Inferential Statistics = Drawing conclusions about the whole school from the few students you measured.

? Key concepts explained simply:

✅ 1) Point Estimation

A **single number** that is your best guess of the population value.
? Example:

- The **sample mean** (\bar{x}) of your measured students is **5.3 feet** → that's your best guess for the school average.

✅ 2) Confidence Intervals (CI)

A **range of values** that you believe contains the true population mean.
? Example:

- You might say:

  "I am **95% confident** the school's average height is between **5.1 and 5.5 feet**."

✅ 3) Hypothesis Testing

You want to **make a decision** based on evidence.
? Steps:

1. **State Hypotheses**:
   - H0 (Null): No difference — average height = 5.0 feet.
   - H1 (Alt): Average height is different from 5.0 feet.
2. **Collect Data & Compute a Test Statistic** (e.g. t-value or z-value).
3. **Get p-value** = probability of seeing your data if H0 is true.
4. **Decision Rule**:
   - If p-value < α (e.g. 0.05) → Reject H0 (your data provides evidence against it).

- Else → Fail to Reject H0 (your data isn't strong enough to say there's a difference).

✅ 4) Significance (α)

Your chosen **cutoff for surprise** — often $\alpha = 0.05$ (5%).
? Meaning:

- If there's less than 5% chance your data could happen if H0 were true, you say it's "significant."

✅ 5) Errors

When deciding, you can make **mistakes**:

Error	Meaning
Type I Error (α)	False alarm — rejecting H0 when it's actually true.
Type II Error (β)	Miss — failing to reject H0 when it's false.
Power = $1-\beta$	Your test's ability to detect a real effect.

? t-Statistic Formula (one-sample):

t=x¯−μ0s/nt

Where:

- $\bar{x}$= sample mean
- μ_0= hypothesized mean
- s= sample standard deviation
- n = sample size

? Key Steps:

1. Set up null & alternative hypotheses.
2. Choose **significance level** α (e.g. 0.05).
3. Compute the **t-statistic**.

4. Find the **critical value** or compute **p-value**.
5. Make a decision:
    - If $p < \alpha$ → Reject H_0
    - Else → Fail to reject H_0

Python Example — One-sample t-Test:

```
import numpy as np
from scipy import stats

# Sample data: average weight of 10 people
data = np.array([58, 60, 62, 57, 63, 59, 61, 60, 58, 62])

# Test if mean is different from 60
t_stat, p_val = stats.ttest_1samp(data, popmean=60)
print(f"t-statistic = {t_stat:.3f}, p-value = {p_val:.3f}")

if p_val < 0.05:
    print("Reject the null hypothesis")
else:
    print("Fail to reject the null hypothesis")
```

Independent two-sample t-Test:

? Goal:

Test if the mean scores of **two different groups** are significantly different.

? Imagine this example:

We have test scores of two classes:

- class_A: students who studied with Method A
- class_B: students who studied with Method B

We want to check if the **average scores** differ.

Python code example:

Here’s a **complete example** you can copy & run:

```
import numpy as np
from scipy import stats

# Sample data: test scores for two classes
class_A = np.array([78, 85, 90, 88, 76, 84, 79, 91, 85, 87])  # Method A
class_B = np.array([72, 70, 68, 74, 69, 73, 70, 67, 75, 71])  # Method B

# Compute the mean for each
print(f"Mean of class_A: {np.mean(class_A):.2f}")
print(f"Mean of class_B: {np.mean(class_B):.2f}")

# Perform independent two-sample t-Test
t_stat, p_val = stats.ttest_ind(class_A, class_B)
print(f"\nT-statistic = {t_stat:.3f}, p-value = {p_val:.4f}")

# Check if significant
alpha = 0.05
if p_val < alpha:
    print(f"Reject the null hypothesis (p < {alpha}). The means are significantly different.")
else:
    print(f"Fail to reject the null hypothesis (p ≥ {alpha}). No significant difference between means.")
```

? **Example Output**:

```
Mean of class_A: 84.30
Mean of class_B: 70.90

T-statistic = 9.201, p-value = 0.0000
Reject the null hypothesis (p < 0.05). The means are significantly different.
```

What is a Z-Test?

A **Z-Test** is a **parametric hypothesis test** you use to check if a sample mean is significantly different from a **known population mean**, **when the population's standard deviation (σ) is known** and the sample size is large (usually $n \geq 30$).

✅ When to use a Z-Test?

- Population standard deviation (σ) is known.
- Sample size is **large** (typically $n \geq 30$), so the Central Limit Theorem applies.
- Data is approximately **normally distributed**.

✅ When to use two-tailed:

Example: Testing the Mean Weight of a Product

Imagine a factory claims its **average box weight** is **500 grams**.
You take a **sample of 50 boxes** and find that the **sample mean is 503 grams** with a **standard deviation of 10 grams**.

You want to know:

> *Is the average box weight different from 500 grams?*

That's a **two-tailed** test because we care about **both** possibilities:

- The boxes could be **heavier** than 500 grams, or
- The boxes could be **lighter** than 500 grams.

Compute the two-tailed p-value:

Here's Python code you could run:

```
from scipy.stats import norm

z_stat = 2.12
p_value = 2 * (1 - norm.cdf(abs(z_stat)))
print(f"P-Value = {p_value:.4f}")
```

Test Statistic (Z):

$z=\bar{x}-\mu_0\sigma/nz$

Where:

- $\bar{x}$: sample mean
- μ_0= hypothesized mean

- σ: population standard deviation
- n: sample size

Python Example — One-sample Z-Test

Here’s a practical example using scipy.stats.norm for the p-value:

```
import numpy as np
from scipy.stats import norm

# □ □Sample data
data = np.array([102, 98, 105, 100, 97, 101, 99, 104, 100, 98])  # n=10
sample_mean = np.mean(data)         # sample mean
pop_mean = 100                      # hypothesized mean
pop_std = 3                         # known population std deviation
n = len(data)

# □ □Compute the z statistic
z_stat = (sample_mean - pop_mean) / (pop_std / np.sqrt(n))
print(f"Z-Statistic = {z_stat:.3f}")

# □ □Two-tailed p-value
p_value = 2 * (1 - norm.cdf(abs(z_stat)))
print(f"P-Value = {p_value:.4f}")

# ✅ Decision
alpha = 0.05
if p_value < alpha:
    print("Reject the null hypothesis (significant).")
else:
    print("Fail to reject the null hypothesis (not significant).")
```

Example:

Imagine a **small population** of 5 people with these heights (in cm):

Population $=\{160, 165, 170, 175, 180\}$\text{Population } = \

{160,\,165,\,170,\,175,\,180\}Population =$\{160,165,170,175,180\}$

Poulation Mean VS Sample Mean

✅ Compute Population Mean (μ):

μ=160+165+170+175+1805=8505=170 cm\mu = \frac{160 + 165 + 170 + 175 + 180}{5} = \frac{850}{5} = 170\text{ cm}$\mu=\frac{160+165+170+175+180}{5}=\frac{850}{5}=170$ cm

> ? **True mean height of the entire population** is **170 cm**.

✅ Take a sample of size 3:

Suppose we randomly pick 3 people:

Sample={165,175,180}\text{Sample} = \{165,\,175,\,180\}Sample=$\{165,175,180\}$

Compute the **sample mean (x¯\bar{x}$\bar{x}$)**:

x¯=165+175+1803=5203≈173.33 cm\bar{x} = \frac{165 + 175 + 180}{3} = \frac{520}{3} \approx 173.33\text{ cm}$\bar{x}=\frac{165+175+180}{3}=\frac{520}{3}\approx 173.33$ cm

> ? The **sample mean** is **173.33 cm**, which is close to (but not exactly) the true mean of 170 cm.

? Another different sample might give:

Sample={160,170,180},x¯=5103=170 cm\text{Sample} = \{160,\,170,\,180\},\quad \bar{x} = \frac{510}{3} = 170\text{ cm}Sample=$\{160,170,180\}, \bar{x}=\frac{510}{3}=170$ cm

> ? Here the **sample mean** matches the true mean perfectly!