Classical and Bayesian Statistics

Problems 13

Problem 13.1

Use the file `stan_beta_compare.R` to check the approximation of the posterior distribution by `stan`. The top figure is the approximated distribution and the bottom figure is the exact posterior distribution we know in this case.

Play with the options `iter=...` (number of steps after tune-in) and `warmup=...` (The first steps that are ignored) around. What can you say about the HDI and mode compared to the exact distribution?

Problem 13.2

The pharmaceutical company Life Co. has developed a new drug to combat ADHD. To determine its effectiveness, the drug was tested with $n = 10$ patients. The current standard method shows an effect in 30 % of the treated patients.

Treatment with the new drug was successful in 4 patients. Carry out a hypothesis test to see if the new drug is more effective than the standard method.

a) Investigate the data using the Bayesian method from the lecture. Make explicit statements about the prior distribution and the ROPE. Justify your answer.

b) Play around with the data so that the zero value is discarded or accepted.

Use the file `stan_beta_rope.R`.

Hint: Run

```
library(rstan)


## Loading required package: StanHeaders

##
## rstan version 2.26.22 (Stan version 2.26.1)

## For execution on a local, multicore CPU with excess RAM we recommend calling
## options(mc.cores = parallel::detectCores()).
## To avoid recompilation of unchanged Stan programs, we recommend calling
## rstan_options(auto_write = TRUE)
```

```
## For within-chain threading using `reduce_sum()` or `map_rect()` Stan functions,
## change `threads_per_chain` option:
## rstan_options(threads_per_chain = 1)

library(bayestestR)
library(latex2exp)
rstan_options(auto_write = TRUE)


plot_posterior <- function(params, Rope = c(.4,.5)){
  dens <- density(params$theta)
  max_dens <- max(dens$y)
  hdi_l <- as.numeric(hdi(params$theta)[2])
  hdi_r <- as.numeric(hdi(params$theta)[3])

  plot(dens,main="Posterior",col="darkseagreen", TeX("$\\theta$"))

  lines(c(hdi_l,hdi_r),c(.12*max_dens,.12*max_dens),col="orange")
  text(hdi_l,.15*max_dens,round(hdi_l,3),cex=.6)
  text(hdi_r,.15*max_dens,round(hdi_r,3),cex=.6)
  text((hdi_l+hdi_r)/2,.15*max_dens,"95% HDI",cex=.6,col="orange")

  lines(c(Rope[1],Rope[2]),c(.08*max_dens,.08*max_dens),col="blue")
  text(Rope[1],.05*max_dens,Rope[1],cex=.6)
  text(Rope[2],.05*max_dens,Rope[2],cex=.6)
  text((Rope[1]+Rope[2])/2,.05*max_dens,"ROPE",cex=.6, col="blue")

}
```

only once after that run only

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
real<lower=0,upper=1> theta ;
}
model {
theta ~ beta(2,4) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 50
```

```
z = 10
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model, data=list(y = y, N = N), iter=2000, warmup=200)

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.6,.8))
```

Problem 13.3

In a pilot medical study, 5 out of 16 patients responded to a *new* treatment. The probability of response to the standard treatment is given as 15 %. Is the new treatment superior to the standard treatment?

a) Investigate the specifications using the Bayesian method from the lecture. Make explicit statements about the prior distribution and the ROPE. Justify your answer.

b) Play around with the data so that the zero value is discarded or accepted.

Use the file **stan_beta_rope.R**.

Problem 13.4

("Quality control of screws") A manufacturer of screws guarantees his customers that the proportion of inferior screws is significantly less than 10 %. For quality assurance purposes, he takes a random sample of fifty screws from a large delivery. It turns out that 3 of these fifty screws are substandard. The problem for the manufacturer is: can he really assume with confidence that the proportion of substandard bolts in the whole delivery is really significantly less than 10 % (at a proportion of 10 % of substandard bolts, the quality standards are no longer met).

a) Investigate the data using the Bayesian method from the lecture. Make explicit statements about the prior distribution and the ROPE. Justify your answer.

b) Play around with the data so that the zero value is discarded or accepted.

Use the file **stan_beta_rope.R**.

Classical and Bayesian Statistic

Sample solution for Problems 13

Solution 13.2

In order to solve the problem with Bayes inference, we need a prior distribution. We choose the beta distribution as prior distribution, where we have to define the two parameter values a and b. In the prior distribution expresses our prior knowledge or our estimates of the efficacy of the drug.

We may well assume that the efficacy of the new drug is probably in the range of the standard method, i.e. around 30 %. To do this, we need to know or estimate how certain our assumption of 30 % is. This information is not included in the task, so we have to make appropriate assumptions here. To do this, we consider the value $\kappa = a + b$: If κ is large, then our certainty is large that the value of 30 % is correct. The beta distribution function then becomes very narrow. If our uncertainty is large, we choose a small value of κ so that the beta distribution function becomes broad.

We specify κ and the mode ω and, based on these two specifications, calculate the parameters a and b for the beta distribution as follows (see script):

$$a = \omega(\kappa - 2) + 1$$

and

$$b = (1 - \omega)(\kappa - 2) + 1$$

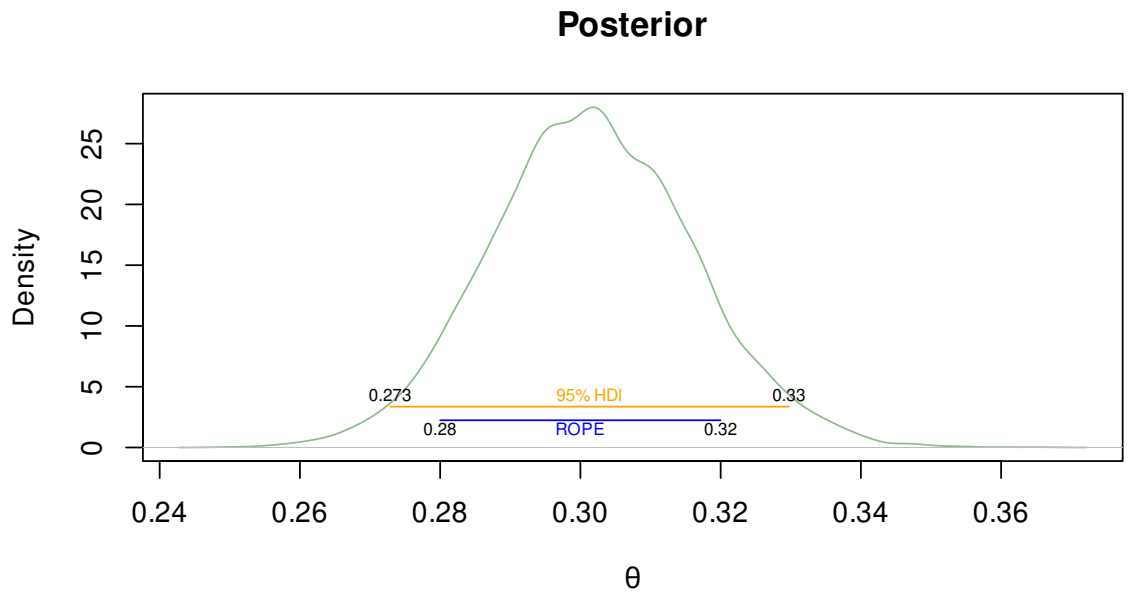
The mode of the prior distribution ω is consequently chosen as 0.3. Now for the choice of κ, which is much more difficult. If we are pretty sure that the standard method is already very good and difficult to improve, we are pretty sure that the efficacy of the new drug should also be around 30 %. We choose in this case $\kappa = 1000$. This gives $a = 300.4$ and $b = 699.6$.

The ROPE indicates which values are equivalent to the zero value 0.3. This information is provided by experts. We choose the ROPE as 0.3 ± 0.02.

We have 10 trials and 4 successes. Consequently, the **rstan** output looks like this:

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
real<lower=0,upper=1> theta ;
```

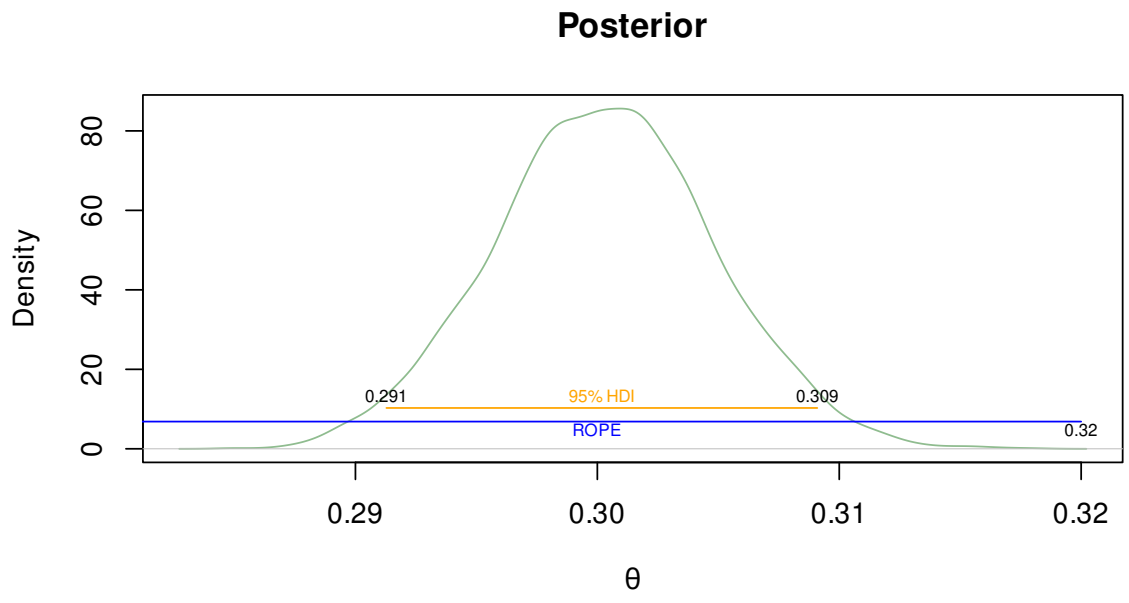
```
}
model {
theta ~ beta(300.4,699.6) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 10
z = 4
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model, data=list(y = y, N = N), iter=2000, warmup=200, refre

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.28,.32))
```



Since we have very little data, it does not have much influence on the prior distribution. The mode has not shifted. The ROPE is fully contained in the 95 %-HDI, i.e. some of the 95 % most likely values are outside the ROPE. In this case, we refuse to decide whether the new treatment method is more successful or equivalent to the standard method.

Let us now try $\kappa = 10000$, i.e. $a = 3000.4$ and $b = 6999.6$.

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
real<lower=0,upper=1> theta ;
}
model {
theta ~ beta(3000.4,6999.6) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 10
z = 4
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model, data=list(y = y, N = N), iter=2000, warmup=200, refre

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.28,.32))
```

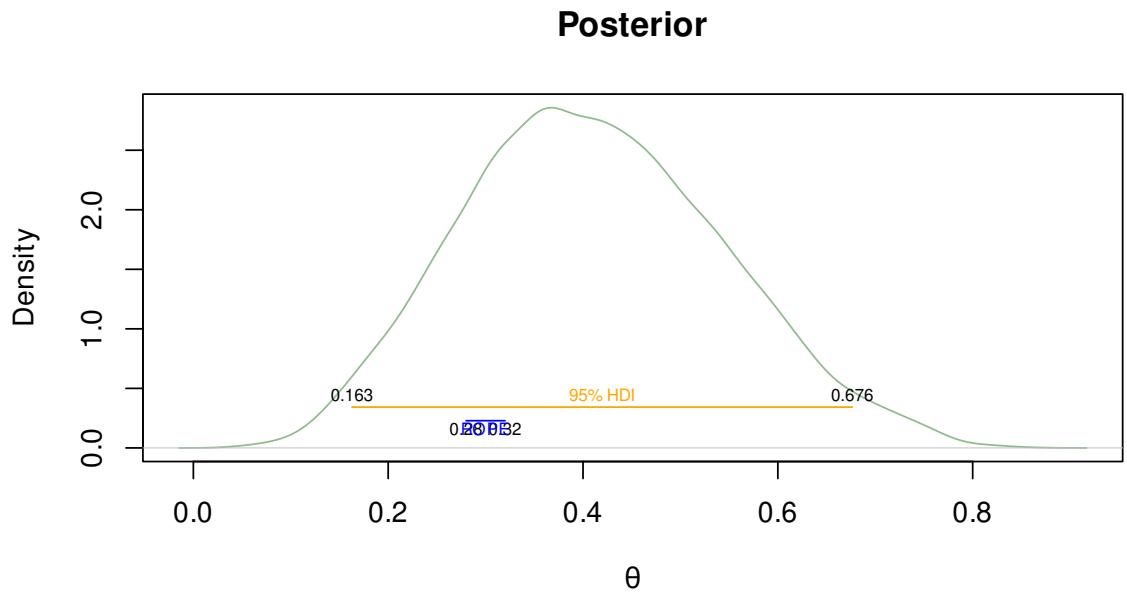


The ROPE now fully contains the 95 % most likely values, and thus we accept the zero value 0.3. Consequently, the efficacy of the new drug is equivalent to the standard

method.

Let us now try a small κ, say $\kappa = 3$, i.e. $b = 1.7$ and $a = 1.3$. In this case, we are very unsure whether the 30 % are correct. Perhaps because the studies on the standard method are unreliable/dubious.

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
real<lower=0, upper=1> theta ;
}
model {
theta ~ beta(1.3, 1.7) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 10
z = 4
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model, data=list(y = y, N = N), iter=2000, warmup=200, refre

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.28,.32))
```



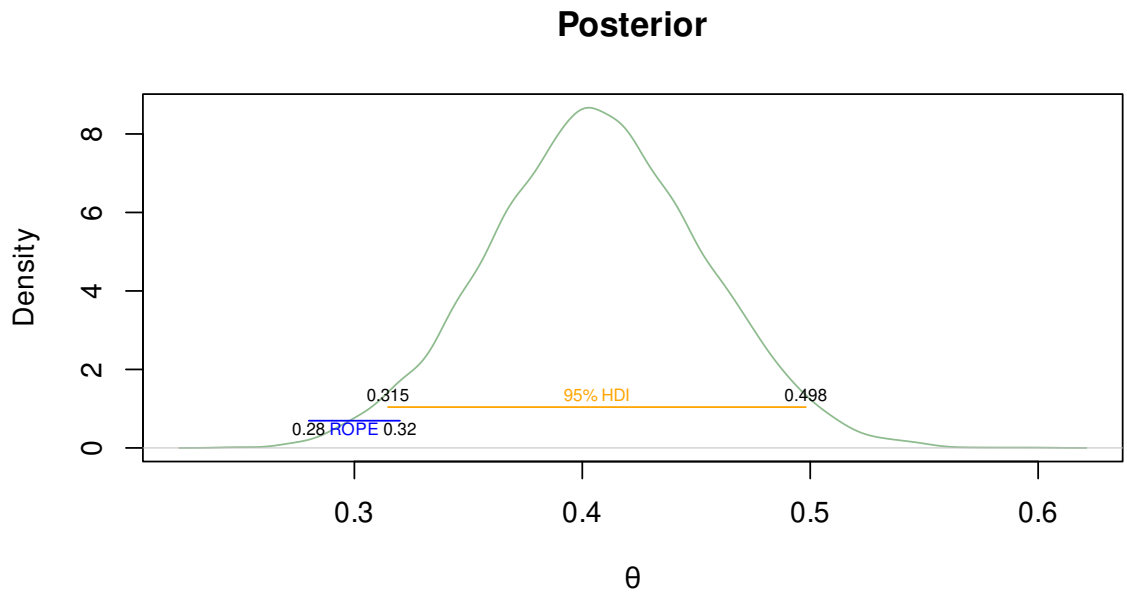
The mode has shifted from 0.3 to 0.39. The ROPE now sweeps only a very small range of the 95 % HDI, and thus very few of the most likely values are in the ROPE. In this case, we refuse to decide whether the new treatment method is more successful or equivalent to the standard method.

The reason why we cannot make a clear decision except for very large κ is because of the small number of trials. If we increase the number of trials, the posterior distribution becomes narrower.

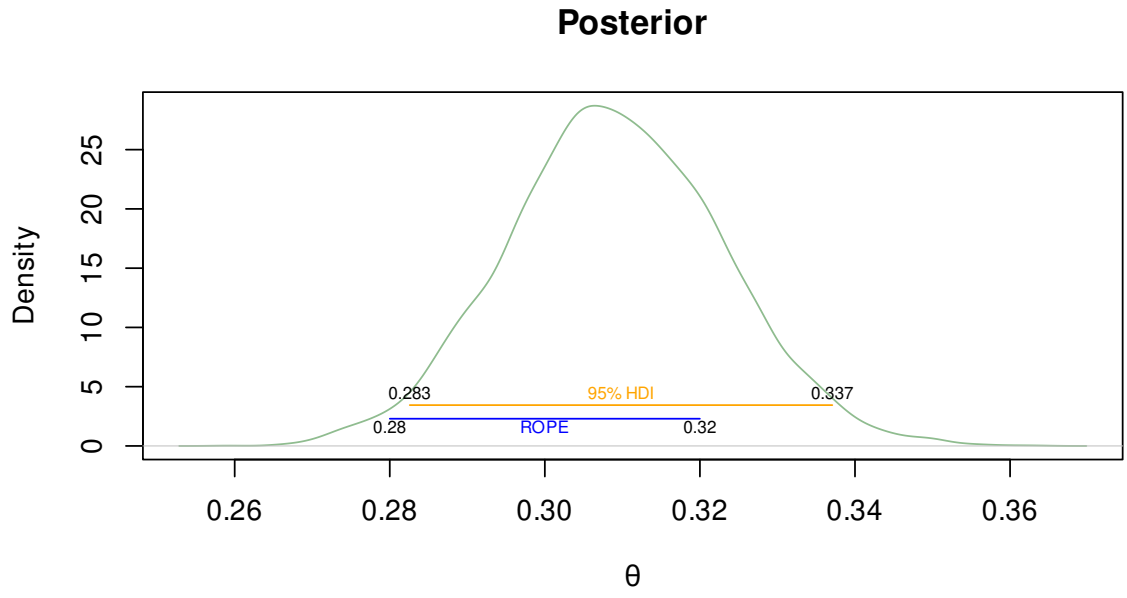
The posterior is always a trade-off between data and the prior:

- Large uncertainty and lots of data: Posterior looks more like the likelihood function (data).
- Large certainty and few data: Posterior looks more like the prior.
- In all other cases, a mixture between likelihood function and prior.

In the following, we consider 100 trials and 40 successes. Thus the ratio of successes to trials remains the same. For $\kappa = 3$ (large uncertainty), i.e. $b = 1.7$ and $a = 1.3$, the posterior is similar to the likelihood function. The ROPE is almost completely outside the HDI, i.e. there is some evidence that the new drug has a higher efficacy than the standard method. However, even in this case we refuse to decide whether the new treatment method is more successful or equivalent to the standard method.

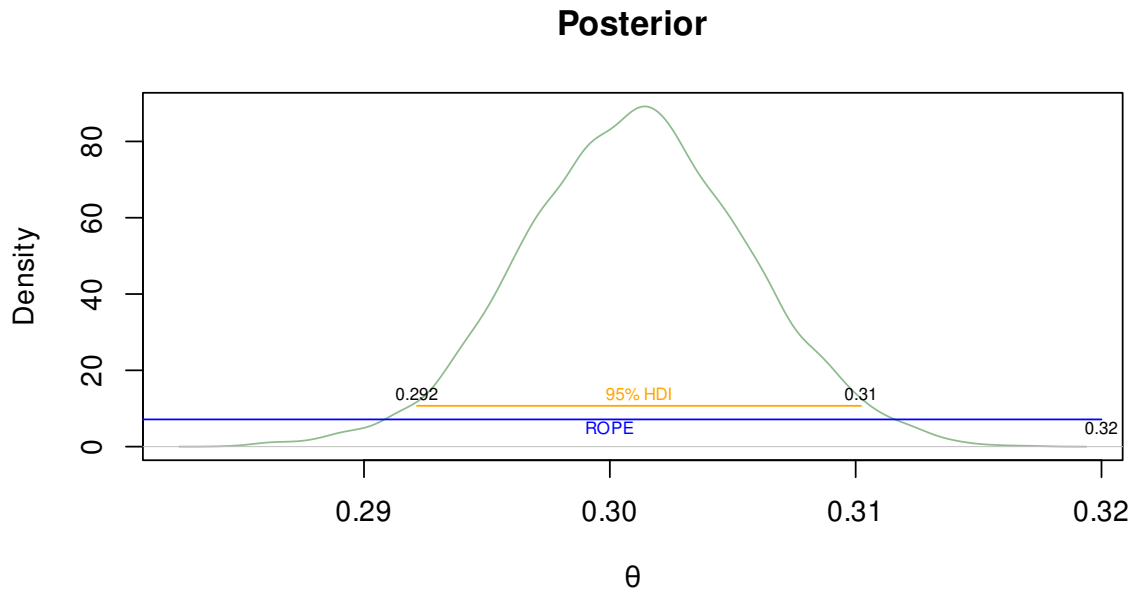


For $\kappa = 1000$ ($a = 300.4$ and $b = 699.6$) the data no longer has the överhand. Since there is a significant overlap between ROPE and HDI, we cannot make a decision on whether the new treatment is also effectively better.



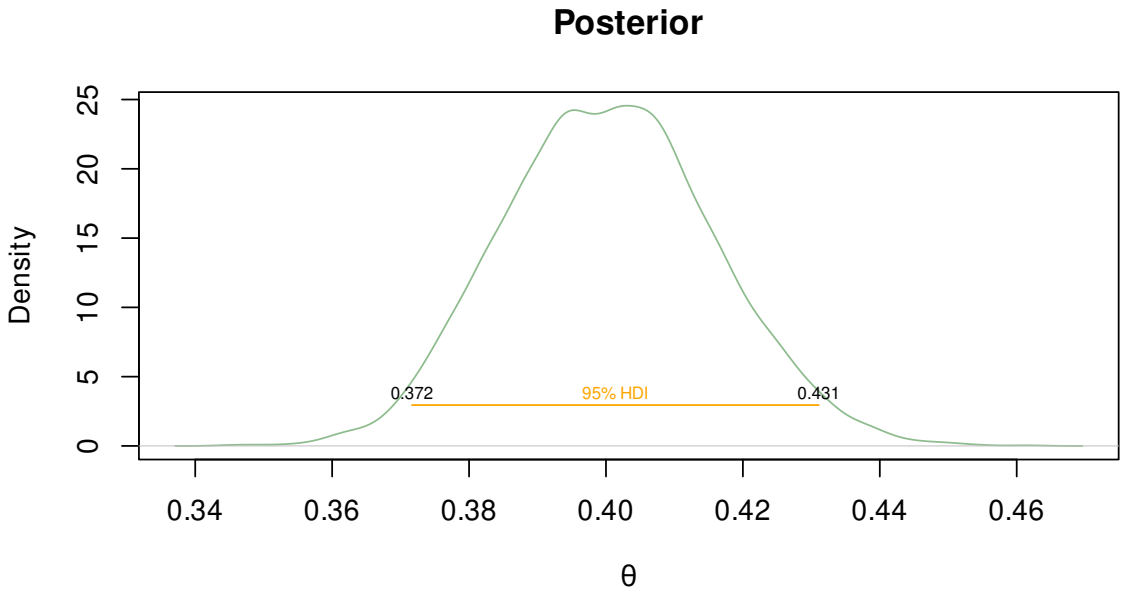
For $\kappa = 10000$ ($a = 3000.4$ and $b = 6999.6$), it does not have enough data to dissuade us from our 0.3 conviction, the ROPE fully contains the HDI. That is, the new drug

is not better than the standard method, but equivalent to it. We accept the zero value 0.3 in this case.

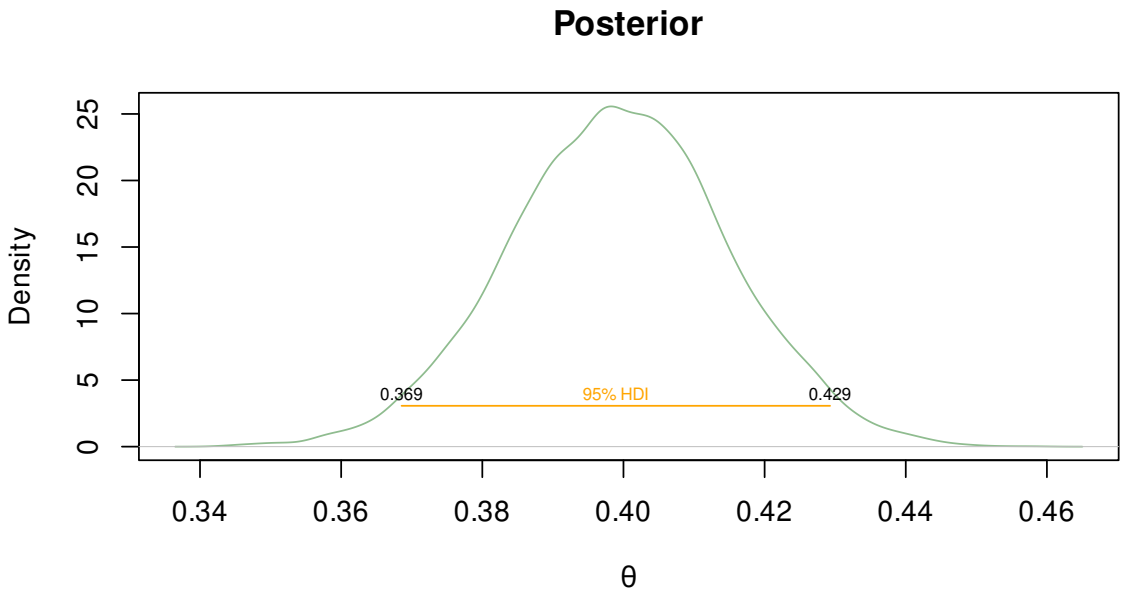


Below we consider 1000 trials and 400 successes and the prior with $\kappa = 3$ ($b = 1.7$ and $a = 1.3$). The data now convince us to abandon our conviction since the ROPE and the HDI do not overlap. We can now assume that the new treatment method is better.

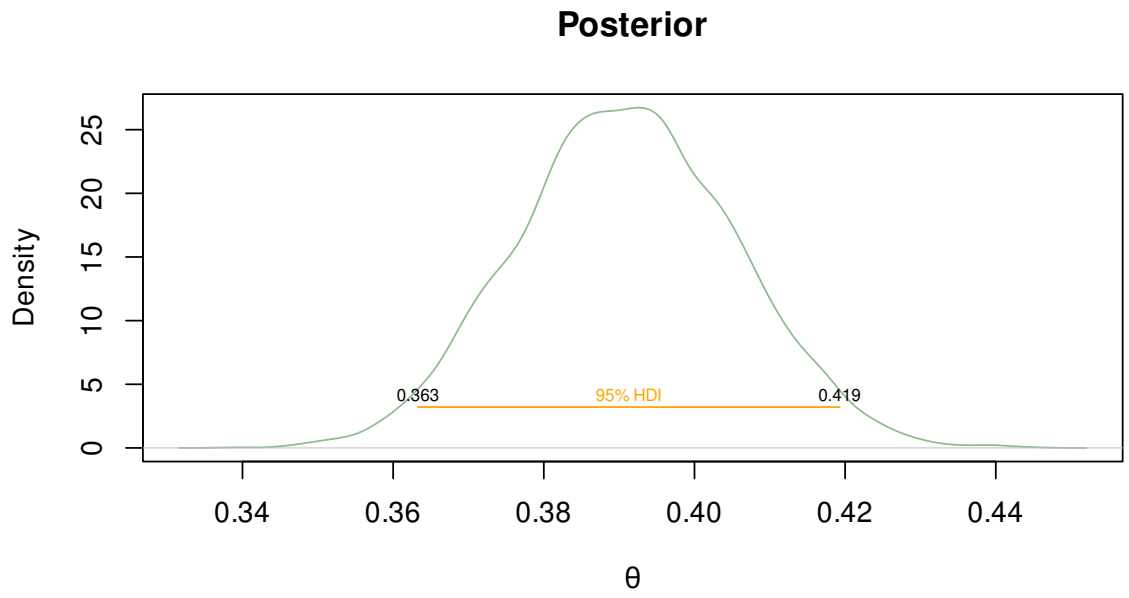
```
## recompiling to avoid crashing R session
```



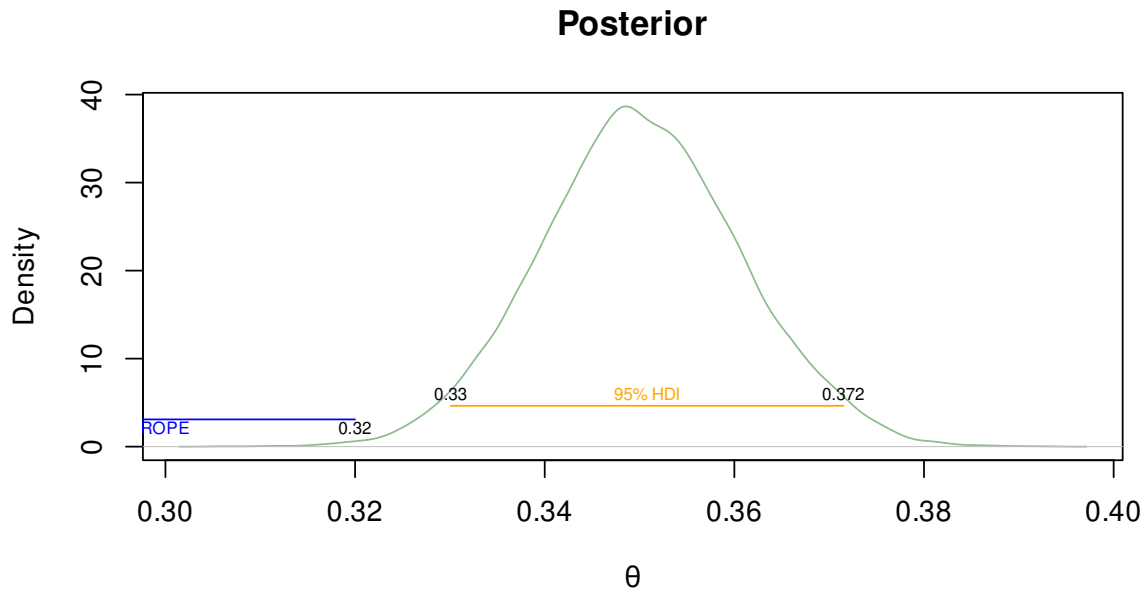
We reach the same conclusion with $\kappa = 10$.



We reach the same conclusion with $\kappa = 100$.

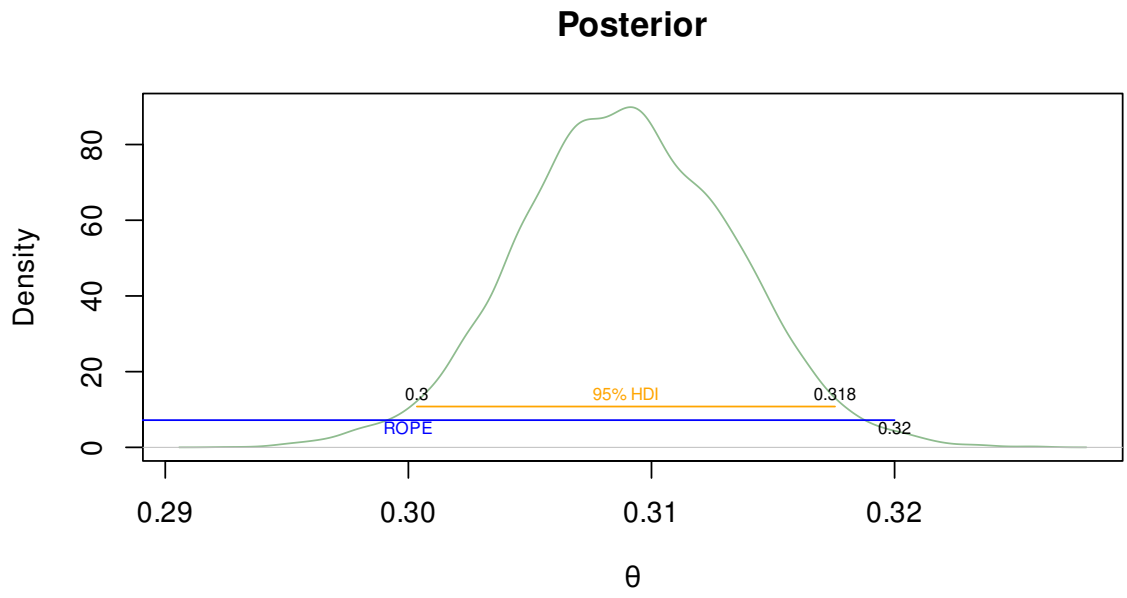


We come to the same conclusion with $\kappa = 1000$



For $\kappa = 10000$ it looks different again. It does not have enough data to dissuade us from our 0.3 conviction, the ROPE fully contains the HDI. That is, the new drug is not better than the standard method, but equivalent to it. We accept the zero value 0.3 in this case.

```
## recompiling to avoid crashing R session
```



Solution 13.3

To solve the problem with Bayesian inference, we need a prior distribution. We choose the beta distribution as prior distribution, where we have to define the two parameter values a and b. In the prior distribution expresses our prior knowledge or our estimates of the efficacy of the drug.

We may well assume that the efficacy of the new drug is probably in the range of the standard method, i.e. by 15 %. To do this, we need to know or estimate how certain our assumption of 15 % is. This information is not included in the task, so we have to make appropriate assumptions here. To do this, we consider the value $\kappa = a + b$: If κ is large, then our certainty is large that the value of 15 % is correct. The beta distribution function then becomes very narrow. If our uncertainty is large, we choose a small value of κ so that the beta distribution function becomes broad.

We specify κ and the mode ω and, based on these two specifications, calculate the parameters a and b for the beta distribution as follows (see script):

$$a = \omega(\kappa - 2) + 1$$

and

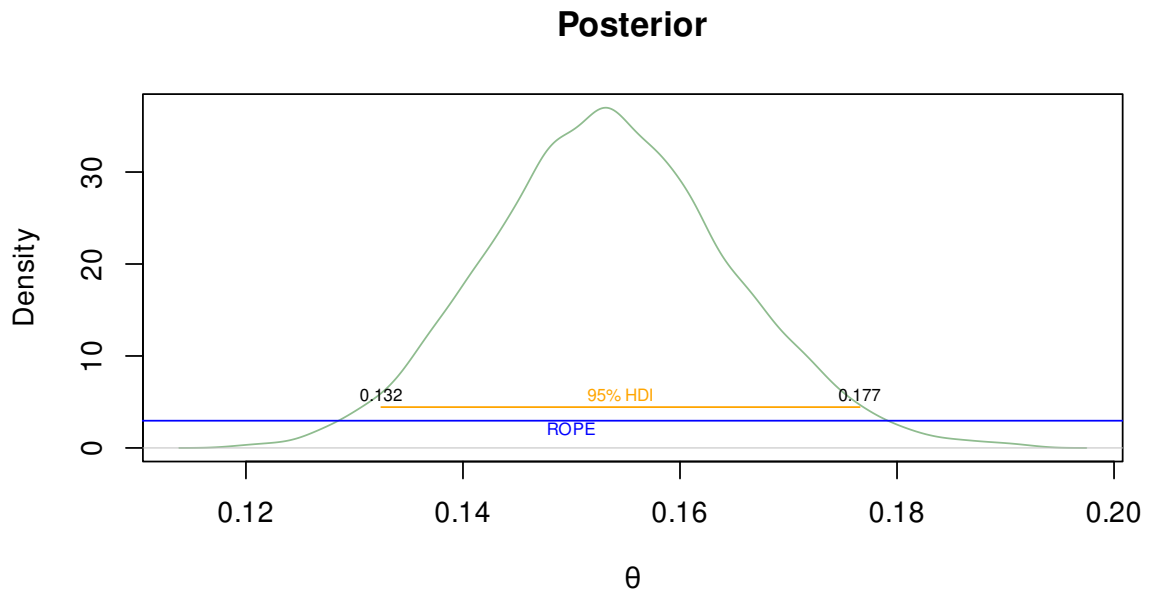
$$b = (1 - \omega)(\kappa - 2) + 1$$

The mode of the prior distribution ω is consequently chosen as 0.15. Now for the choice of κ, which is much more difficult. If we are pretty sure that the standard method is already very good and difficult to improve, we are pretty sure that the efficacy of the new drug should also be around 15 %. We choose in this case $\kappa = 1000$. This gives $a = 150.7$ and $b = 849.3$.

The ROPE indicates which values are equivalent to the zero value 0.15. This information must be provided by experts. We choose the ROPE as 0.15 ± 0.06.

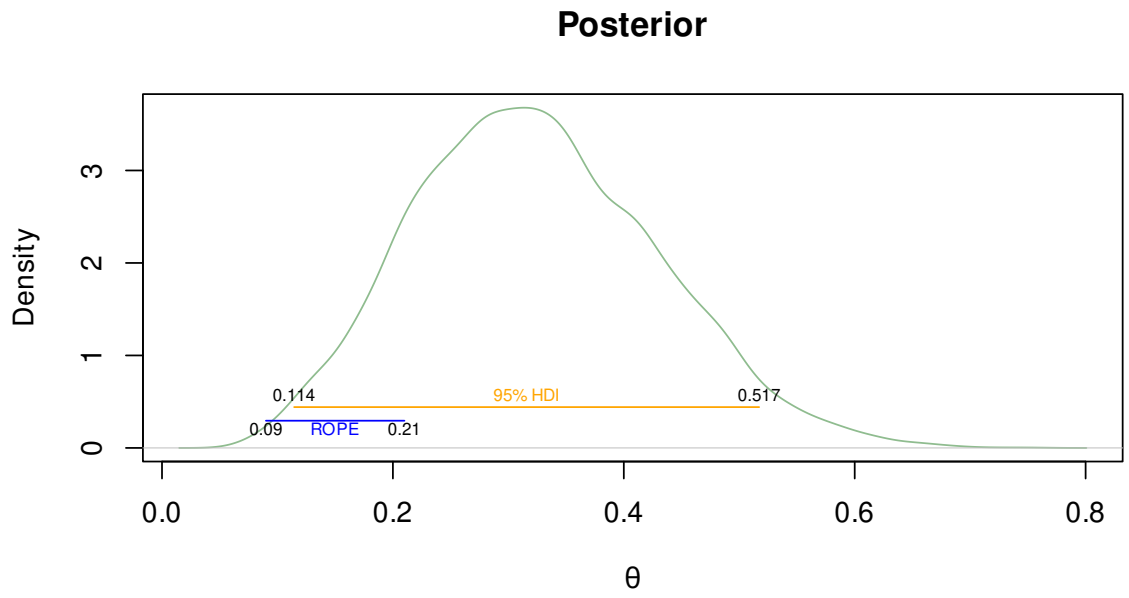
We have 16 trials and 5 successes. Consequently, the **rstan** input looks like this:

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
real<lower=0, upper=1> theta ;
}
model {
theta ~ beta(150.7, 849.3) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 16
z = 5
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model, data=list(y = y, N = N), iter=2000, warmup=200, refre

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.09,.21))
```



Since we have very little data, it does not have much impact on the prior distribution. The mode has not shifted. The 95 %-HDI is fully contained in the ROPE, i.e. all of the 95 % most likely values are within the ROPE. In this case, we accept the zero value and conclude that the new treatment type is equivalent to the standard method.

Let us now try a small κ, say $\kappa = 3$, i.e. $b = 1.85$ and $a = 1.15$, and increase the number of trials: 160 trials and 50 successes. In this case, we are very unsure whether the 15 % are correct. Perhaps because the studies on the standard method are unreliable/dubious. In addition, we now have much more data.



The mode has shifted from 0.15 to 0.31. The ROPE intersects with the 95 % HDI. In this case, based on the data, we cannot decide whether we accept the zero value or not.

Solution 13.4

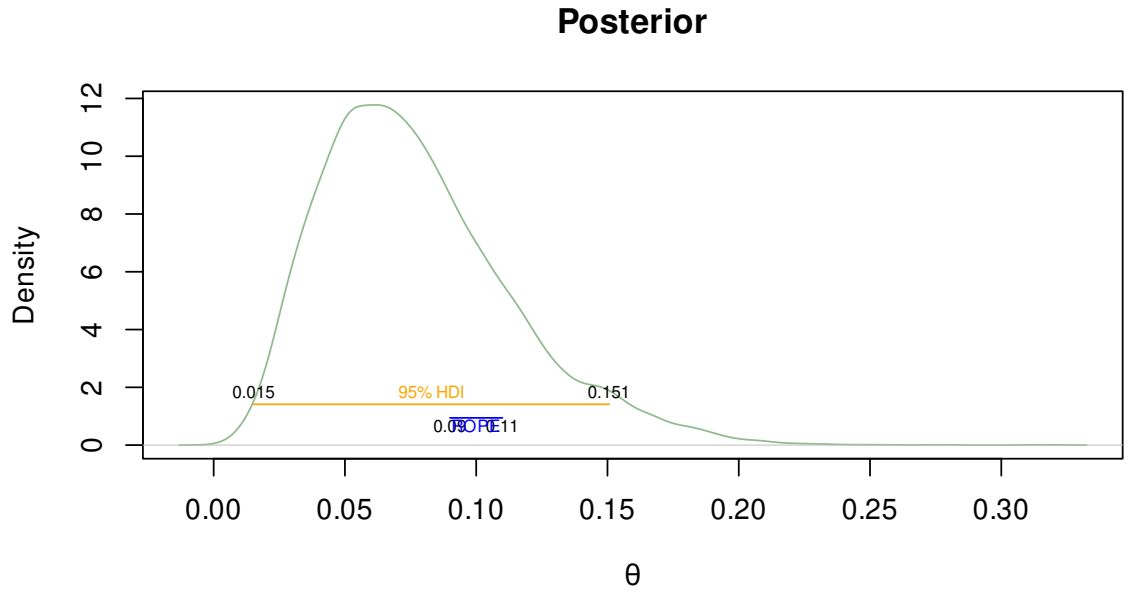
To solve the problem with Bayesian inference, we need a prior distribution. We choose the beta distribution as prior distribution, where we have to define the two parameter values a and b. In the prior distribution expresses our prior knowledge or our estimates of the efficacy of the drug. In this task, we assume complete ignorance of the proportion of inferior bolts. We consequently choose the Uniform Distribution, i.e. $a = 1$ and $b = 1$.

The ROPE indicates which values are equivalent to the zero value 0.1. This information must be provided by material testing experts. We choose the ROPE from 0.09 to 0.11. If the percentage of substandard bolts falls within this range, then we consider the quality standards not met.

We have 50 samples and 3 substandard bolts. Consequently, the **rstan** output looks like this:

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
```

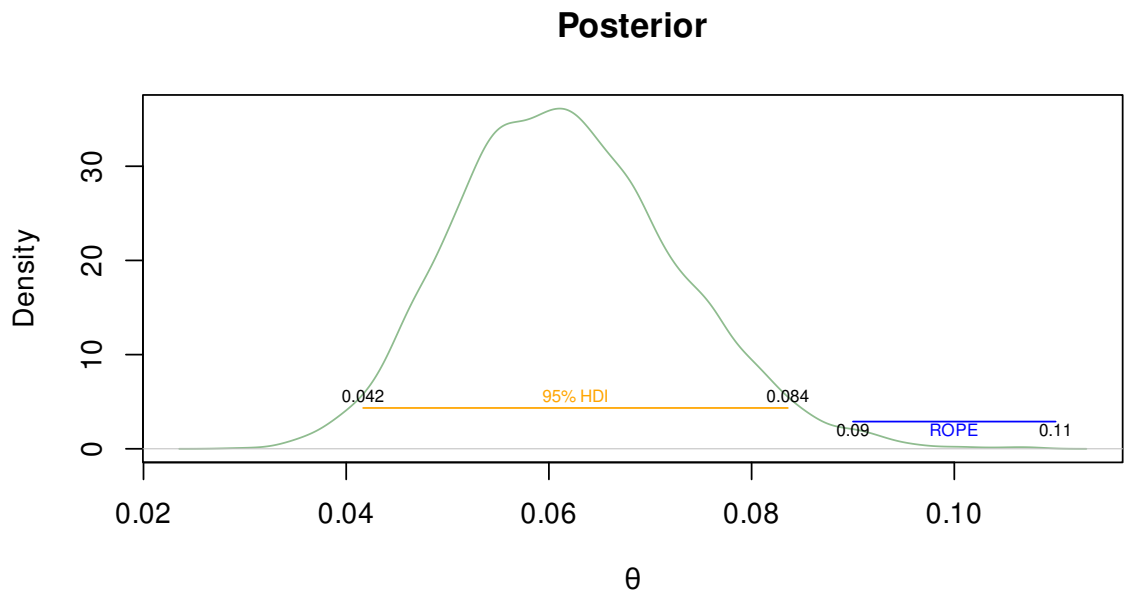
```
real<lower=0,upper=1> theta ;
}
model {
theta ~ beta(1,1) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 50
z = 3
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model , data=list( y = y , N = N ), iter=2000, warmup=200, r

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.09,.11))
```



Since we have chosen a uniform distribution for the prior distribution, the data has a very large influence on the posterior distribution. The mode of the posterior distribution is now at the percentage of inferior bolts in the sample. The ROPE overlaps with the 95 %-HDI, i.e. some of the 95 % most likely values lie outside the ROPE. In this case, we refuse to decide whether the bolts meet the quality standards.

Suppose we drew a sample of 500 screws and 30 inferior screws.

```
modelString = "
data{
int<lower=0> N ;
int y[N] ; // y is a length-N vector of integers
}
parameters {
real<lower=0,upper=1> theta ;
}
model {
theta ~ beta(1,1) ;
y ~ bernoulli(theta) ;
}
" # close quote for modelString

model <- stan_model(model_code=modelString)

N = 500
z = 30
y = c(rep(1,z),rep(0,N-z))

stanFit = sampling( object=model , data=list( y = y , N = N ), iter=2000 , warmup=200,

params = rstan::extract(stanFit)

plot_posterior(params, Rope=c(.09,.11))
```



The ROPE and the HDI are separate in this case. We discard the zero value 0.1 here and conclude that the screws meet the quality standards.