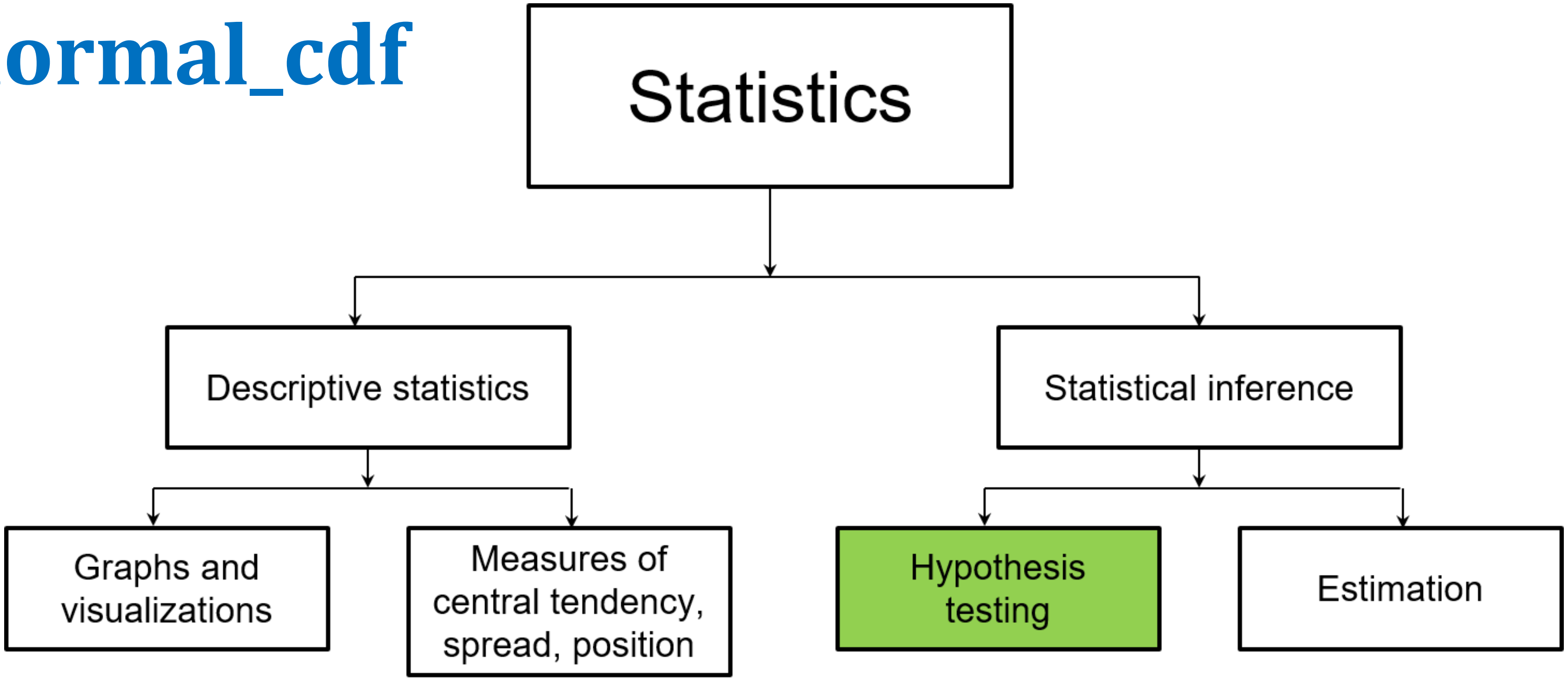
Syllabus

Unit II

Statistical Hypothesis Testing, Example: Flipping a Coin, p-Values, Confidence Intervals, p-Hacking, Example: Running an A/B Test, Bayesian Inference, Gradient Descent, The Idea Behind Gradient Descent Estimating the Gradient, Using the Gradient, Choosing the Right Step Size, Using Gradient Descent to Fit Models, Minibatch and Stochastic Gradient Descent.

normal_cdf



- Hypothesis testing plays a crucial role in statistical analysis and decision-making.
- By providing a structured framework for evaluating assumptions and drawing conclusions, it enables researchers and data analysts to make informed choices based on evidence.
- Two key concepts underpin hypothesis testing: **the null hypothesis and the alternative hypothesis.**

Statistical Hypothesis Testing

- Often, as data scientists, want to test whether a certain hypothesis is likely to be true.
- For our purposes, hypotheses are assertions like “this coin is fair” or “data scientists prefer Python to R” or “people are more likely to navigate away from the page without ever reading the content if we pop up an irritating interstitial advertisement with a tiny, hard-to-find close button” that can be translated into statistics about data.
- In the classical setup, we have a null hypothesis, H_0, that represents some default position, and some alternative hypothesis, H_1, that we’d like to compare it with.
- We use statistics to decide whether we can reject H0 as false or not.

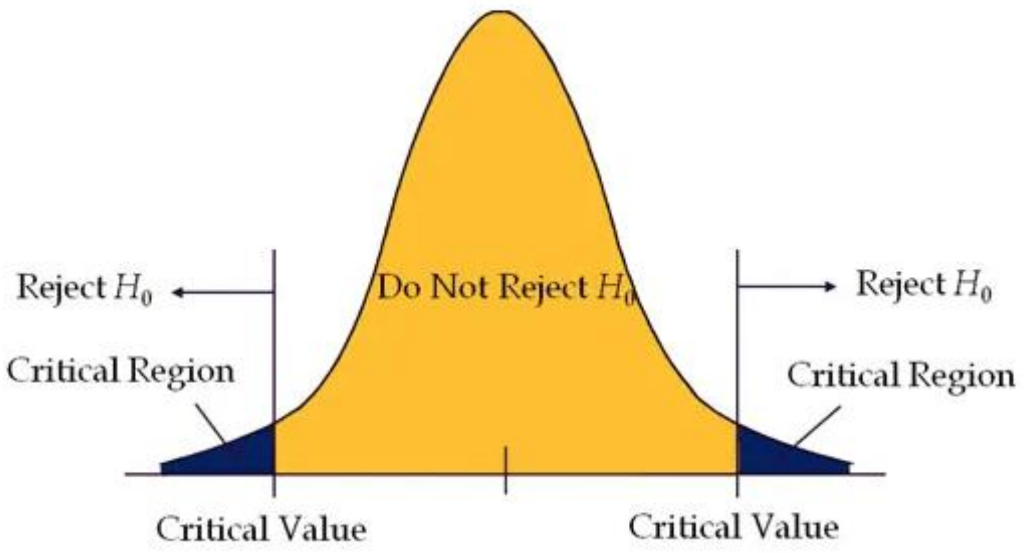
Example: Flipping a Coin

- Imagine we have a coin and we want to test whether it's fair.
- We'll make the assumption that the coin has some probability p of landing heads, and so our **null hypothesis is that the coin is fair—that is, that p = 0.5.**
- We'll test this against the **alternative hypothesis p ≠ 0.5.**
- Test will involve **flipping the coin some number, n,** times and counting the number of heads, X.
- Each coin flip is a Bernoulli trial, which means that X is a Binomial(n, p) random variable, we can approximate using the normal distribution:

```
def normal_approximation_to_binomial(n, p):
    """finds mu and sigma corresponding to a Binomial(n, p)"""
    mu = p * n
    sigma = math.sqrt(p * (1 - p) * n)
    return mu, sigma
```

Methods to Calculate Hypothesis Testing:

Rejection Region Approach:



In a hypothesis test, critical regions are ranges of the distributions where the values represent statistically significant results. If the test statistic falls in the critical region, reject the null hypothesis.

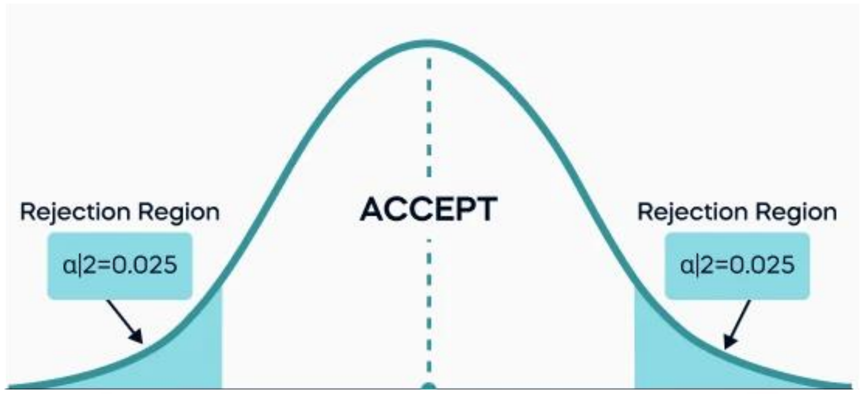
The rejection region approach is one of the commonly used methods to conduct hypothesis testing. It involves determining a critical region or rejection region, which serves as a threshold for making decisions based on test statistics.

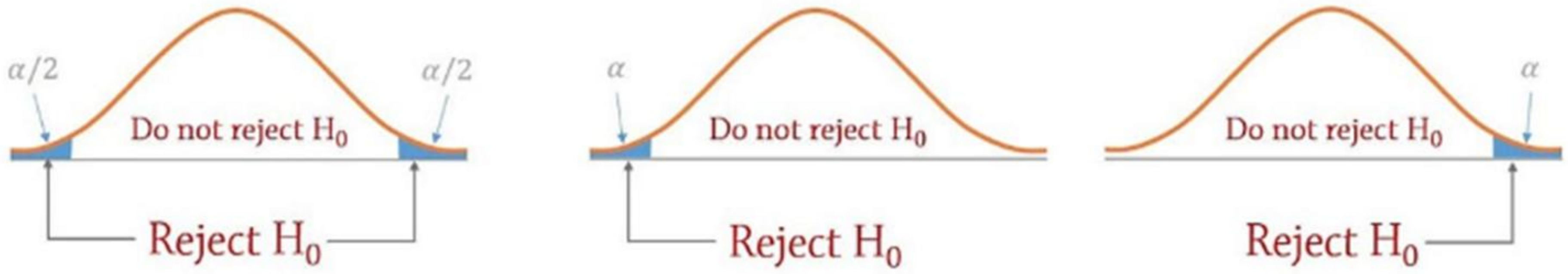
1. Setting Up the Hypothesis Test

- **Null Hypothesis (H_0)**: The coin is fair (unbiased), meaning it has a 50% probability of landing on heads or tails.
- **Alternative Hypothesis (H_1)**: The coin is biased, meaning it does not have a 50% probability of landing on heads or tails.

2. Choosing the Significance Level (α)

- The significance level (α) represents the probability of rejecting H_0 when it is actually true (Type I error).
- You have set **α = 0.05 (5%)**, which is a common threshold in hypothesis testing.





Hypothesis Testing: Flipping Coin Example

3. Interpreting the p-value (2.28%)

- The **p-value (0.0228 or 2.28%)** is the probability of observing a result as extreme as (or more extreme than) the one obtained, assuming H_0 is true.
- If **p-value** $\leq$ **α**, we reject H_0.
- If **p-value** $>$ **α**, we fail to reject H_0.

Since **2.28% (p-value) is less than 5% (α)**, we **reject H_0**.

4. Conclusion: The Coin Might Be Biased

- Rejecting H_0 suggests that the observed data provides strong enough evidence against the assumption that the coin is fair.
- This does **not** prove the coin is biased with absolute certainty, but it strongly suggests that it is.

normal_cdf

- Whenever a random variable follows a normal distribution, we can use ***normal_cdf*** to figure out the probability that its realized value lies within or outside a particular interval:
- **Python program using normal_cdf to figure out that the probability value lies within or outside a particular interval.**

```
from math import erf, sqrt
from typing import Union
def normal_cdf(x: float, mu: float = 0, sigma: float = 1) -> float:
    """Computes the CDF of a normal distribution."""
    return (1 + erf((x - mu) / (sigma * sqrt(2)))) / 2
# The normal_cdf is the probability the variable is below a threshold
normal_probability_below = normal_cdf

# It's above the threshold if it's not below the threshold
def normal_probability_above(lo: float, mu: float = 0, sigma: float = 1)
-> float:
    """The probability that an N(mu, sigma) is greater than lo."""
    return 1 - normal_cdf(lo, mu, sigma)
# It's between if it's less than hi, but not less than lo
def normal_probability_between(lo: float, hi: float, mu: float = 0,
sigma: float = 1) -> float:
    """The probability that an N(mu, sigma) is between lo and hi."""
    return normal_cdf(hi, mu, sigma) - normal_cdf(lo, mu, sigma)
```

normal_cdf

```
# It's outside if it's not between
def normal_probability_outside(lo: float, hi: float, mu: float = 0,
sigma: float = 1) -> float:
    """The probability that an N(mu, sigma) is not between lo and
hi."""
    return 1 - normal_probability_between(lo, hi, mu, sigma)
print(normal_probability_below(1.0))  # Probability that X < 1
(assuming standard normal distribution)
print(normal_probability_above(1.0))  # Probability that X > 1
print(normal_probability_between(-1.0, 1.0))  # Probability that -1 < X
< 1
print(normal_probability_outside(-1.0, 1.0))  # Probability that X is
not between -1 and 1
```

normal_cdf : flipping Coin Example

Compute the Normal Approximation

Using function:

```
def normal_approximation_to_binomial(n: int, p: float) -> Tuple
[float, float]:
    """Returns mu and sigma corresponding to a Binomial(n, p)"""
    mu = p * n
    sigma = math.sqrt(p* (1-p) * n)
    return mu, sigma
```

mu, sigma = normal_approximation_to_binomial(100, 0.5)

print(mu, sigma) # Output: 50.0, 5.0

So, under H0, the expected number of heads is **50**, with a standard deviation of **5**.

Compute the Probability of Getting 60 or More Heads

We calculate:

Using the normal CDF:

probability = normal_probability_above(60, mu, sigma)

print(probability) # Output: 0.0228

This means that if the coin were fair, there would be **only a 2.28% chance** of getting 60 or more heads.

Inverse normal_cdf

- Python program using Inverse normal_cdf to find either the nontail region or the (symmetric) interval around the mean that accounts for a certain level of likelihood given the probability

```
def  normal_upper_bound(probability: float, mu: float = 0, sigma: float = 1) ->
float:
  """Returns the z for which P(Z <= z) = probability"""
  return inverse_normal_cdf(probability, mu, sigma)
def  normal_lower_bound(probability: float, mu: float = 0, sigma: float = 1) ->
float:
  """Returns the z for which P(Z >= z) = probability"""
  return inverse_normal_cdf(1 - probability, mu, sigma)

def normal_two_sided_bounds(probability: float, mu: float = 0, sigma: float = 1):
   """Returns the symmetric (about the mean) bounds that contain the specified
probability"""
  # Compute the tail probability before using it
  tail_probability = (1 - probability) / 2
  print(tail_probability)
  # Now use tail_probability in functions
  upper_bound = normal_lower_bound(tail_probability, mu, sigma)
  lower_bound = normal_upper_bound(tail_probability, mu, sigma)
  return lower_bound, upper_bound
mu,sigma=normal_approximation_to_binomial(1000,0.5)
print(mu,sigma)
lower,upper=normal_two_sided_bounds(0.95,mu,sigma)
```

- In particular, let's say that we choose to flip the coin n = 1,000 times.
- If our hypothesis of fairness is true, X should be distributed approximately normally with mean 500 and standard deviation 15.8:

```python
mu_0, sigma_0 = normal_approximation_to_binomial(1000, 0.5)

```

- We need to make a decision about significance—how willing we are to make a type 1 error ("false positive"), in which we reject H0 even though it's true.
- For reasons lost to the annals of history, this willingness is often set at 5% or 1%. Let's choose 5%.
- Consider the test that rejects H0 if X falls outside the bounds given by:

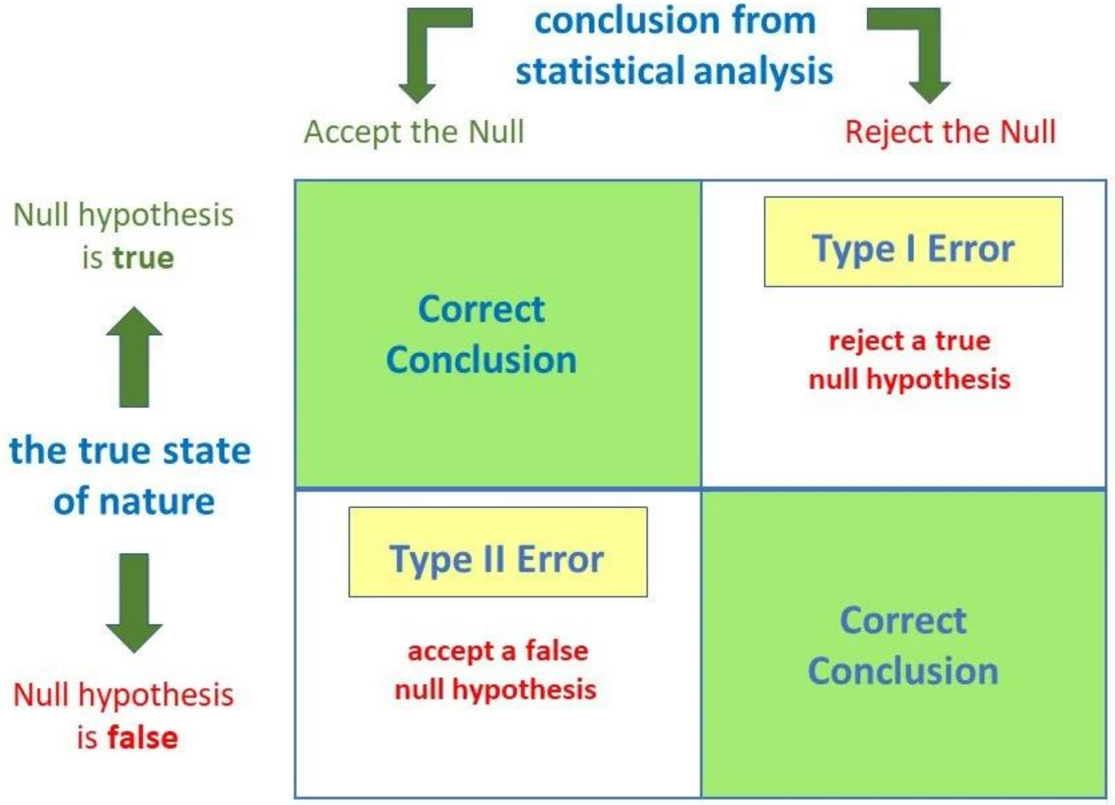
```python
# (469, 531)
lower_bound, upper_bound = normal_two_sided_bounds(0.95, mu_0, sigma_0)

```

- Assuming p really equals 0.5 (i.e., H0 is true), there is just a 5% chance we observe an X that lies outside this interval, which is the exact significance we wanted.

Types of Errors

Type 1 and Type 2 errors are inherent risks in hypothesis testing.

- **Type I error** means rejecting the null hypothesis when it's actually true,
- **Type II error** means failing to reject the null hypothesis when it's actually false



Types of Errors

A **Type 1 error** occurs when we reject a true null hypothesis (**H_0**). Let's apply this to a **coin tossed 1,000 times** scenario.

Hypothesis Setup

- **H_0 (Null Hypothesis):** The coin is fair (P(Heads) = 0.5).
- **H_1 (Alternative Hypothesis):** The coin is biased (P(Heads) ≠ 0.5).
- **Significance Level (α):** 0.05 (5%)

Scenario

- We toss the coin **1,000 times** and record the number of heads.
- If the coin is truly fair, the expected number of heads is **500** (since 1000 × 0.5 = 500).
- However, due to randomness, we may get slightly different results, say **530 or 470 heads**, which might still be reasonable for a fair coin.
- Suppose we set a decision rule:
  - If the number of heads is **outside the range 470–530**, we reject H_0 and conclude the coin is biased.

Types of Errors

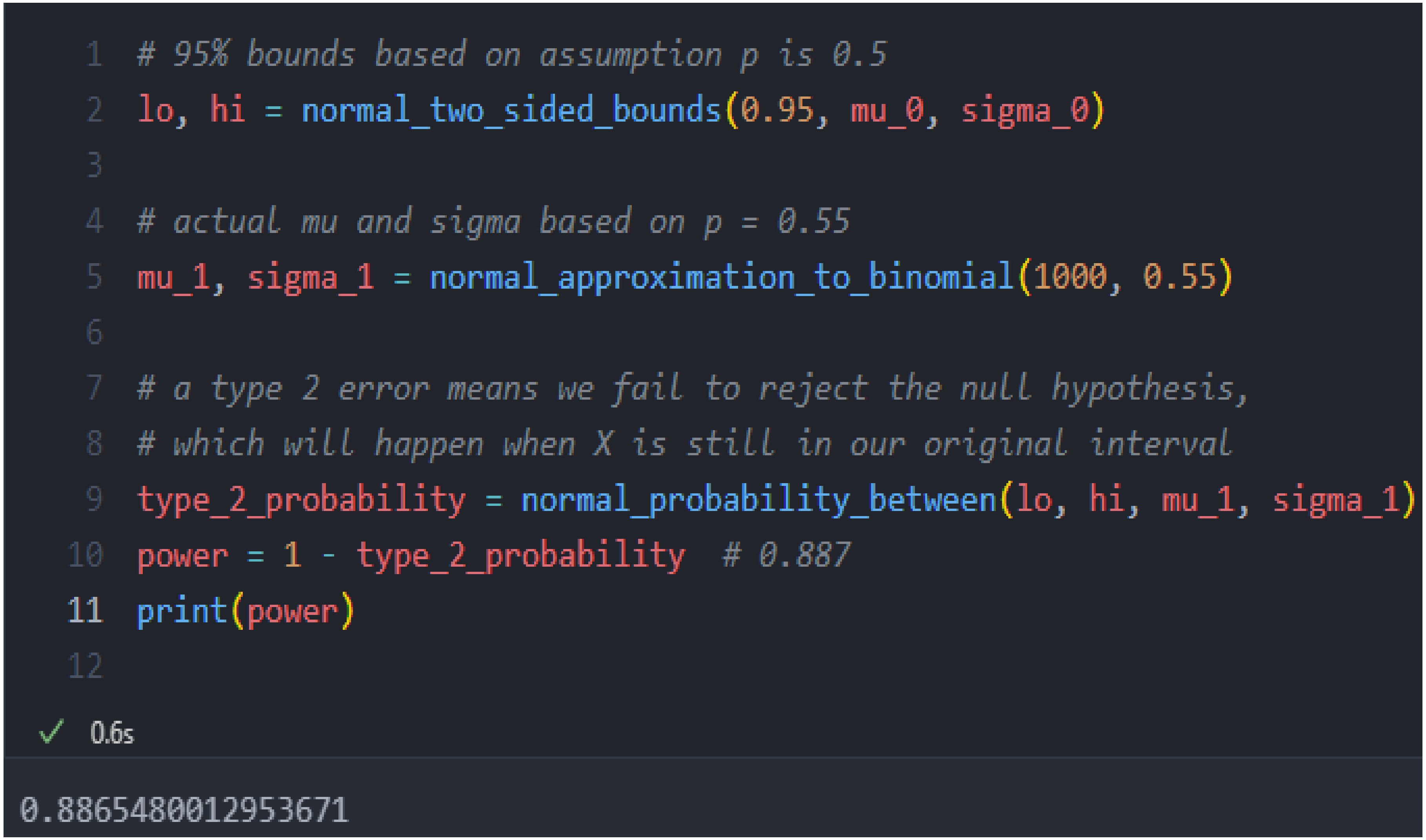
Type 1 Error (False Positive)

- The coin is actually **fair** (H_0 is true).
- Due to randomness, we observe **540 heads** (which is outside the accepted range of 470–530).
- We **incorrectly reject** H_0 and conclude the coin is biased.
- **This is a Type 1 error because we rejected a true null hypothesis.**

Type 2 Error (False Negative)

- The coin is actually **biased** (H_0 is false), and suppose P(Heads) = **0.55** instead of 0.5.
- The expected number of heads is **550** (since 1000 × 0.55 = 550).
- However, we happen to observe **525 heads**, which **falls within our acceptance range (470–530).**
- We **fail to reject** H_0 and incorrectly conclude that the coin is fair.
- **This is a Type 2 error because we failed to detect a biased coin when it was actually biased.**

Power of the test



```python
# 95% bounds based on assumption p is 0.5
lo, hi = normal_two_sided_bounds(0.95, mu_0, sigma_0)

# actual mu and sigma based on p = 0.55
mu_1, sigma_1 = normal_approximation_to_binomial(1000, 0.55)

# a type 2 error means we fail to reject the null hypothesis,
# which will happen when X is still in our original interval
type_2_probability = normal_probability_between(lo, hi, mu_1, sigma_1)
power = 1 - type_2_probability  # 0.887
print(power)

```

✓ 0.6s

```
0.8865480012953671
```

Power of a Hypothesis Test

The **power of a test** is the probability of correctly rejecting the null hypothesis (H_0) when the alternative hypothesis (H_1) is true. In other words, it measures how well the test detects a real effect (such as a biased coin).

$$\text{Power} = 1 - P(\text{Type 2 Error})$$

Since a **Type 2 error** (β) occurs when we fail to reject H_0 even though it is false, the power of the test is:

$$\text{Power} = 1 - \beta$$

Power Calculation for the Coin Toss Example (n = 1000, p = 0.55)

From our previous calculation:

- **Type 2 error probability (β) ≈ 0.102 (10.2%)**

Thus, the power of the test is:

$$\text{Power} = 1 - 0.102 = 0.898$$

So, the **power of this test is 89.8%**, meaning there is an **89.8% probability that we correctly detect the biased coin** when P(Heads) = 0.55.

p-Values

1. What is a p-Value?

A **p-value** (probability value) is a measure used in **hypothesis testing** to determine the strength of evidence against the **null hypothesis** (H_0). It answers the question:

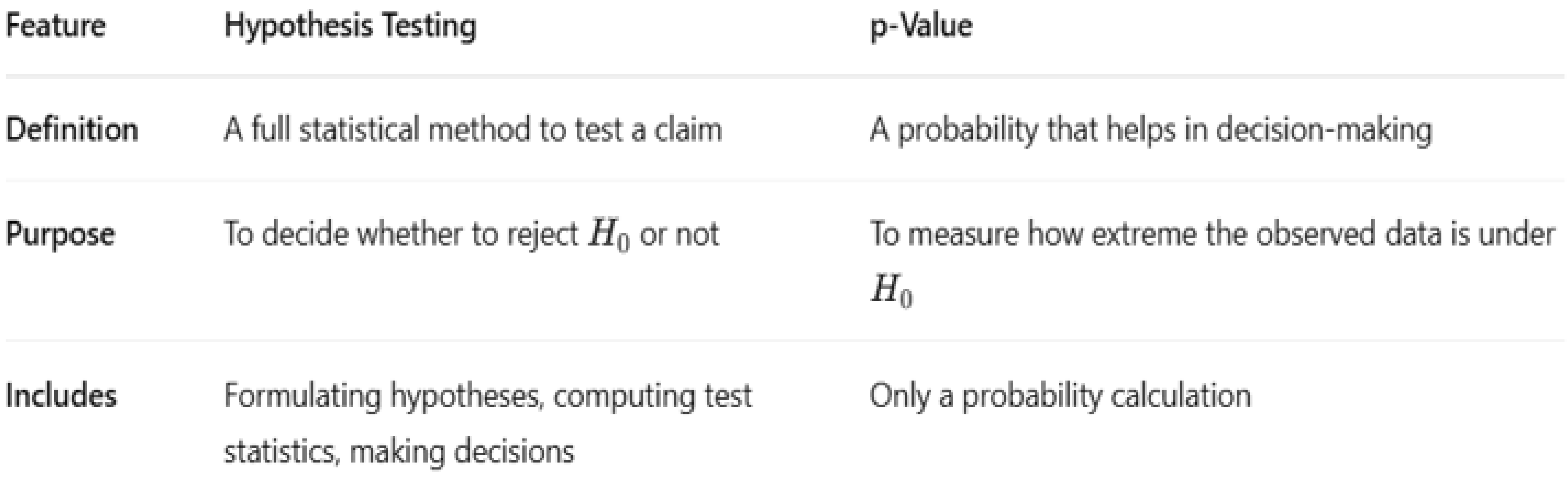
> **"If the null hypothesis were true, what is the probability of observing a test statistic at least as extreme as the one obtained?"**

- **A small p-value (typically ≤ 0.05)** indicates **strong evidence against** H_0, leading us to **reject the null hypothesis**.
- **A large p-value** (> 0.05) suggests **weak evidence against** H_0, meaning we **fail to reject** H_0.

p-value ≤ 0.05 → Reject H_0 (Strong evidence against H_0).

p-value > 0.05 → Fail to reject H_0 (Not enough evidence to conclude H_1).

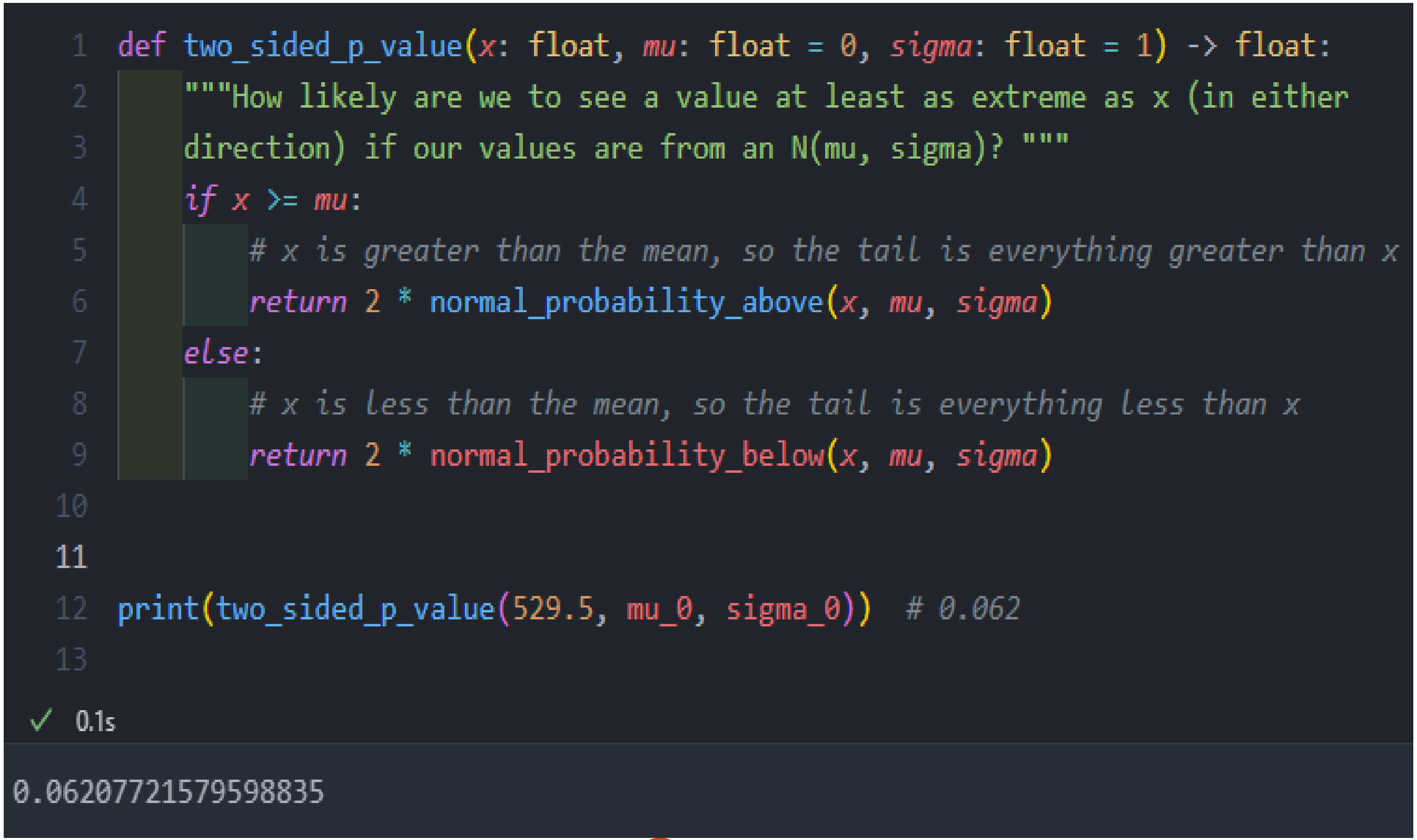
p-Values



Feature	Hypothesis Testing	p-Value
Definition	A full statistical method to test a claim	A probability that helps in decision-making
Purpose	To decide whether to reject H_0 or not	To measure how extreme the observed data is under H_0
Includes	Formulating hypotheses, computing test statistics, making decisions	Only a probability calculation

p-Values

- For our two-sided test of whether the coin is fair, we compute:
- **Python code snippet for two sided test to check whether coin is fair using p-values.**



```python
def two_sided_p_value(x: float, mu: float = 0, sigma: float = 1) -> float:
    """How likely are we to see a value at least as extreme as x (in either
    direction) if our values are from an N(mu, sigma)? """
    if x >= mu:
        # x is greater than the mean, so the tail is everything greater than x
        return 2 * normal_probability_above(x, mu, sigma)
    else:
        # x is less than the mean, so the tail is everything less than x
        return 2 * normal_probability_below(x, mu, sigma)


print(two_sided_p_value(529.5, mu_0, sigma_0))  # 0.062

```

✓ 0.1s

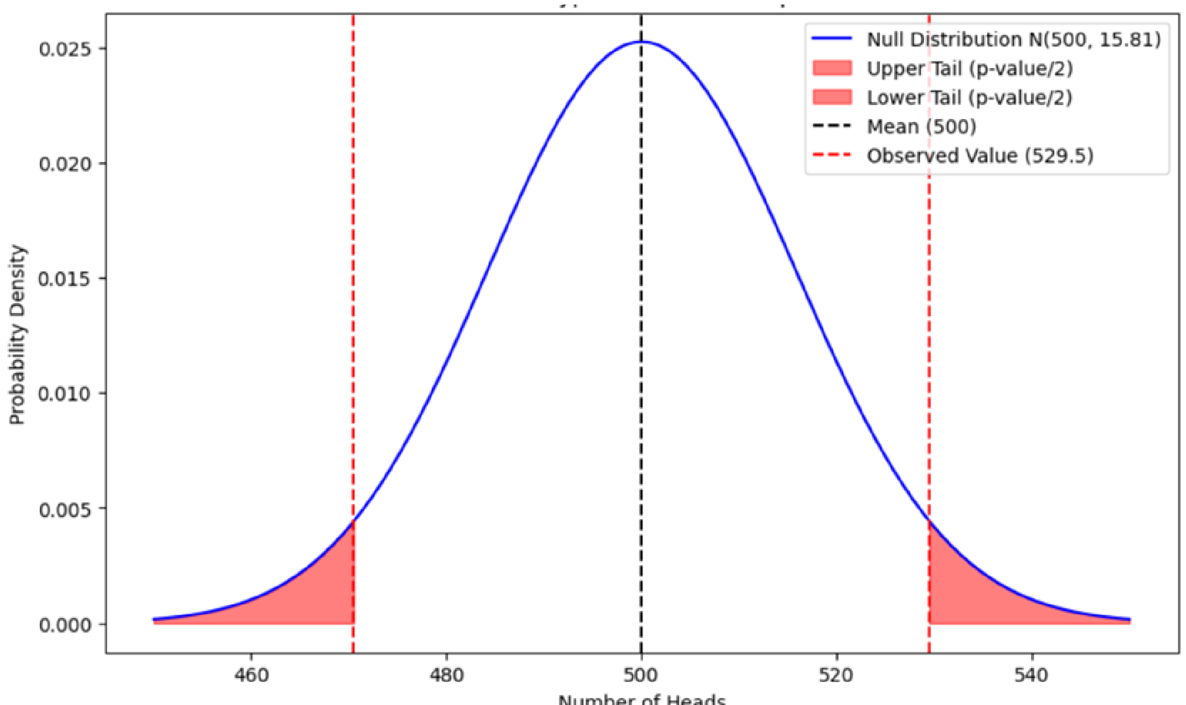
```
0.06207721579598835
```

Scenario: Testing If a Coin Is Biased

Suppose we flip a coin **1,000 times** and observe **570 heads.**

We want to test whether the coin is fair:

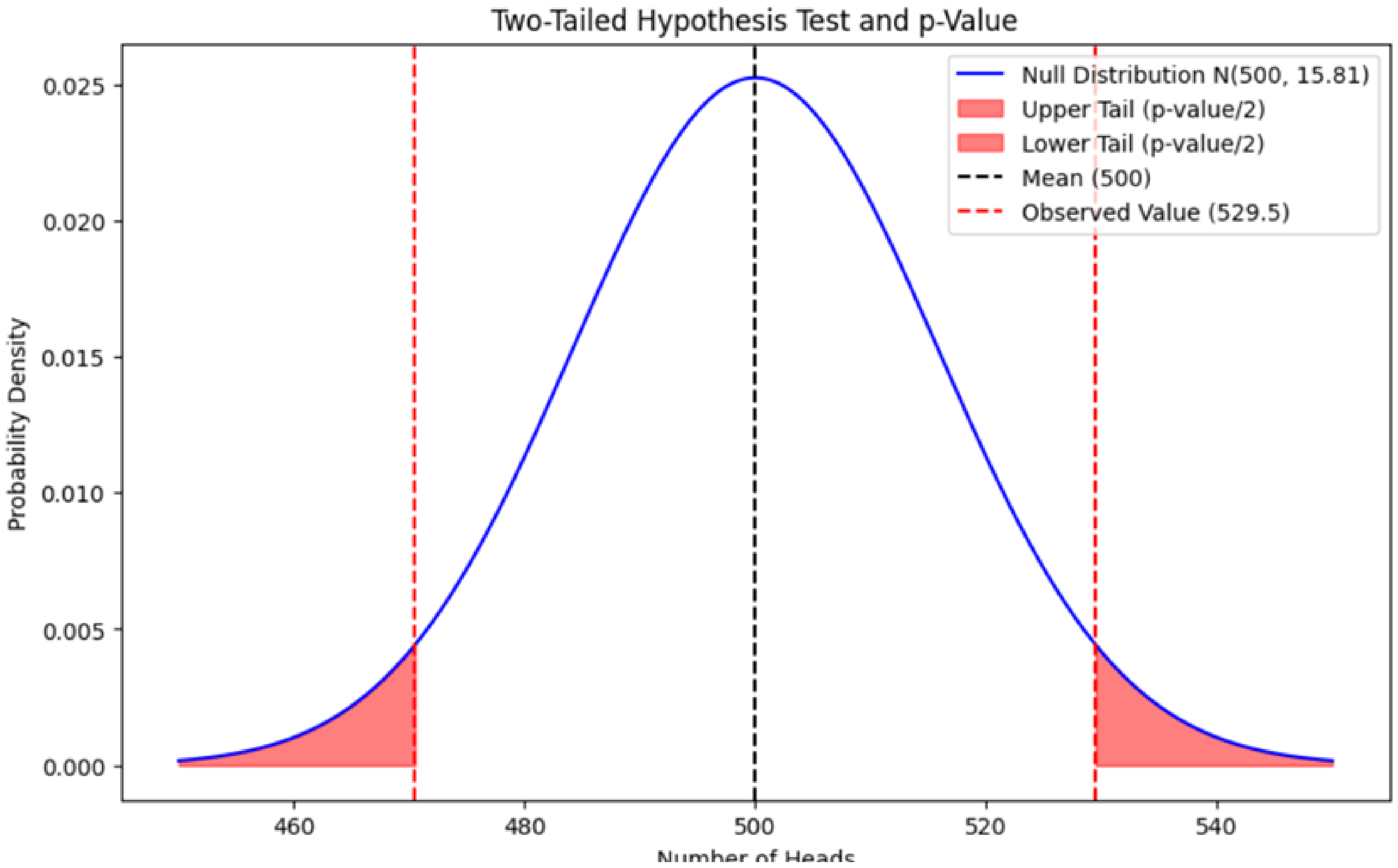
- **H_0 (Null Hypothesis):** The coin is fair → $P(\text{Heads}) = 0.5.$
- **H_1 (Alternative Hypothesis):** The coin is biased → $P(\text{Heads}) \neq 0.5.$
- **p-value = 0.000018** (very small, much less than 0.05).
- This means that **if the coin were fair**, the probability of observing **570 heads or more (or 430 heads or fewer)** is **0.0018%**.
- Since this is an **extremely unlikely** event under H_0, we **reject H_0.**
- **Conclusion: The coin is biased**—there is **strong evidence against fairness.**



```
print(two_sided_p_value(529.5, mu_0, sigma_0))  # 0.062
```

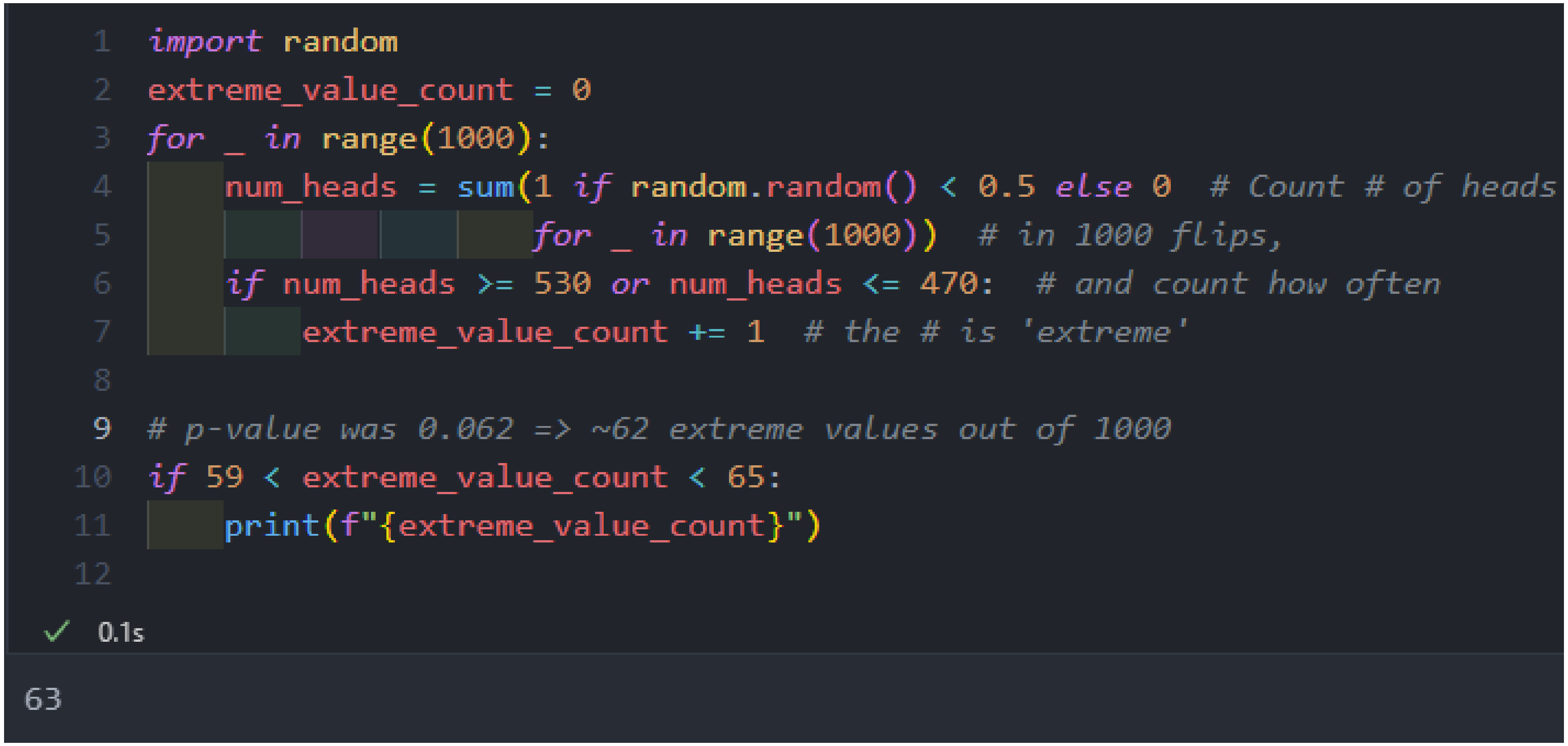
- The p-value is **0.062 (6.2%)**.
- This means that **if H_0 were true**, the probability of observing a result as extreme as **529.5** (in either direction) is **6.2%**.
- Since **0.062 > 0.05**, we **fail to reject H_0** at the 5% significance level.

Conclusion: There is **not enough evidence** to say the coin is biased.



p-Values

- One way to convince yourself that this is a sensible estimate is with a simulation:



```python
import random
extreme_value_count = 0
for _ in range(1000):
    num_heads = sum(1 if random.random() < 0.5 else 0  # Count # of heads
                    for _ in range(1000))  # in 1000 flips,
    if num_heads >= 530 or num_heads <= 470:  # and count how often
        extreme_value_count += 1  # the # is 'extreme'

# p-value was 0.062 => ~62 extreme values out of 1000
if 59 < extreme_value_count < 65:
    print(f"{extreme_value_count}")

```

✓ 0.1s

```
63
```

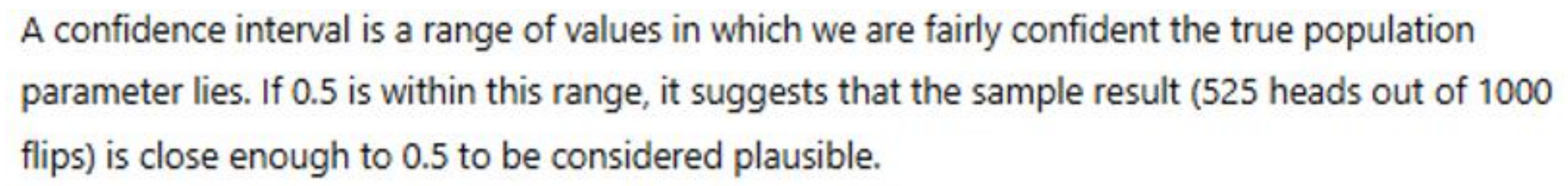
Confidence Intervals

- We’ve been testing hypotheses about the value of the heads probability p, which is a parameter of the unknown “heads” distribution.
- Another approach is to construct a **confidence interval around the observed value of the parameter.**
- A **confidence interval (CI)** is a range of values that is likely to contain the **true population parameter** (e.g., mean, proportion) with a certain level of confidence (usually **95% or 99%**).
- In hypothesis testing, confidence intervals help us determine:
  - ❖ Whether we **reject or fail to reject H_0**.
  - ❖ The **uncertainty** in our estimate of the population parameter.

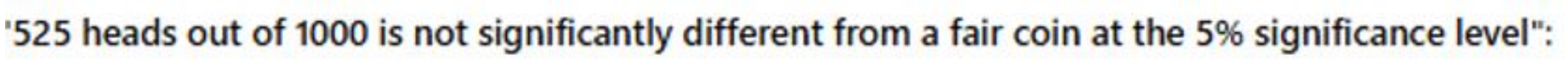
Confidence Intervals

- we observe 525 heads out of 1,000 flips, then we estimate *p* equals 0.525:
- **Python code snippet to find confidence Intervals for 525 heads observed out of 1000 coin flips**

```
p_hat = 525 / 1000
mu = p_hat
sigma = math.sqrt(p_hat * (1 - p_hat) / 1000) # 0.0158
normal_two_sided_bounds(0.95, mu, sigma)
# [0.4940, 0.5560]
```



A confidence interval is a range of values in which we are fairly confident the true population parameter lies. If 0.5 is within this range, it suggests that the sample result (525 heads out of 1000 flips) is close enough to 0.5 to be considered plausible.



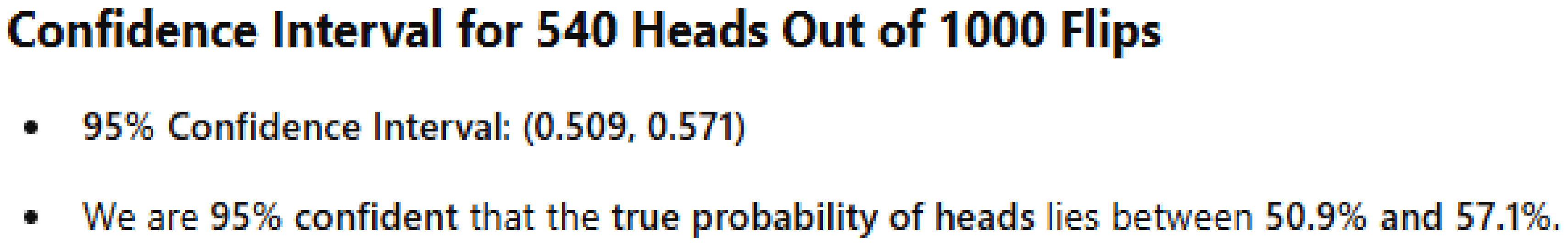
'525 heads out of 1000 is not significantly different from a fair coin at the 5% significance level":

Confidence Intervals

- If instead we'd seen 540 heads, then we'd have:

Python code snippet to find confidence Intervals for 540 heads observed out of 1000 coin flips

```
p_hat = 540 / 1000
mu = p_hat
sigma = math.sqrt(p_hat * (1 - p_hat) / 1000) # 0.0158
normal_two_sided_bounds(0.95, mu, sigma)
# [0.5091, 0.5709]
```



Confidence Interval for 540 Heads Out of 1000 Flips

- 95% Confidence Interval: (0.509, 0.571)
- We are 95% confident that the true probability of heads lies between 50.9% and 57.1%.

p-Hacking

- P-hacking, also known as **data snooping**, is the misuse of statistical analysis to find patterns in data that appear significant, even if they are not, by manipulating data collection and analysis
- P-hacking involves strategies to manipulate data analysis to achieve statistically significant results ($p < 0.05$), even when no real effect exists.
- **Examples of p-hacking**:
  - ❖ **Selective reporting**: Only reporting results that show significance while ignoring non-significant findings.
  - ❖ **Data dredging**: Running multiple statistical tests on the same data and only reporting the ones that yield significant results.
  - ❖ **Outlier removal**: Removing data points that don't fit the desired outcome.
  - ❖ **Altering** sample size or statistical models after initial analyses.
- **Real-world analogy:**
- **Imagine flipping a coin 100 times in secret and only showing the part where it lands heads 8 out of 10 times.**

p-Hacking

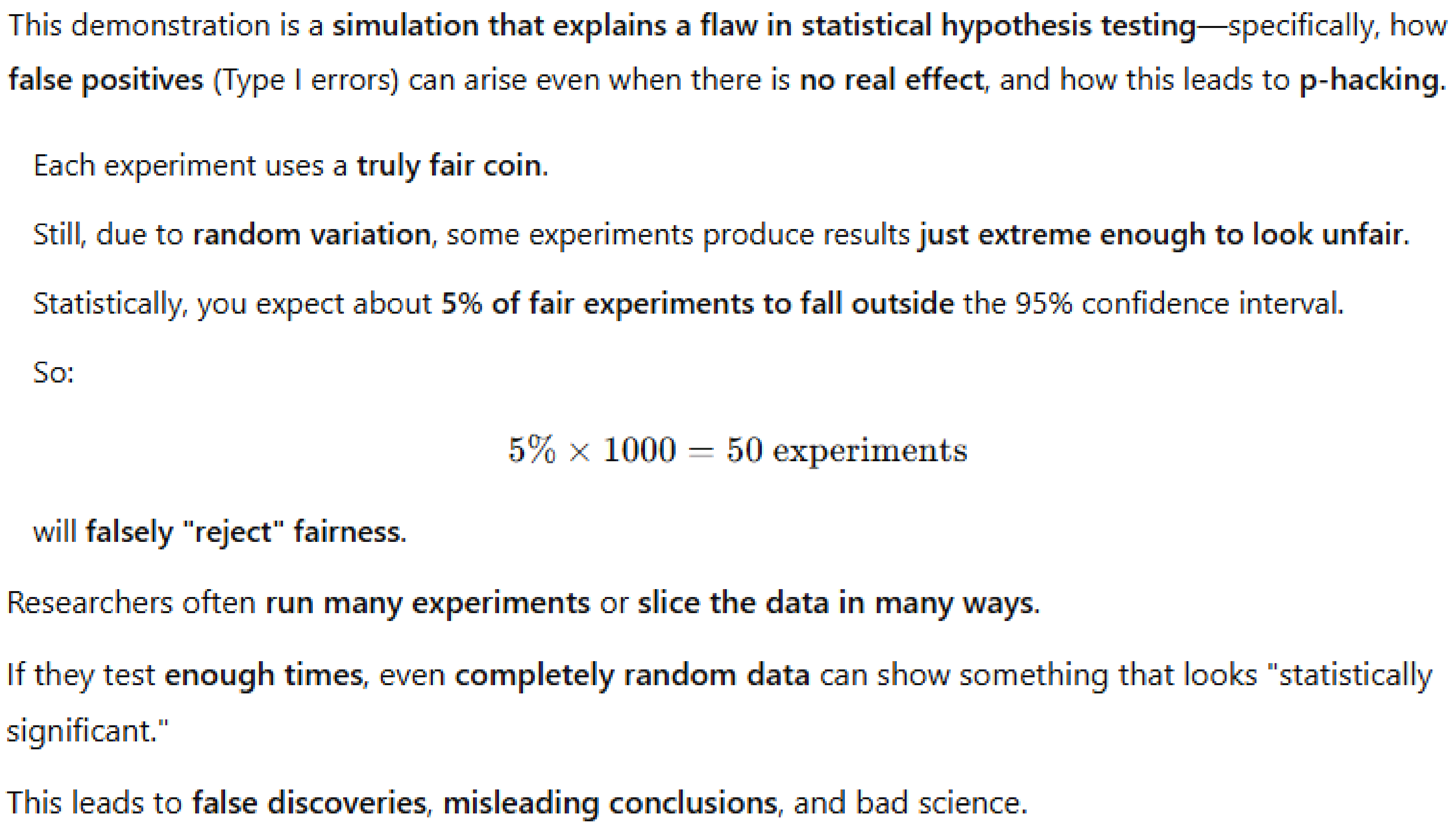
Python code snippet to demonstrate p-Hacking

```
import random
from typing import List
def run_experiment() -> List[bool]:
    """Flips a fair coin 1000 times, True = heads, False = tails"""
    return [random.random() < 0.5 for _ in range(1000)]
def reject_fairness(experiment: List[bool]) -> bool:
    """Uses a 5% significance level (two-tailed test) to check if the coin is fair"""
    num_heads = len([flip for flip in experiment if flip])
    print(num_heads)
     return num_heads < 469 or num_heads > 531  # 5% significance range for 1000
flips
random.seed(0)  # For reproducibility
# Run 1000 experiments
experiments = [run_experiment() for _ in range(1000)]
# Count how many experiments "reject" the fair coin hypothesis
num_rejections = len([ experiment for experiment in experiments if
reject_fairness(experiment)])
print(f"Number of false positives (rejecting a fair coin): {num_rejections}")
```

```
Number of false positives (rejecting a fair coin): 46
```

p-Hacking

- **What it demonstrates**



This demonstration is a **simulation that explains a flaw in statistical hypothesis testing**—specifically, how **false positives** (Type I errors) can arise even when there is **no real effect**, and how this leads to **p-hacking**.

Each experiment uses a **truly fair coin**.

Still, due to **random variation**, some experiments produce results **just extreme enough to look unfair**.

Statistically, you expect about **5% of fair experiments to fall outside** the 95% confidence interval.

So:

$$5\% \times 1000 = 50 \text{ experiments}$$

will **falsely "reject" fairness**.

Researchers often **run many experiments** or **slice the data in many ways**.

If they test **enough times**, even **completely random data** can show something that looks "statistically significant."

This leads to **false discoveries**, **misleading conclusions**, and bad science.

Example: Running an A/B Test

- One of your primary responsibilities at Data Sciencester is experience optimization.
- One of the advertisers has developed a new energy drink targeted at data scientists, and the VP of Advertisements wants your help choosing between advertisement A ("tastes great!") and advertisement B ("less bias!").
- Being a scientist, you decide to run an experiment by randomly showing site visitors one of the two advertisements and tracking how many people click on each one.
- If 990 out of 1,000 A-viewers click their ad, while only 10 out of 1,000 B-viewers click their ad, you can be pretty confident that A is the better ad.

Example: Running an A/B Test

- But what if the differences are **not so stark**? Here's where you'd use statistical inference.
- Let's say that N_A people see ad A, and that n_A of them click it.
- We can think of each ad view as a Bernoulli trial where $\boldsymbol{p_A}$ is the probability that someone clicks ad A.
- $\boldsymbol{p_A = n_A/N_A}$ is approximately a normal random variable with mean $\boldsymbol{p_A}$
- standard deviation $\sigma_A = \sqrt{p_A(1-p_A)/N_A}$

Example: Running an A/B Test

- Similarly, n_B/N_B is approximately a normal random variable with mean p_B and standard deviation

$$\sigma_B = \sqrt{p_B(1 - p_B)/N_B}$$

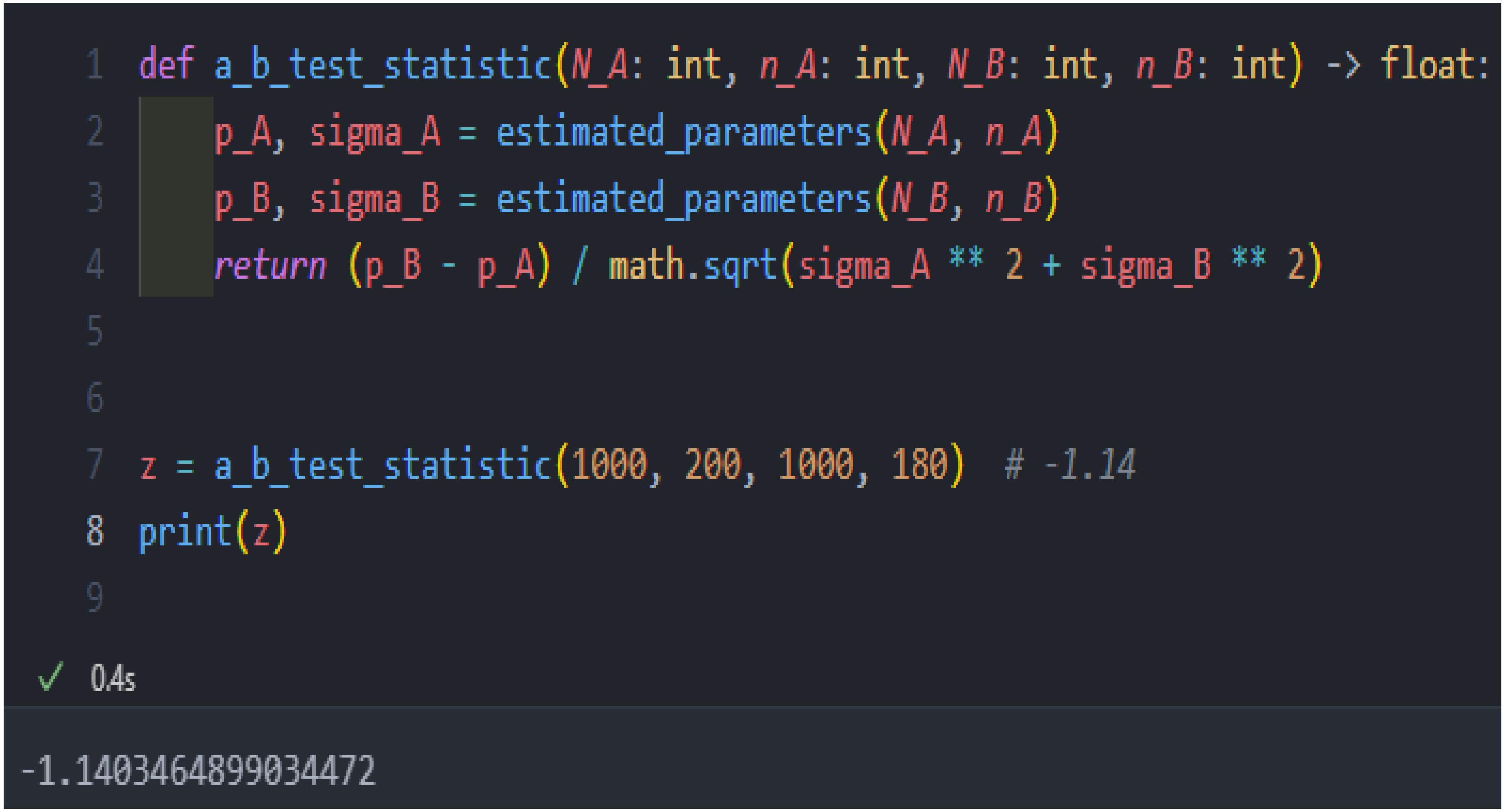
- We can express this in code as:

```
def estimated_parameters(N, n):
    p = n / N                          # observed proportion
    sigma = math.sqrt(p * (1 - p) / N)   # standard deviation of the
proportion
    return p, sigma
```

This tells you how far apart the two proportions (p_B and p_A) are **in terms of standard deviation** units — basically, how surprising the difference is

Example: Running an A/B Test

Python code snippet to Running an A/B Test



```
def a_b_test_statistic(N_A: int, n_A: int, N_B: int, n_B: int) -> float:
    p_A, sigma_A = estimated_parameters(N_A, n_A)
    p_B, sigma_B = estimated_parameters(N_B, n_B)
    return (p_B - p_A) / math.sqrt(sigma_A ** 2 + sigma_B ** 2)


z = a_b_test_statistic(1000, 200, 1000, 180)  # -1.14
print(z)

```

✓ 0.4s

```
-1.1403464899034472
```

Example: Running an A/B Test

Example 1: Not a Big Difference

"Tastes great" gets 200 clicks out of 1000 views ⟶ p_A = 0.20

"Less bias" gets 180 clicks out of 1000 views ⟶ p_B = 0.18

z = a_b_test_statistic(1000, 200, 1000, 180) # ≈ -1.14

two_sided_p_value(z) # ≈ 0.254

Interpretation:

A z-score of -1.14 means the observed difference is only 1.14 standard deviations below the mean (i.e., not very surprising).

A p-value of 0.254 = 25.4% chance of seeing such a difference due to random chance, even if both ads are equally effective.

Conclusion: The difference is not statistically significant.

Example: Running an A/B Test

Example 2: Likely a Real Difference

"Tastes great" gets 200 clicks out of 1000 views → p_A = 0.20“

Less bias" gets 150 clicks out of 1000 views → p_B = 0.15

z = a_b_test_statistic(1000, 200, 1000, 150) # ≈ -2.94

two_sided_p_value(z) # ≈ 0.003

Interpretation: A z-score of -2.94 means the difference is almost 3 standard deviations away.

A p-value of 0.003 = 0.3% chance this could happen just by random chance.

Conclusion: Statistically significant difference.

Bayesian Inference

- Statements about our *tests we made were like:*
- "*there's only a 5% chance you'd observe such an extreme statistic if our null hypothesis were true.*"
- An alternative approach to inference involves treating the unknown parameters as random variables.
- **The analyst (that's you) starts with a prior distribution for the parameters and then uses the observed data and Bayes's Theorem to get an updated posterior distribution for the parameters.**

Bayesian Inference

- The **Beta distribution** is often used as a **prior probability distribution** in **Bayesian statistics** — especially when you're modeling the probability of **binary outcomes**, like success/failure or heads/tails.
- The Beta distribution is a way to model beliefs about a probability (like the chance of a coin landing heads):
  - alpha = how many "successes" (e.g., heads) you believe in.
  - beta = how many "failures" (e.g., tails) you believe in.
  - Beta(1, 1) prior → this is uniform across [0, 1], meaning you have no preference or knowledge.
  - Beta(5, 2) → this encodes your belief that the probability of heads is likely around 70%.

Bayesian Inference

The Beta function, is used to normalize the Beta distribution. Makes sure the total area under the curve equals 1 (which is a requirement for any probability distribution).

$$B(\alpha, \beta) = \frac{\Gamma(\alpha) \cdot \Gamma(\beta)}{\Gamma(\alpha + \beta)}$$

Where:

- `Γ(n)` is the **Gamma function**, which generalizes factorial:

$$\Gamma(n) = (n-1)!$$

(only for positive integers)

Calculate `B(2, 3)`

$$B(2,3) = \frac{\Gamma(2) \cdot \Gamma(3)}{\Gamma(5)} = \frac{1! \cdot 2!}{4!} = \frac{1 \cdot 2}{24} = \frac{2}{24} = 0.0833$$

Bayesian Inference

Python code snippet for Beta Function

```
import math
def B(alpha, beta):
   return math.gamma(alpha) * math.gamma(beta) / math.gamma(alpha + beta)
```

Bayesian Inference

- The PDF gives the shape of the distribution —
  - ❖ It tells you how likely different values of the parameter (e.g., a coin's probability of heads) are.
- For the posterior, the PDF tells you:
  - ❖ “Given the data I’ve seen, how likely is each possible value of the parameter?”

Bayesian Inference

It's a **continuous probability distribution** used to model probabilities themselves. Represent uncertainty about a proportion, like:

$$f(x;\alpha,\beta) = \frac{x^{\alpha-1}(1-x)^{\beta-1}}{B(\alpha,\beta)} \quad \text{for } x \in [0,1]$$

Symbol	Meaning
x	The value you're evaluating (a probability between 0 and 1)
α	Shape parameter: related to prior "successes"
β	Shape parameter: related to prior "failures"
$B(\alpha,\beta)$	**Beta function** (a normalization constant so the total area under the curve = 1)
$x^{\alpha-1}(1-x)^{\beta-1}$	Shapes the distribution based on your belief about probability

Interpretation:

This formula gives the **height** (density) of the Beta distribution at any point $x \in [0,1]$.

The values of α and β **control the shape** of the distribution:

- High α: pushes the peak toward 1
- High β: pushes the peak toward 0
- Equal $\alpha = \beta$: makes it symmetric

Bayesian Inference

It's a **continuous probability distribution** used to model probabilities themselves. Represent uncertainty about a proportion, like:

$$f(x;\alpha,\beta) = \frac{x^{\alpha-1}(1-x)^{\beta-1}}{B(\alpha,\beta)} \quad \text{for } x \in [0,1]$$

Python code snippet for Continuous Probability Distribution in Bayesian Inference

```
def beta_pdf(x, alpha, beta):
    if x < 0 or x > 1: # no weight outside of [0, 1]
    return 0
    return x ** (alpha - 1) * (1 - x) ** (beta - 1) / B(alpha, beta)
```

Bayesian Inference

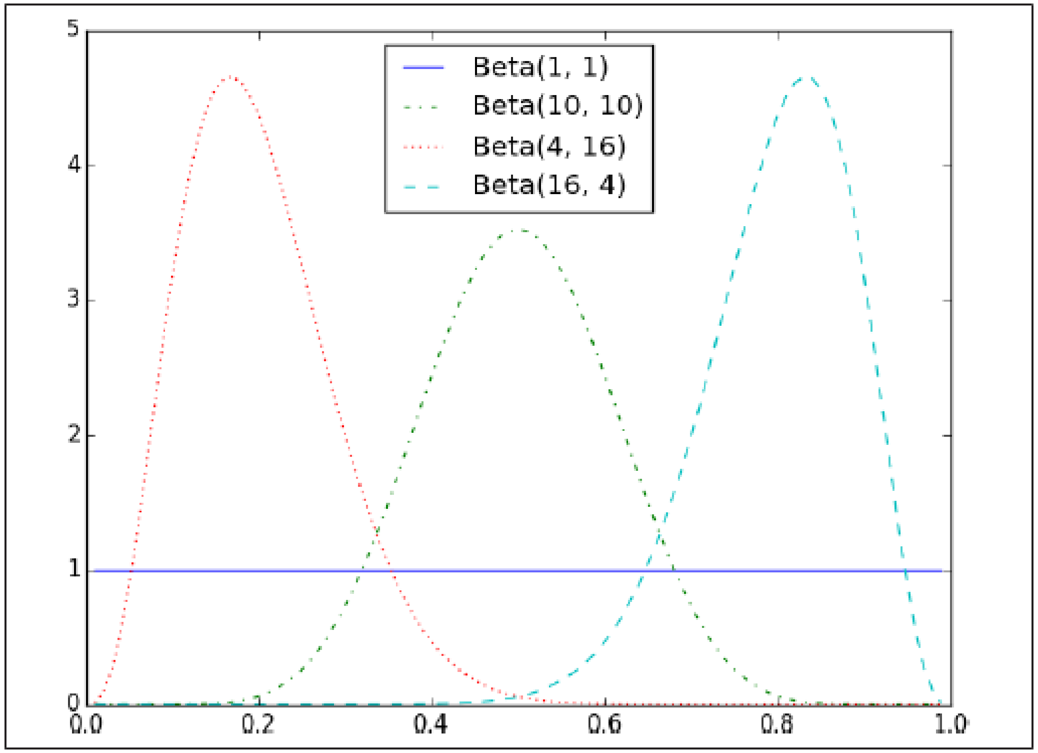


Figure 7-1. Example Beta distributions

- If alpha and beta are both 1, it's just the uniform distribution (centered at 0.5, very dispersed).
- If alpha is much larger than beta, most of the weight is near 1.
- And if alpha is much smaller than beta, most of the weight is near zero

Bayesian Inference

Bayes's Theorem Tells us that the posterior distribution for p is again a Beta distribution but with parameters alpha + h and beta + t.

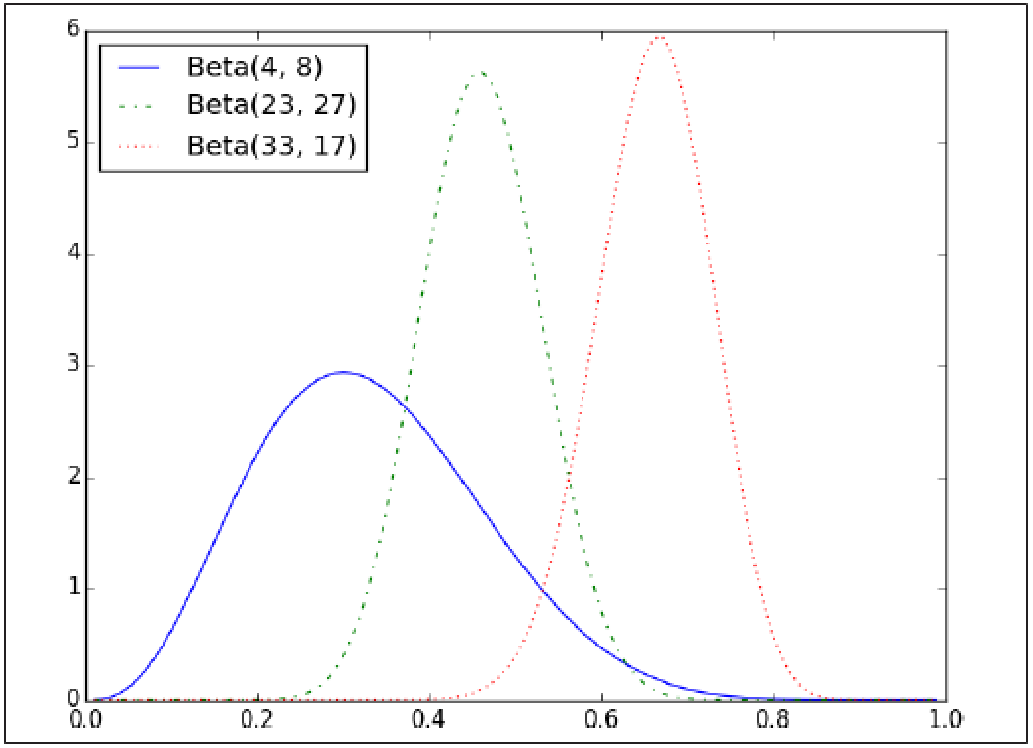


Figure 7-2. Posteriors arising from different priors

- Flip the coin 10 times and see only 3 heads.
- If you started with the uniform Beta(1,1) prior your posterior distribution would be a Beta(4, 8), centered around 0.33 your best guess is something pretty close to the observed probability.
- If you started with a Beta(20, 20) (expressing the belief that the coin was roughly fair), your posterior distribution would be a Beta(23, 27), centered around 0.46, indicating a revised belief that maybe the coin is slightly biased toward tails.
- And if you started with a Beta(30, 10) (expressing a belief that the coin was biased to flip 75% heads), your posterior distribution would be a Beta(33, 17), centered around 0.66

Gradient Descent

- Frequently when doing data science, we try to the find the **best model** for a certain situation.
- And usually "best" will mean something like "**minimizes the error of its predictions**" or "**maximizes the likelihood of the data.**"
- In other words, it will represent the solution to some sort of **optimization problem**.
- This means we'll need to solve a number of optimization problems. And need to solve them from scratch.
- Our approach will be a technique called ***gradient descent***, which lends itself pretty well to a from scratch treatment.

- Gradient descent is an optimization algorithm used in machine learning to find the minimum of a function, typically a cost or loss function, by iteratively adjusting the model's parameters.
- It works by moving in the direction of the steepest descent, akin to rolling downhill on a hill, until a minimum is reached.
- It's an iterative process where the algorithm repeatedly adjusts the parameters of a model in the direction that decreases the cost function, aiming to find the optimal parameter values.

The Idea Behind Gradient Descent

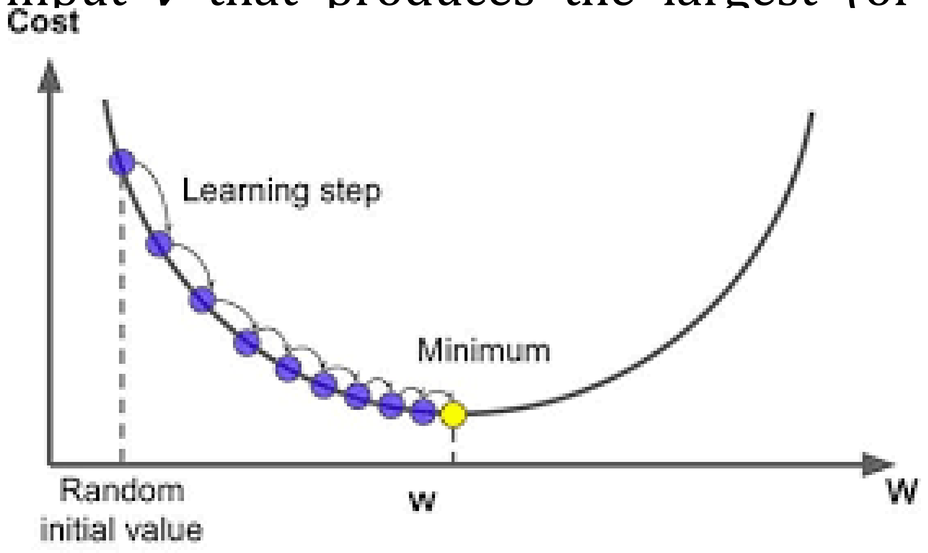
- Suppose we have some function ***f*** that takes as input a vector of real numbers and outputs a single real number. One simple such function is:

def *sum_of_squares(v):*

"""computes the sum of squared elements in v"""

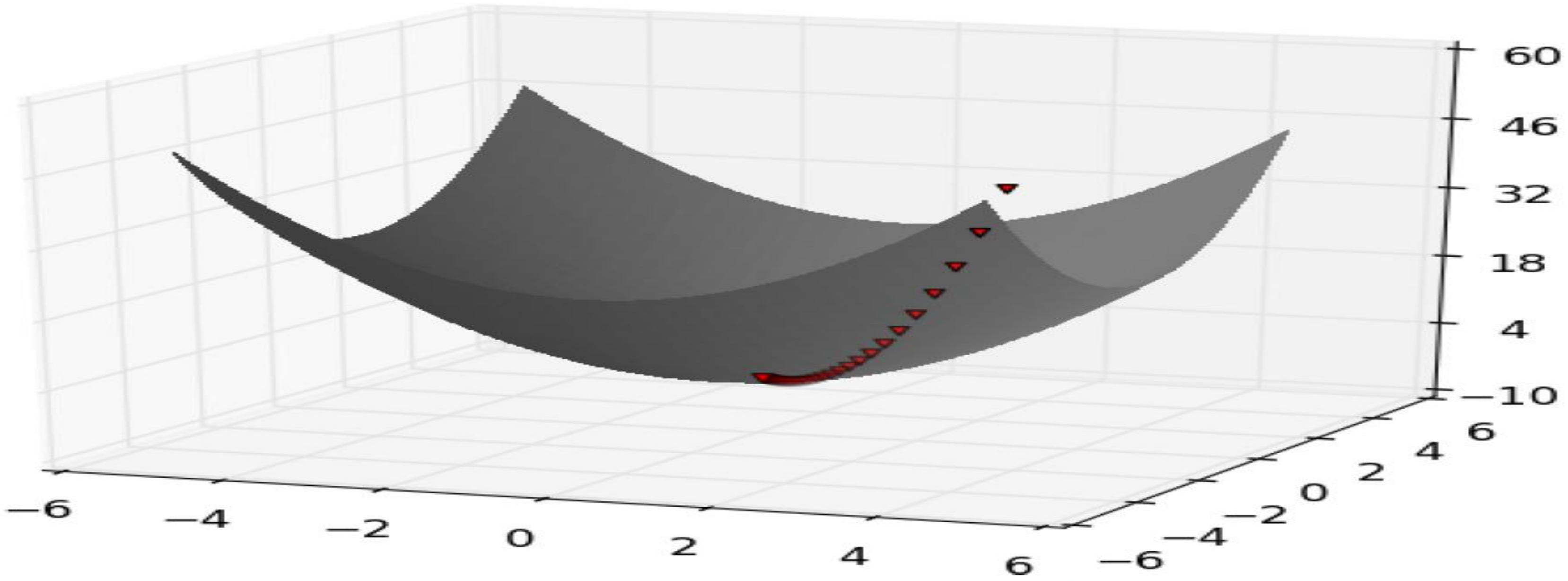
return *sum(v_i ** 2* ***for*** *v_i* ***in*** *v)*

- We'll frequently need to maximize or minimize such functions.
- That is, we need to find the input ***v*** that produces the largest (or smallest) possible value.



The Idea Behind Gradient Descent

- For functions like ours, the gradient (if you remember your calculus, this is the vector of partial derivatives) gives the input direction in which the function most quickly increases.
- Accordingly, one approach to maximizing a function is to pick a random starting point, compute the gradient, take a small step in the direction of the gradient (i.e., the direction that causes the function to increase the most), and repeat with the new starting point.
- Similarly, you can try to minimize a function by taking small steps in the opposite direction, as shown in Figure



Finding a minimum using gradient descent

Estimating the Gradient

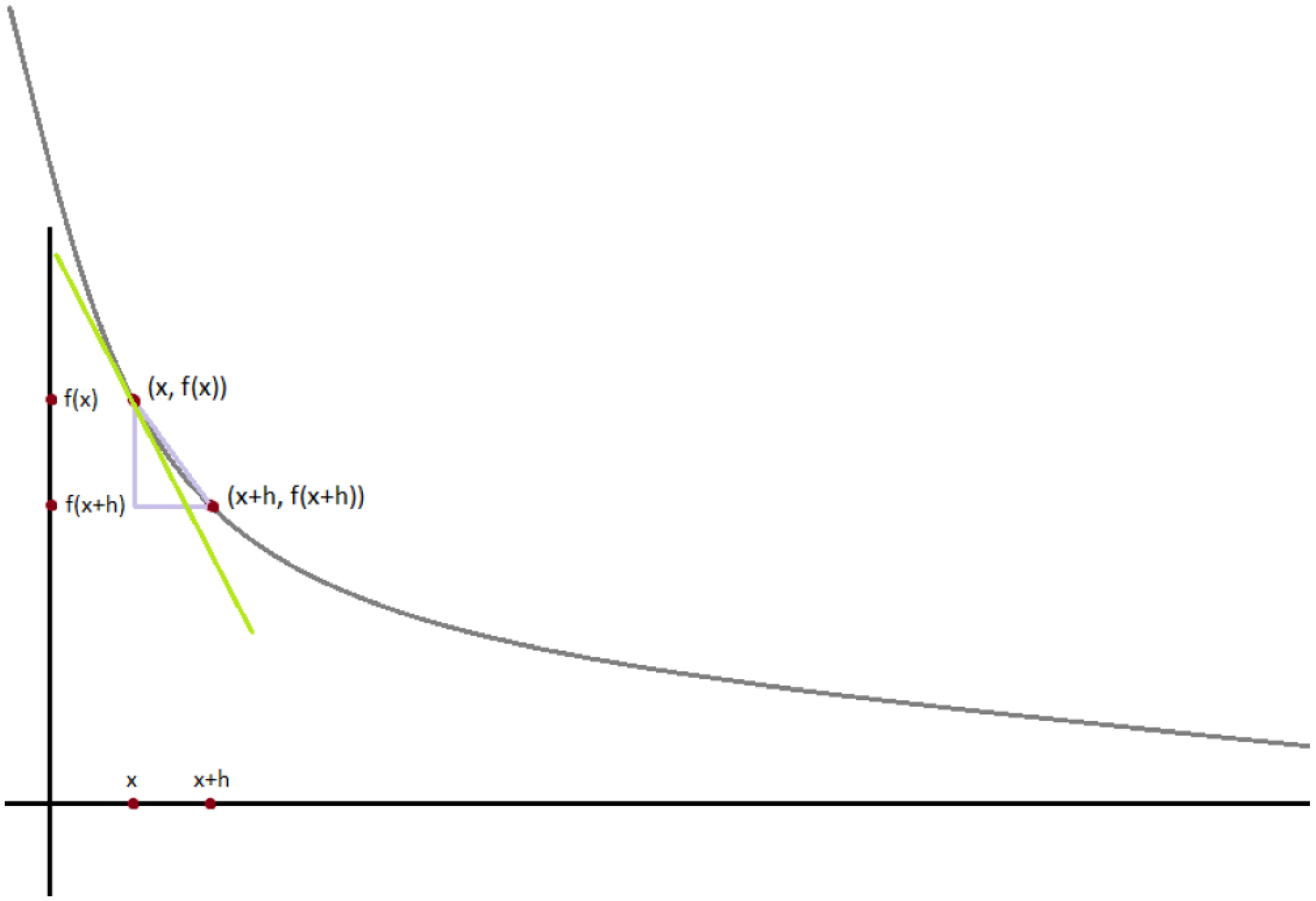
- If ***f*** is a function of one variable, its derivative at a point ***x*** measures how ***f(x)*** changes when we make a very small change to ***x***.
- The derivative is defined as the limit of the difference quotients:

```
def square(x):
        return x * x
def derivative(x):
        return 2 * x
def difference_quotient(f, x, h):
        return (f(x + h) - f(x)) / h
```

as h approaches zero.

- The derivative is the slope of the tangent line at (x, f(x)), while the difference quotient is the slope of the not-quite-tangent line that runs through (x + h, f(x + h)).
- As h gets smaller and smaller, the not-quite-tangent line gets closer and closer to the tangent line

Estimating the Gradient

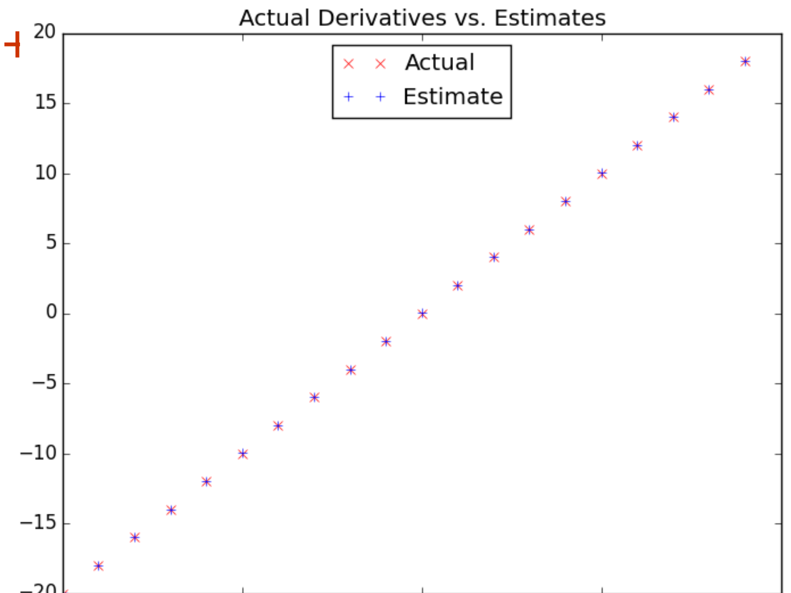


Approximating a derivative with a difference quotient

Estimating the Gradient

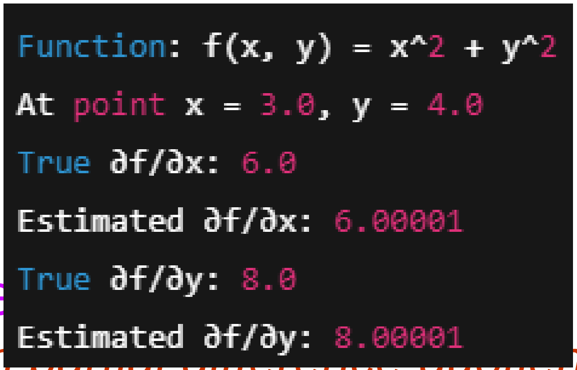
Python code snippet for estimating gradient for X^2 and plot the graph for Actual Derivatives Vs Estimates

```
derivative_estimate = partial(difference_quotient, square, h=0.00001)
# plot to show they're basically the same
import matplotlib.pyplot as plt
x = range(-10,10)
plt.title("Actual Derivatives vs. Estimates")
plt.plot(x, map(derivative, x), 'rx', label='Actual') # red x
plt.plot(x, map(derivative_estimate, x), 'b+
plt.legend(loc=9)
plt.show()
```



Estimating the Gradient

- When ***f*** is a function of many variables, it has multiple partial derivatives, each indicating how ***f*** changes when we make small changes in just one of the input variables.



```
Function: f(x, y) = x^2 + y^2
At point x = 3.0, y = 4.0
True ∂f/∂x: 6.0
Estimated ∂f/∂x: 6.00001
True ∂f/∂y: 8.0
Estimated ∂f/∂y: 8.00001
```

```
def partial_differe                              :
    """compute the ith                   t of f at v"""
    w = [v_j + (h if j == i else 0) for j, v_j in enumerate(v)]
    return (f(w) - f(v)) / h
def estimate_gradient(f, v, h=0.00001):
  return [partial_difference_quotient(f, v, i, h) for i, _ in enumerate(v)]
```

- We calculate its ***i***th partial derivative by treating it as a function of just its ***i***th variable, holding the other variables fixed:

Using Gradient Descent

- It’s easy to see that the ***sum_of_squares*** function is smallest when its input ***v*** is a vector of zeros.
- But imagine we didn’t know that.
- Let’s use gradients to find the minimum among all three-dimensional vectors.
- We’ll just pick a random starting point and then take tiny steps in the opposite direction of the gradient until we reach a point where the gradient is very small:

Using Gradient Descent

Python Program to find the minimum among all three-dimensional vectors using gradients

```
import random
from scratch.linear_algebra import distance, add, scalar_multiply
def gradient_step(v: Vector, gradient: Vector, step_size: float) -> Vector:
	"""Moves `step_size` in the `gradient` direction from `v`"""
	assert len(v) == len(gradient)
	step = scalar_multiply(step_size, gradient)
	return add(v, step)
def sum_of_squares_gradient(v: Vector) -> Vector:
	 return [2 * v_i for v_i in v]
# pick a random starting point
v = [random.uniform(-10, 10) for i in range(3)]
for epoch in range(1000):
	grad = sum_of_squares_gradient(v) # compute the gradient at v
	v = gradient_step(v, grad, -0.01) # take a negative gradient step
	print(epoch, v)
assert distance(v, [0, 0, 0]) < 0.001 # v should be close to 0
```

Choosing the right step size

- Although the rationale for moving against the gradient is clear, how far to move is not.
- Indeed, choosing the right step size is more of an art than a science.
- Popular **options** include:
  - Using a fixed step size
  - Gradually shrinking the step size over time
  - At each step, choosing the step size that minimizes the value of the objective function
- The last approach sounds great but is, in practice, a costly computation.
- To keep things simple, we'll mostly just use **a fixed step size.**
- The step size that "works" depends on the problem—too small, or too big, **will need to experiment**.

Choosing the right step size

- We’ll be using gradient descent to fit parameterized models to data.
- In the usual case, we’ll have some dataset and some (hypothesized) model for the data that depends (in a differentiable way) on one or more parameters.
- We’ll also have a loss function that measures how well the model fits our data. (Smaller is better.)
- If we think of our data as being fixed, then our loss function tells us how good or bad any particular model parameters are.
- This means we can use gradient descent to find the model parameters that make the loss as small as possible.

Using Gradient Descent to Fit Models

- Let’s think about what that gradient means.
- Imagine for some x our prediction is too large. In that case the error is positive.
- The second gradient term, 2 * error, is positive, which reflects the fact that small increases in the intercept will make the (already too large) prediction even larger, which will cause the squared error (for this x) to get even bigger.
- The first gradient term, 2 * error * x, has the same sign as x.
- Sure enough, if x is positive, small increases in the slope will again make the prediction (and hence the error) larger.

Using Gradient Descent to Fit Models

- If x is negative, though, small increases in the slope will make the prediction (and hence the error) smaller.
- Now, that computation was for a single data point. For the whole dataset we'll look at the mean squared error.
- And the gradient of the mean squared error is just the mean of the individual gradients.
- So, here's what we're going to do:
    1. Start with a random value for theta.
    2. Compute the mean of the gradients.
    3. Adjust theta in that direction.
    4. Repeat.

Using Gradient Descent to Fit Models

- Let’s look at a simple example:

Python Program to demonstrate use of gradient descent is used to fit parameterized model Y=20X+5

```
# x ranges from -50 to 49, y is always 20 * x + 5
inputs = [(x, 20 * x + 5) for x in range(-50, 50)]
def linear_gradient(x: float, y: float, theta: Vector) -> Vector:
    slope, intercept = theta
    predicted = slope * x + intercept # The prediction of the model.
    error = (predicted - y) # error is (predicted - actual).
    squared_error = error ** 2 # We'll minimize squared error
    grad = [2 * error * x, 2 * error] # using its gradient.
    return grad
```

Using Gradient Descent to Fit Models

After a lot of epochs (what we call each pass through the dataset), we should learn something like the correct parameters:

```
 from scratch.linear_algebra import vector_mean
# Start with random values for slope and intercept
theta = [random.uniform(-1, 1), random.uniform(-1, 1)]
learning_rate = 0.001
for epoch in range(5000):
    # Compute the mean of the gradients
    grad = vector_mean([linear_gradient(x, y, theta) for x, y in inputs])
    # Take a step in that direction
    theta = gradient_step(theta, grad, -learning_rate)
    print(epoch, theta)
slope, intercept = theta
assert 19.9 < slope < 20.1, "slope should be about 20"
assert 4.9 < intercept < 5.1, "intercept should be about 5"
```

Minibatch Gradient Descent

- One drawback of the preceding approach is that we had to evaluate the gradients on the entire dataset before we could take a gradient step and update our parameters.
- In this case it was fine, because our dataset was only 100 pairs and the gradient computation was cheap.
- Your models, however, will frequently have large datasets and expensive gradient computations.
- In that case you’ll want to take gradient steps more often.
- We can do this using a technique called ***minibatch gradient descent***, in which we compute the gradient (and take a gradient step) based on a “minibatch” sampled from the larger dataset:

Minibatch Gradient Descent

Python Code Snippet to demonstrate use of Minibatch gradient descent to fit parameterized model Y=20X+5

```
from typing import TypeVar, List, Iterator
T = TypeVar('T') # this allows us to type "generic" functions
def minibatches(dataset: List[T], batch_size: int, shuffle: bool = True) ->
Iterator[List[T]]:
    """Generates `batch_size`-sized minibatches from the dataset"""
    # start indexes 0, batch_size, 2 * batch_size, ...
    batch_starts = [start for start in range(0, len(dataset),batch_size)]
    if shuffle: random.shuffle(batch_starts) # shuffle the batches
    for start in batch_starts:
        end = start + batch_size
        yield dataset[start:end]
```

Minibatch Gradient Descent

```
theta = [random.uniform(-1, 1), random.uniform(-1, 1)]
for epoch in range(1000):
    for batch in minibatches(inputs, batch_size=20):
        grad = vector_mean([linear_gradient(x, y, theta) for x, y in
        batch])
        theta = gradient_step(theta, grad, -learning_rate)
        print(epoch, theta)
slope, intercept = theta
assert 19.9 < slope < 20.1, "slope should be about 20"
assert 4.9 < intercept < 5.1, "intercept should be about 5"
```

- **Stochastic Gradient Descent**
- Using the batch approach, each gradient step requires us to make a prediction and compute the gradient for the **whole data set**, which makes each step take a long time.
- Now, usually these error functions are additive, which means that the predictive error on the whole data set is simply the sum of the predictive errors for each data point.
- When this is the case, we can instead apply a technique called stochastic gradient descent, which computes the gradient (and takes a step) for only one point at a time.
- It cycles over our data repeatedly until it reaches a stopping point.

Stochastic Gradient Descent

Stochastic Gradient Descent

Python Code Snippet to demonstrate use of Stochastic gradient descent to fit parameterized model Y=20X+5

```
theta = [random.uniform(-1, 1), random.uniform(-1, 1)]
for epoch in range(100):
        for x, y in inputs:
                grad = linear_gradient(x, y, theta)
                theta = gradient_step(theta, grad, -learning_rate)
        print(epoch, theta)
slope, intercept = theta
assert 19.9 < slope < 20.1, "slope should be about 20"
assert 4.9 < intercept < 5.1, "intercept should be about 5"
```