

Lecture 5: Parametric Hypothesis Testing

GENOME 560, Spring 2026

Saori Sakaue (sakaue@uw.edu)

Section 1

Recap

Collinearity (Recap from Lecture 4)

- Two or more predictor variables closely related
- Difficult to separate out individual effects
- Power reduced due to inflated standard errors

Categorical Independent Variables

Use **dummy variables** for k categories $\rightarrow k - 1$ indicators

Example: Three levels $\{A, B, C\}$

$$Y = \beta_0 + \beta_1 D_A + \beta_2 D_B + \epsilon$$

Reference category C is captured by β_0 .

Categorical Variables — ABO Blood Type

Four choices: {A, B, O, AB}

	D_A	D_B	D_{AB}
Type A	1	0	0
Type B	0	1	0
Type AB	0	0	1
Type O (ref)	0	0	0

Collinearity in Dummy Variables

If you include all k dummy variables (instead of $k - 1$), one predictor is a linear combination of the others.

$$D_O = 1 - D_A - D_B - D_{AB}$$

This causes **perfect collinearity** $\rightarrow \mathbf{X}^T \mathbf{X}$ is singular (not invertible).

Variance of the Sum of Two Variables

$$\text{Var}(A + B) = \text{Var}(A) + \text{Var}(B) + 2\text{Cov}(A, B)$$

If A and B are **independent**:

$$\text{Var}(A + B) = \text{Var}(A) + \text{Var}(B)$$

$$\text{Var}(A - B) = \text{Var}(A) + \text{Var}(B)$$

Section 2

Hypothesis Testing

Hypothesis Testing

- Examine H_0 (null) and H_A (alternative)
- They are **mutually exclusive and exhaustive**

The Null and Alternative Hypothesis

H_0 : States the assumption to be tested (contains “=”)

H_A : The opposite of the null (never contains just “=”)

Example

A diabetes cohort: compare blood glucose between cases and controls.

$$H_0 : \mu_{\text{case}} = \mu_{\text{control}}$$

$$H_A : \mu_{\text{case}} \neq \mu_{\text{control}}$$

One- and Two-Sided Tests

One-sided (directional):

$$H_0 : \mu = \mu_0 \quad \text{vs.} \quad H_A : \mu > \mu_0 \quad (\text{or } \mu < \mu_0)$$

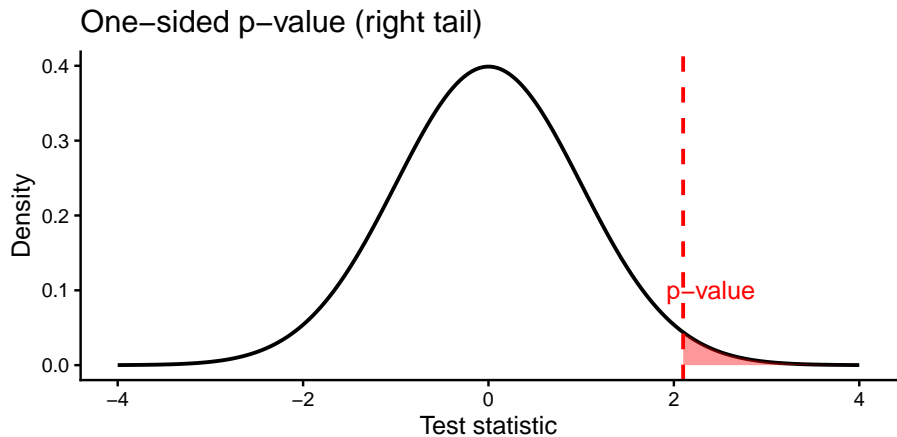
Two-sided (non-directional):

$$H_0 : \mu = \mu_0 \quad \text{vs.} \quad H_A : \mu \neq \mu_0$$

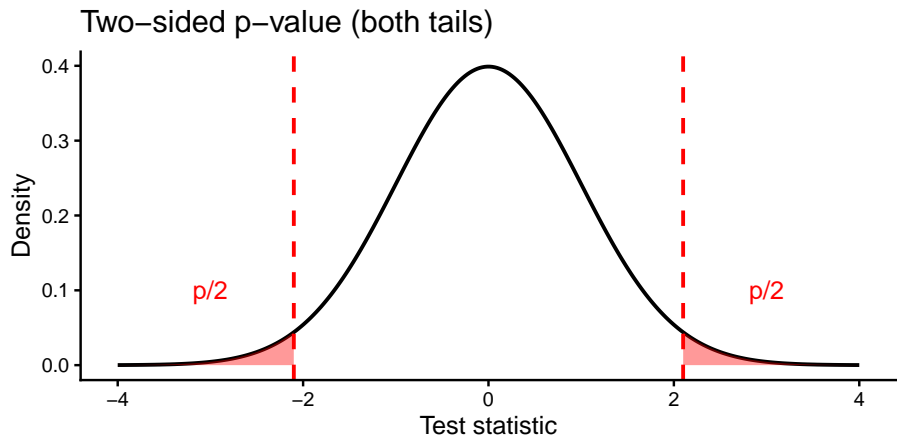
P-values

- 1 Calculate a **test statistic** from the data
- 2 Compare to the distribution of the test statistic **under** H_0
- 3 The **p-value** = probability of observing a test statistic as extreme (or more) under H_0

One-sided Test P-values



Two-sided Test P-values

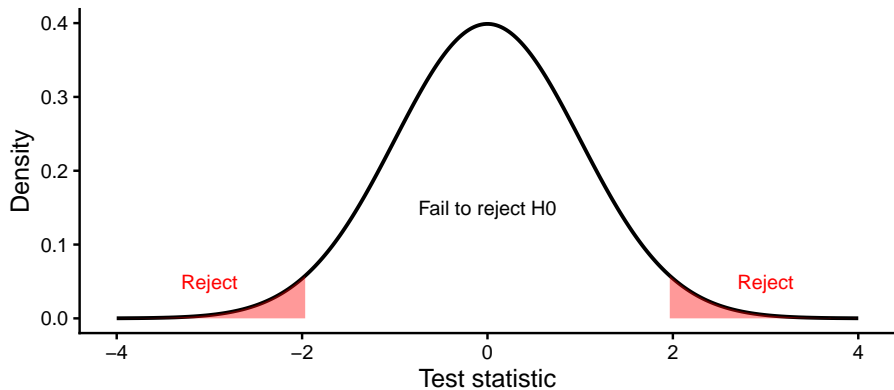


When To Reject H_0

- Set a **significance level** α (commonly 0.05)
- If p-value $< \alpha$, reject H_0
- The **rejection region** is the set of test statistic values leading to rejection

When To Reject H_0 (continued)

Two-sided test, $\alpha = 0.05$



Why 0.05?

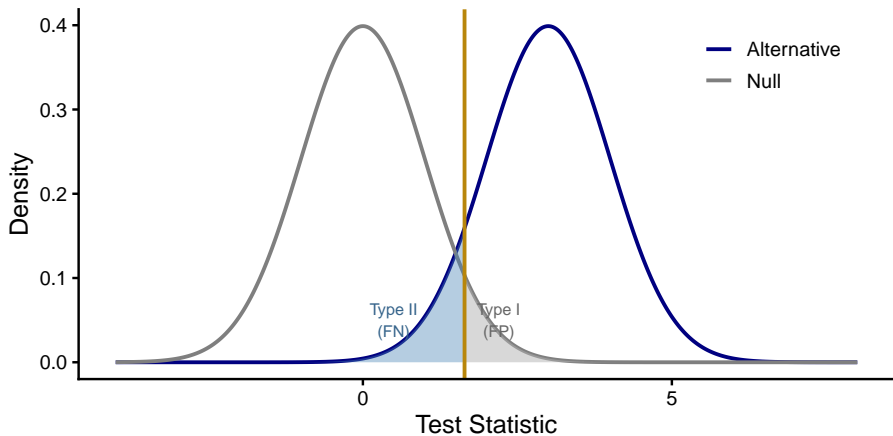
“...it is convenient to draw the line at about the level at which we can say: ‘Either there is something in the treatment, or a coincidence has occurred such as does not occur more than once in twenty trials.’” — R.A. Fisher

Errors in Hypothesis Testing

	H_0 True	H_0 False
Do Not Reject H_0	Correct ($1 - \alpha$)	Type II Error (β)
Reject H_0	Type I Error (α)	Correct ($1 - \beta$)

- **Type I Error (α):** False Positive
- **Type II Error (β):** False Negative

Errors in Hypothesis Testing — Visualized



Section 3

Parametric Tests

Parametric and Non-parametric Tests

Parametric tests:

- Rely on theoretical distributions (normal, t , χ^2 , F)
- Assume normality of the data or residuals

Non-parametric tests:

- Do not assume a specific distribution
- Often use ranks instead of raw values

One-Sample Hypothesis Tests

Example: Systolic blood pressure in a population.

$$H_0 : \mu = 120 \quad H_A : \mu \neq 120$$

Given n observations with sample mean \bar{x} and sample SD $\hat{\sigma}$:

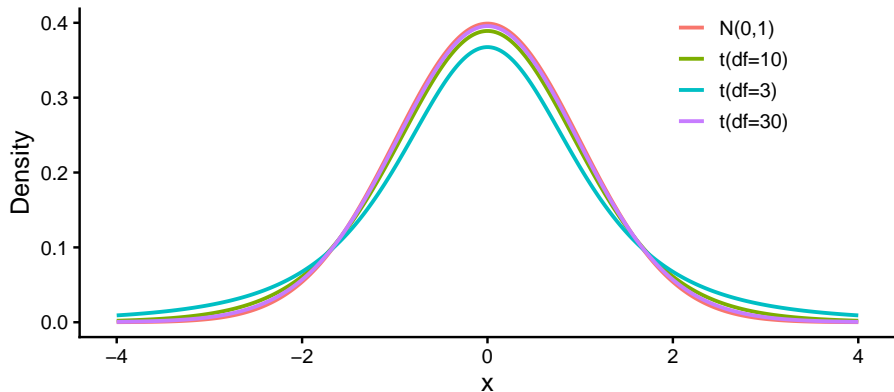
The t-Statistic

$$t = \frac{\bar{x} - \mu_0}{\hat{\sigma} / \sqrt{n}}$$

- **Numerator:** How far is \bar{x} from μ_0 ? (signal)
- **Denominator:** Standard error (noise)
- t follows the **Student's t -distribution** with $n - 1$ degrees of freedom

Student's t -Distribution

t -distribution approaches normal as df increases



Student's t -Distribution (continued)

- Heavier tails than normal \rightarrow accounts for uncertainty in estimating σ
- As $n \rightarrow \infty$ ($df \rightarrow \infty$), t -distribution \rightarrow normal
- For $df > 30$, practically indistinguishable from normal

Standardizing Normal RV (Recap)

If $X \sim N(\mu, \sigma^2)$:

$$Z = \frac{X - \mu}{\sigma} \sim N(0, 1)$$

The Central Limit Theorem (Recap)

$$\bar{X} \xrightarrow{d} N\left(\mu, \frac{\sigma^2}{n}\right) \quad \text{as } n \rightarrow \infty$$

This justifies using t -tests even when the population isn't perfectly normal (for large n).

Section 4

Two-Sample t-Tests

Two-Sample t-Test

Paired: Same size, natural pairing

- Before/after drug treatment
- Expression levels of same genes in two conditions

Unpaired: Independent samples from two populations

Paired Two-Sample t-Test

Expression levels of n genes, before and after drug treatment.

$$d_i = x_i - y_i$$

$$H_0 : \mu_d = 0 \quad t = \frac{\bar{d}}{\hat{\sigma}_d / \sqrt{n}} \sim t_{n-1}$$

Unpaired Two-Sample t-Test

Independent samples from two populations:

$$H_0 : \mu_X = \mu_Y$$

$$t = \frac{\bar{X} - \bar{Y}}{\sqrt{\text{Var}(\bar{X} - \bar{Y})}}$$

Since samples are independent: $\text{Var}(\bar{X} - \bar{Y}) = \text{Var}(\bar{X}) + \text{Var}(\bar{Y})$

Pooled Variances

Assume $\sigma_X^2 = \sigma_Y^2 = \sigma^2$ (homogeneity of variances):

$$\hat{\sigma}_{\text{pooled}}^2 = \frac{(n_X - 1)\hat{\sigma}_X^2 + (n_Y - 1)\hat{\sigma}_Y^2}{n_X + n_Y - 2}$$

$$t = \frac{\bar{X} - \bar{Y}}{\hat{\sigma}_{\text{pooled}} \sqrt{\frac{1}{n_X} + \frac{1}{n_Y}}} \sim t_{n_X + n_Y - 2}$$

Key Assumptions in the t-Test

- 1 **Random sampling** from the population
- 2 **Independence** of observations
- 3 **Homogeneity of variances** (for pooled test)
- 4 **Normality** (approximately) of the data

Plot your data! Visual inspection can reveal violations.

Unpooled Variances (Welch's t-Test)

When $\sigma_X^2 \neq \sigma_Y^2$, replace with sample variances:

$$t = \frac{\bar{X} - \bar{Y}}{\sqrt{\frac{\hat{\sigma}_X^2}{n_X} + \frac{\hat{\sigma}_Y^2}{n_Y}}}$$

Degrees of freedom (Welch-Satterthwaite approximation):

$$\nu = \frac{\left(\frac{\hat{\sigma}_X^2}{n_X} + \frac{\hat{\sigma}_Y^2}{n_Y}\right)^2}{\frac{(\hat{\sigma}_X^2/n_X)^2}{n_X-1} + \frac{(\hat{\sigma}_Y^2/n_Y)^2}{n_Y-1}}$$