

Chapter 3 – Sampling The Imaginary

3.1 Sampling from a grid-approximate posterior

- R Code 3.2:

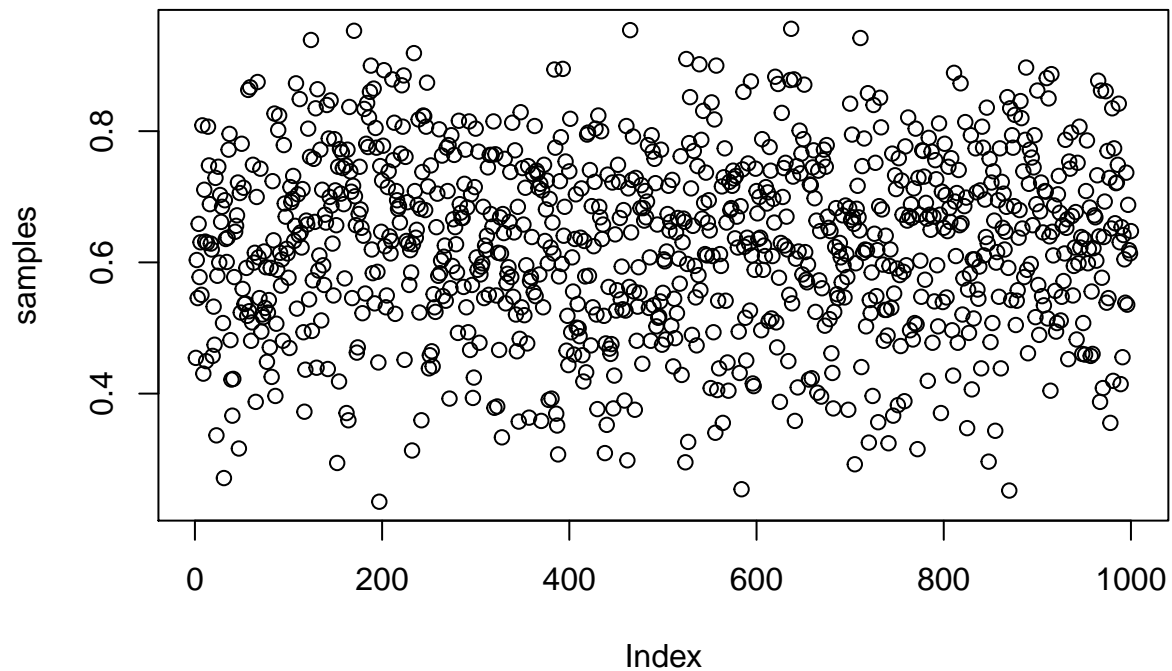
```
n = 1000
p_grid <- seq(from=0, to=1, length.out=n)
prior <- rep(1, n)
likelihood <- dbinom(x=6, size=9, prob=p_grid)
posterior_notnorm <- likelihood * prior
posterior <- posterior_notnorm / sum(posterior_notnorm)
```

Draw 10,000 samples: * R Code 3.3:

```
samples_orig <- sample(p_grid, prob=posterior, size=n, replace=T)
samples = samples_orig
```

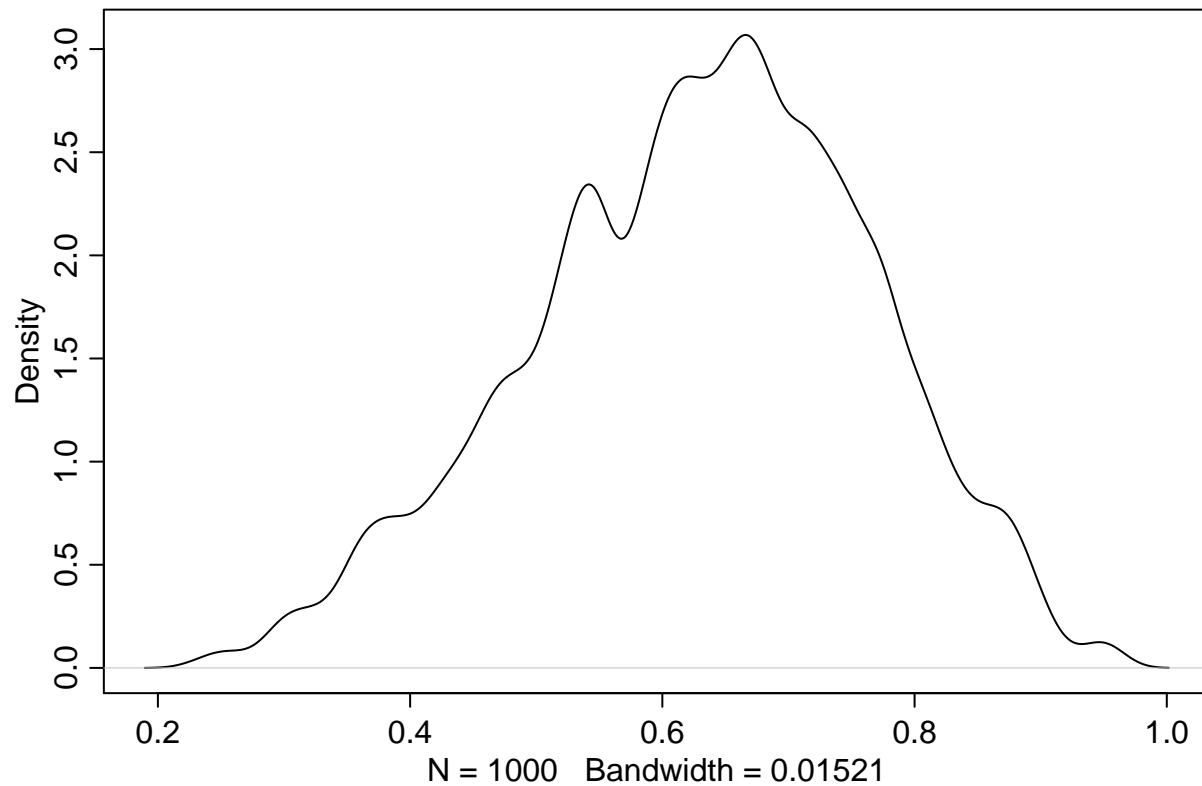
- 3.4:

```
plot(samples)
```



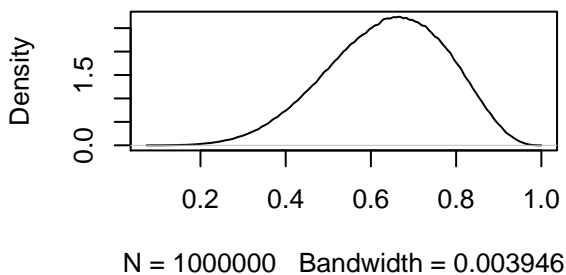
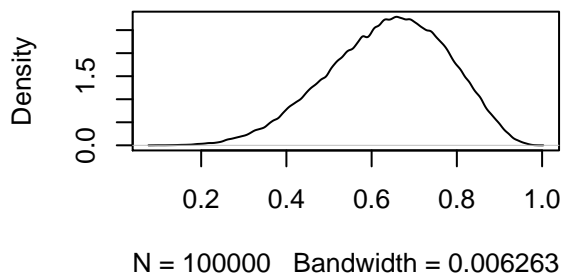
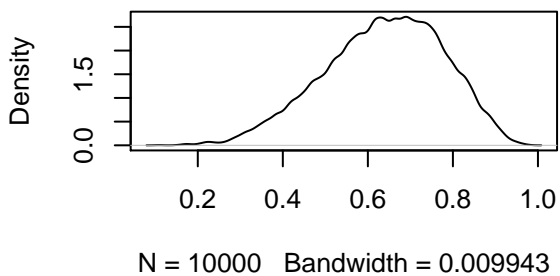
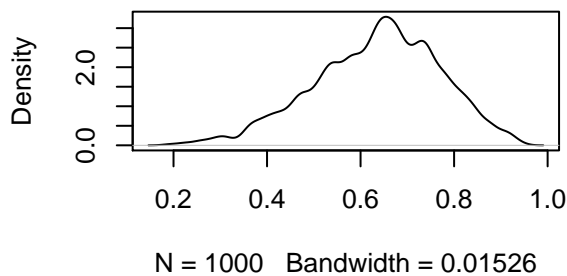
- 3.5:

```
dens(samples)
```



Let's try more samples:

```
par(mfrow=c(2, 2))
dens(sample(p_grid, prob=posterior, size=1e3, replace=T))
dens(sample(p_grid, prob=posterior, size=1e4, replace=T))
dens(sample(p_grid, prob=posterior, size=1e5, replace=T))
dens(sample(p_grid, prob=posterior, size=1e6, replace=T))
```



3.2 Sampling to Summarize

3.2.1. Intervals of defined boundaries.

The posterior probability that the proportion of water is less than 0.5:

- 3.6:

```
p_grid < 0.5
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [12] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [23] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [34] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [45] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [56] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [67] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [78] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [89] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [100] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [111] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [122] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [133] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [144] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [155] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
## [166] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

[illegible]

```
## [771] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [782] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [793] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [804] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [815] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [826] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [837] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [848] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [859] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [870] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [881] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [892] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [903] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [914] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [925] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [936] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [947] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [958] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [969] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [980] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [991] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

```
sum(posterior[p_grid < 0.5])
```

```
## [1] 0.1718746
```

Samples array:

```
head(samples, 100)
```

```
## [1] 0.4544545 0.6036036 0.5455455 0.6586587 0.5775776 0.6306306 0.5505506
## [8] 0.8088088 0.4304304 0.7107107 0.6316316 0.4494494 0.6296296 0.8068068
## [15] 0.7477477 0.6886887 0.6286286 0.6196196 0.4574575 0.5325325 0.4744745
## [22] 0.7287287 0.3363363 0.5795796 0.7457457 0.5995996 0.7027027 0.6616617
## [29] 0.6846847 0.5075075 0.2712713 0.6946947 0.6356356 0.6006006 0.6376376
## [36] 0.7717718 0.7957958 0.4814815 0.4214214 0.3663664 0.4224224 0.5775776
## [43] 0.6466466 0.6556557 0.6716717 0.7217217 0.3163163 0.7057057 0.5235235
## [50] 0.7807808 0.5595596 0.7137137 0.5365365 0.5375375 0.5915916 0.5185185
## [57] 0.8628629 0.5255255 0.8668669 0.4804805 0.5085085 0.7487487 0.5995996
## [64] 0.6146146 0.3873874 0.6996997 0.8748749 0.6076076 0.5455455 0.7427427
## [71] 0.4944945 0.5205205 0.5165165 0.6166166 0.5305305 0.5925926 0.4484484
## [78] 0.5235235 0.5425425 0.4704705 0.5915916 0.4254254 0.7237237 0.6336336
## [85] 0.8268268 0.3963964 0.5065065 0.5885886 0.8018018 0.8238238 0.6146146
## [92] 0.5645646 0.6046046 0.4804805 0.7787788 0.6896897 0.6696697 0.6206206
## [99] 0.6136136 0.5765766
```

The same calculation using samples. Add up all samples that lie in the grid < 0.5 , and divide by the total number of samples to get the frequency \sim probability:

- 3.7:

```
n = 1e4
samples = sample(p_grid, prob=posterior, size=n, replace=T)
sum(samples < 0.5) / n
```

```
## [1] 0.1705
```

How much probability lies between 0.5 and 0.75: * 3.8:

```
sample_points = sum(samples > 0.5 & samples < 0.75)
sample_points
```

```
## [1] 6044
```

```
sample_points / n
```

```
## [1] 0.6044
```

3.2.2. Intervals of defined mass.

Boundaries of the lower 80% posterior probability lies:

- 3.9:

```
quantile(samples, probs = .8)
```

```
##          80%
```

```
## 0.7607608
```

Middle 80%, i.e. lying between 10% and 90%:

```
# 3.10
```

```
quantile(samples, probs = c(0.1, 0.9))
```

```
##          10%          90%
```

```
## 0.4484484 0.8128128
```

The above are PERCENTILE INTERVALS. Percentiles can be misleading if the distribution is highly skewed.

```
# 3.11
```

```
n <- 10000
```

```
p_grid <- seq(0, 1, length.out = n)
```

```
prior <- rep(1, n)
```

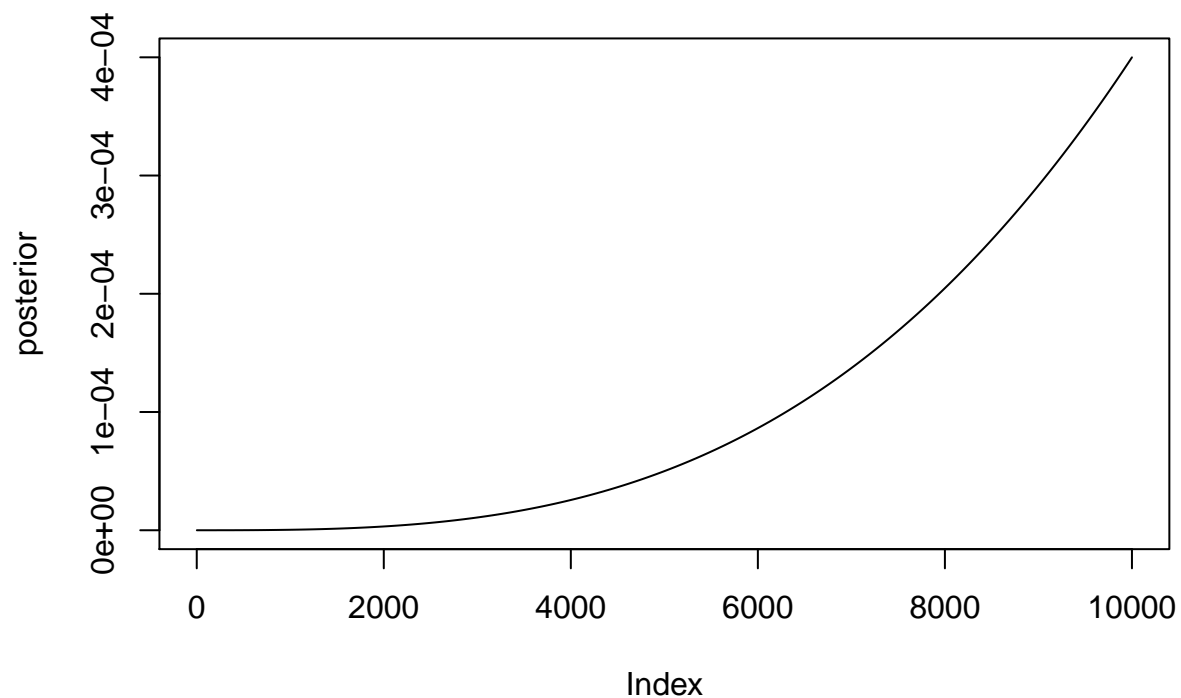
```
likelihood <- dbinom(3, size=3, prob=p_grid)
```

```
posterior_notnorm <- likelihood * prior
```

```
posterior <- posterior_notnorm / sum(posterior_notnorm)
```

```
samples <- sample(p_grid, size=1e5, replace=T, prob=posterior)
```

```
plot(posterior, type='l')
```



```
# 3.12
```

```
PI(samples, prob=0.5)
```

```
##      25%      75%
## 0.7099710 0.9314931
```

Highest Posterior Density Interval described the distribution better. It's the *narrowest* interval containing the specified probability mass, e.g. 50%.

```
# 3.13
```

```
HPDI(samples, prob=0.5)
```

```
##      |0.5      0.5|
## 0.8427843 1.0000000
```

3.2.3. Point Estimates

A parameter with the highest posterior probability is called a *maximum a posteriori* estimate, or *MAP*.

```
# 3.14
```

```
which.max(posterior)
```

```
## [1] 10000
```

```
p_grid[which.max(posterior)]
```

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

Use samples to get the same (or similar) result:

```
# 3.15
chainmode(samples, adj=0.01)
```

```
## [1] 0.9894167
```

```
# 3.16
mean(samples)
```

```
## [1] 0.801751
```

```
median(samples)
```

```
## [1] 0.8427843
```

If the loss function is the absolute difference, then the posterior loss for $p = 0.5$ is

```
# 3.17
sum(posterior * abs(0.5 - p_grid))
```

```
## [1] 0.3125375
```

```
# 3.18
loss <- sapply(p_grid, function(d) sum(posterior * abs(d - p_grid)))
```

```
# 3.19
which.min(loss)
```

```
## [1] 8410
```

```
p_grid[which.min(loss)]
```

```
## [1] 0.8409841
```

The posterior median minimizes the abs loss function. Let's test the quadratic loss function:

```
loss2 <- sapply(p_grid, function(d) sum(posterior * (d - p_grid)^2))
which.min(loss2)
```

```
## [1] 8001
```

```
p_grid[which.min(loss2)]
```

```
## [1] 0.80008
```

This is a mean.

3.3. Sampling to Simulate Prediction

3.3.1. Dummy Data

```
# 3.20
dbinom(0:2, size=2, prob=0.7)
```

```
## [1] 0.09 0.42 0.49
```

We can sample from this distribution:

```
# 3.22
rbinom(10, size=2, prob=0.7)
```

```
## [1] 1 1 2 1 1 0 1 2 2 1
```

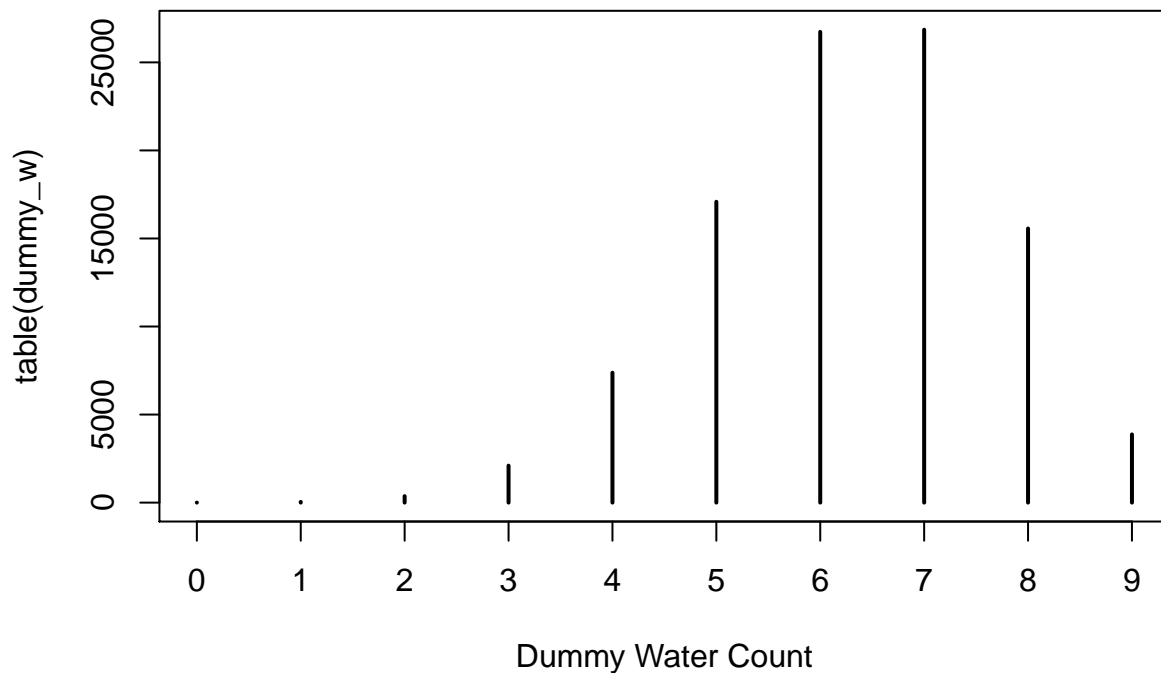

Let's generate 100,000 dummy observations to verify that each values 0, 1, and 2 appear in proportion to its likelihood:

```
# 3.23
dummy_w <- rbinom(1e5, size=2, prob=0.7)
table(dummy_w) / 1e5
```

```
## dummy_w
##      0      1      2
## 0.08912 0.42157 0.48931
```

Let's simulate the sample with 9 tosses:

```
# 3.24
dummy_w <- rbinom(1e5, size=9, prob=0.7)
plot(table(dummy_w), xlab="Dummy Water Count")
```



```
table(dummy_w)
```

```
## dummy_w
##      0      1      2      3      4      5      6      7      8      9
##      2     40    367   2100   7378  17085  26733  26855  15567   3873
```

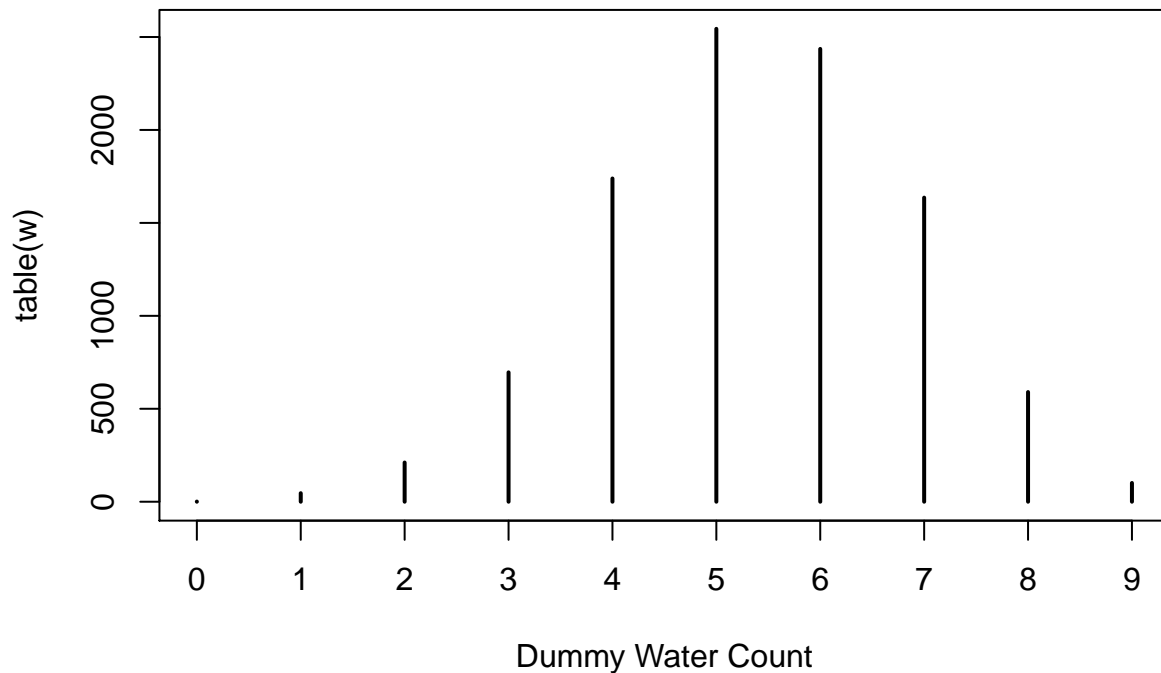
```
dummy_w[1:100]
```

```
##      [1] 5 5 7 7 8 4 7 5 4 8 8 7 8 7 4 5 7 6 4 8 5 5 7 5 5 7 8 9 6 5 7 7 9 4 7
##     [36] 8 9 6 7 4 6 6 8 9 8 5 4 7 5 5 4 7 4 6 8 5 5 6 7 6 6 7 7 5 5 7 8 6 7 7
##     [71] 7 5 9 6 6 5 6 6 8 7 8 2 6 7 6 6 3 6 5 7 4 7 7 7 6 9 5 7 8 7
```

3.2. Model Checking

Below is a misleading distribution plot. While $p = 0.6$ is the likeliest estimate, if we simply use it as a point estimate we will obtain a much more narrow, “overly confident” predictions:

```
# 3.25
w <- rbinom(1e4, size=9, prob=0.6)
plot(table(w), xlab="Dummy Water Count")
```



The correct way to generate predictions is to incorporate our uncertainty about p . We can do it by using sampled values of p , and averaging over all of them. The sampled values will appear with the right frequency, described by our posterior. Samples from the *posterior* distribution of p :

```
samples[1:20]
```

```
## [1] 0.9022902 0.2151215 0.7202720 0.9247925 0.9942994 0.7457746 0.8035804
## [8] 0.8390839 0.8042804 0.6967697 0.8024802 0.7568757 0.9796980 0.6420642
## [15] 0.9236924 0.8105811 0.6538654 0.7180718 0.4230423 0.6872687
```

```
# 3.26
w2 <- rbinom(1e4, size=9, prob=samples_orig)
table(w2)
```

```
## w2
##  0   1   2   3   4   5   6   7   8   9
## 26 113 371 768 1324 1797 2061 1912 1161 467
```

```
par(mfrow=c(1, 2))
plot(table(w), xlab="Overly confident")
plot(table(w2), xlab="Correct")
```

