Informative Hypotheses

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Contents

Chapter 1

Introduction

This is a template GitBook based on *A GitBook Example for Teaching* and *bookdown: Authoring Books and Technical Documents with R Markdown.*

Chapter 2

Monte Carlo Simulations

```r
library(tidyverse)
# {-} no chapter number
# see Appendix.Rmd how to make parts in a book
# don't forget library(bookdown)
# R - help -cheatsheets
```

2.1 The Confidence Interval

In this exercise I will try to repeat the example given by Gerko Vink

The main idea of this exercise is to illustrate the nature of the *Confidence Interval* as described by Neyman (1934)

We set a seed to make our results reproducible:

```r
set.seed(6465)
```

- The first step is to take 100 samples (in this case of size 800) from a *normal distributuon* with $\mu = 0$ and $\sigma = 1$:

```r
samples <-plyr::rlply(100, rnorm(800, 0, 1))
```

- Secondly, we need to calculate for the mean of each sample: the absolute bias; standard error lower bound of the 95% confidence interval and upper bound of the 95% confidence interval.

Table 2.1: Here is a table of the samples

Mean	Bias	Std.Err	Lower	Upper	Covered
-0.0945589	0.0945589	0.0353553	-0.1639592	-0.0251585	0
0.0740058	0.0740058	0.0353553	0.0046055	0.1434062	0

We can construct a function that does this:

```r
samp_function <- function(x) {

  m <- mean(x)
  n <- length(x)
  se <- 1/sqrt(n)
  bias <- abs(-0 - m)
  df <- n - 1
  interval <- qt(.975, df) * se
  return(c(m, bias, se, m - interval, m + interval))

}

format <- c("Mean" = 0, "Bias" = 0, "Std.Err" = 0, "Lower" = 0, "Upper" = 0)
```

Now we use the constructed function `samp_function` on all 100 samples contained in the object `samples`. And we also add a new column to the results that indicates which CI of the respective samples does contain μ.

```r
results <- samples %>%
  vapply(., samp_function, format) %>%
  t %>%
  as_tibble %>%
  mutate(Covered = ifelse(Lower < 0 & Upper > 0, 1, 0))
```

We can also add a table with the sample statistics of the samples whose CI's do not contain μ.

```r
# the results contains the table content that is piped into the table
results %>%
  filter(Covered ==0) %>%
  kableExtra::kable(caption = "Here is a table of the samples" )
```

And finally we can also make a nice plot illustrating everything that we did so far.

```
# in the line above also the size of the figure can be adjusted
lims <- aes(ymax = results$Upper, ymin = results$Lower)
ggplot(results, aes(y=Mean, x=1:100, colour = Covered)) +
  geom_hline(aes(yintercept = 0)) +
  geom_pointrange(lims) +
  xlab("Simulations") +
  ylab("Means and 95% Confidence Intervals")
```

```
## Warning: Use of 'results$Upper' is discouraged. Use 'Upper' instead.
```

```
## Warning: Use of 'results$Lower' is discouraged. Use 'Lower' instead.
```
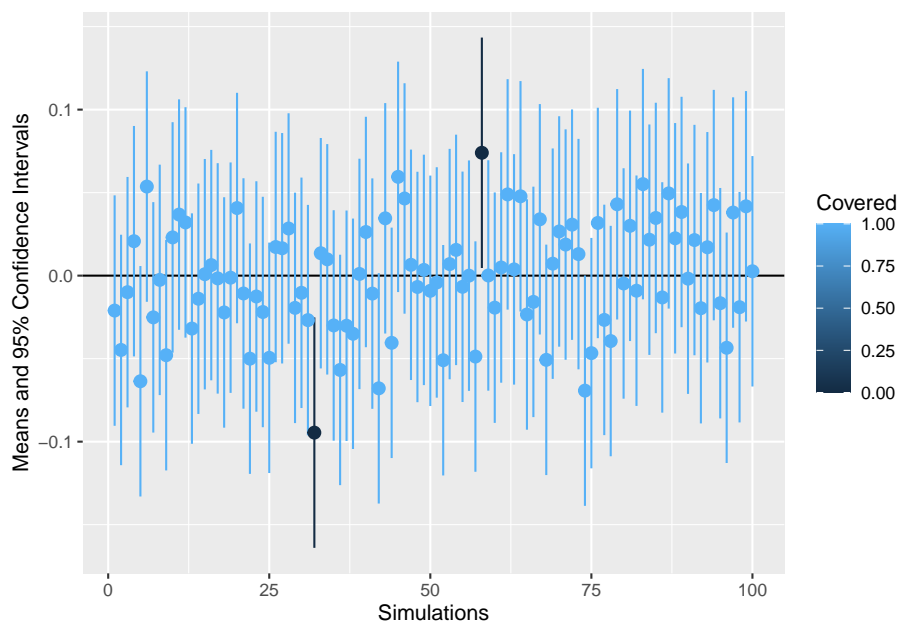

In this case only two out of 100 CI's do not include the true population mean.

2.2 The Central Limit Theorem

Here we will also try to illustrate the Central Limit Theorem, in it's most basic form, with a very simple example.

First we draw 1000 samples (again of size 800), form , say, a *Poisson* distribution, of course we could've drawn them from a uniform or an exponential as well.

Now we calculate the mean for each sample:

```
means <- samples_2 %>%
  lapply(., mean) %>%
  as.data.frame() %>%
  t()
```

And now we plot a histogram of the resulting means:
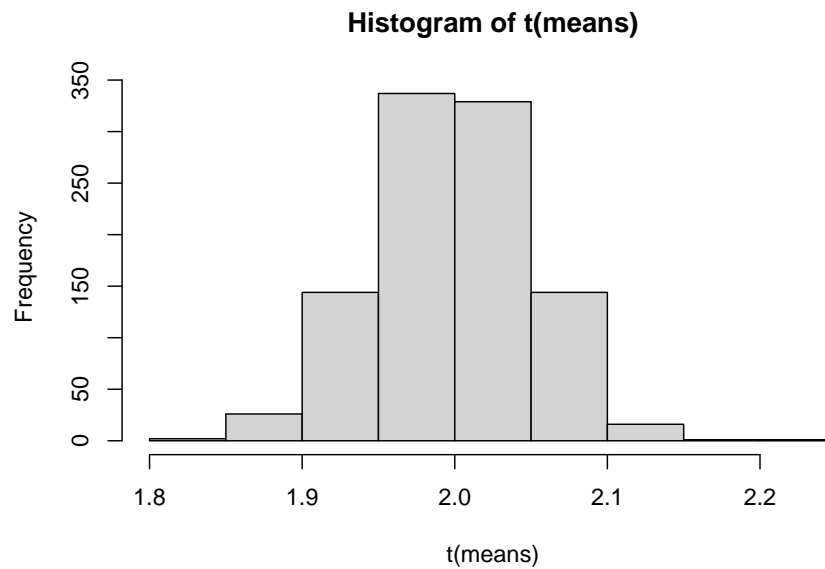
```
hist(t(means))
```


Figure 2.1: Histogram of the sampling distribution of the mean

Literature

Appendix A