Lecture 7: Hypothesis testing part I

Statistical Methods for Data Science

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Today

1. Terminology
   - Experiment and parameter of interest
   - Null hypothesis and alternative hypothesis
   - Test statistic
   - Null distribution $f(s \mid H_0)$
   - Significance level α, power and p-value
2. Example
3. p-hacking
4. Summary

Learning outcome

- Be able to explain the following terminology
  - Null hypothesis H_0 and alternative hypothesis H_A
  - Test statistic s
  - Null distribution $f(s \mid H_0)$
  - Significance level α and power
  - p-value
- Be able to design and interpret the one-sample z-test
- Be able to explain the concept of p-hacking

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- What if company A tested drug D on 100 ducks and the average weight loss after one month is 2.3 kg?

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- What if company A tested drug D on 100 ducks and the average weight loss after one month is 2.3 kg?
- Now company B tested drug E on 30 ducks and the average weight loss after one month is 2.5 kg, while drug D results in 2.3 kg weight loss with the same setup, would you buy drug E instead of drug D?

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How would you make your decision?

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  - The test is based on sample statistics, which are computed from data
  - Hypothesis + data $\rightarrow$ decision on rejecting/not rejecting the hypothesis

Hypothesis testing: a list to go through

- A "boring" statement
- Experiment
- Data x, random variable X
- Parameter of interest θ
- Parameter estimate $\hat{\theta}$
- Null hypothesis H_0
- Alternative hypothesis H_A
- Test statistic s
- Null distribution $f(s \mid H_0)$
- Significance level α
- p-value

Experiment and parameter of interest

Experiment design

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  Then we can use $\bar{x}$ to approximate μ_D and check if it is greater than diet control (2.1 kg)

Experiment design (cont.)

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  Then we use $\bar{x}$ and $\bar{y}$ to approximate μ_D and μ_E to see if they are the same

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  - Example 2: drug E and drug D work the same on average (5 sec)

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- **Alternative hypothesis H_A**: a complementary alternative explanation to the "boring" statement
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  - Example 2: drug E and drug D do not work the same on average (5 sec)

Hypotheses H_0 and H_A

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- **Alternative hypothesis** H_A: a complementary alternative explanation to the "boring" statement
  - Example 1: drug D is more effective than regular diet on average (5 sec)

$$H_A : \mu_D > 2.1$$

  - Example 2: drug E and drug D do not work the same on average (5 sec)

$$H_A : \mu_D \neq \mu_E$$

Hypotheses H_0 and H_A (cont.)

Questions:

- Question 1: why are $H_A : \mu_D > 2.1$ and $H_0 : \mu_D = 2.1$ complementary to each other? What about $H_A : \mu_D < 2.1$?

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  Answer: an implicit assumption here is that μ_D will not be smaller than 2.1
- Question 2: can H_0 and H_A be ANYTHING I want? Like a magic mirror!?

Hypotheses H_0 and H_A (cont.)

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- Question 1: why are $H_A : \mu_D > 2.1$ and $H_0 : \mu_D = 2.1$ complementary to each other? What about $H_A : \mu_D < 2.1$?
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  Answer: no
- Follow up question: what are the choices for H_0 and H_A?

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    For example, is classifier A better than classifier B? $H_0 : p_A = p_B$
- We have seen one-sample test and two-sample test in the Q-Q plot lecture
- In practice, you can narrow down your choice of hypotheses by making a Q-Q plot

Choices for H_A

Given

$$H_0 : \theta = \beta$$

where β can be either a constant (one-sample test) or a parameter from another data distribution (two-sample test)

- **Alternative hypothesis H_A**: H_A can be **one-tailed** or **two-tailed**
  - **One-tailed**:

$$H_A : \quad \theta > \beta$$

or

$$H_A : \quad \theta < \beta$$

  - **Two-tailed**:

$$H_A : \quad \theta \neq \beta \iff \theta < \beta \text{ or } \theta > \beta$$

Summary: choices for H_0 and H_A

Putting everything together,

	One-sample test	Two-sample test
Two-tailed	$H_0: \theta = c,\ H_A: \theta \neq c$	$H_0: \theta_1 = \theta_2,\ H_A: \theta_1 \neq \theta_2$
One-tailed	$H_0: \theta = c,\ H_A: \theta > c$	$H_0: \theta_1 = \theta_2,\ H_A: \theta_1 > \theta_2$
	$H_0: \theta = c,\ H_A: \theta < c$	$H_0: \theta_1 = \theta_2,\ H_A: \theta_1 < \theta_2$

where θ, θ_1, θ_2 are the parameters of interest and c is a constant

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Note: in this course, we only deal with null hypothesis where we are able to express the PDF/PMF $f(s \mid H_0)$, i.e. H_0 with an equal sign in them

Test statistic (cont.)

Example 1. one-sample test

- Data: $x_1, \cdots, x_N$
- Random variable: $X_1, \cdots, X_N$ i.i.d. Gaussian with known σ
- Parameter of interest: μ_D
- Parameter estimate: $\bar{x}$
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Standardize $\bar{x}$ (15 sec)

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Standardize $\bar{x}$ (15 sec)

$$z = \frac{\bar{x} - 2.1}{\sigma / \sqrt{N}}$$

Test statistic (cont.)

Example 2. two-sample test

- **Data**: $x_1, \cdots, x_{N_D}$ and $y_1, \cdots, y_{N_E}$
- **Random variable**: $X_1, \cdots, X_{N_D}$ i.i.d. **Gaussian with known σ_D**; $Y_1, \cdots, Y_{N_E}$ i.i.d. **Gaussian with known σ_E**; X_i and Y_j independent
- **Parameter of interest**: μ_D, μ_E
- **Parameter estimate**: $\bar{x}$, $\bar{y}$
- **Null hypothesis**: $H_0 : \mu_D = \mu_E \iff H_0 : \mu_D - \mu_E = 0$
- **Test statistic**: standardized $\bar{x} - \bar{y}$ assuming the null hypothesis

$$z = \frac{\bar{x} - \bar{y}}{\sqrt{\sigma_D^2/N_D + \sigma_E^2/N_E}} \text{ (explained later)}$$

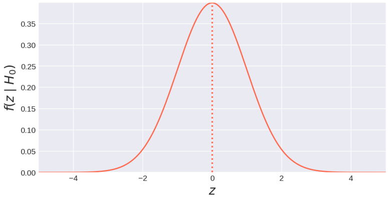
Null distribution $f(s \mid H_0)$

Null distribution

- **Null distribution** $f(s \mid H_0)$: the distribution of the test statistic given the null hypothesis
- Example:
  - **Data**: $x_1, \cdots, x_N$
  - **Random variable**: $X_1, \cdots, X_N$ i.i.d. Gaussian with known σ
  - **Parameter of interest**: μ
  - **Parameter estimate**: $\bar{x}$
  - **Null hypothesis**: $H_0 : \mu = \mu_0$
  - **Test statistic**:

$$z = \frac{\bar{x} - \mu_0}{\sigma/\sqrt{N}}$$

  - **Null distribution**: standard Gaussian distribution



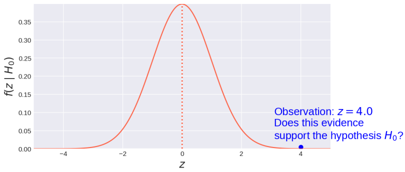
Significance level α, power and p-value

Significance level

Given a null hypothesis $H_0 : \mu = 2.1$ and the null distribution $f(s \mid H_0)$, we decide if we reject the hypothesis or not by observing data

- Run some experiments and collect data $x_1, \cdots, x_N$
- Estimate the parameter of interest $\hat{\theta}$, e.g. $\hat{\mu} = \bar{x} = \frac{1}{N} \sum_{i=1}^{N} x_i$
- Standardize $\hat{\theta}$ assuming H_0 to compute the test statistic, e.g.

$$z = \frac{\bar{x} - 2.1}{\sigma / \sqrt{N}} = 4.0$$



- Does this evidence support the hypothesis H_0?

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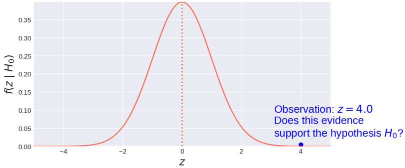
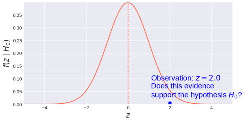


- Does this evidence support the hypothesis H_0? Probably not since it's so far away from the center?

Significance level (cont.)

- What about this observation?



Significance level (cont.)

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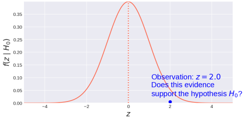

- To be able to answer the question, you need to decide where you draw the line

Significance level (cont.)

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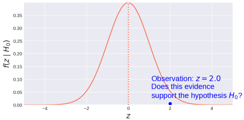

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Significance level (cont.)

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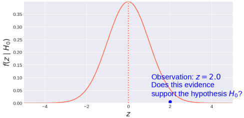

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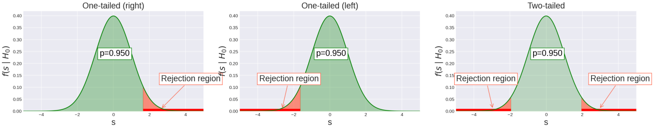
- **Significance level** α: red area under the curve



In these three images, $\alpha = 0.05$

Significance level (cont.)

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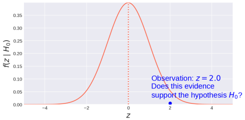

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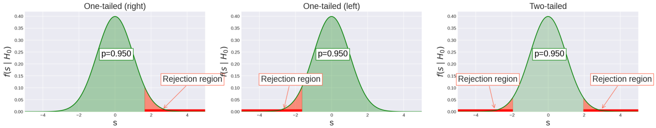

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More conservative $\Rightarrow$ less probable to reject H_0, which indicates a smaller rejection region

Significance level (cont.)

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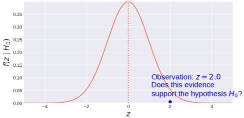

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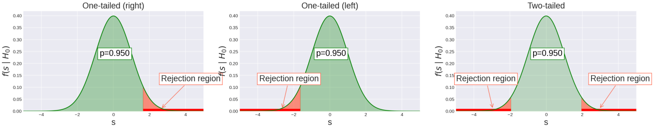

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More conservative $\Rightarrow$ less probable to reject H_0, which indicates a smaller rejection region
Two-tailed H_A is more conservative

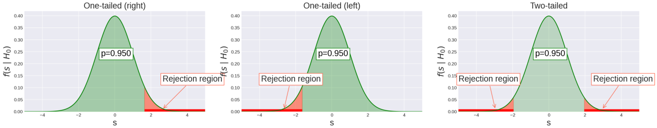
Significance level (cont.)

What is needed for choosing a meaningful α?

- Null distribution
- H_A one-tailed or two-tailed

Interpretation of α

- $\alpha = P(\textit{reject } H_0 \mid H_0 \textit{ is true})$ - the probability of making such a mistake



  - The rejection region indicates that H_0 is **unlikely**, but the probability is not zero
  - It is possible that H_0 is true, but our observation happens to fall in the rejection region
  - If H_0 is true and our observation falls in the rejection region, we will **mistakenly** reject H_0
  - The probability of making this type of mistakes is α
- Similar to the confidence interval, $1 - \alpha$ is called the **confidence level**

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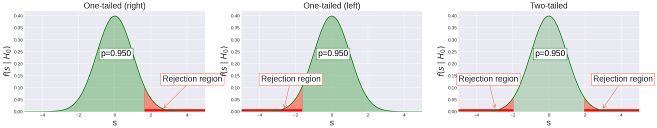

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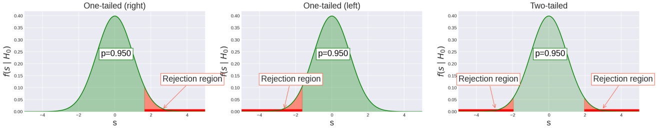
  - The probability of making this type of mistakes is α
- Similar to the confidence interval, $1 - \alpha$ is called the **confidence level** - "with 95% confidence, rejecting H_0 is the right thing to do"

Interpretation of α

- $\alpha = P(\textit{reject } H_0 \mid H_0 \textit{ is true})$ - the probability of making such a mistake



  - The rejection region indicates that H_0 is **unlikely**, but the probability is not zero
  - It is possible that H_0 is true, but our observation happens to fall in the rejection region
  - If H_0 is true and our observation falls in the rejection region, we will **mistakenly** reject H_0
  - The probability of making this type of mistakes is α
- Similar to the confidence interval, $1 - \alpha$ is called the **confidence level** - "with 95% confidence, rejecting H_0 is the right thing to do"
- Define the significance level **before you run the experiments** so that you can't cheat!

Significance level and power

- Contingency table:

	$y = H_A$	$y = H_0$
$\hat{y}$ = reject H_0	**TP**	**FP** (Type I error)
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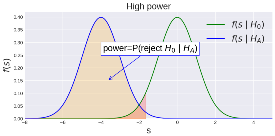

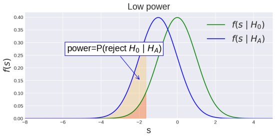

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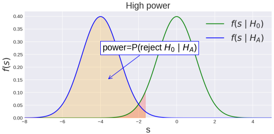

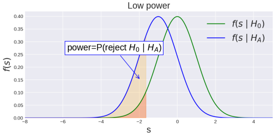

- What is needed for computing the power?

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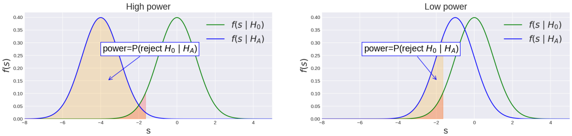

- What is needed for computing the power? $f(s \mid H_0)$, $f(s \mid H_A)$

p-value

- ***p*-value**:
  - One-tailed:
    - Right tail: $p = P(S \geq s \mid H_0)$, e.g. 1-stats.norm.cdf(s, 0, 1)
    - Left tail: $p = P(S \leq s \mid H_0)$, e.g. stats.norm.cdf(s, 0, 1)
  - Two-tailed:
    - $p = 2\min\left(P(S \leq s \mid H_0), P(S \geq s \mid H_0)\right)$, e.g. 2*min(stats.norm.cdf(s, 0, 1), 1-stats.norm.cdf(s, 0, 1))

    Note: for example, if $f(s \mid H_0)$ is symmetric around zero and $s < 0$,

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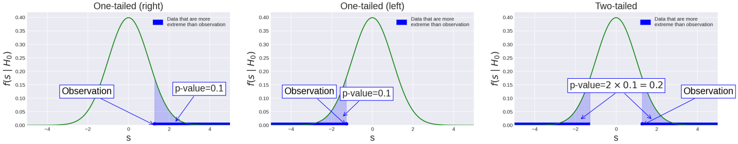

- What is needed for computing the p-value? (10 sec)

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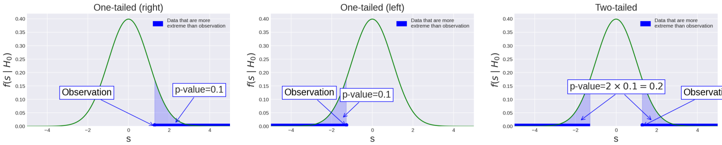

- What is needed for computing the p-value? (10 sec)
  - Null distribution
  - Alternative hypothesis H_A to know one-tailed or two-tailed
  - Observation - test statistic computed from data

Summary: steps for hypothesis testing

- Step 1 Make a "boring" statement
- Step 2 Design an **experiment**
- Step 3 Describe the **data** generated from the experiment and the corresponding random variables
- Step 4 Describe the parameter of interest and their estimates
- Step 5 Translate the "boring" statement into a statistical hypothesis and call it the **null hypothesis** H_0
- Step 6 Find the expression for the **test statistic** s
- Step 7 Find the expression for the **null distribution**
- Step 8 Define **an alternative hypothesis** H_A: one-tailed or two-tailed
- Step 9 Choose a **significance level** α (the tail), which defines the **rejection region**
- Step 10 Collect **data**
- Step 11 Compute the test statistic from data
- Step 12 Compute the p-value
- Step 13 If p-value$< \alpha$, i.e. the test statistic falls in the rejection region of the null distribution, then we reject the hypothesis H_0; otherwise, we fail to reject H_0.

Today

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$$z_0 = \frac{2.2 - 2.1}{0.6/\sqrt{30}} = 0.91$$

Example (cont.)

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- **For** $H_A : \mu_D > 2.1$ **(one-tailed):** $p = P(Z \geq z_0 \mid H_0) = 0.1807 > \alpha$

Example (cont.)

Step 12 Compute the *p*-value (20 secs):

- **For** $H_A : \mu_D > 2.1$ **(one-tailed):** $p = P(Z \geq z_0 \mid H_0) = 0.1807 > \alpha$
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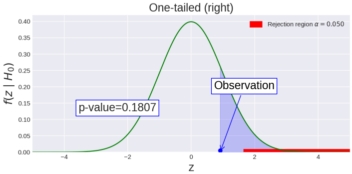

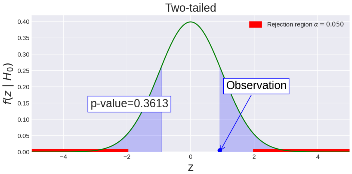

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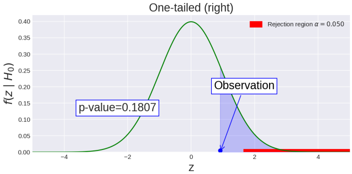

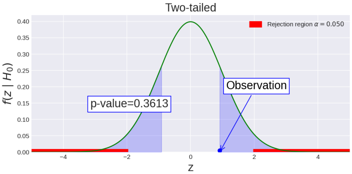

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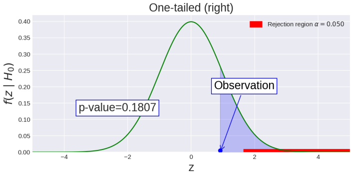

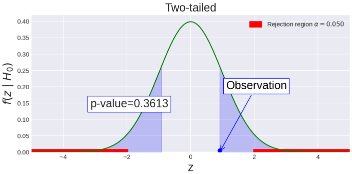

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What does it mean? - Based on this test, you will stick to diet control instead of buying drug D.

Example (cont.)

What if $\bar{x} = 2.3$?

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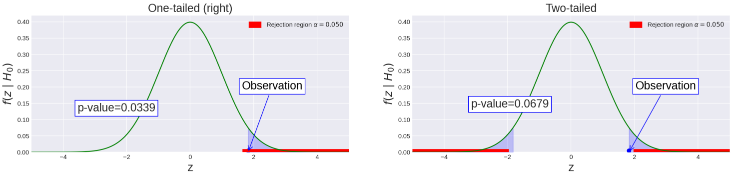

Reject H_0 for one-tailed H_A; do not reject H_0 for two-tailed H_A for the same confidence level $1 - \alpha = 95\%$

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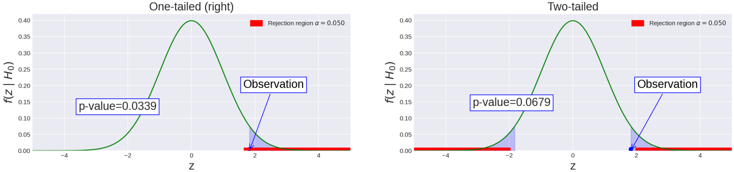

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Note: the two-tailed test is more conservative - if the data passes a two-tailed test, it is more conclusive than one-tailed test for the same confidence level

Example (cont.)

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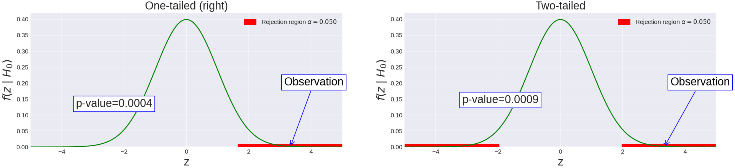

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Note:

- With more data, it becomes more certain that we should reject H_0 in favor of H_A given the observation $\bar{x} = 2.3$

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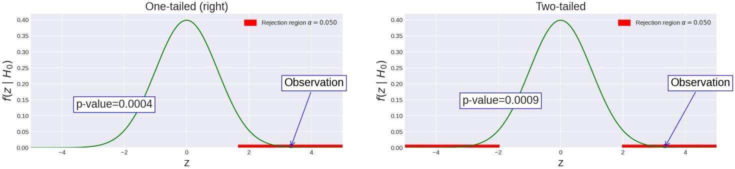

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Note:

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This test is called one-sample z-test

Today

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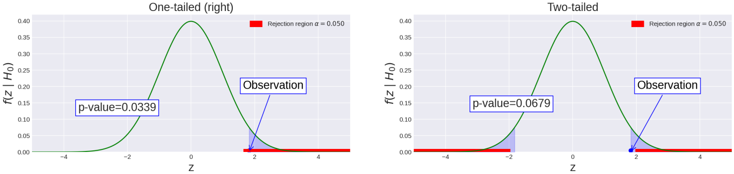

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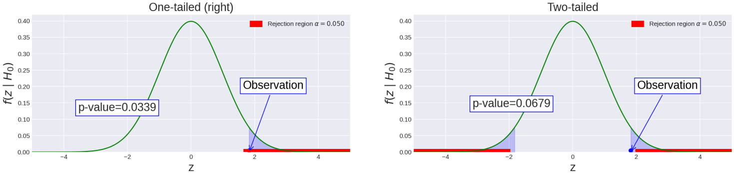

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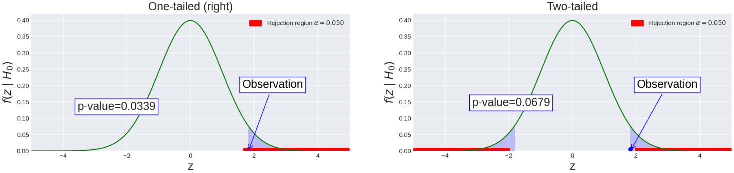

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- The conclusion we draw depends on which test we conduct

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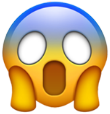
- p-value is computed from data
- Data is random - **p-value is random**
- With the same experiment set up, if we switch to a different sample, p-value will be different

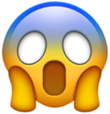
p-hacking

- Many factors can result in a different p-value
- p-hacking refers to situations where researchers are **trying multiple things until they get the desired result**
- This action can be a conscious decision, a subconscious decision or even an unconscious action
- p-hacking can be tricky to identify
- Suggestions to avoid p-hacking, e.g. one should always **report effect sizes and confidence intervals**
- Reference:
  - `https://www.nature.com/news/scientific-method-statistical-errors-1.14700`
  - Why Most Published Research Findings Are False?

p-hacking (cont.)

What should I do!? 

p-hacking (cont.)



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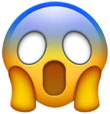

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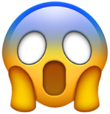
What should I do!? 

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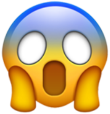

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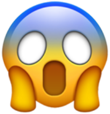
What should I do!? 

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Today

1. Terminology
2. Example
3. p-hacking
4. Summary

Summary

So far:

- Data types and data containers
- Descriptive data analysis: descriptive statistics, visualization
- Probability distributions, events, random variables, PMF, PDF, parameters
- CDF, Q-Q plot, how to compare two distributions (data vs theoretical, data vs data)
- Modeling
- Parameter estimation: maximum likelihood estimation (MLE) and maximum a posteriori estimation (MAP)
- Classification, multinomial naive Bayes classifier, Gaussian naive Bayes classifier
- Central limit theorem, interval estimation
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Before next lecture:

- Steps for hypothesis testing