Summarizing the Posterior

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Summarizing the Posterior

- Once our Bayesian model produces a posterior distribution, it is necessary to summarize and interpret it.
- However, a posterior distribution is (usually) a high dimensional object that is hard to visualize and work with [Murphy, 2021].
- In this class we will learn how to draw estimates (e.g., point estimates, intervals) to summarize and interpret a posterior distribution.
- Exactly how it is summarized depends upon our purpose.
- Common questions include:
  - How much posterior probability lies below some parameter value?
  - How much posterior probability lies between two parameter values?
  - Which parameter value marks the lower 5% of the posterior probability?
  - Which range of parameter values contains 90% of the posterior probability?
  - Which parameter value has highest posterior probability?

Sampling to summarize

- These questions can be usefully divided into questions about:
  - intervals of defined boundaries
  - intervals of defined probability mass
  - point estimates
- In the theoretical world (when the posterior has a closed mathematical expressions), answering these questions implies calculating complicated integrals to cancel out (or average) different variables.
- In the practical world, however, the same results can be approximated using **samples** from the posterior.
- In this class we will approach the above questions using samples from the posterior.
- Another reason to learn to work with posterior samples is that methods like MCMC produce nothing but samples from the posterior.
- This class is based on Chapter 3 of [McElreath, 2020].

Sampling from a grid-approximate posterior

- Before beginning to work with samples, we need to generate them.
- Here's a reminder for how to compute the posterior for the globe tossing model, using grid approximation:

```
p_grid <- seq( from=0 , to=1 , length.out=1000 )
prior <- rep( 1 , 1000 )
likelihood <- dbinom( 6 , size=9 , prob=p_grid )
posterior <- likelihood * prior
posterior <- posterior / sum(posterior)
```

- Now we wish to draw 10,000 samples from this posterior.
- Imagine the posterior is a bucket full of parameter values, numbers such as 0.1, 0.7, 0.5, 1, etc.
- Within the bucket, each value exists in proportion to its posterior probability, such that values near the peak are much more common than those in the tails.

Sampling from a grid-approximate posterior

- We're going to scoop out 10,000 values from the bucket.
- Provided the bucket is well mixed, the resulting samples will have the same proportions as the exact posterior density.
- Therefore the individual values of p will appear in our samples in proportion to the posterior plausibility of each value.
- Here's how you can do this in R, with one line of code:

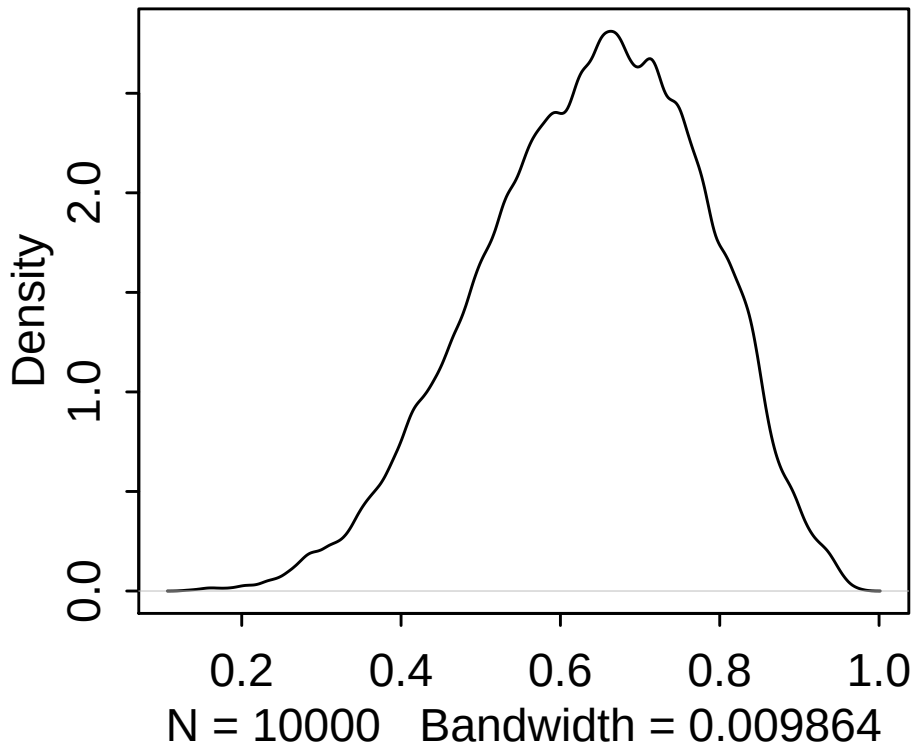
```
samples <- sample( p_grid , prob=posterior , size=1e4 ,
replace=TRUE )
```

- We are randomly pulling values from the grid of parameter values where the probability of each value is given by the posterior.

Sampling from a grid-approximate posterior

- We can visualize a density plot of our posterior sample as follows:

```
library(rethinking)
dens(samples)
```



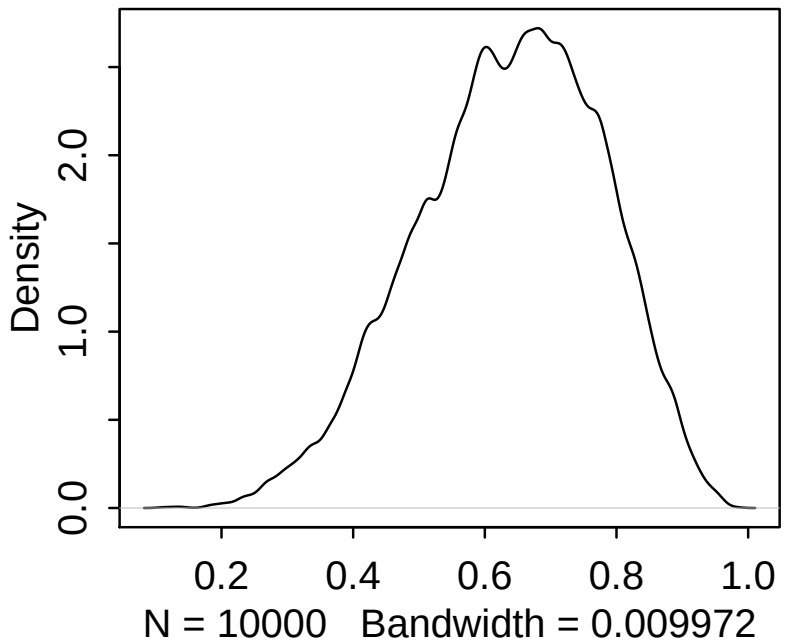
- We can see that the estimated density is very similar to to ideal posterior we computed via grid approximation in previous class.

Sampling from the theoretical posterior

- We could get the same results by sampling from the theoretical posterior using the beta distribution:

```
teo.samples<-rbeta(1e4,7,4)
dens(teo.samples)
```

- We can see that the estimated density is very similar to the theoretical posterior obtained from the beta distribution:



- However, we should keep in mind that for complex models we will not have access to the posterior closed form, so it is better to get used to working with samples.

Intervals of defined boundaries

- Suppose I ask you for the posterior probability that the proportion of water is less than 0.5.
- We could calculate this from the theoretical posterior:

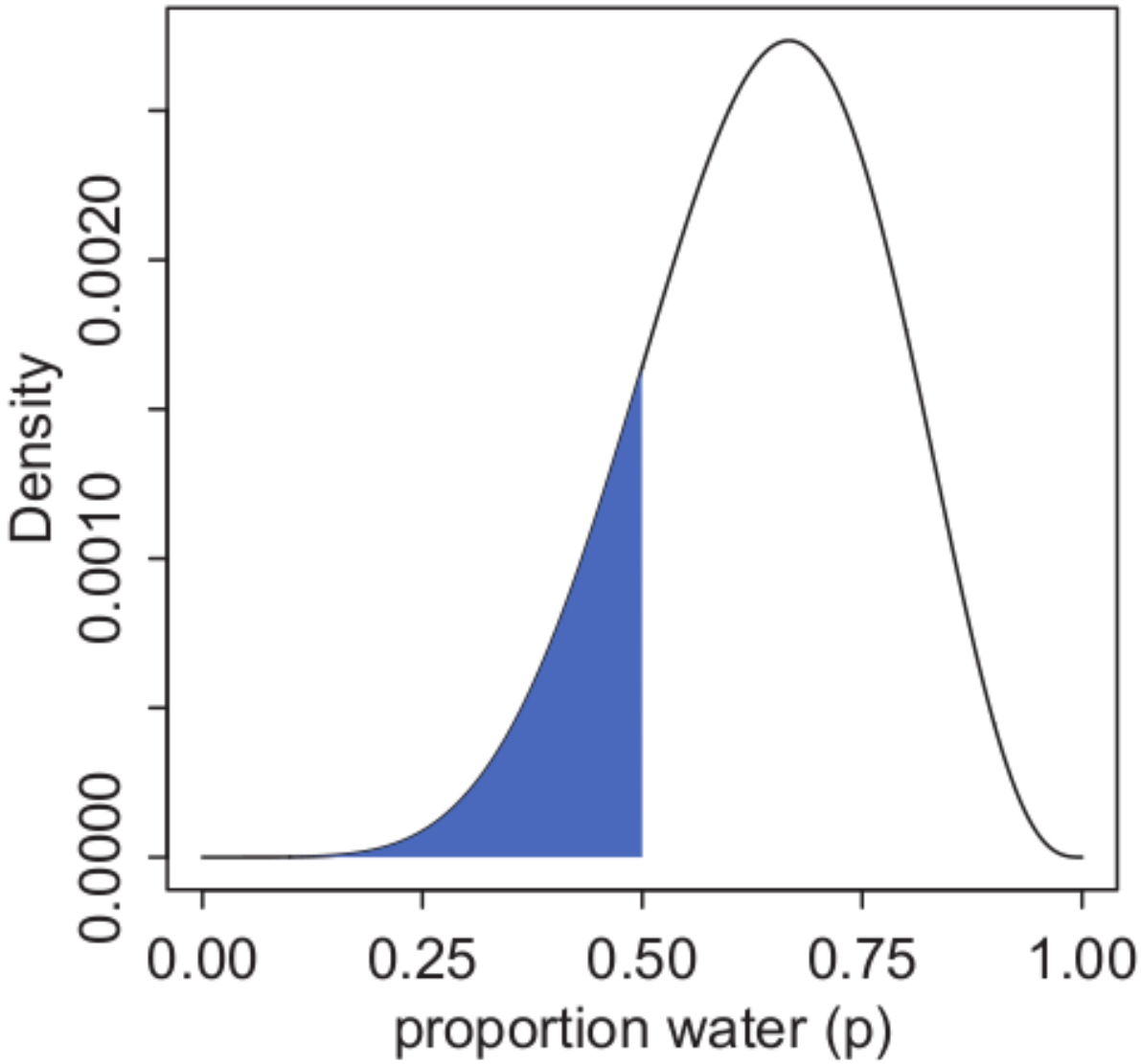
```
> pbeta(0.5,7,4)
[1] 0.171875
```

- Or alternatively we could calculate it from the grid-approximate posterior by adding up all of the probabilities where the corresponding parameter value is less than 0.5.

```
> sum( posterior[ p_grid < 0.5 ] )
[1] 0.1718746
```

- So about 17% of the posterior probability is below 0.5.

Intervals of defined boundaries



Intervals of defined boundaries

- Now, let's perform the same calculation, using samples from the posterior.
- Recall than in more complex models neither a grid-approximation nor a closed-form posterior will be available.
- All we have to do is add up all samples less than 0.5 and divide the resulting count by the total number of samples.

```
> sum( samples < 0.5 ) / 1e4
[1] 0.1752
```

- In R, the condition `samples < 0.5` returns a logical vector, so since R treats TRUE values as 1, `sum` will count all the samples satisfying the condition.

Intervals of defined boundaries

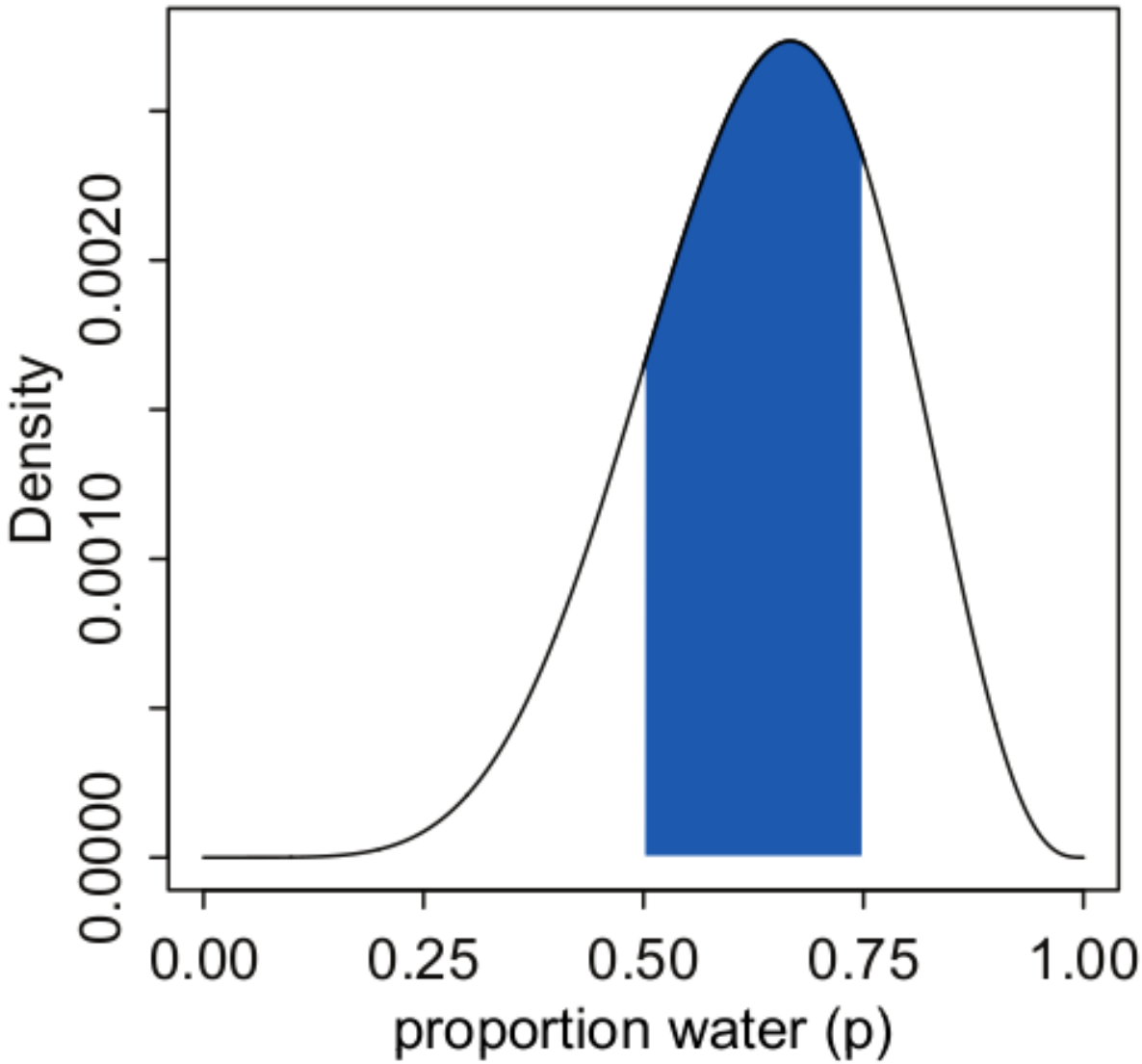
- Now, we can ask our sample how much posterior probability lies between 0.5 and 0.75.

```
> sum( samples > 0.5 & samples < 0.75 ) / 1e4
[1] 0.6043
```

- So about 61% of the posterior probability lies between 0.5 and 0.75.
- Let's validate this result using the exact posterior:

```
> pbeta(0.75,7,4)-pbeta(0.5,7,4)
[1] 0.6040001
```

Intervals of defined boundaries



Intervals of defined probability

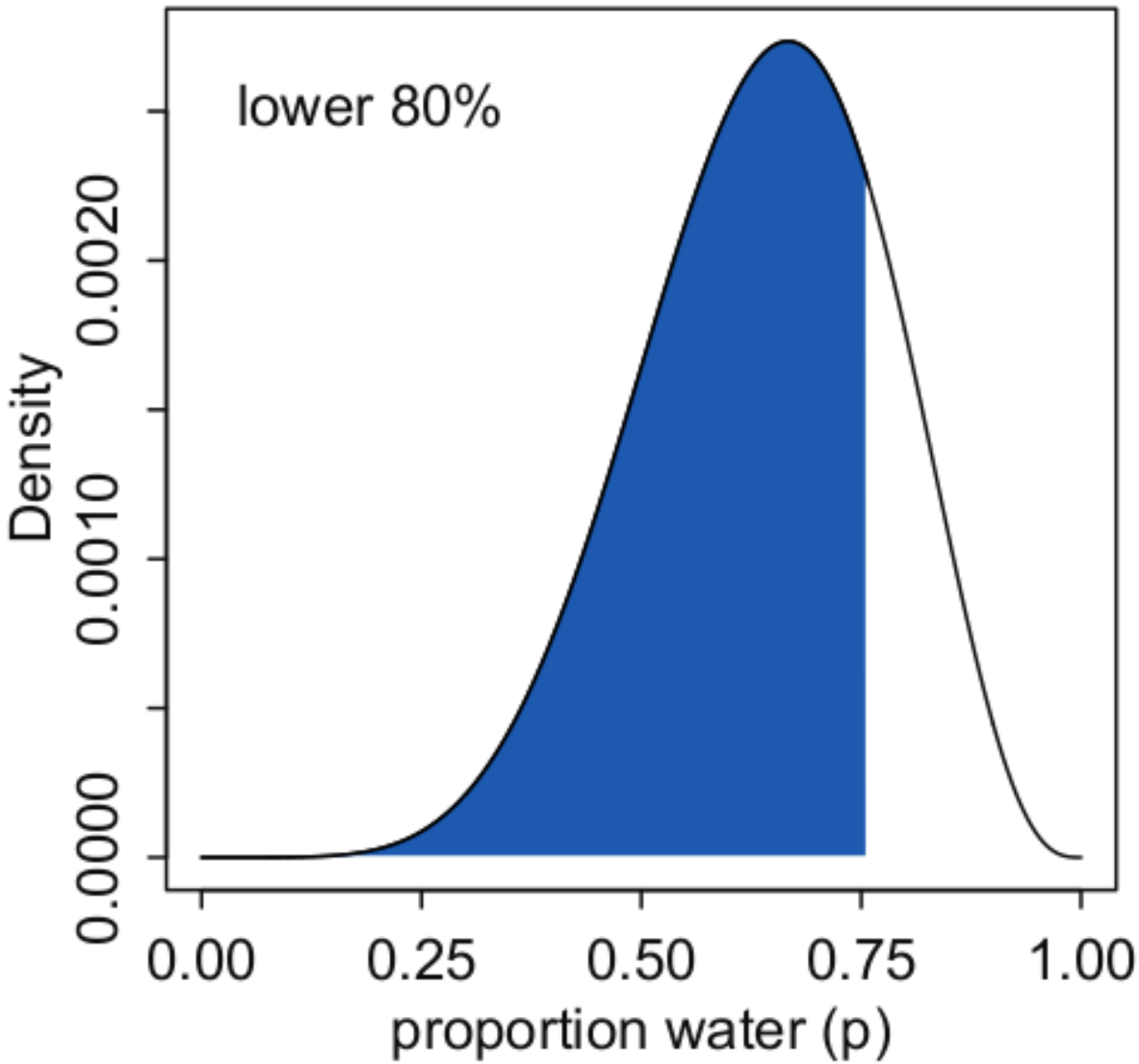
- Suppose we want to know the boundaries of the lower 80% posterior probability.
- We can answer this by obtaining the 80-th percentile of the posterior sample:

```
> quantile( samples , 0.8 )
      80%
0.7577578
```

- Or alternatively, using the quantile function of the beta distribution (the distribution of the exact posterior):

```
> qbeta(0.8,7,4 )
[1] 0.7605588
```

Intervals of defined boundaries



Intervals of defined probability

- Similarly, we can calculate the middle 80% interval that lies between the 10th percentile and the 90th percentile.

```
> quantile( samples , c( 0.1 , 0.9 ) )
      10%       90%
0.4504505 0.8148148
```

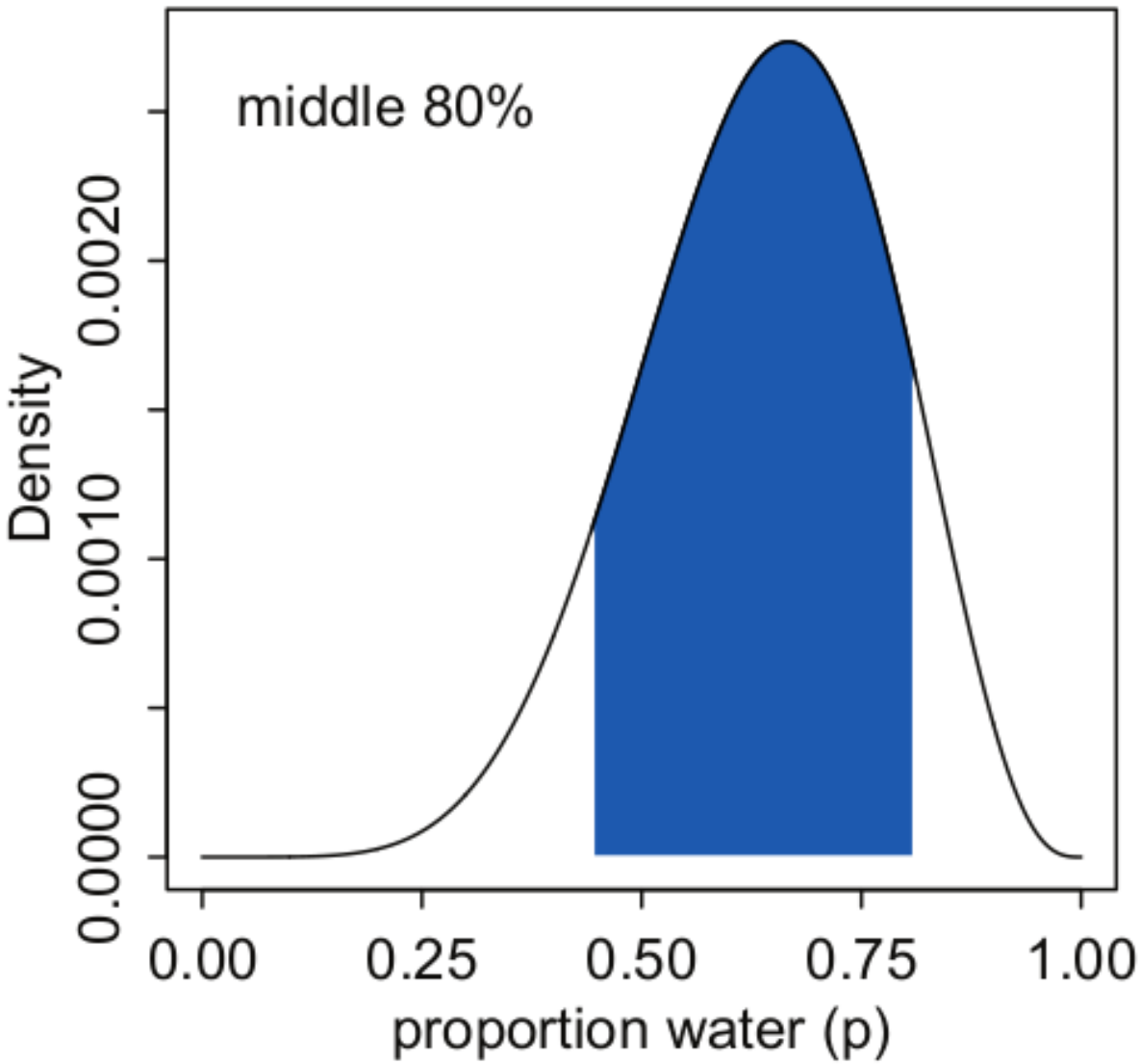
- The "rethinking" package provides the function `PI` (from percentile interval) to calculate this type of interval:

```
> PI( samples , prob=0.8 )
      10%       90%
0.4504505 0.8148148
```

- Notice that we are assigning $(1 - 0.8)/2 = 0.1$ of probability above and below the interval.
- We can also obtain the exact interval from the exact posterior:

```
> c("10%"=qbeta(0.1,7,4 ),"90%"=qbeta(0.9,7,4 ))
      10%       90%
0.4482692 0.8124377
```

Intervals of defined boundaries



Credible Intervals

- The intervals of posterior probability that assign equal probability to each tail are called **credible interval**.
- These posterior intervals report two parameter values that contain between them a specified amount of posterior probability.
- What the interval indicates is a range of parameter values compatible with the model and data.
- Credible intervals resemble very much the confidence intervals seen in previous lectures on frequentist inference.
- The interpretations are very different though.
- A confidence interval is a region[1] that after infinitely repeating the data sampling experiment will contain the true parameter with a certain chance.
- In contrast, a credible interval is a range of values that we believe our parameter can take with a certain probability according to both our prior beliefs and the evidence given by the data.

[1] Notice that the region will vary from one experiment to another.

Credible Intervals

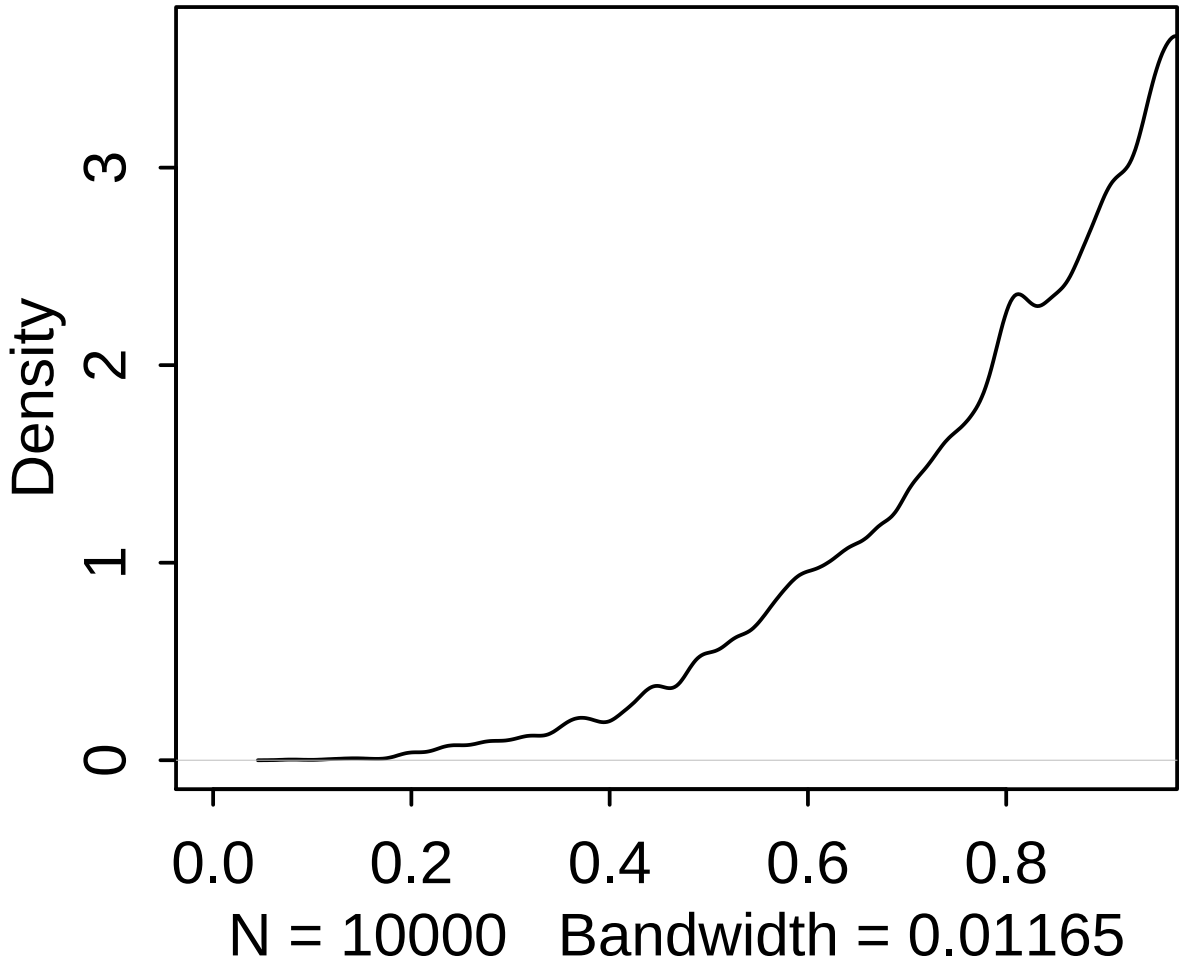
- Equal-tailed credible intervals do a good job of communicating the shape of a distribution, as long as the distribution isn't too asymmetrical.
- Suppose that in our globe tossing experiment we had observed 3 W and 0 L.
- If we again consider a flat prior, we will get a highly skewed posterior distribution with its maximum value at the boundary, $p = 1$.

```
p_grid.a <- seq( from=0 , to=1 , length.out=1000 )
prior.a <- rep(1,1000)
likelihood.a <- dbinom( 3 , size=3 , prob=p_grid.a )
posterior.a <- likelihood.a * prior.a
posterior.a <- posterior.a / sum(posterior.a)
samples.a <- sample( p_grid.a , size=1e4 ,
replace=TRUE , prob=posterior.a )
dens(samples.a,xlim=c(0,0.935))
```

- Alternatively we could sample from the exact posterior $Beta(\alpha + W, \beta + L)$ = $Beta(1 + 3, 1 + 0)$ = $Beta(4, 1)$:

```
teo.samples.a<-rbeta(1e4,4,1)
dens(teo.samples.a,xlim=c(0,0.935))
```

Credible Intervals



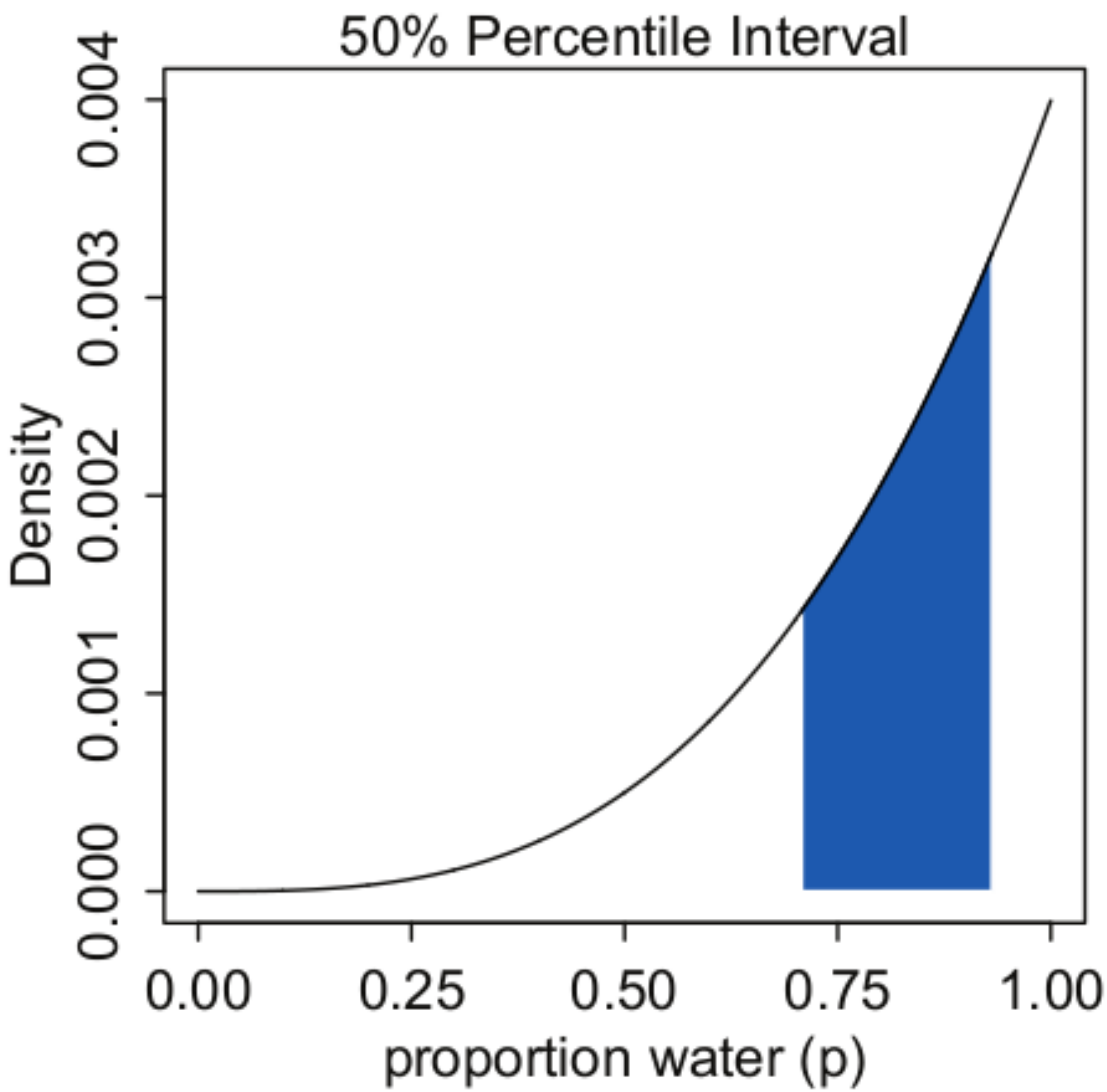
Credible Intervals

- Let's compute a 50% equal-tailed credible interval for this posterior:

```
> PI( samples.a , prob=0.5 )
      25%       75%
0.7037037 0.9309309
```

- This interval assigns 25% of the probability area above and below the interval.
- So it provides the central 50% probability.
- But in this example, it ends up excluding the most probable parameter values, near $p = 1$.
- So, in terms of describing the shape of the posterior distribution it can be misleading.

Credible Intervals



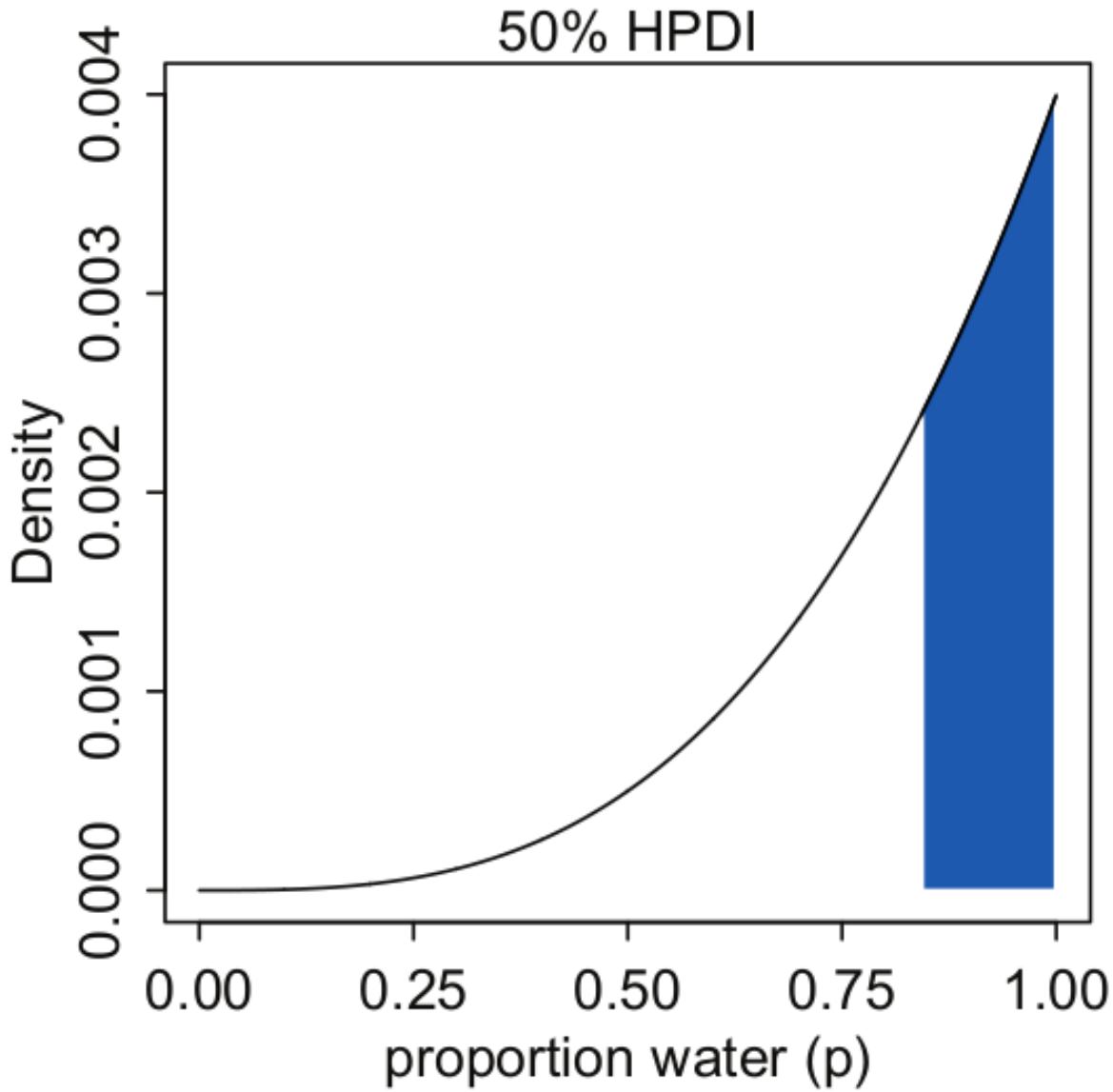
Highest Posterior Density Intervals

- An alternative type of credible interval is the Highest Posterior Density Interval (HPDI).
- If we relax the restriction of assigning equal probability to each tail, we obtain an infinite number of intervals containing the specified probability area.
- The HPDI is the narrowest of those possible interval.
- It can be calculated from posterior samples using the HPDI function from the rethinking package.

```
> HPDI( samples.a , prob=0.5 )
     |0.5      0.5|
0.8368368 1.0000000
```

- This interval captures the parameters with highest posterior probability, as well as being noticeably narrower: 0.16 in width rather than 0.23 for the equal-tailed credible interval.

Highest Posterior Density Intervals



Highest Posterior Density Intervals

- A disadvantage of the HPDI, is that it is more computationally intensive than the equal-tailed credible interval.
- Apart from the cases when the posterior distribution is highly skewed, these two types of intervals are similar.
- For example, let's calculate an 80% HPDI for the the original posterior with 6 W and 3 L:

```
> HPDI( samples , prob=0.8 )
     |0.8       0.8|
0.4694695 0.8298298
```

- This interval is very similar to the equal-tailed credible interval calculated before.

Point estimates

- The idea of point estimation in a Bayesian setting is to summarize the posterior with a single value.
- The three most common options here:
  - The mode, which is the value with highest posterior probability, also known as the maximum a posteriori (MAP) estimate.
  - The mean
  - The median
- Let's calculate them for the globe tossing experiment in which we observe 3 waters out of 3 tosses.

Point estimates

- We can compute the MAP from the grid approximation of the posterior as follows:

```
 > p_grid[ which.max(posterior.a) ]
[1] 1
```

- Or we can approximate it using posterior samples:

```
> dd <- density(samples.a,adj=0.01)
> dd$x[which.max(dd$y)]
[1] 0.9971593
```

- The same procedure can be done more easily using the chainmode function from the rethinking package:

```
> chainmode( samples.a , adj=0.01 )
[1] 0.9971593
```

Point estimates

- Now the posterior mean:

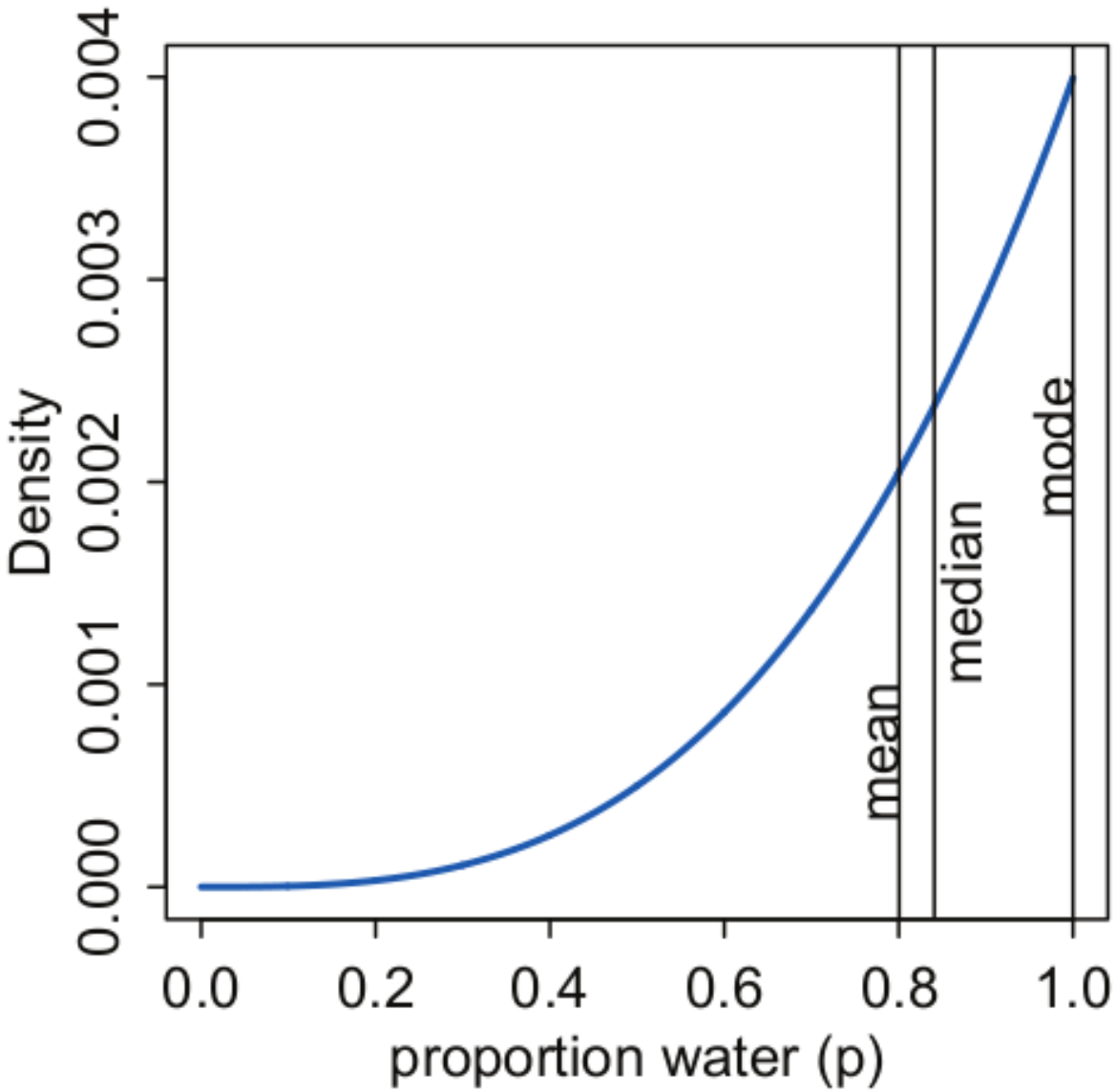
```
> mean(samples.a)
[1] 0.7988011
```

- and the median:

```
> median(samples.a)
[1] 0.8408408
```

- The same procedure can be done more easily using the chainmode function from the rethinking package:
- Which of these values should we report?
- Recall that our ultimate goal is to report the shape of the posterior
- Hence, it is better to communicate as much as we can about it.
- For example: density plots, HPDI, MAP estimates, mean, mode, etc..

Point Estimates



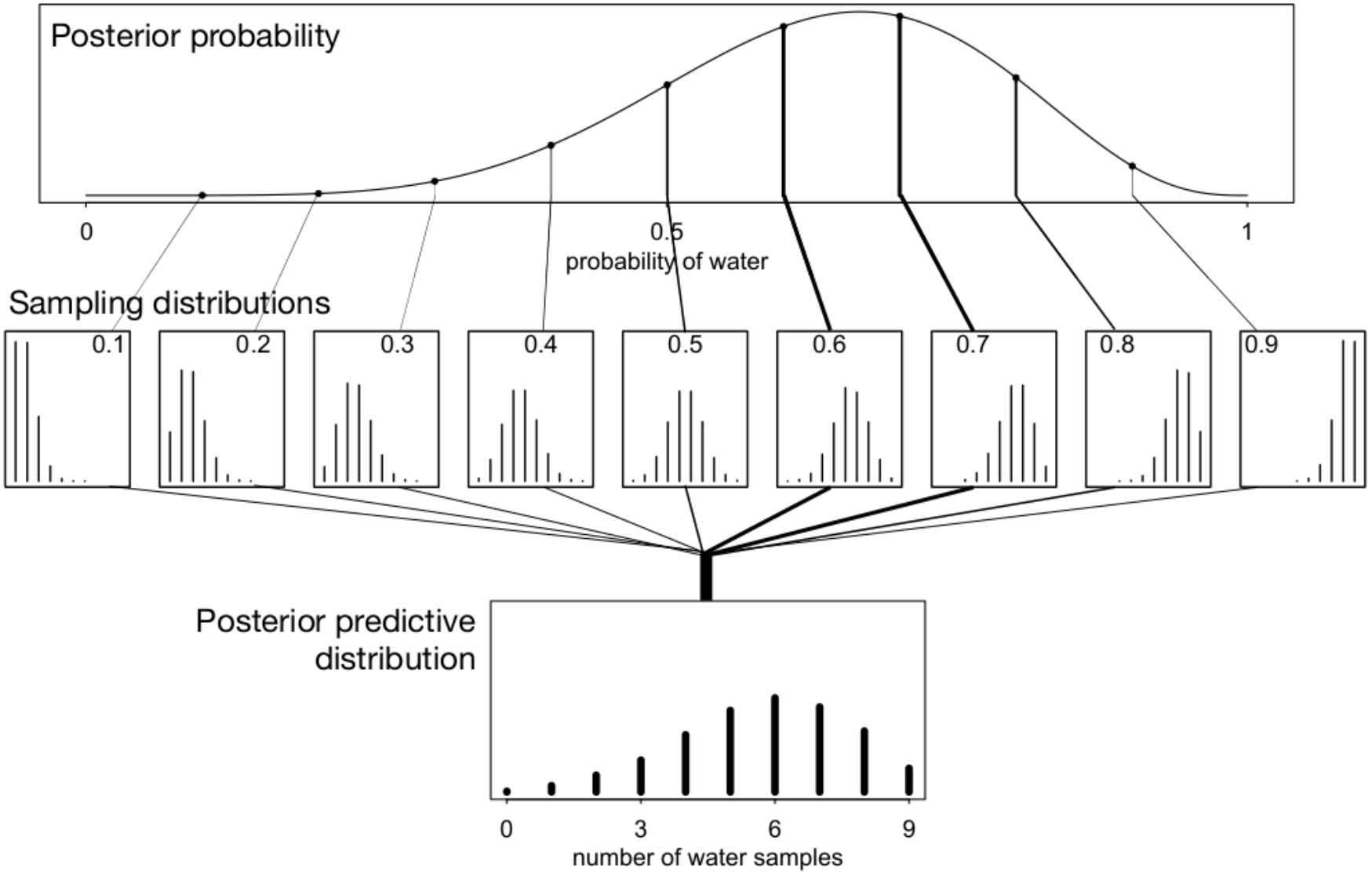
Sampling to Simulate Prediction

- We expect to do better when we use the entire posterior distribution, not just some point estimate derived from it.
- Why? Because there is a lot of information about uncertainty in the entire posterior distribution.
- We lose this information when we pluck out a single parameter value and then perform calculations with it.
- This loss of information leads to overconfidence.

Sampling to Simulate Prediction

$$\begin{aligned} f(\tilde{d}|d) &= \int_\theta f(\tilde{d}, \theta|d) d\theta \\ &= x \end{aligned}$$

Posterior Predictive Distribution



Conclusions

- Blablaag

References I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