

# Hypothesis testing with simulation, Part 2

*Put your name here*

*Put the date here*

## Introduction

Now that we have learned about hypothesis testing, we'll explore a different example. Although the rubric for performing the hypothesis test will not change, the individual steps will be implemented in a different way due to the research question we're asking and the type of data used to answer it.

## Instructions

Presumably, you have already created a new project and downloaded this file into it. Please knit the document and work back and forth between this R Markdown file and the PDF output as you work through this module.

When you are finished with the assignment, knit to PDF one last time, proofread the PDF file **carefully**, export the PDF file to your computer, and then submit your assignment.

Sometimes you will be asked to add your own R code. That will appear in this document as a code chunk with a request for you to add your own code, like so:

```
## Add code here to [do some task]...
```

Be sure to remove the line `## Add code here to [do some task]...` when you have added your own code.

Sometimes you will be asked to type up your thoughts. That will appear in the document as follows:

Please write up your answer here.

Again, please be sure to remove the line “Please write up your answer here” when you have written up your answer. In these areas of the assignment, please use contextually meaningful full sentences/paragraphs (unless otherwise indicated) and proper spelling, grammar, punctuation, etc. This is not R code, but rather a free response section where you talk about your analysis and conclusions. If you need to use some R code as well, you can use inline R code inside the block between `\begin{answer}` and `\end{answer}`, or if you need an R code chunk, please go outside the `answer` block and start a new code chunk.

## Load Packages

We load the `MASS` package to access the `Melanoma` data on patients in Denmark with malignant melanoma, and the `mosaic` package for simulation tools.

```
library(MASS)
library(mosaic)
```

As explained in an earlier module, we will set the seed so that our results are reproducible.

```
set.seed(42)
```

## Our research question

We know that certain types of cancer are more common among females or males. Is there a sex bias among patients with malignant melanoma?

Let's jump into the "Exploratory data analysis" part of the rubric first.

## Exploratory data analysis

Use data documentation (help files, code books, Google, etc.), the `str` command, and other summary functions to understand the data.

At the console, type `library(MASS)` and then `?Melanoma` to see the help file on the `Melanoma` data set. In particular, note that the `sex` variable is coded as "1 = male" and "0 = female".

Use `str` to examine the structure of the data:

```
str(Melanoma)

## 'data.frame':    205 obs. of  7 variables:
## $ time      : int  10 30 35 99 185 204 210 232 232 279 ...
## $ status    : int  3 3 2 3 1 1 1 3 1 1 ...
## $ sex       : int  1 1 1 0 1 1 1 0 1 0 ...
## $ age       : int  76 56 41 71 52 28 77 60 49 68 ...
## $ year      : int  1972 1968 1977 1968 1965 1971 1972 1974 1968 1971 ...
## $ thickness: num  6.76 0.65 1.34 2.9 12.08 ...
## $ ulcer     : int  1 0 0 0 1 1 1 1 1 1 ...
```

### Prepare the data for analysis.

It appears that `sex` is coded as an integer. You will recall that we need to convert it to a factor variable since it is categorical, not numerical. If we have a preconceived idea of which category is considered the "success" category, we should list it first in the `factor` command. It doesn't matter in this case, so since the first number 0 is "female", we will take that to be our "success" and measure the proportion of malignant melanoma patients who are female.

Although it seems silly to create a data frame with only one variable in it, our analysis in R will work better if it's set up like that.

```
sex <- factor(Melanoma$sex, levels = c(0, 1), labels = c("Female", "Male"))
sex_df <- data.frame(sex)
```

### Make tables or plots to explore data visually.

We only have one categorical variable, so we only need a frequency table. Since we are concerned with proportions, we'll also look at a relative frequency table.

```
table(sex_df$sex)

##
## Female    Male
##    126      79
```

```
prop.table(table(sex_df$sex))
```

```
##  
##      Female      Male  
## 0.6146341 0.3853659
```

## The logic of inference and simulation

This is a good place to pause and remember why statistical inference is important. There are certainly more females than males in this data set. So why don't we just show the table above, declare females are more likely to have malignant melanoma, and then go home?

Think back to coin flips. Even though there was a 50% chance of seeing heads, did that mean that we always saw exactly half of our flips as heads? No. We have to acknowledge *sampling variability*: even if the truth were 50%, when we sample, we could accidentally get more or less than 50%, just by pure chance alone. Perhaps these 205 patients just happen to have more females than average.

The key, then, is to figure out if 61.4634146% is *significantly* larger than 50%, or if a number like 61.4634146% (or one even more extreme) could easily come about from random chance.

As we know from Part 1 of this assignment, we can run a formal hypothesis test to find out. As we do so, make note of the things that are the same and the things that have changed from the last hypothesis tests you run. For example, we are not comparing two groups anymore. We have one group of patients, and all we're doing is measuring the percentage of this group that is female. It's tempting to think that we're comparing males and females, but that's not the case. We are not using `sex` to divide our data into two groups for the purpose of exploring whether some other variable differs between men and women. We just have one sample. "Female" and "Male" are simply categories in a single categorical variable. Also, because we are only asking about one variable (`sex`), the mathematical form of the hypotheses will look a little different.

Because this is no longer a question about two variables being independent or associated, the "shuffling" idea we've been using no longer makes sense. So what does make sense?

It helps to start by figuring out what our null hypothesis is. Remember, our question of interest is whether there is a sex bias in malignant melanoma. In other words, are there more or fewer females than males with malignant melanoma? As this is our research question, it will be the alternative hypothesis. So what is the null? What is the "default" situation in which nothing interesting is going on? Well, there would be no sex bias. In other words, there would be the same number of females and males with malignant melanoma. Or another way of saying that—with respect to the "success" condition of being female that we discussed earlier—is that females comprise 50% of all patients with malignant melanoma.

Okay, given our philosophy about the null hypothesis, let's take the skeptical position and assume that, indeed, 50% of all malignant melanoma patients in our population are female. Then let's take a sample of 205 patients. We can't get exactly 50% females from a sample of 205 (that would be 102.5 females!), so what numbers can we get?

Simulation will tell us. What kind of simulation? As we come across each patient in our sample, there is a 50% chance of them being female. So what if instead of sampling real patients, we just flipped a coin? A coin flip will come up heads just as often as our patients will be female.

So this brings us full circle, back to the first simulation idea you explored. We can simulate coin flips (using the `mosaic` package in R with the `rflip` function), graph our results, and calculate a P-value. More specifically, we'll flip a coin 205 times to represent sampling 205 patients. Then we'll use the `do` command to do this a bunch of times and establish a range of plausible percentages that can come about by chance from this procedure.

Let's dive back into the remaining steps of the formal hypothesis test.

## Hypotheses

**Identify the sample (or samples) and a reasonable population (or populations) of interest.**

The sample consists of 205 patients from Denmark with malignant melanoma. Our population is presumably all patients with malignant melanoma, although in checking conditions below, we'll take care to discuss whether patients in Denmark are representative of patients elsewhere.

**Express the null and alternative hypotheses as contextually meaningful full sentences.**

$H_0$  : The null hypothesis states that half of all malignant melanoma patients are female.

$H_A$  : The alternative hypothesis states that there is a sex bias among patients with malignant melanoma (meaning that females are either overrepresented or underrepresented).

**Express the null and alternative hypotheses in symbols.**

$H_0 : p = 0.5$

$H_A : p \neq 0.5$

## Model

**Check the relevant conditions to ensure that the model assumptions are met.**

- Random
  - As mentioned above, these 205 patients are not a random sample of all people with malignant melanoma. We don't even have any evidence that they are a random sample of melanoma patients in Denmark. Without such evidence, we have to hope that these 205 patients are representative of all patients who have malignant melanoma. Unless there's something special about Danes in terms of their genetics or diet or something like that, one could imagine that their physiology makes them just as susceptible to melanoma as anyone else. More specifically, though, our question is about females and males getting malignant melanoma. Perhaps there are more female sunbathers in Denmark than in other countries. That might make Danes unrepresentative in terms of the gender balance among melanoma patients. We should be cautious in interpreting any conclusion we might reach in light of these doubts.
- 10%
  - Whether in Denmark or not, given that melanoma is a fairly common form of cancer, I assume 205 is less than 10% of all patients with malignant melanoma.

## Mechanics

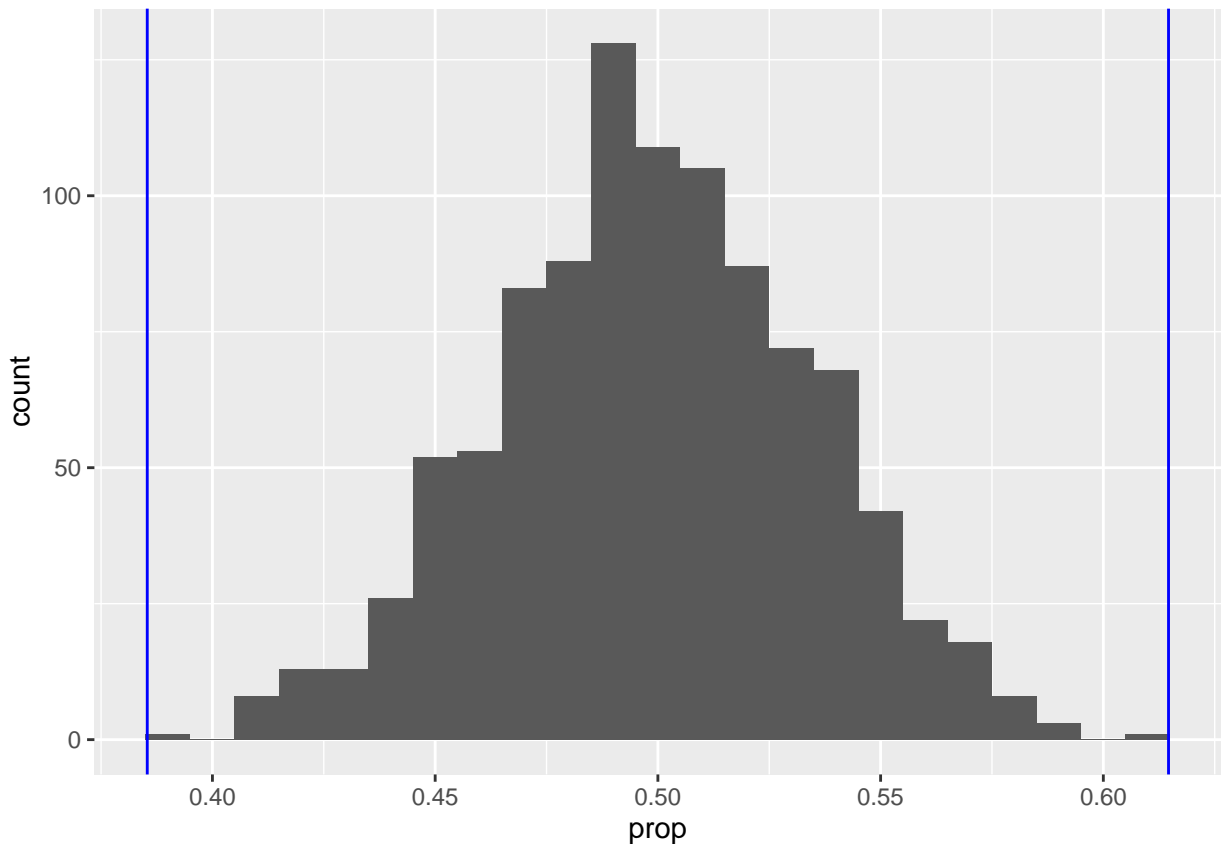
**Compute the test statistic.**

```
females <- prop(sex, data = sex_df)
females
```

```
##      Female
## 0.6146341
```

Plot the simulated values of the null distribution.

```
sims <- do(1000) * rflip(205, prob = 0.5)
# Strictly speaking, you don't need prob = 0.5 because
# that's the default for rflip. However, I'm showing you
# the syntax because your null hypothesis won't always
# be  $p = 0.5$ .
ggplot(sims, aes(x = prop)) +
  geom_histogram(binwidth = 0.01) +
  geom_vline(xintercept = females, color = "blue") +
  geom_vline(xintercept = 1 - females, color = "blue")
```



(The last line above requires a little explanation. The proportion of successes is 0.6146341, but we're running a two-sided test. So we also need to plot another blue line at a value that's as extreme as 0.6146341, but on the other side of 50%. That number is 0.3853659.)

Calculate the P-value.

```
2 * prop(sims$prop >= females)
```

```
## TRUE
##    0
```

Three observations here:

1. We multiplied by 2 because this is a two-sided test.
2. We need “greater than or equal to ( $\geq$ )” here because the simulated values that are more extreme than 0.6146341 are lying *above* 0.6146341, in the right tail of the simulated sampling distribution.
3. The P-value appears to be zero. Indeed, among the 5000 simulated values, we saw none that exceeded 0.6146341. However, a true P-value can never be zero. If you did millions or billions of simulations (please don’t try!), surely there would be one or two with even more extreme values.

In cases when the P-value is really, really tiny, it is traditional to report  $P < 0.001$ .

It is **incorrect** to say  $P = 0$ .

## Conclusion

**State the statistical conclusion.**

We reject the null hypothesis.

**State (but do not overstate) a contextually meaningful conclusion.**

There is sufficient evidence that there is a sex bias in patients who suffer from malignant melanoma.

**Identify the possibility of either a Type I or Type II error and state what making such an error means in the context of the hypotheses.**

As we rejected the null, we run the risk of making a Type I error. If we have made such an error, that would mean that patients with malignant melanoma are equally likely to be male or female, but that we got a sample with an unusual number of female patients.

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## Your turn

Determine if the percentage of patients in Denmark with malignant melanoma who also have an ulcer is significantly different from 50%.

As before, you have the outline of the rubric for inference below. Some of the steps will be the same or similar to steps in the example above. It is perfectly okay to copy and paste R code, making the necessary changes. It is **not** okay to copy and paste text. You need to put everything into your own words.

The template below is exactly the same as in the file `Rubric_for_inference.pdf`.

## Exploratory data analysis

Use data documentaton (help files, code books, Google, etc.), the `str` command, and other summary functions to understand the data.

```
## Add code here to understand the data.
```

Prepare the data for analysis.

```
## Add code here to prepare the data for analysis.
```

Make tables or plots to explore data visually.

```
## Add code here to make tables or plots.
```

## Hypotheses

Identify the sample (or samples) and a reasonable population (or populations) of interest.

Please write up your answer here.

Express the null and alternative hypotheses as contextually meaningful full sentences.

$H_0$  : Null hypothesis goes here.

$H_A$  : Alternative hypothesis goes here.

Express the null and alternative hypotheses in symbols.

$H_0$  : *math*

$H_A$  : *math*

## Model

Check the relevant conditions to ensure that the assumptions are met.

Please write up your answer here.

## Mechanics

Compute the test statistic.

```
## Add code here to compute the test statistic.
```

Plot simulated values of the null distribution.

```
## Add code here to plot simulated values of the null distribution.
```

**Calculate the P-value.**

```
## Add code here to calculate the P-value.
```

## Conclusion

**State the statistical conclusion.**

Please write up your answer here.

**State (but do not overstate) a contextually meaningful conclusion.**

Please write up your answer here.

**Identify the possibility of either a Type I or Type II error and state what making such an error means in the context of the hypotheses.**

Please write up your answer here.

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## Conclusion

Now you have seen two fully-worked examples of hypothesis tests using simulation, and you have created two more examples on your own. Hopefully, the logic of inference and the process of running a formal hypothesis test are starting to make sense.

Keep in mind that the outline of steps will not change. However, the way each step is carried out will vary from problem to problem. Not only does the context change (one example involved smoking mothers and the other, melanoma patients), but the statistics you compute also change (one example compared proportions from two samples and the other only had one proportion from a single sample). Pay close attention to the research question and the data that will be used to answer that question. That will be the only information you have to help you know which hypothesis test applies.