ANOVA and Linear Regression

Ling250: Data Science for Linguistics
C.M. Downey
Spring 2025

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  - There are ways to **check** those assumptions, but we won't
  - If you use these for real, there are **nitty-gritty details** to be considered

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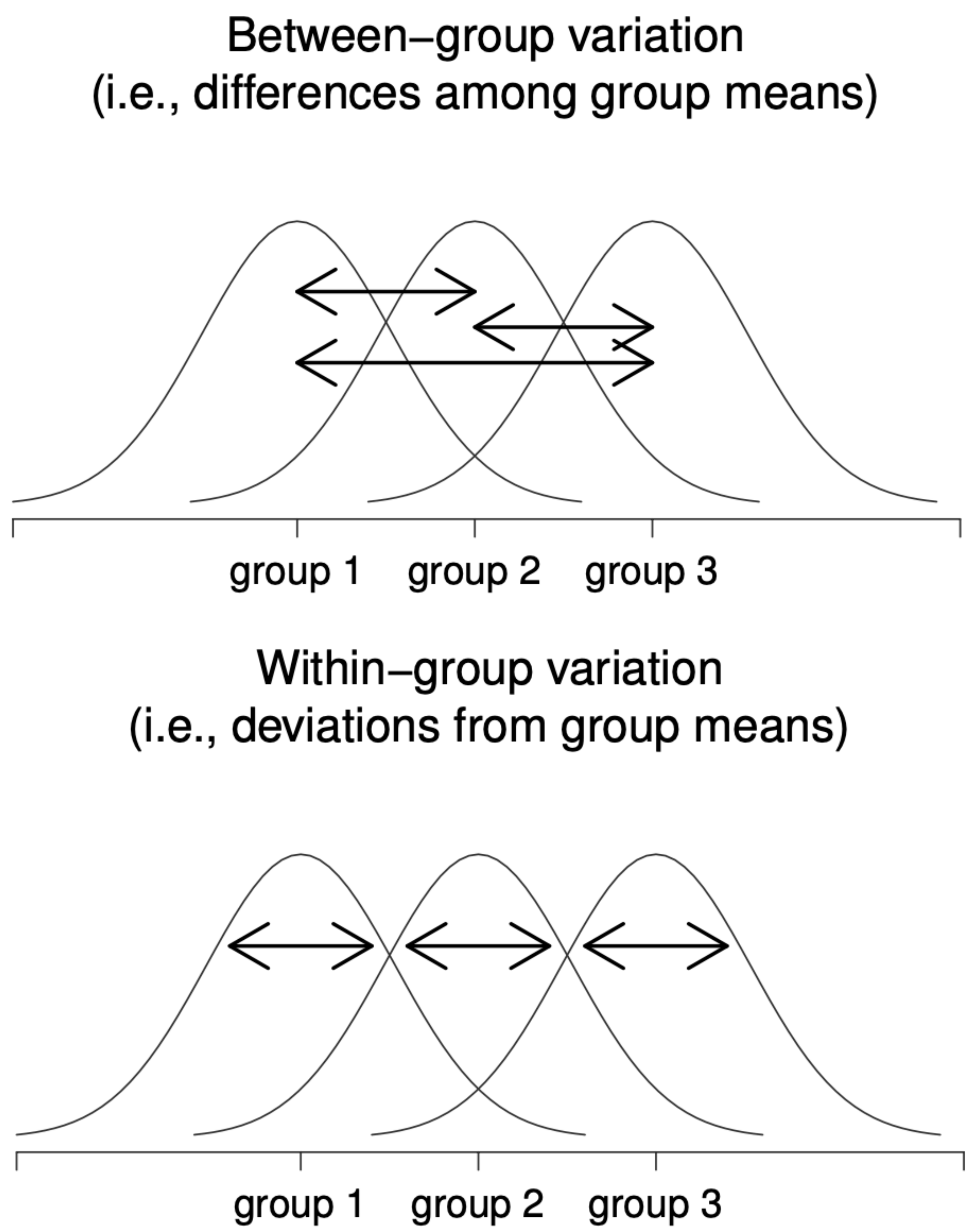
  - There are ways to **check** those assumptions, but we won't
  - If you use these for real, there are **nitty-gritty details** to be considered
- We'll focus on **when to use** these tests, and how to **use them in R**
  - Our goal is to practice the basics

ANOVA

ANOVA


Between–group variation
(i.e., differences among group means)
group 1
group 2
group 3
Within–group variation
(i.e., deviations from group means)
group 1
group 2
group 3

ANOVA

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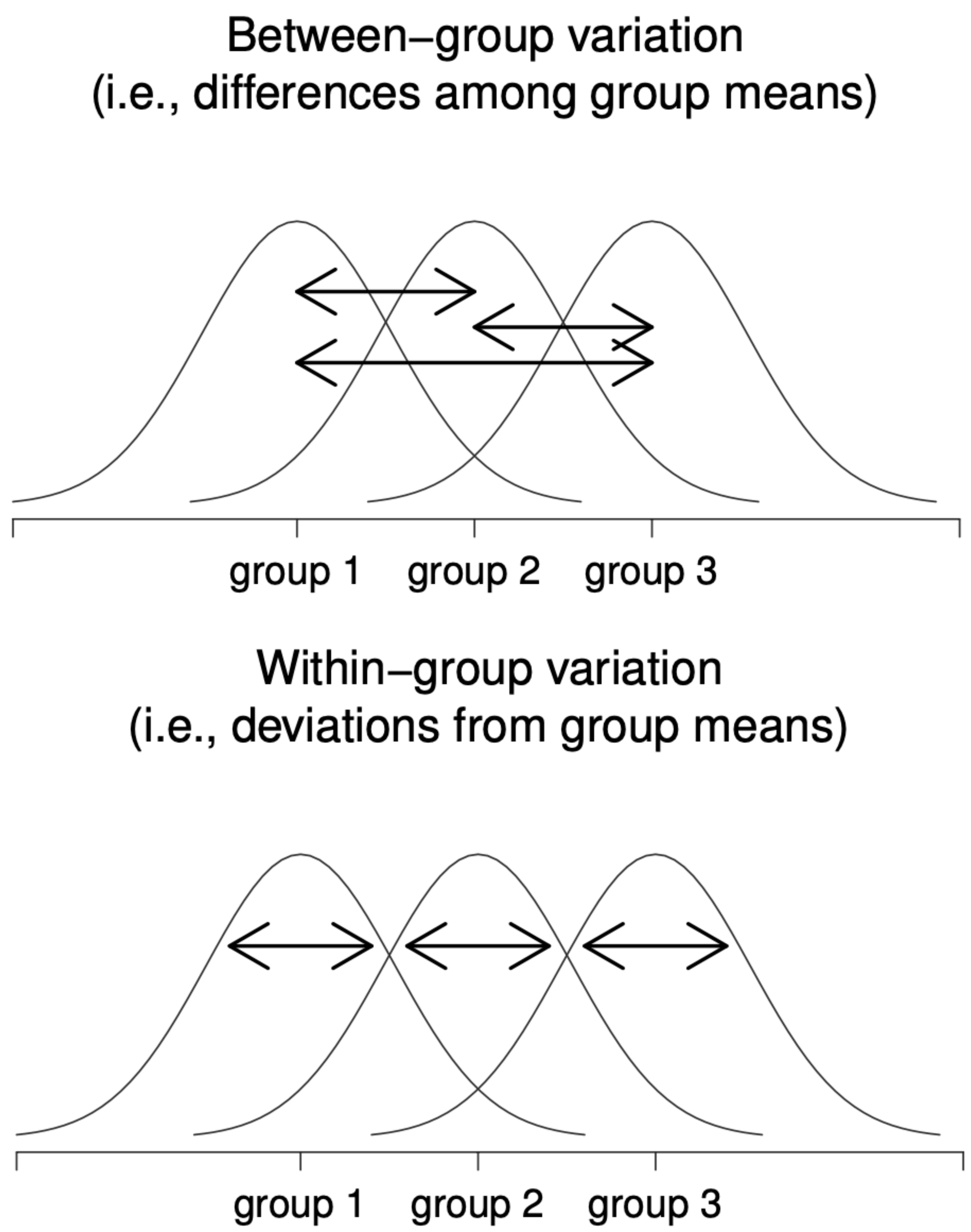

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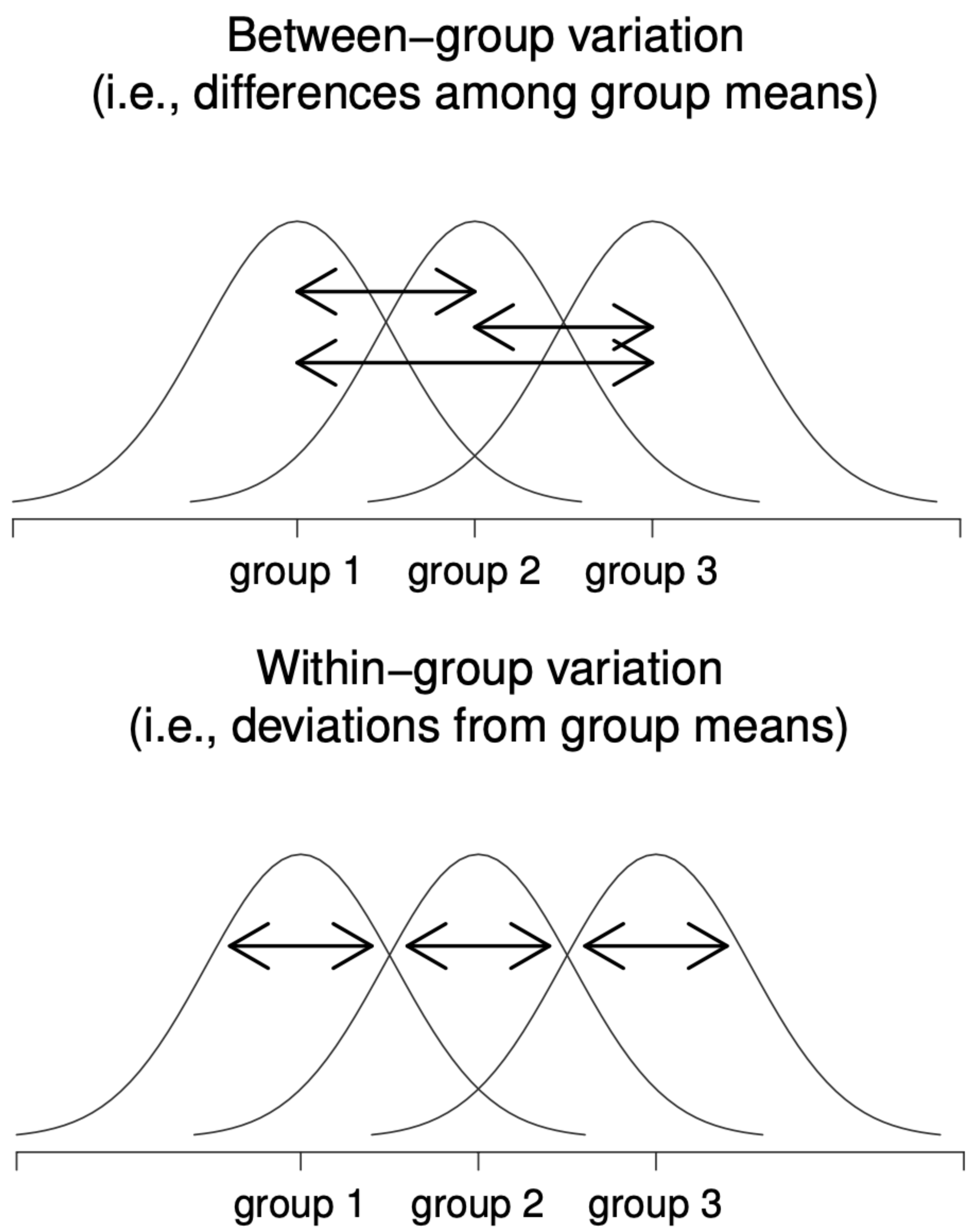

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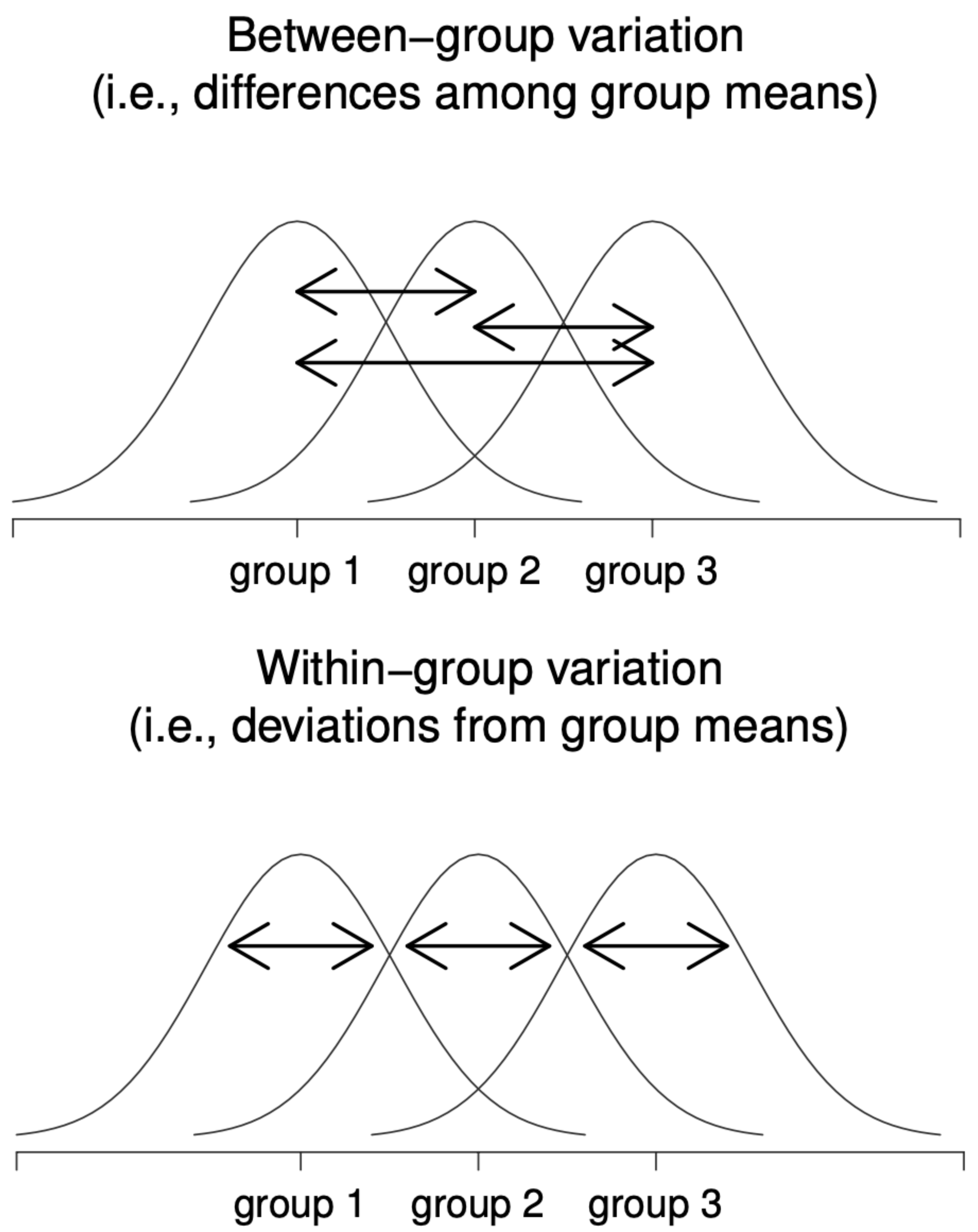

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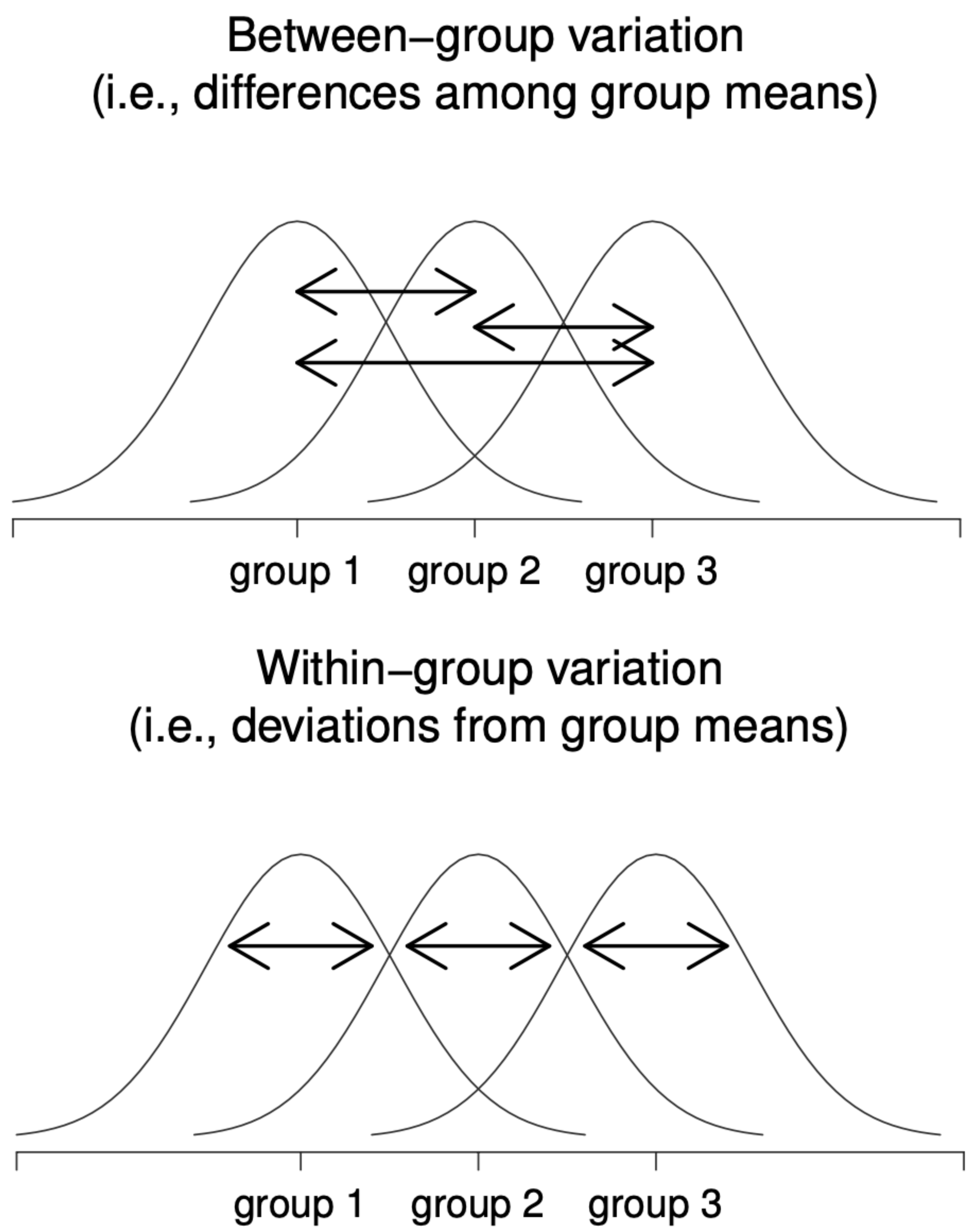

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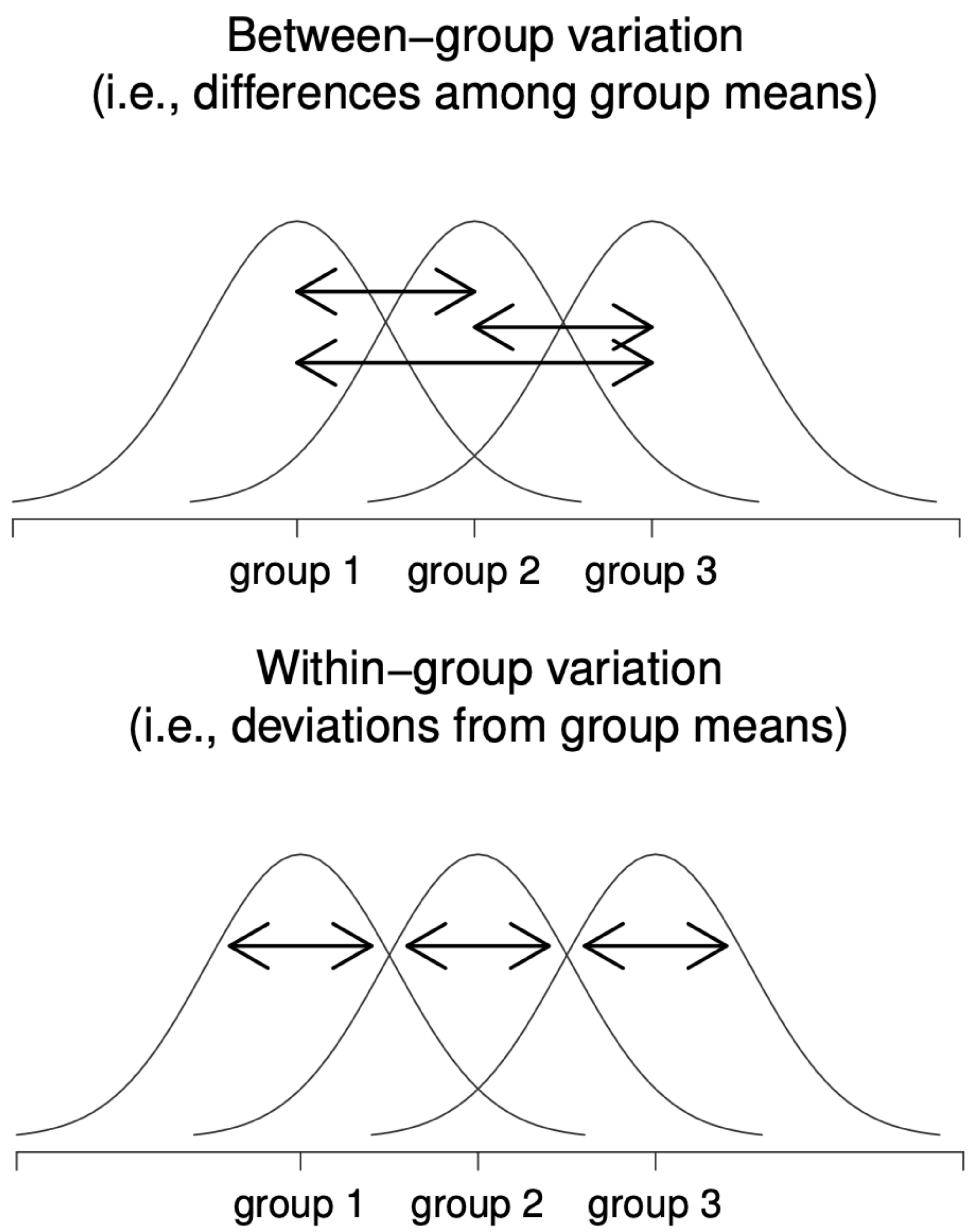

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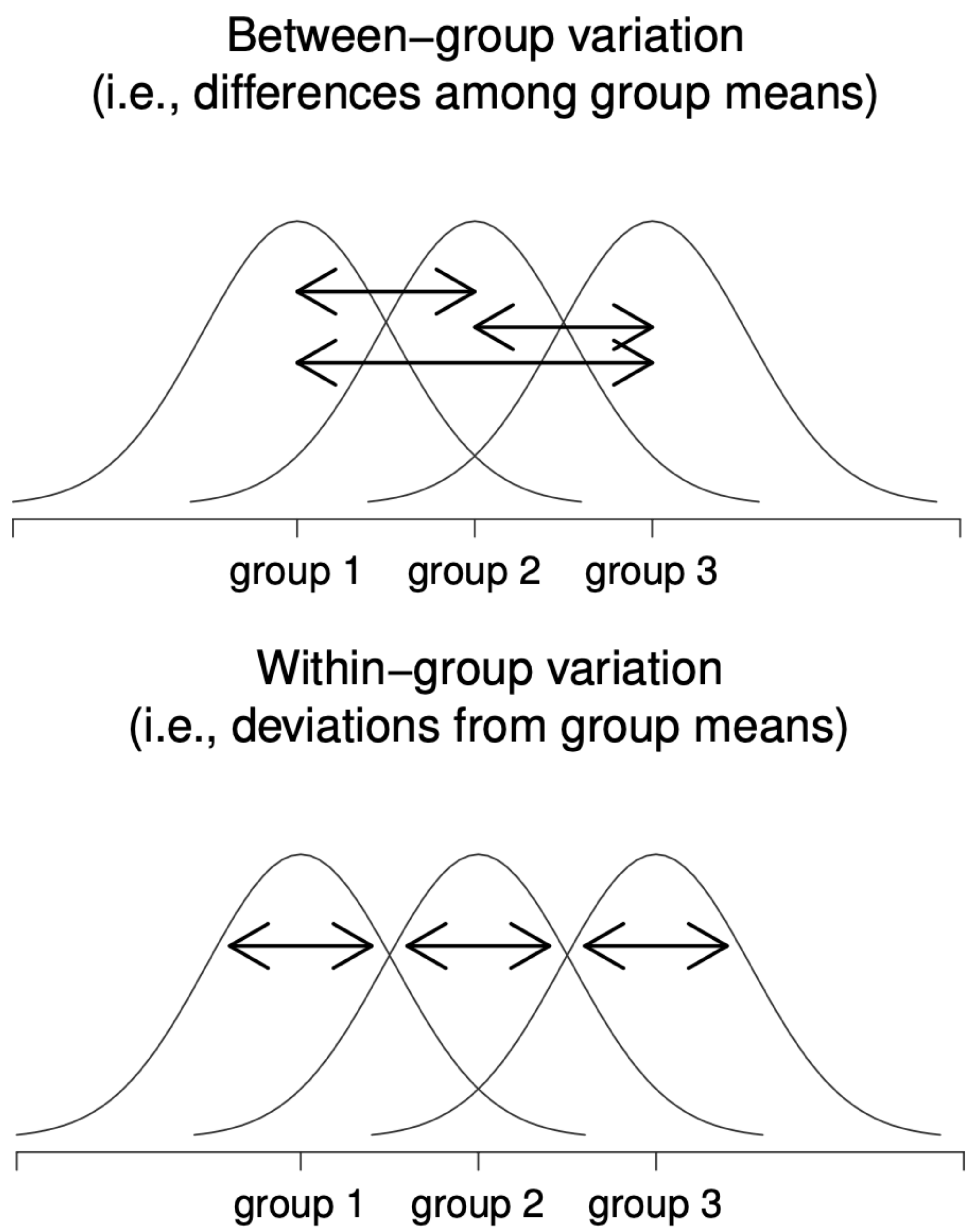

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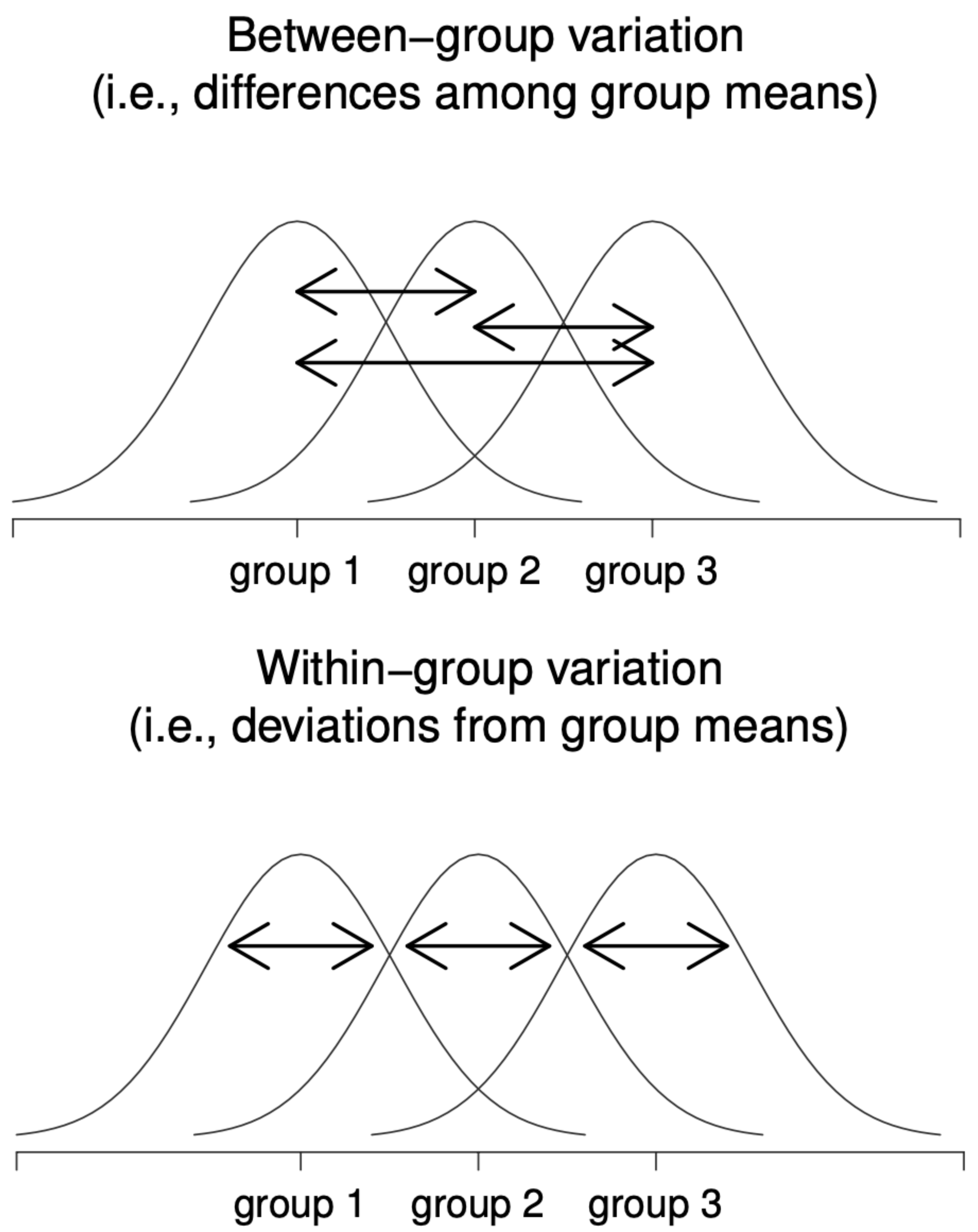
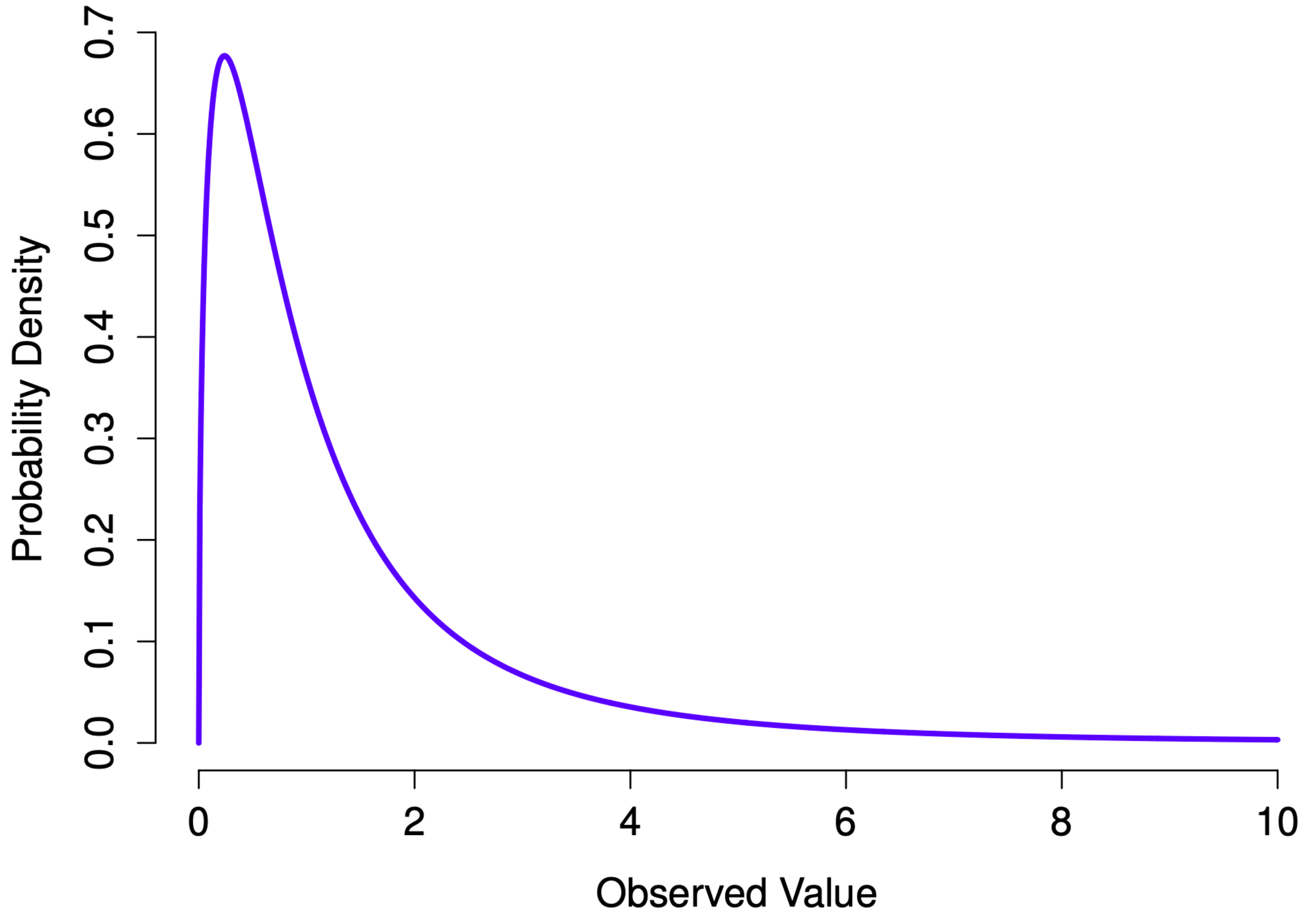
- Hypotheses
  - $H_0 : \mu_1 = \mu_2 \ldots = \mu_G$
  - H_1 : Not $(\mu_1 = \mu_2 \ldots = \mu_G)$
  - (H_1 is a **different hypothesis** than $\mu_1 \neq \mu_2 \ldots \neq \mu_G$)

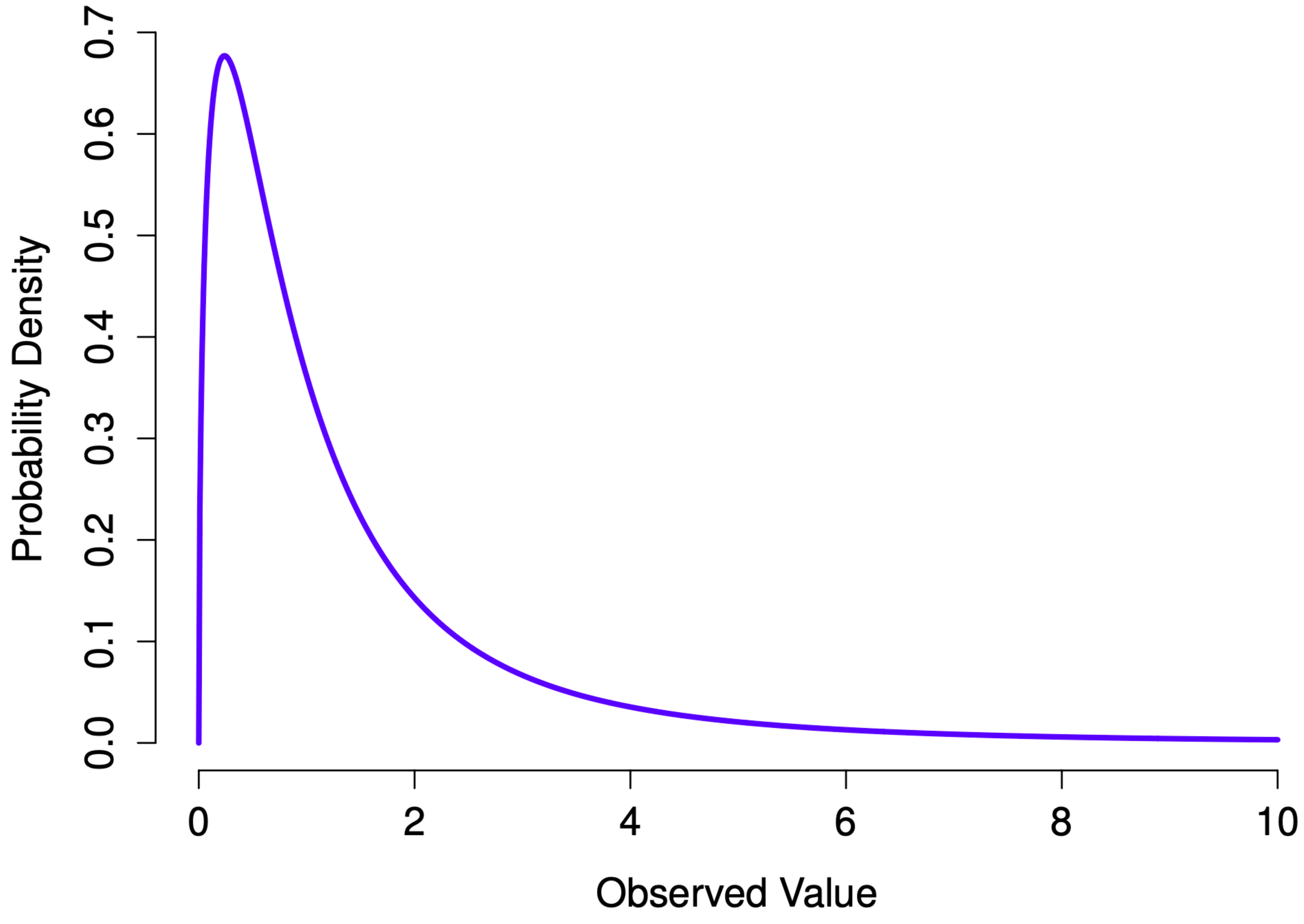


F-statistic


Probability Density
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0
2
4
6
8
10
Observed Value

F-statistic

- We test the hypothesis with a **ratio** called the **F-statistic**
  - Compares the **between-group variation** (MS_b) with **within-group variation** (MS_w)
  - Computed as MS_b/MS_w
  - **F-distribution** gives us significance values
  - Higher F → lower p-value



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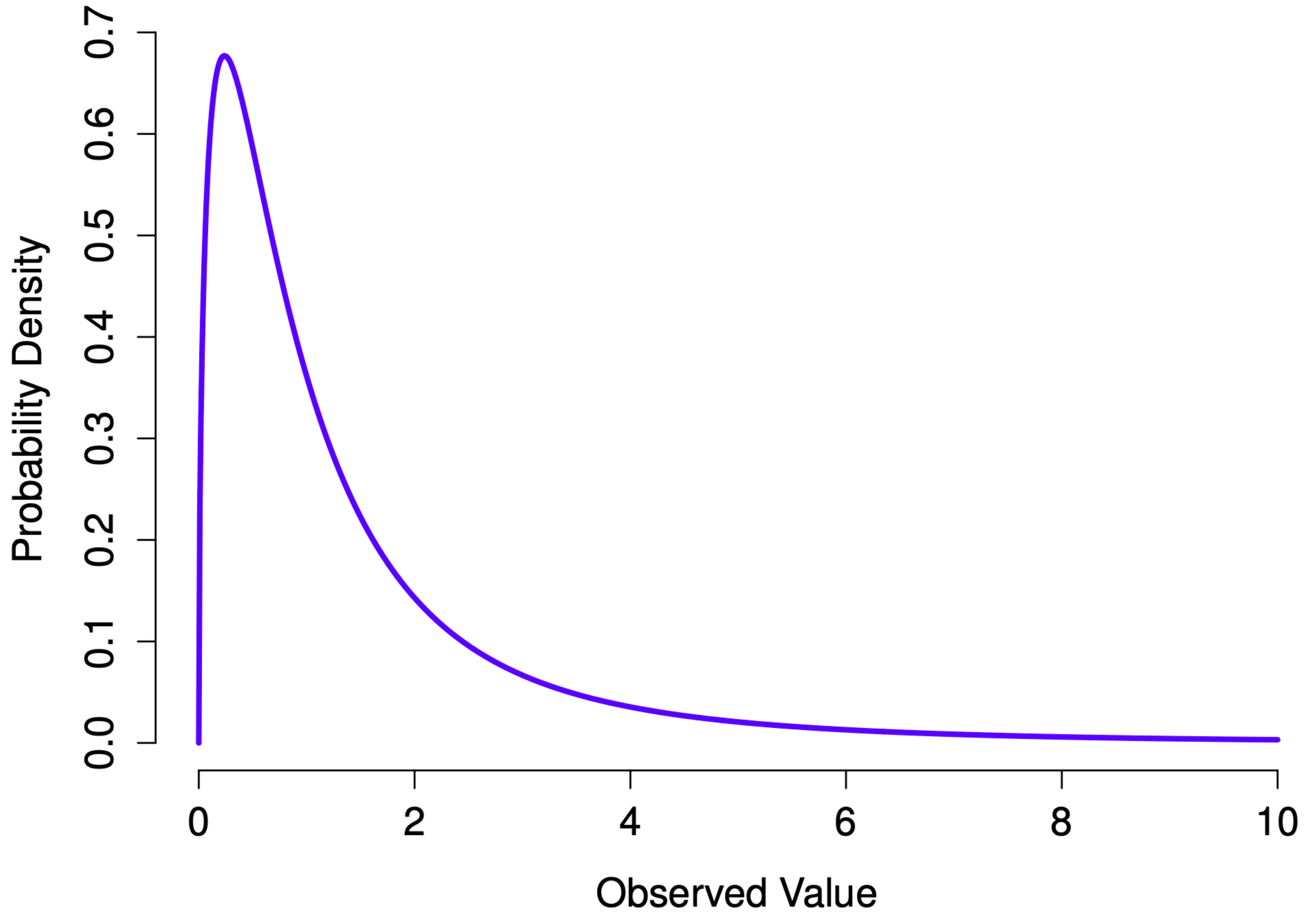
- Purposefully **glossing over** where MS_b and MS_w come from



Example in R

	drug	therapy	mood.gain
1	placebo	no.therapy	0.5
2	placebo	no.therapy	0.3
3	placebo	no.therapy	0.1
4	anxifree	no.therapy	0.6
5	anxifree	no.therapy	0.4
6	anxifree	no.therapy	0.2
7	joyzepam	no.therapy	1.4
8	joyzepam	no.therapy	1.7
9	joyzepam	no.therapy	1.3
10	placebo	CBT	0.6
11	placebo	CBT	0.9
12	placebo	CBT	0.3
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14	anxifree	CBT	0.8
15	anxifree	CBT	1.2
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- Groups: **two drugs and a placebo** in a clinical trial
  - Encoded as categorical variable

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Example in R

- Groups: **two drugs and a placebo** in a clinical trial
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- Outcome measure: **mood improvement**
- R command: **`aov()`**
  - `formula`: outcome variable distributed by group
  - Returns **complex R object**

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Example in R

```
> print(my_anova)
Call:
   aov(formula = mood_gain ~ drug, data = clin_trial)

Terms:
                    drug Residuals
Sum of Squares  3.453333  1.391667
Deg. of Freedom        2        15

Residual standard error: 0.3045944
Estimated effects may be unbalanced

> summary(my_anova)
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drug         2  3.453  1.7267   18.61 8.65e-05 ***
Residuals   15  1.392  0.0928                     
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Signif. codes:
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- The result of `print` is **not very informative**
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Example in R

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- Can get **p-values** with `summary(my_anova)`
  - F-statistic is here too

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- Null can be rephrased as "drugs don't have an affect on mood"
- What if we want to be **more specific?**

Multiple comparisons

possibility:	is $\mu_P = \mu_A$?	is $\mu_P = \mu_J$?	is $\mu_A = \mu_J$?	which hypothesis?
1	✓	✓	✓	null
2	✓	✓		alternative
3	✓		✓	alternative
4	✓			alternative
5		✓	✓	alternative
6		✓		alternative
7			✓	alternative
8				alternative

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8				alternative

Multiple comparisons

- 3 groups gives us **8 possible hypotheses!**
  - ANOVA **combines** 7 of them
- Can test all with **pair-wise t-tests**

```
> pairwise.t.test( x = clin.trial$mood.gain,    # outcome variable
+                  g = clin.trial$drug,         # grouping variable
+                  p.adjust.method = "none"     # which correction to use?
+ )

        Pairwise comparisons using t tests with pooled SD

data:  clin.trial$mood.gain and clin.trial$drug

         placebo anxifree
anxifree 0.15021 -
joyzepam 3e-05   0.00056
```

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- The issue with pair-wise tests: **p-value "fishing"**
  - We do a **large number** of pair-wise comparisons, so a few are likely to be **significant by random chance!**
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  - Idea: p-values adjusted as if it were **one big test** rather than multiple
  - The book recommends **Holm Correction** (can be applied in R)
- Why not just run corrected pair-wise tests rather than ANOVA?
  - ANOVA encourages **well-formulated hypotheses**

Corrected pair-wise t-tests

```
> pairwise.t.test(
+     x = clin_trial$mood_gain,
+     g = clin_trial$drug,
+     p.adjust.method = "holm"
+ )

        Pairwise comparisons using t tests with pooled SD

data:  clin_trial$mood_gain and clin_trial$drug

          anxifree joyzepram
joyzepram 0.0011   -
placebo   0.1502   9.1e-05

P value adjustment method: holm
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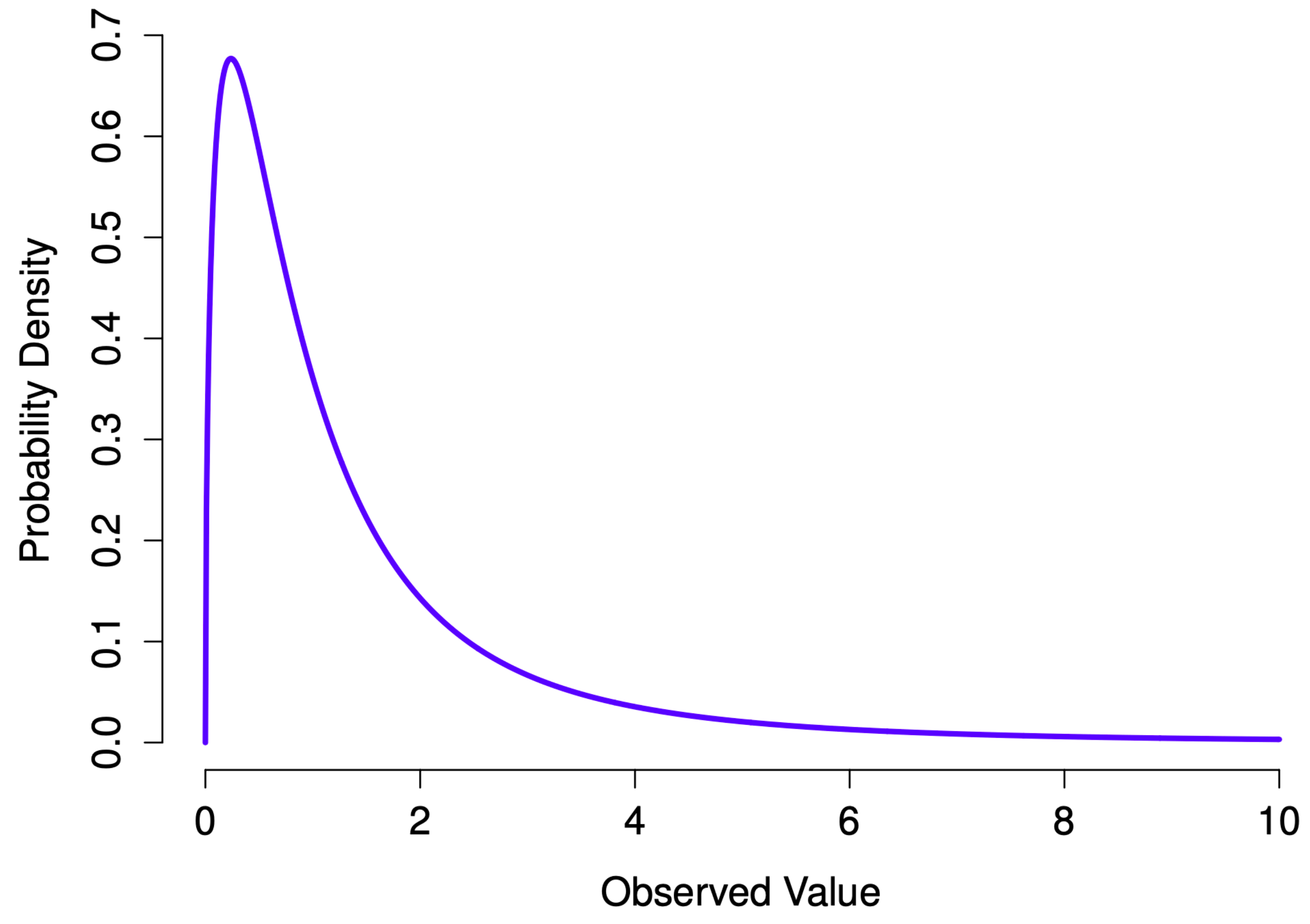
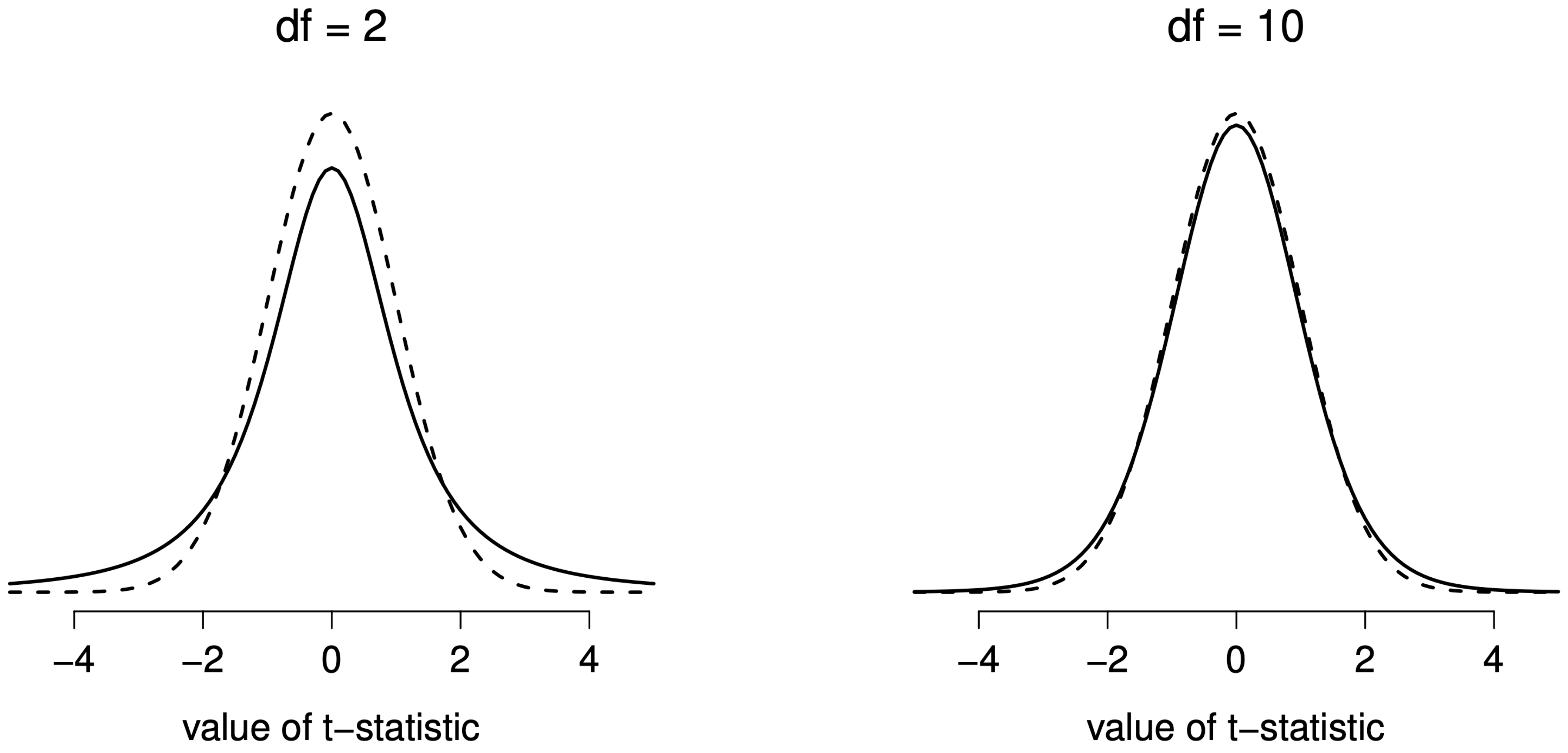
  - Like t-tests, there's a version of ANOVA that **removes this assumption**
  - Called the **Welch One-way Test**
  - R command is named unhelpfully: `oneway.test()`
- Groups are **Normally distributed**
  - This is a **strong assumption**, but there are **methods to check it**
  - (We won't bother checking Normality in this course. **This is a <u>simplification</u>**)

ANOVA and t-test

- With **two groups** the ANOVA is **mathematically equivalent** to the **Student's t-test**
  - Student's t-test can be considered a **simplified case** of ANOVA
  - Of mathematical interest: equivalence between test based on F-statistic and t-statistic





Linear regression

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- "Linear" refers to the fact that effects of predictors are **summed together**

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$$\underbrace{y}_{\text{response}} = \beta \underbrace{x}_{\text{predictor}} + \alpha$$

Linear regression

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learned
coefficients

$$y = \beta x + \alpha$$

response

predictor

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slope

intercept / bias

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response

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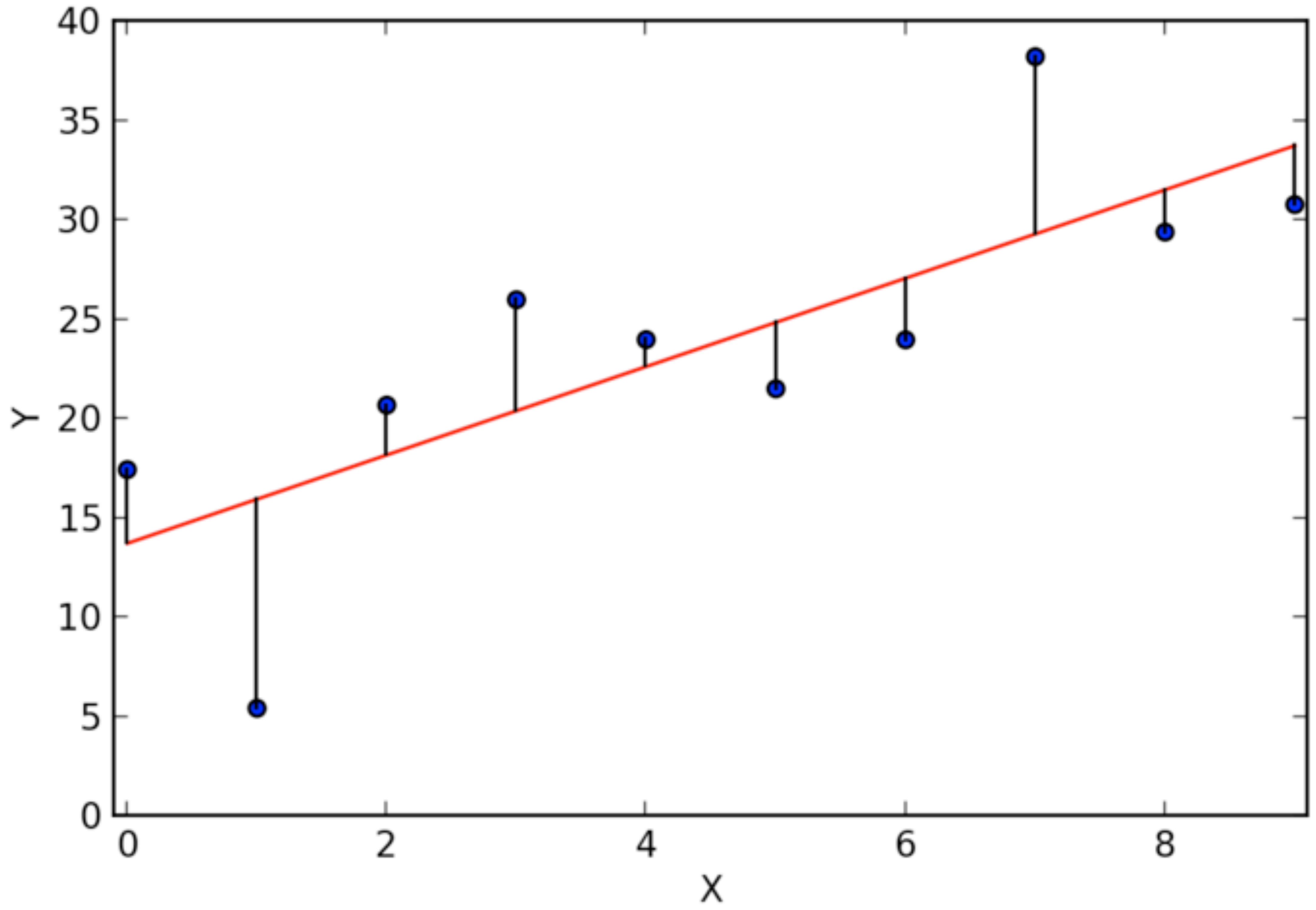
$$\underbrace{y}_{\text{response}} = \overbrace{\beta}^{\text{slope}}\underbrace{x}_{\text{predictor}} + \overbrace{\alpha}^{\text{intercept / bias}} \qquad (y = mx + b)$$

Error minimization



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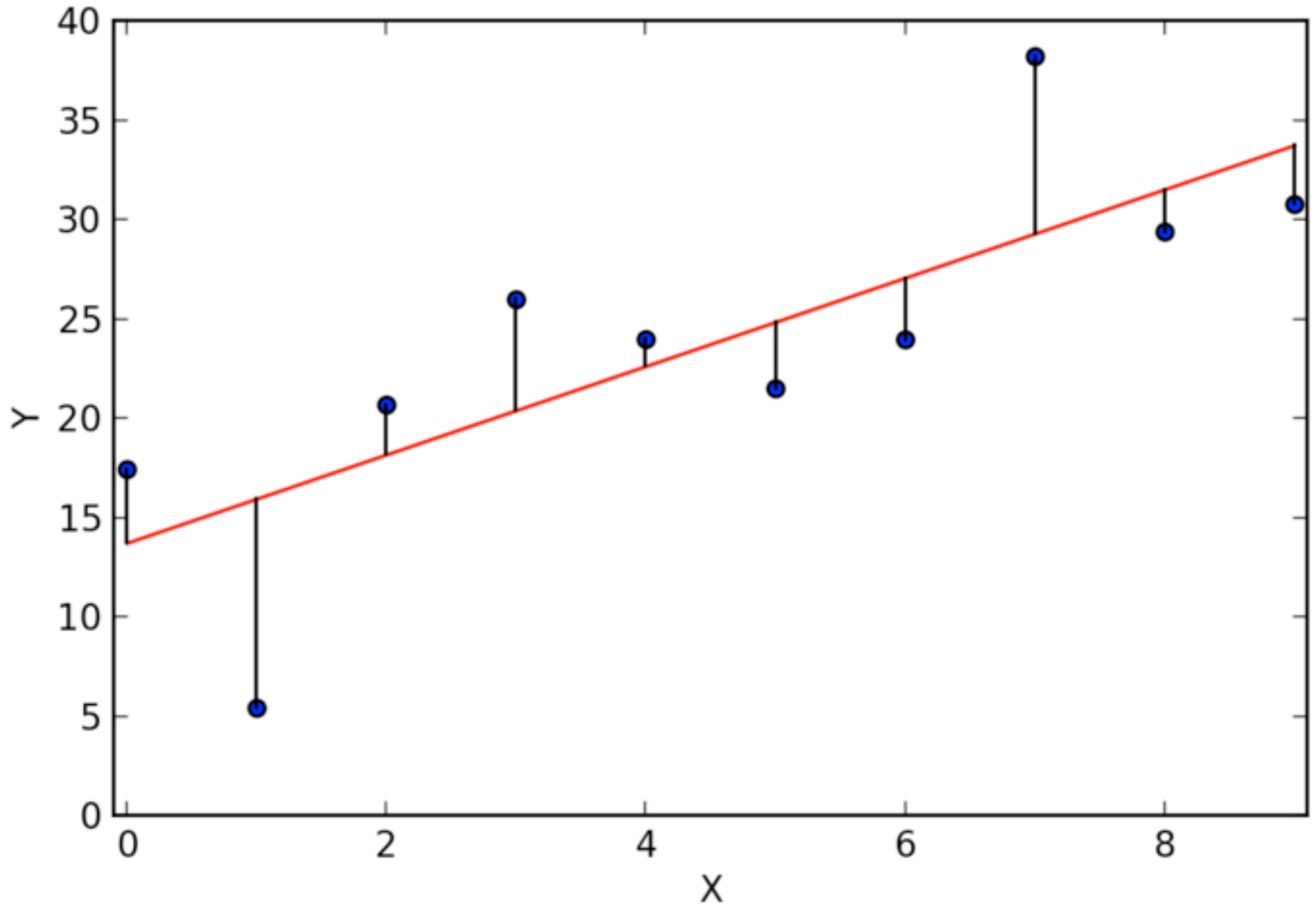

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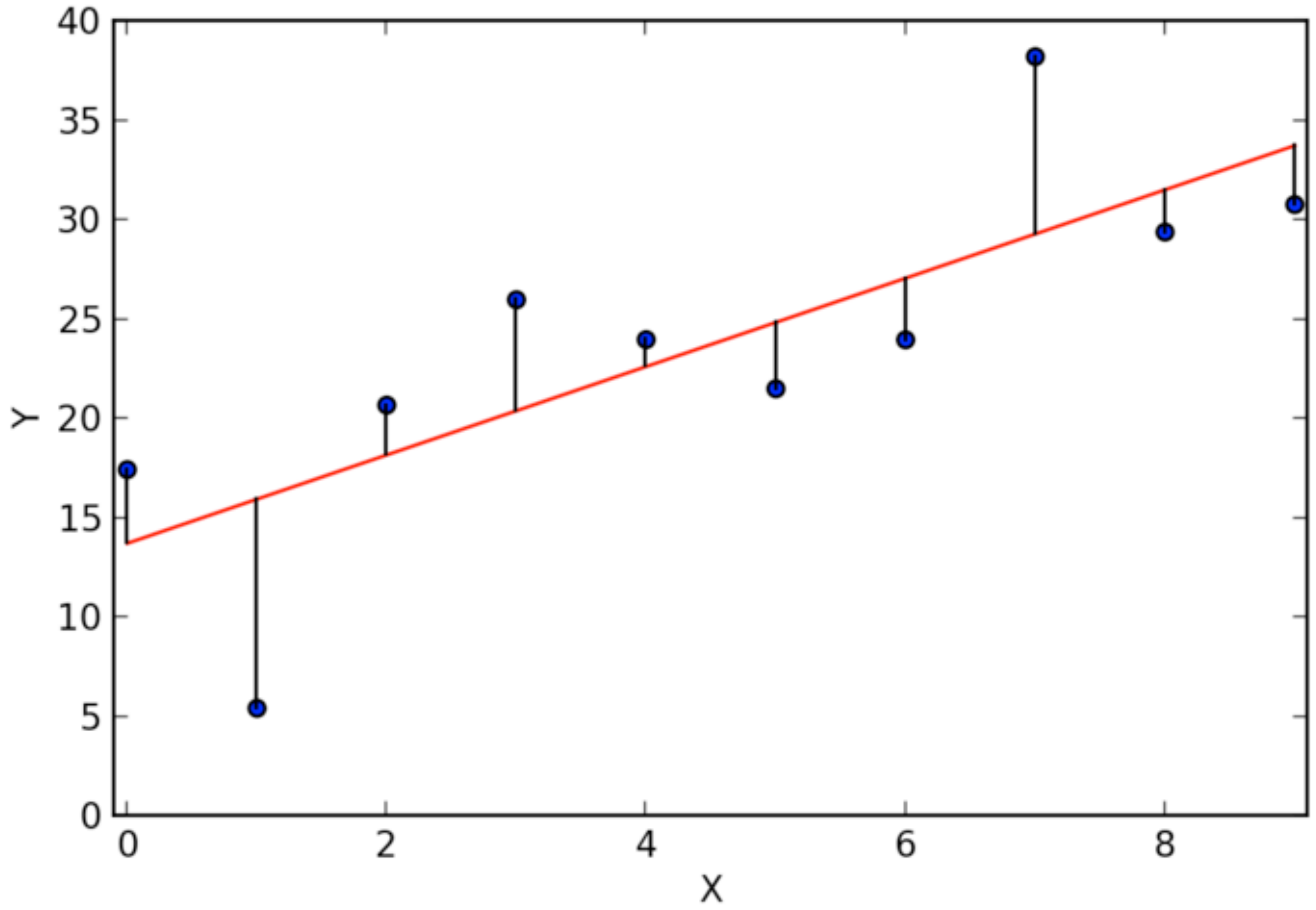

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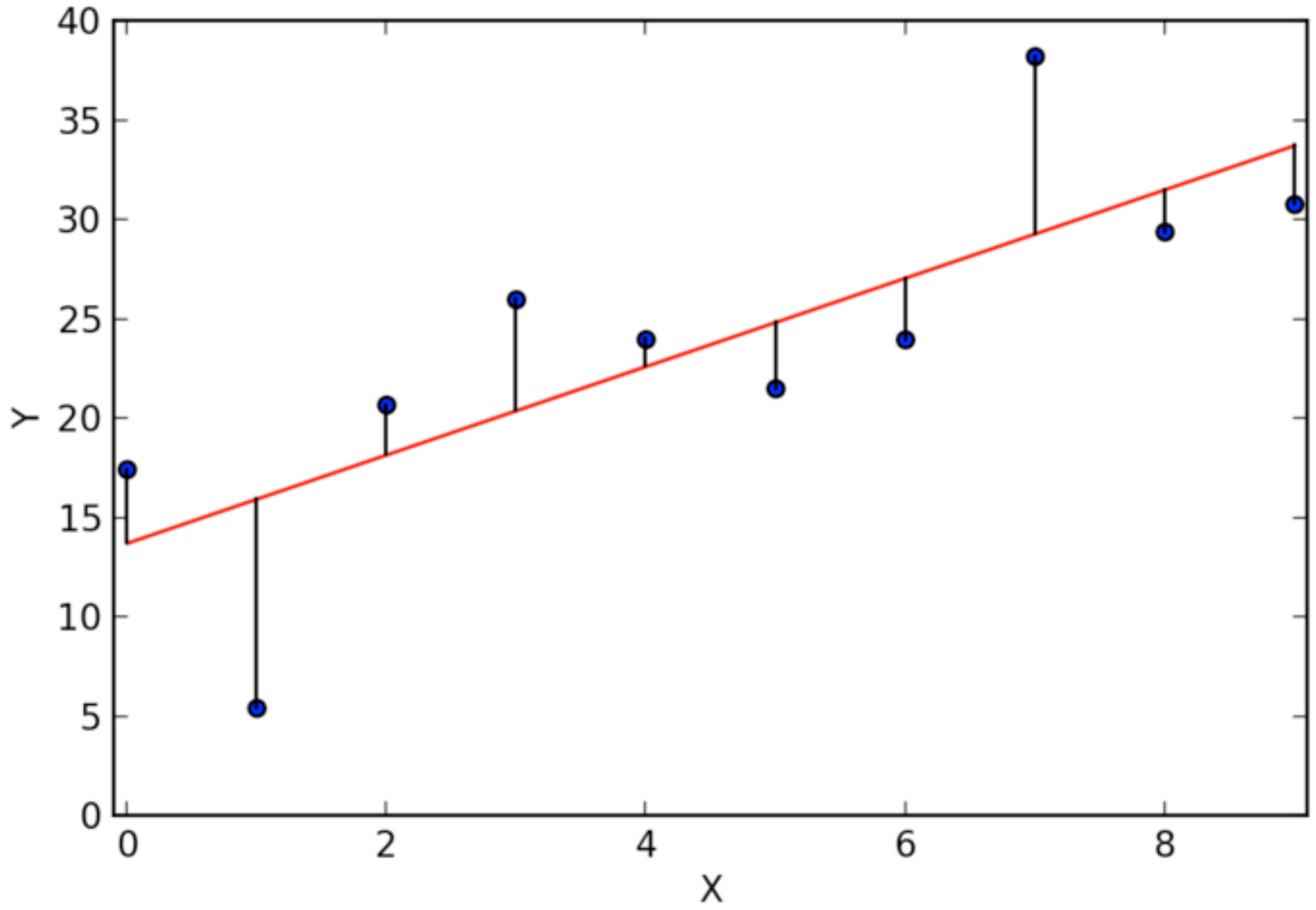

Error minimization

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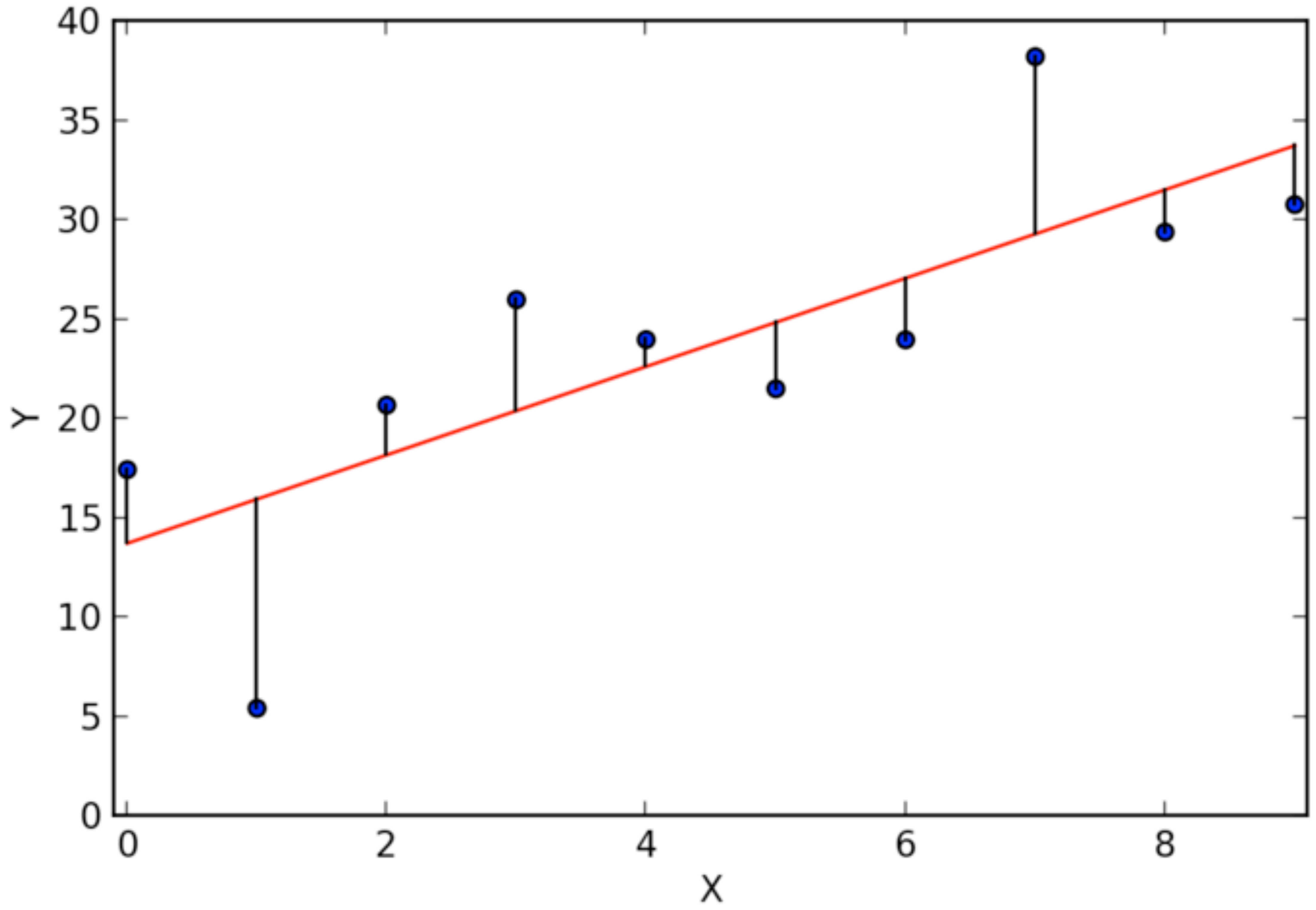
- This is called the **residual error**
- Yields the "**best fit line**"
- Sometimes explicitly modeled:
  - $y = \beta x + \alpha + \epsilon$
  - where ϵ is residual error



Multivariable regression

Multivariable regression

- Formula straightforwardly generalizes to **multiple predictors**
  - $y = \alpha + \beta_1 x_1 + \beta_2 x_2 + \ldots + \epsilon$
  - Matrix notation: $Y = X\beta + \epsilon$
  - Can be **solved in the same way**

Multivariable regression

- Formula straightforwardly generalizes to **multiple predictors**
  - $y = \alpha + \beta_1 x_1 + \beta_2 x_2 + \ldots + \epsilon$
  - Matrix notation: $Y = X\beta + \epsilon$
  - Can be **solved in the same way**
- R code
  - `model = lm(y ~ variable)`
  - `model = lm(y ~ variable_1 + variable_2)`

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- What is the result of this "dummy" encoding?

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- With the dummy encoding, α is the **mean of pond 1**
  - Implicitly assumes **pond 1** is the **“baseline/control” group**
  - β is the **difference** between pond 1 and pond 2

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- ($n - 1$ dummy variables used to represent n values)

R example

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> pond_data
   fertilizer pond     algae
1   7.6990327    1 13.910031
2   6.2655237    1 11.260629
3   3.0759136    1  5.283725
4   4.2035496    1  7.677377
5   9.5885167    1 19.556104
6   3.2948473    1  2.923524
7   1.0155064    1  1.319341
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- **Null hypothesis** is that α and β are zero

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Residuals:
     Min       1Q   Median       3Q      Max 
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Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  0.12995    0.50861   0.256    0.802    
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.9967 on 13 degrees of freedom
Multiple R-squared:  0.9827,	Adjusted R-squared:   0.98 
F-statistic: 368.3 on 2 and 13 DF,  p-value: 3.58e-12
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$$\text{algae} = 2.05 \cdot \text{fertilizer} + 3.37 \cdot \text{pond2} + 0.13$$