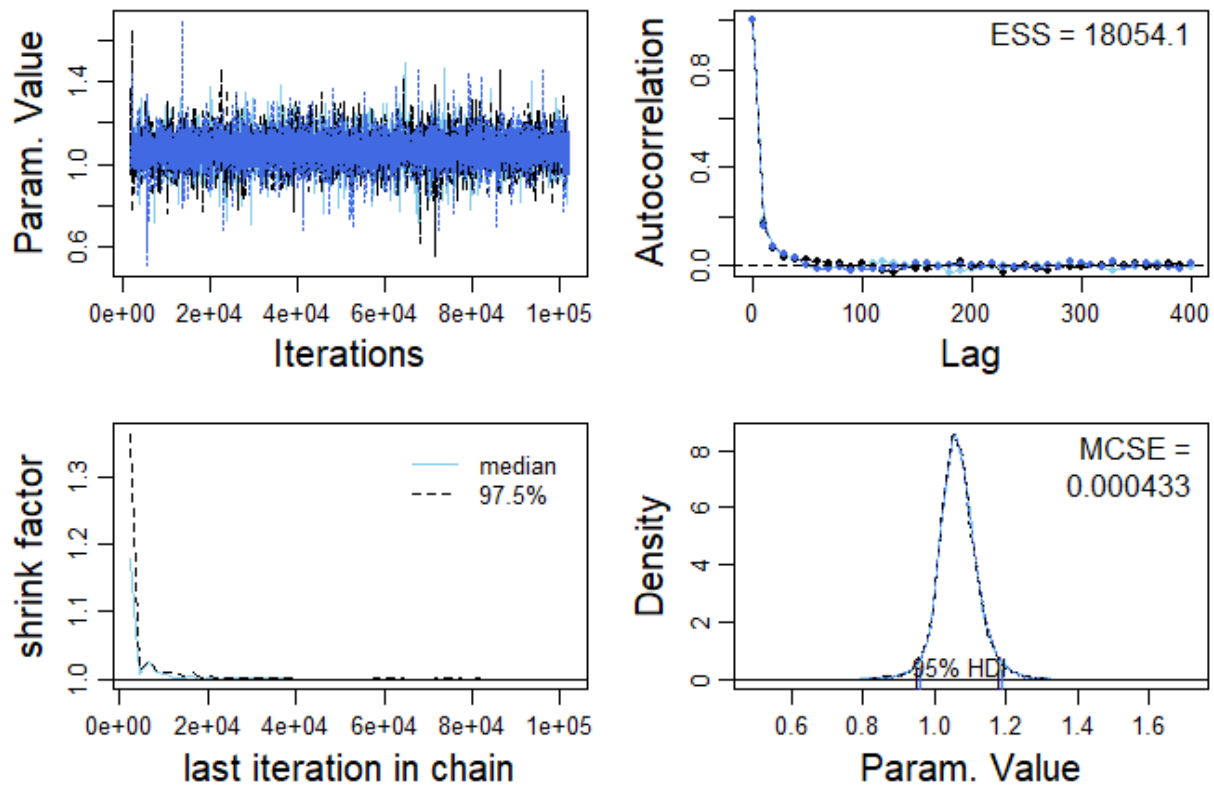Figure 7:

muMeta

Figure 8: