

Managing Things You Cannot Control (SOC 412)

Week 10 Lecture 7

Sherrerd Hall 306



J. Nathan Matias

@natematias

civilservant.io

jmatias@princeton.edu



What we will cover today

Cluster randomization

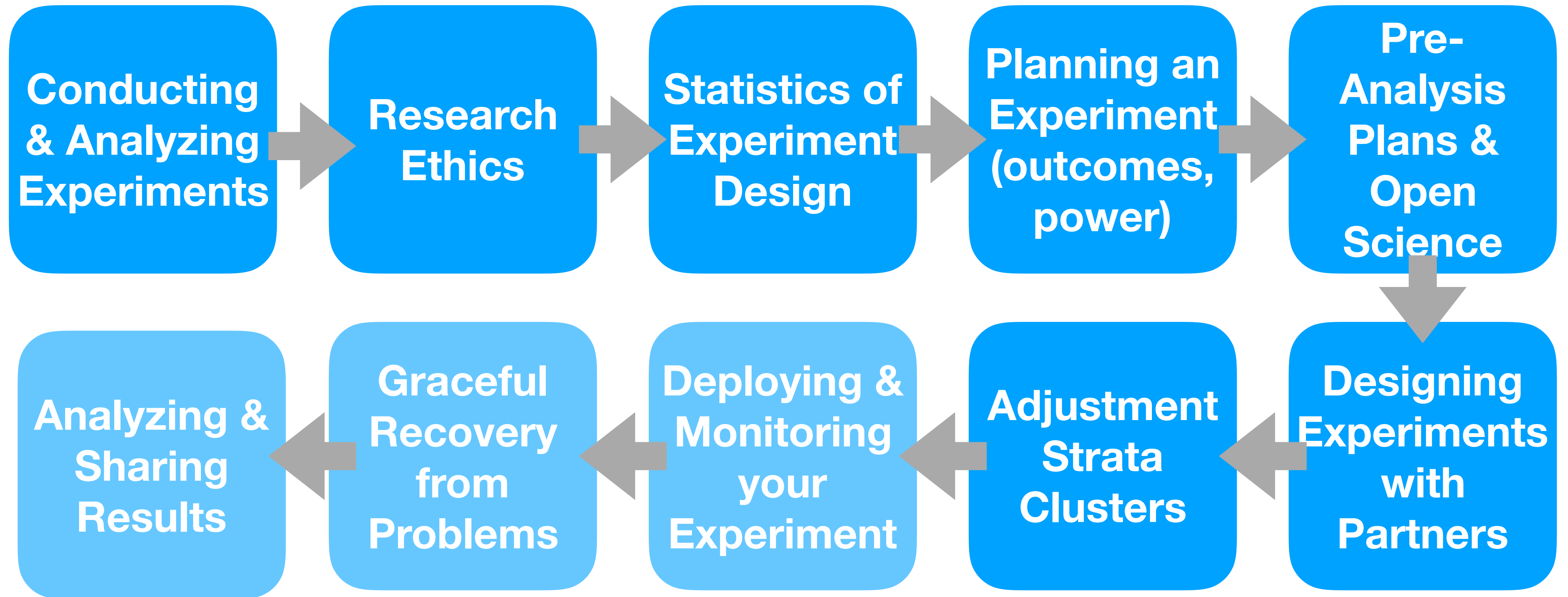
Block randomization

Regression adjustment

Bonferroni Adjustment

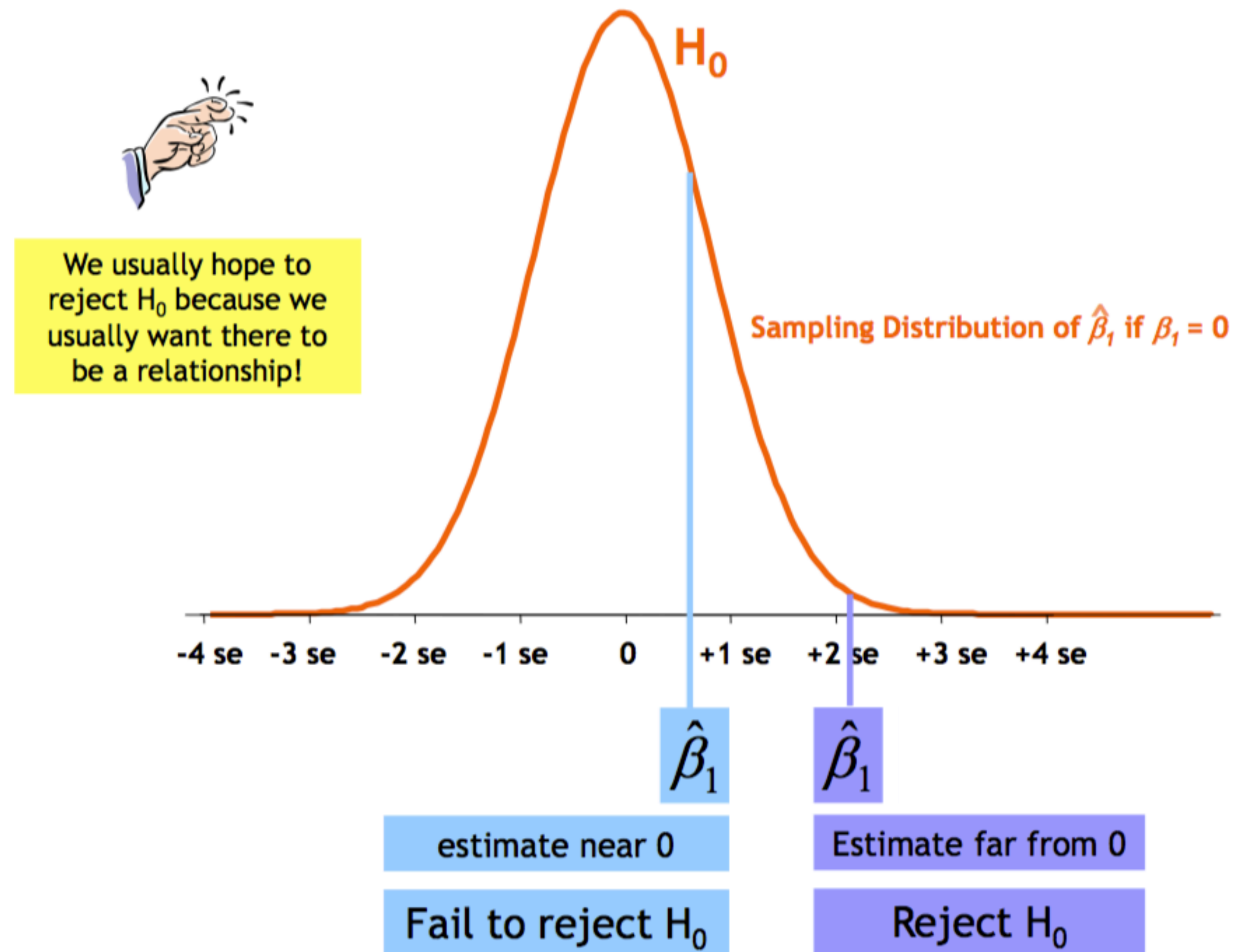
Final Projects

Experiment Plan



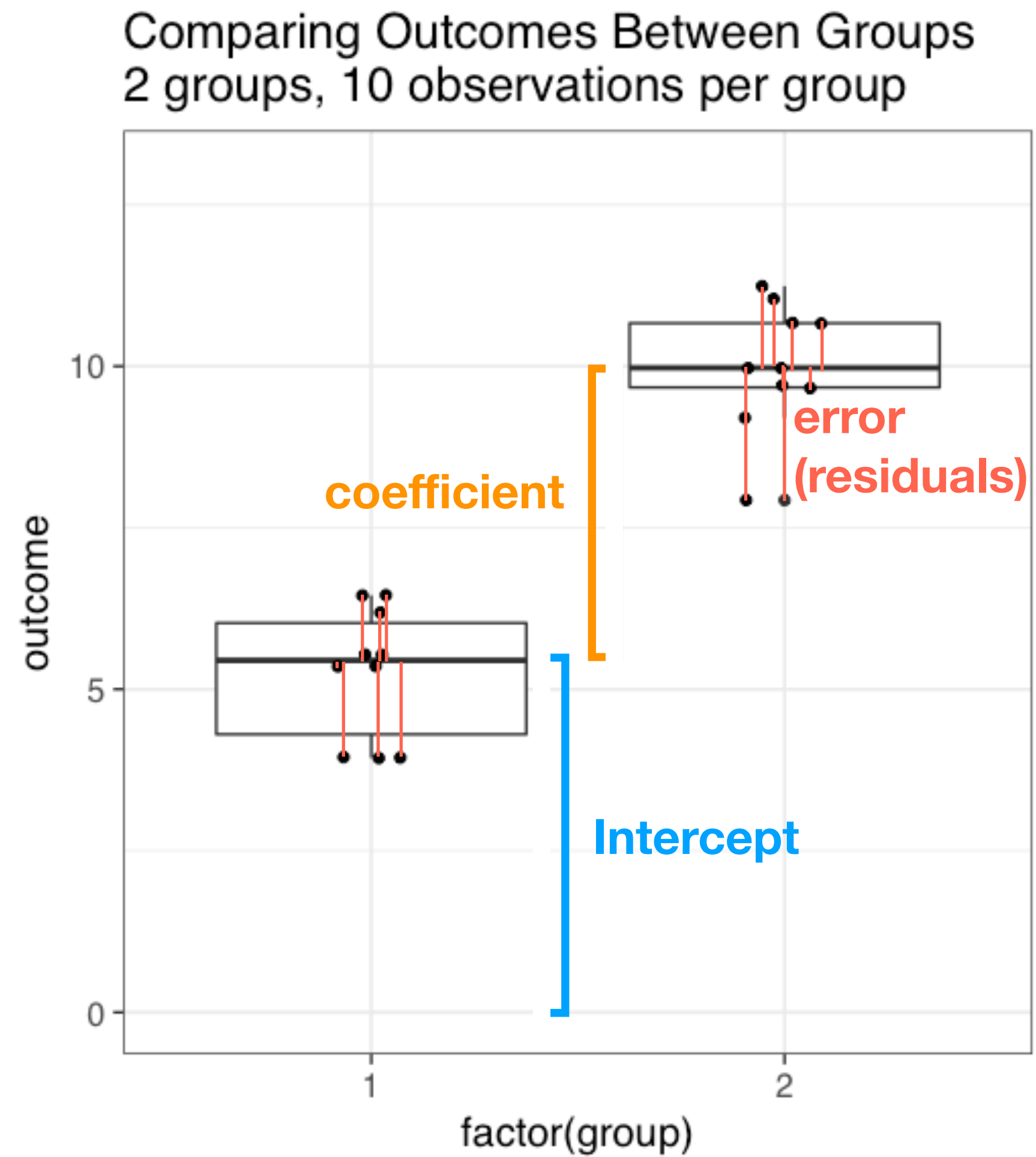
Null Hypothesis Testing

revisiting basics of OLS linear regression



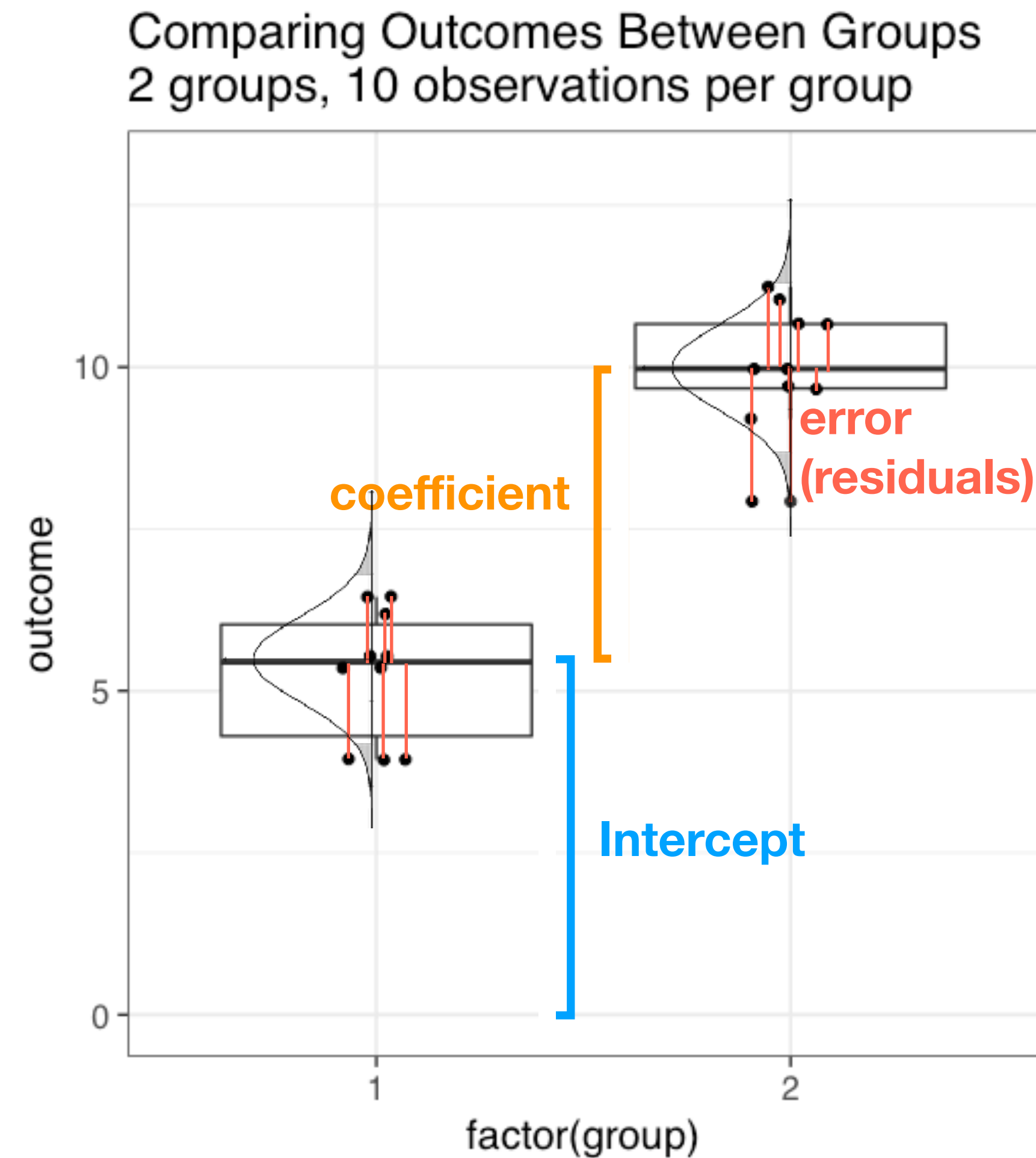
Error

revisiting basics of OLS linear regression



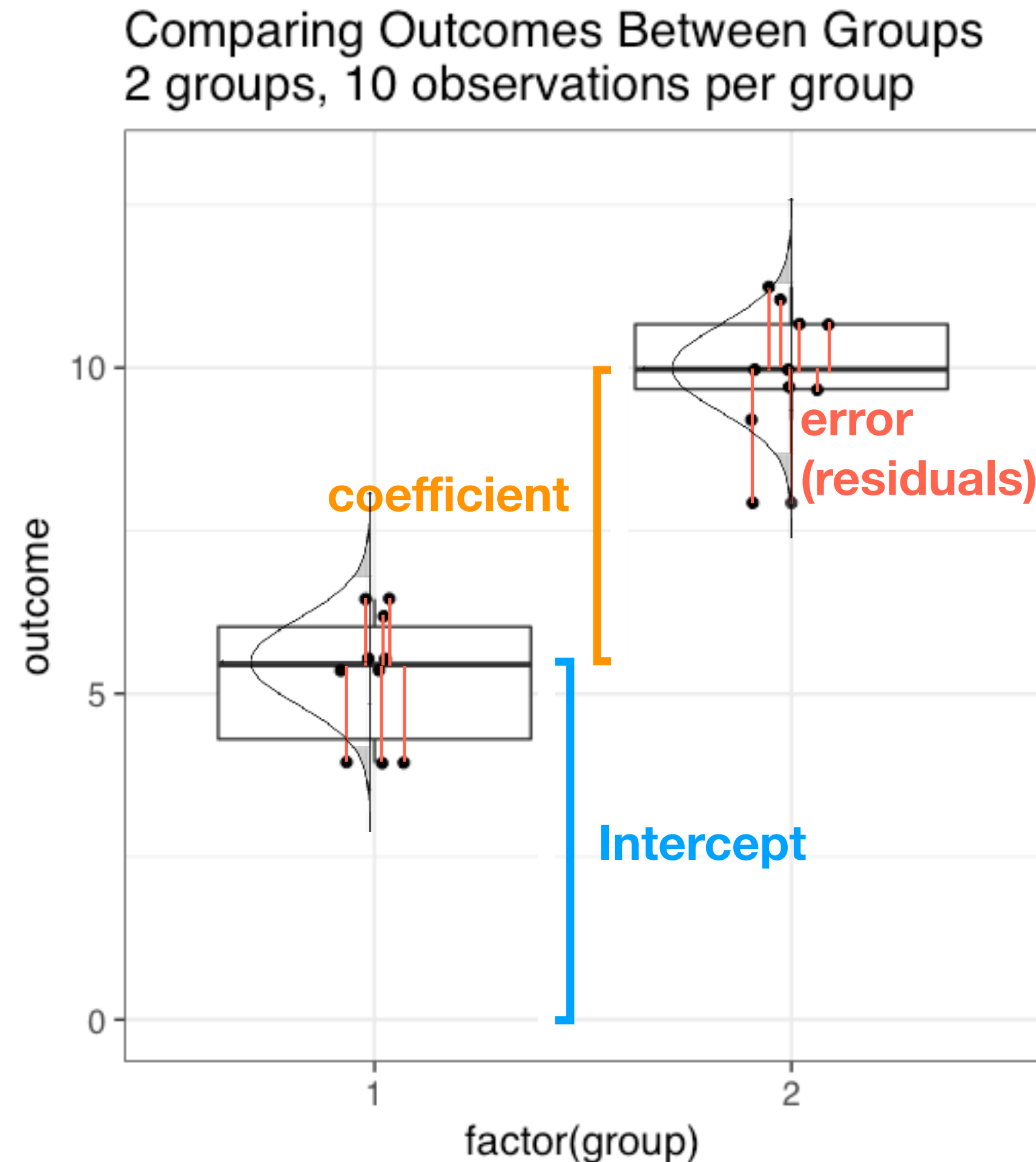
Distribution of Errors

assumption of OLS: error is normally distributed & homoscedastic



Root Mean Square Error

the estimated standard deviation of the residuals

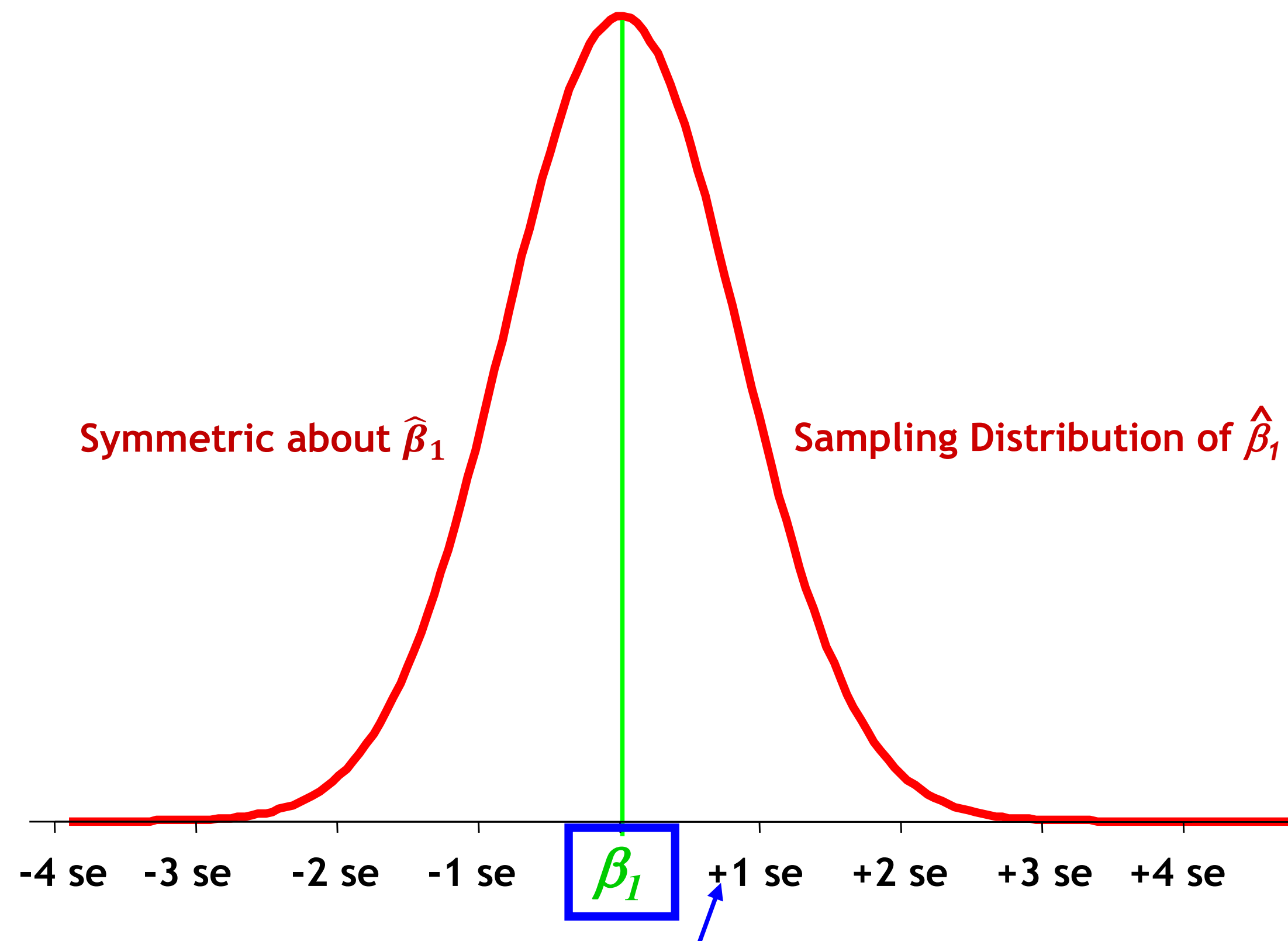


```
m1 <- lm(outcome ~  
          group == 2 ,  
          data=posts)
```

```
rmse <- sqrt(  
  sum(m1$residuals^2) /  
  length(m1$residuals)  
)
```


Standard Error

The standard deviation of the sampling distribution (of a particular statistic)



Definition: The *standard deviation of a sampling distribution* is known as a “standard error,” commonly abbreviated as “se”

$$se(\hat{\beta}) = \frac{\sigma}{\sqrt{(n - 1) \times Var(X)}}$$

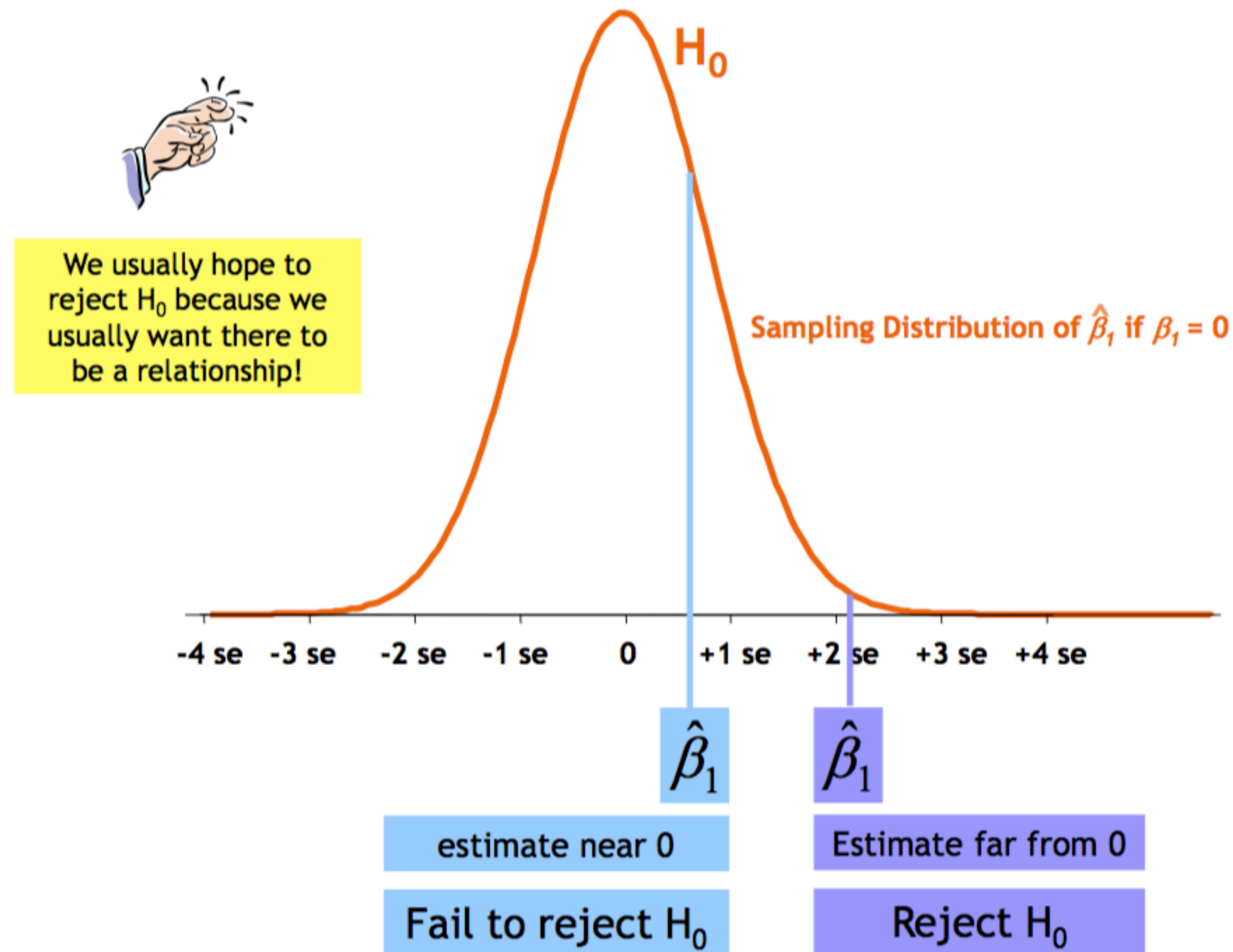
$$\sigma = RMSE$$

$n = \text{num of observations}$

$Var(X) = \text{variance of predictor (TREAT)}$

Null Hypothesis Testing

revisiting basics of OLS linear regression



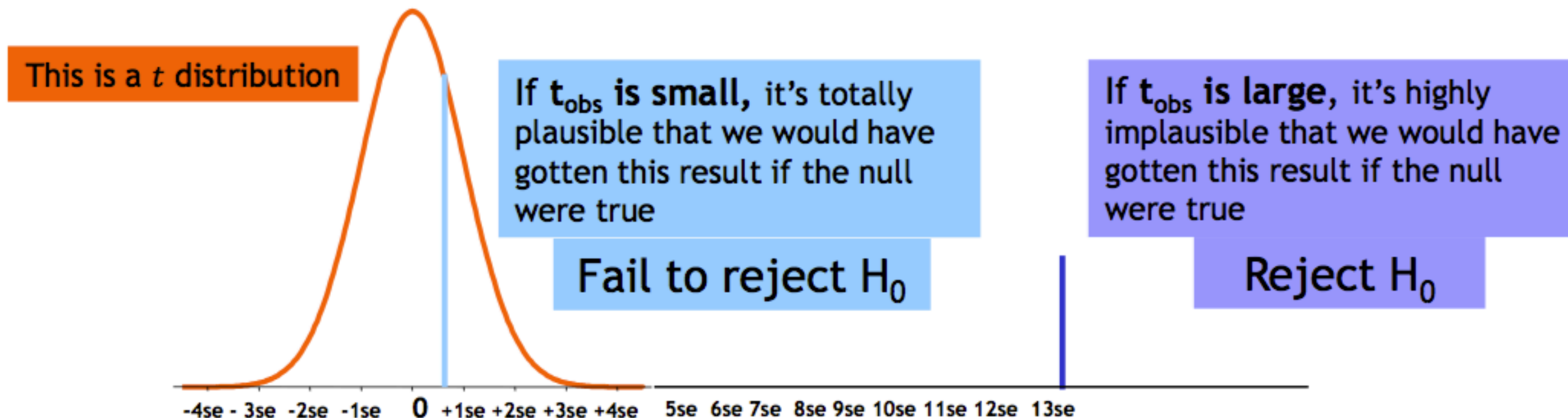
t-statistic

revisiting basics of OLS linear regression

$$t_{obs} = \frac{\hat{\beta} - \beta}{se(\hat{\beta})} \text{ where } H_0: \beta = 0$$

So t_{obs} tells us how many standard errors away from 0 our sample estimate is.

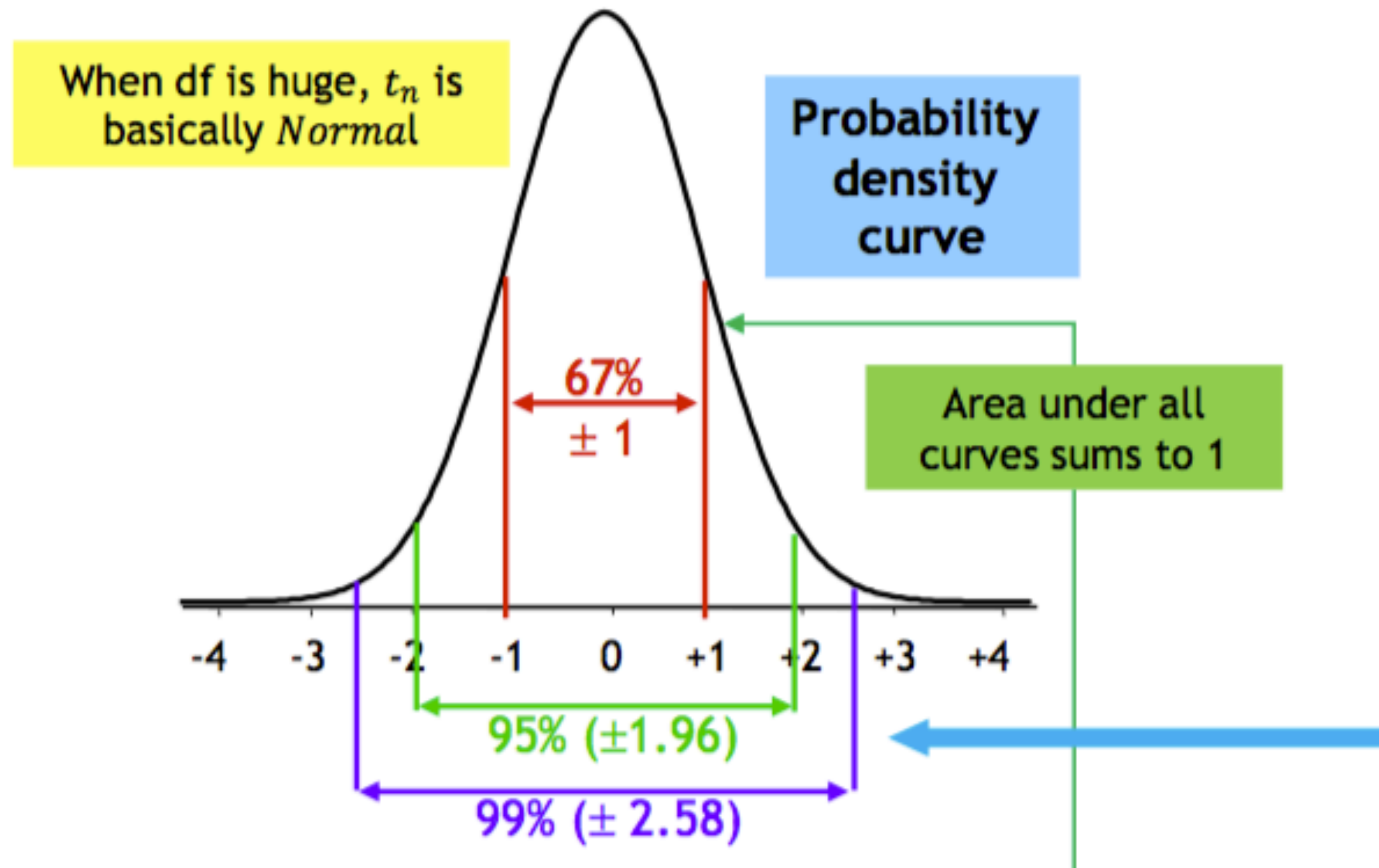
There's nothing magical about $H_0: \beta_1 = 0$, it could be anything (e.g., $H_0: \beta_1 = 1$)



t-distribution

revisiting basics of OLS linear regression

$$t_{obs} = \frac{\hat{\beta} - \beta}{se(\hat{\beta})} \text{ where } H_0: \beta = 0$$



How large is large? Critical values of $t_{observed}$			
df	Two-sided probability level, p		
	0.10	0.05	0.01
10	1.81	2.23	3.17
20	1.72	2.09	2.85
30	1.70	2.04	2.75
50	1.68	2.01	2.68
100	1.66	1.98	2.63
infinite	1.64	1.96	2.58

confidence intervals

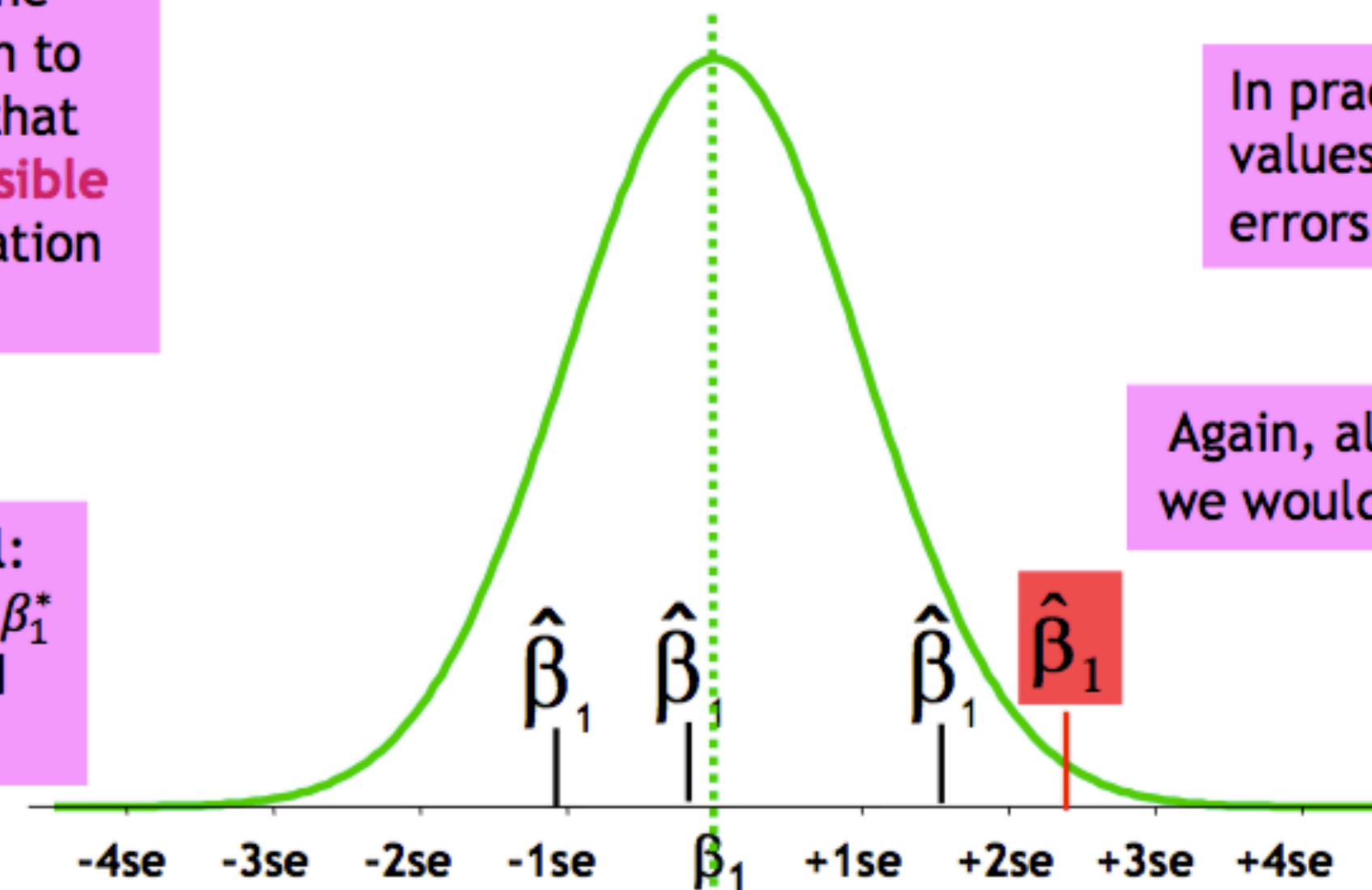
Idea: Can we use the sampling distribution to construct intervals that offer a **range of plausible values** for the population parameter?

Yes!

Confidence interval:
Set of all values of β_1^* for which we would reject $H_0: \beta_1 = \beta_1^*$

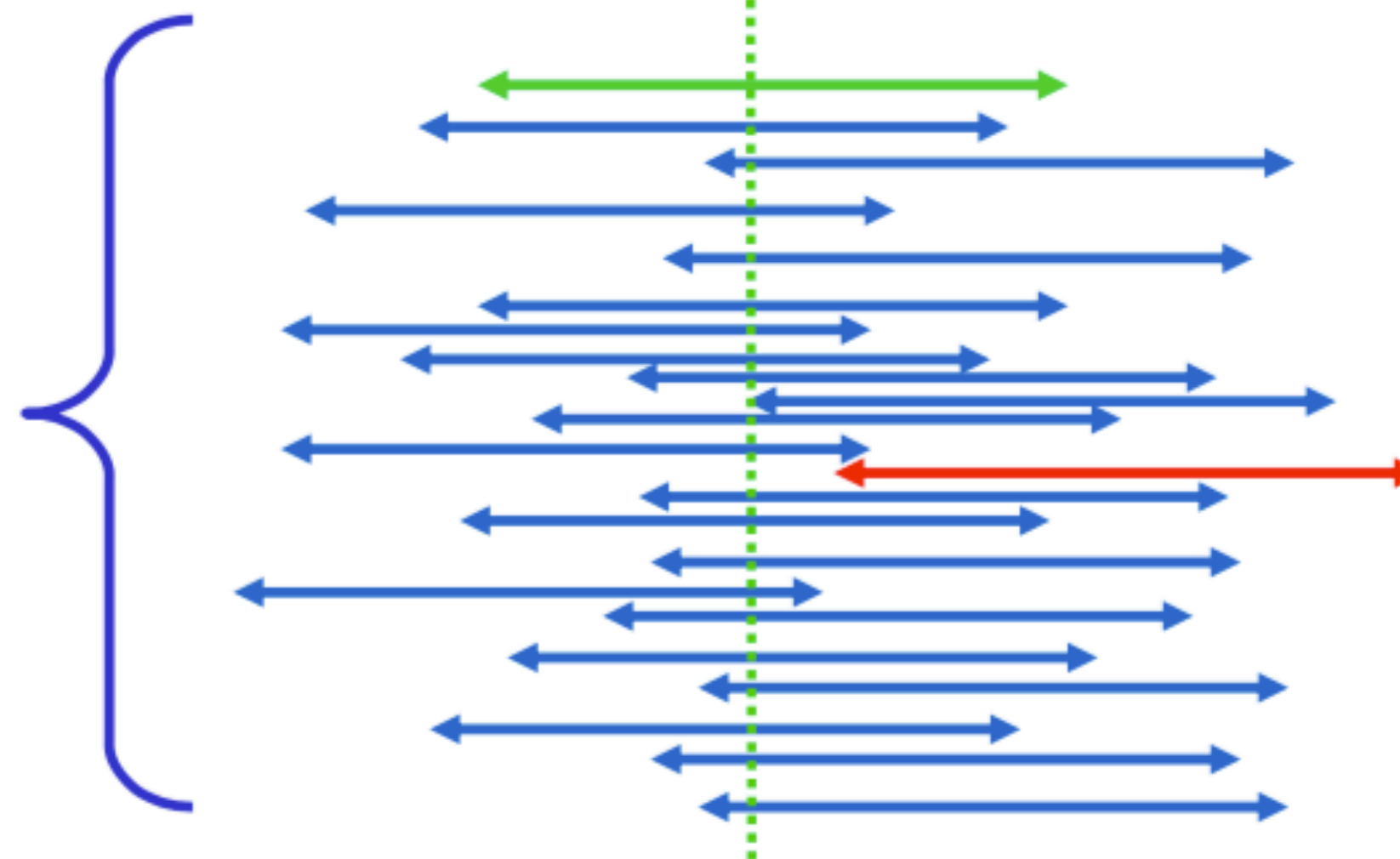
In practice: Take all possible values of β_1 within ~ 2 standard errors of $\hat{\beta}_1$

Again, all values of $\beta_{possible}$ for which we would fail to reject $H: \beta = \beta_{possible}$



$$95\% \text{ conf interval} = \hat{\beta} \pm 1.96 \text{ se}(\hat{\beta})$$

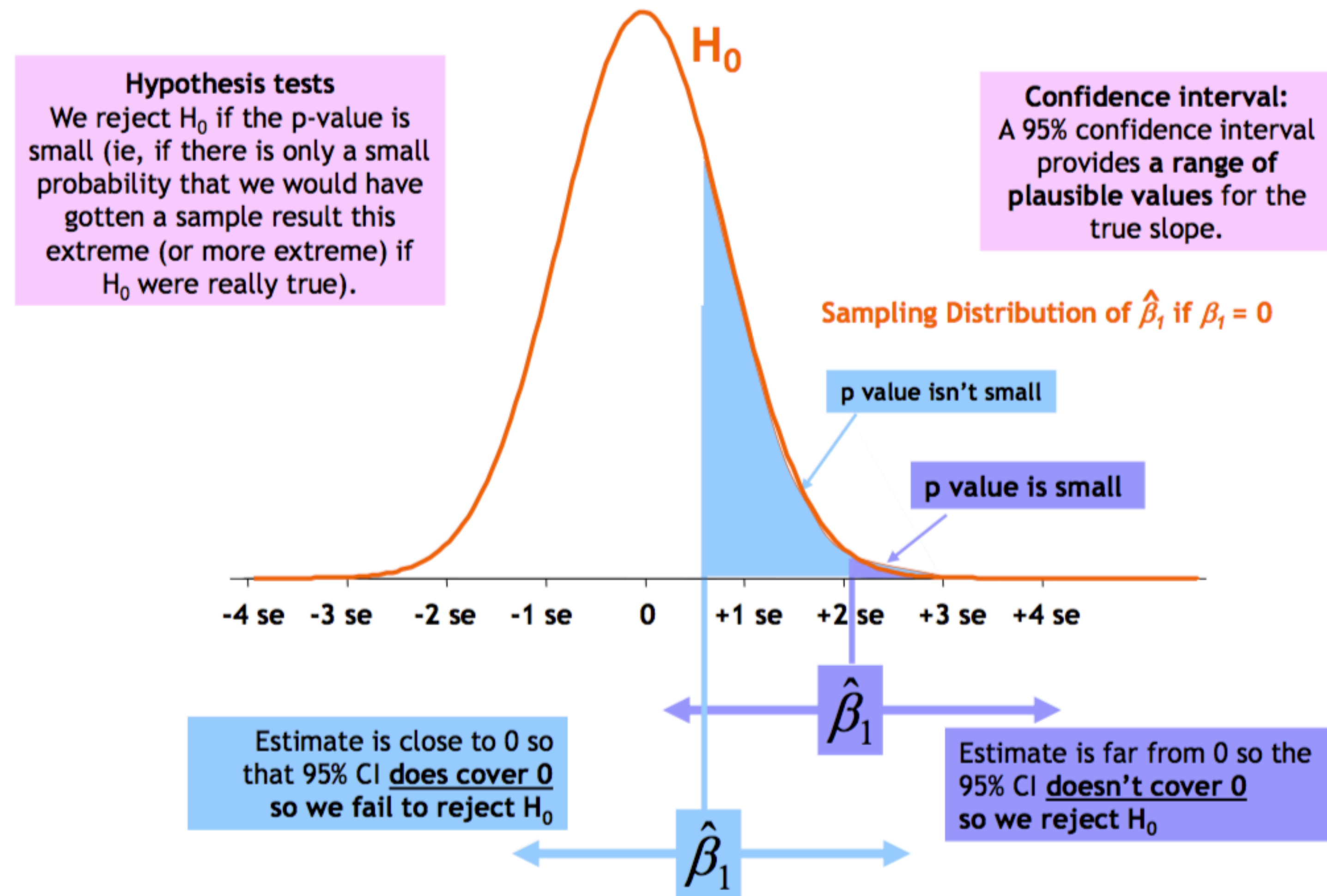
For every 20 95% confidence intervals we construct, we estimate that an average of 1 won't cover the true value of β_1



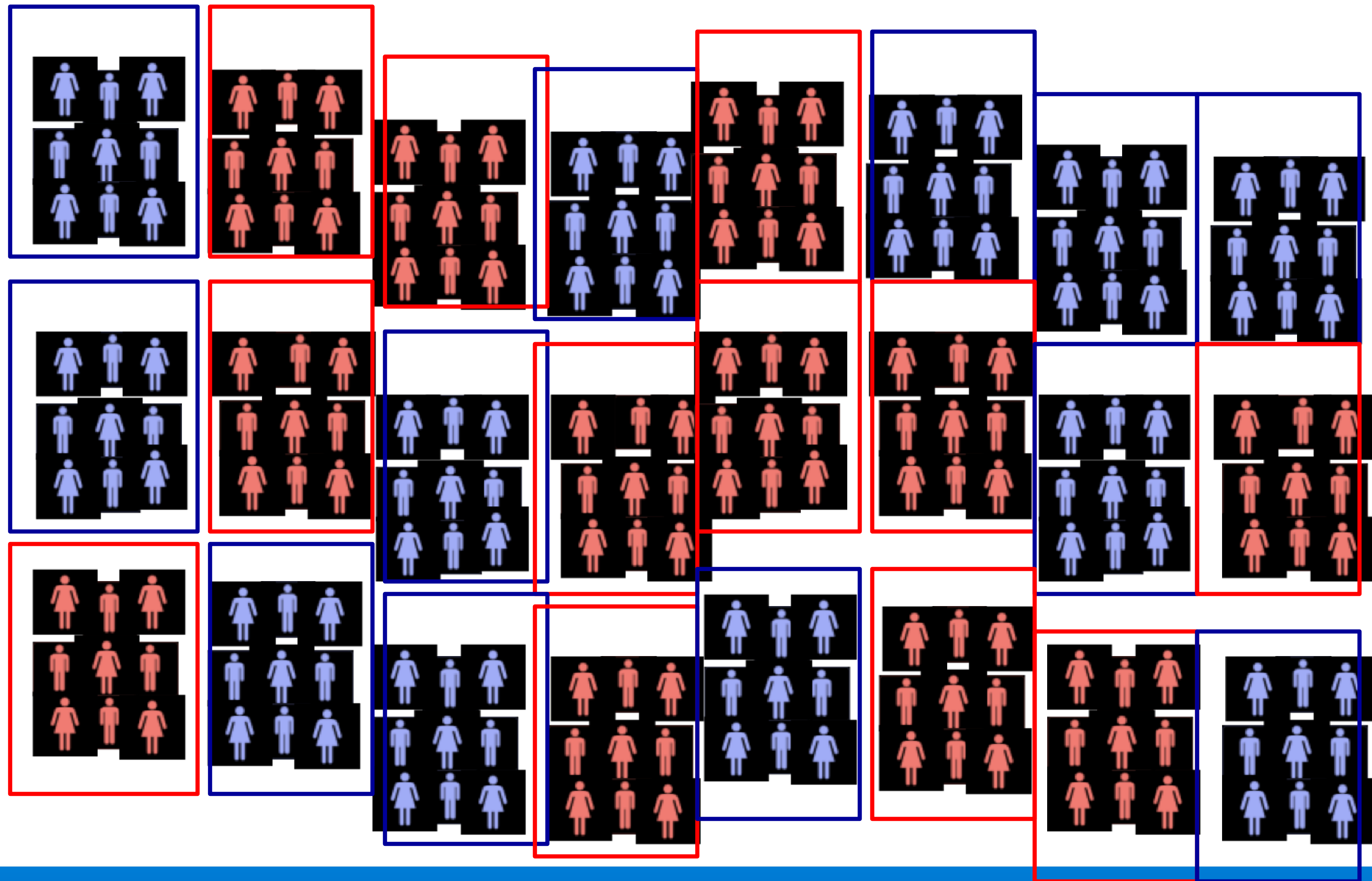
We don't know whether this is one of the lucky 95% that do cover the true value or the unfortunate 5% that don't

p-value

probability of observing a coefficient this extreme if the null hypothesis were true



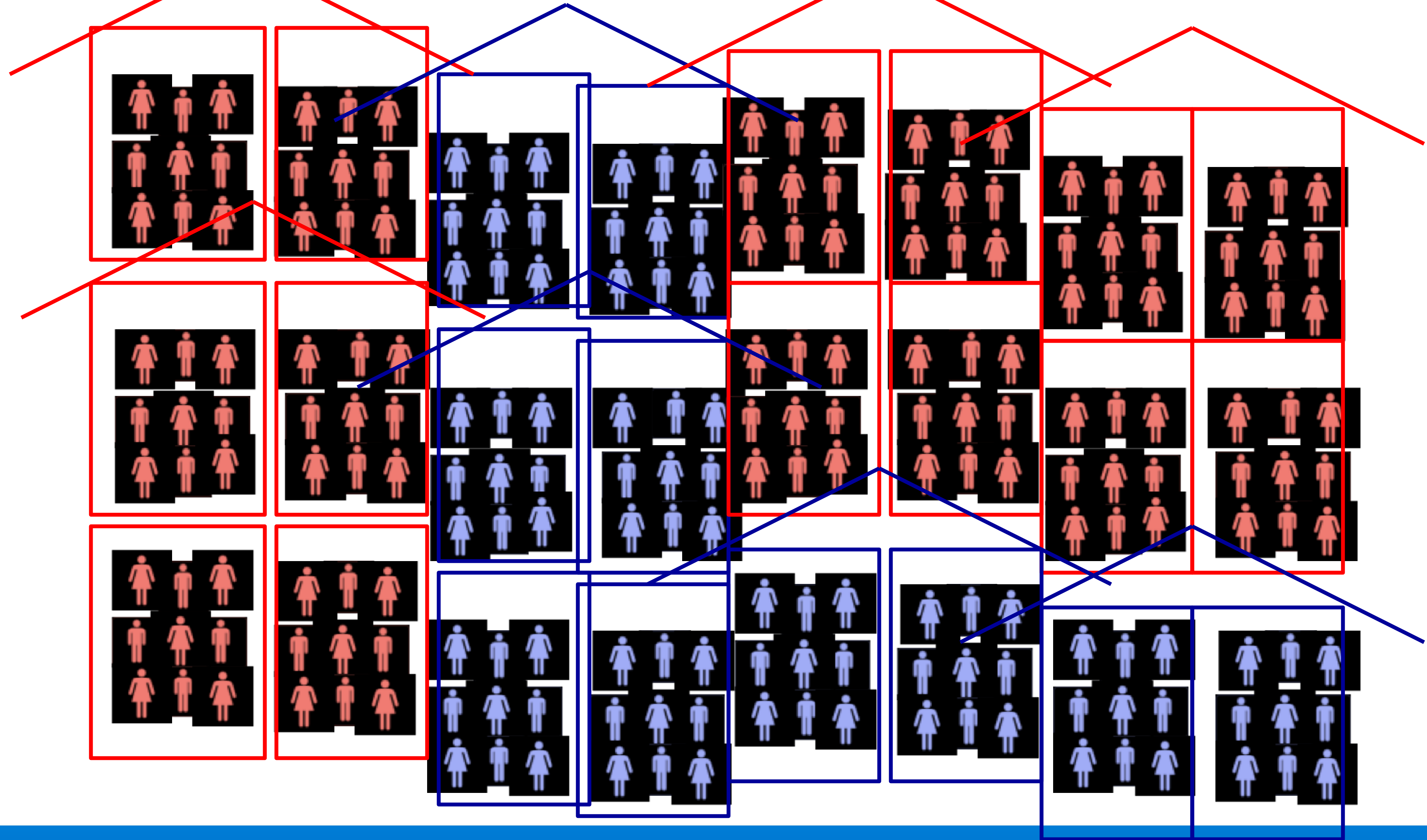
Clustered Randomization: Class



Clustered Randomization: School



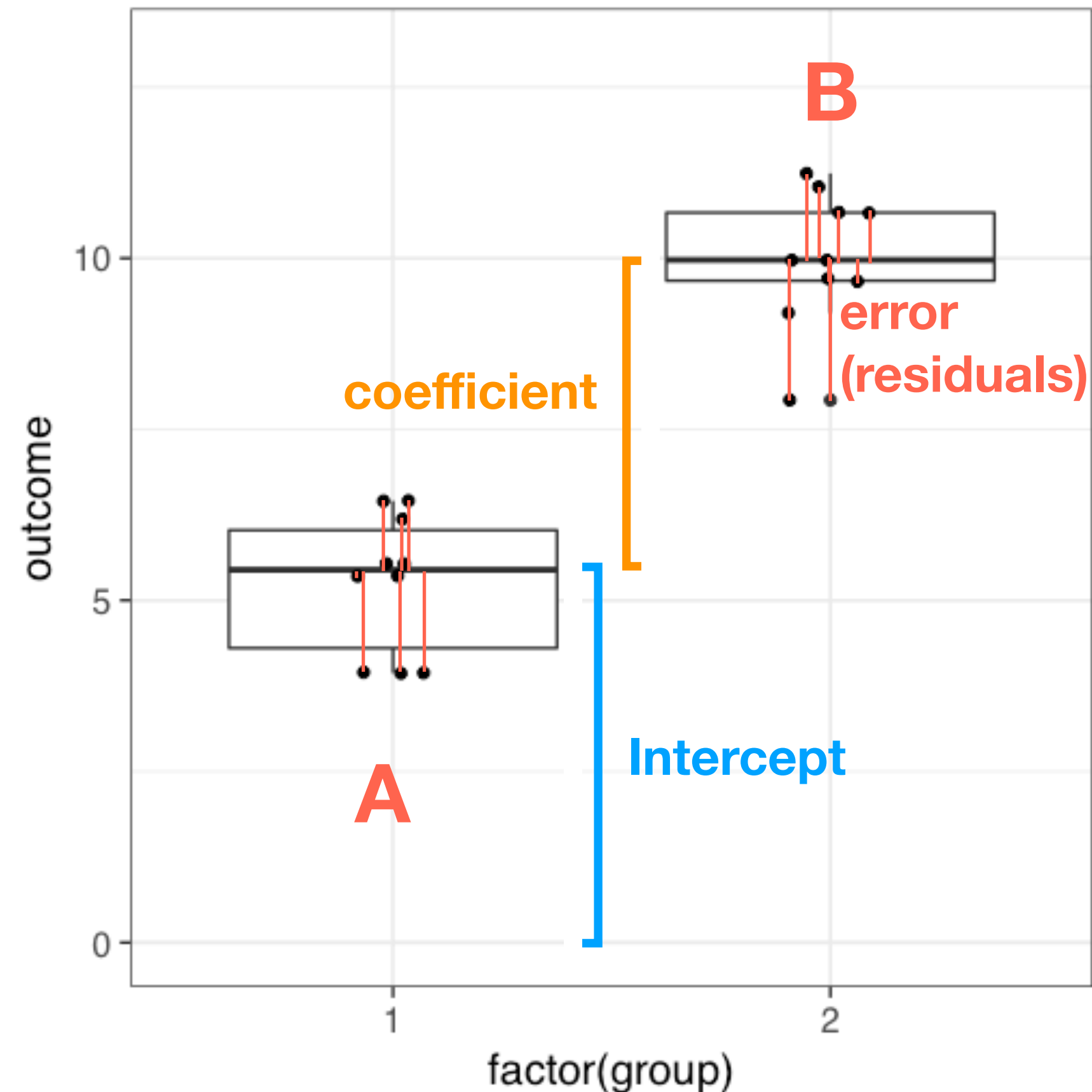
Clustered Randomization: School



Estimating ATE from Cluster Randomization

we are estimating the ATE, not looking for correlations

Comparing Outcomes Between Groups
2 groups, 10 observations per group



Standard Error

$$se(\hat{\beta}) = \frac{\sigma}{\sqrt{(n - 1) \times Var(X)}}$$

$\sigma = RMSE$

$n = \text{num of observations}$

$Var(X) = \text{variance of predictor (TREAT)}$

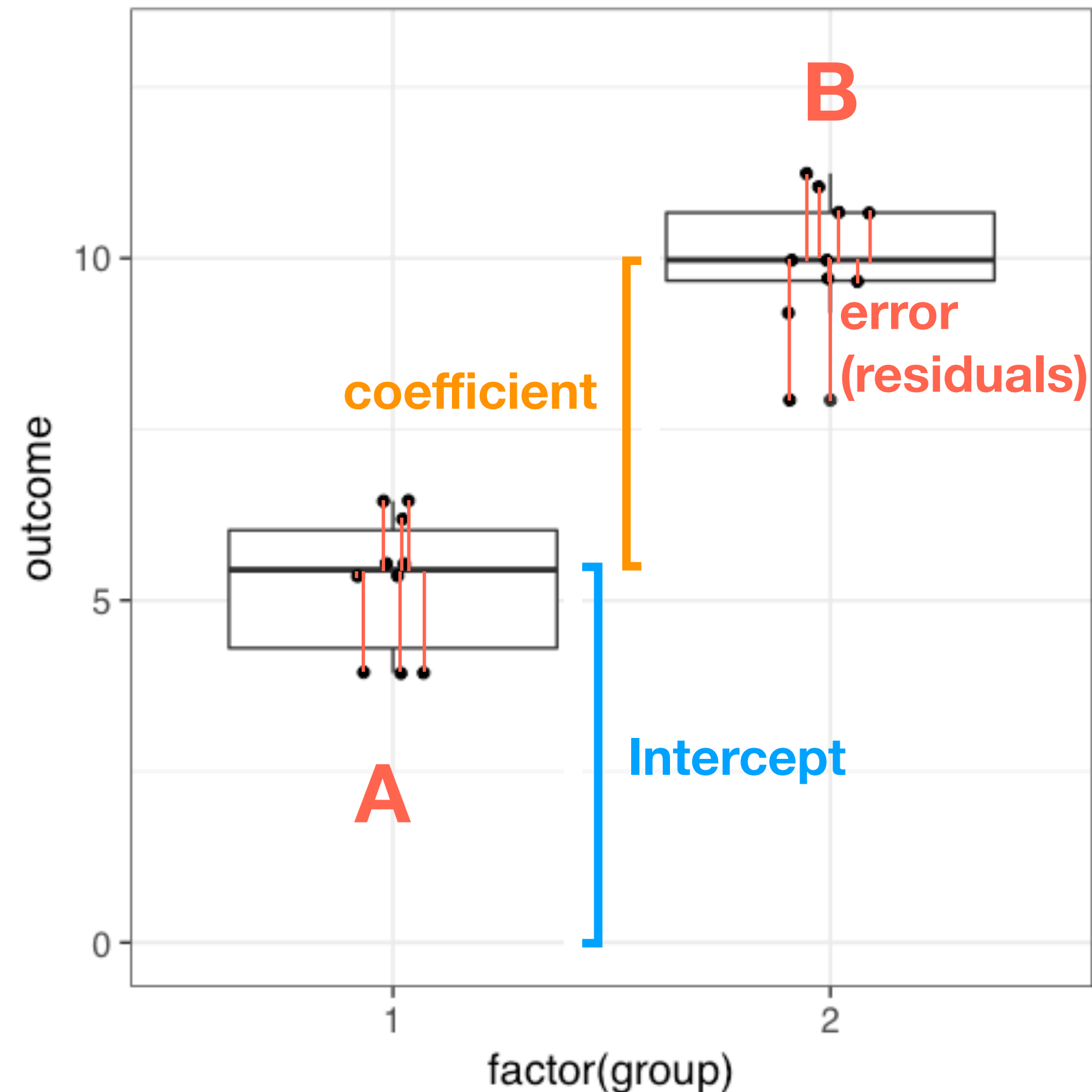
How many observations
do we **really** have?

20 observations or **2**?

Estimating ATE from Cluster Randomization

we are estimating the ATE, not looking for correlations

Comparing Outcomes Between Groups
2 groups, 10 observations per group



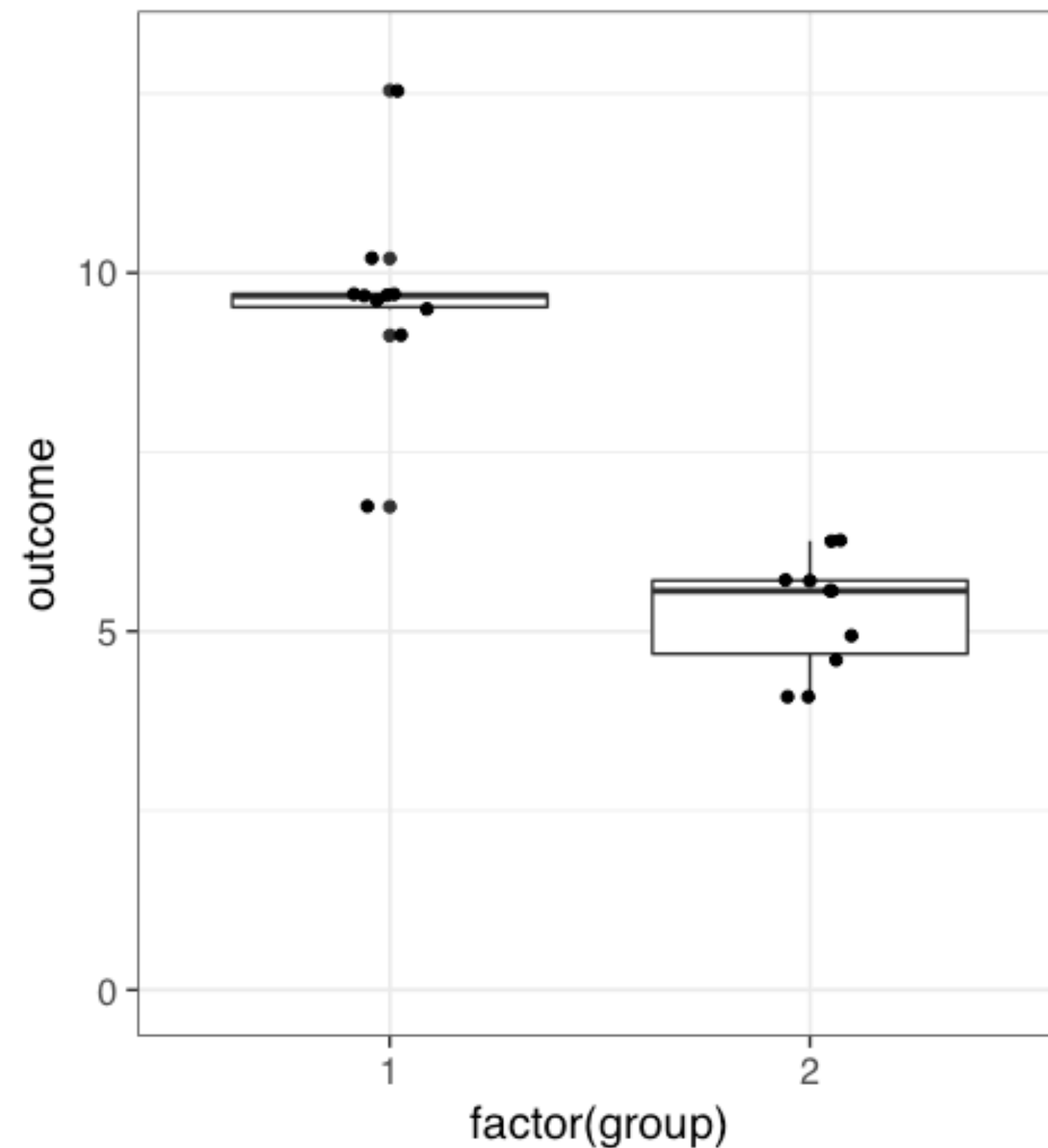
Assumptions of Linear Regression

- Linearity of residuals
- **Independence of Outcomes**
- Homoscedasticity
- Normality of errors

Simulating Group Randomization

(examples in R at simulated-cluster-randomization-example.R)

Comparing Outcomes Between Groups
2 groups, 10 observations per group



Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	5.2787	0.3599	14.666	1.88e-11	***
group%%2	4.3698	0.5090	8.585	8.85e-08	***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

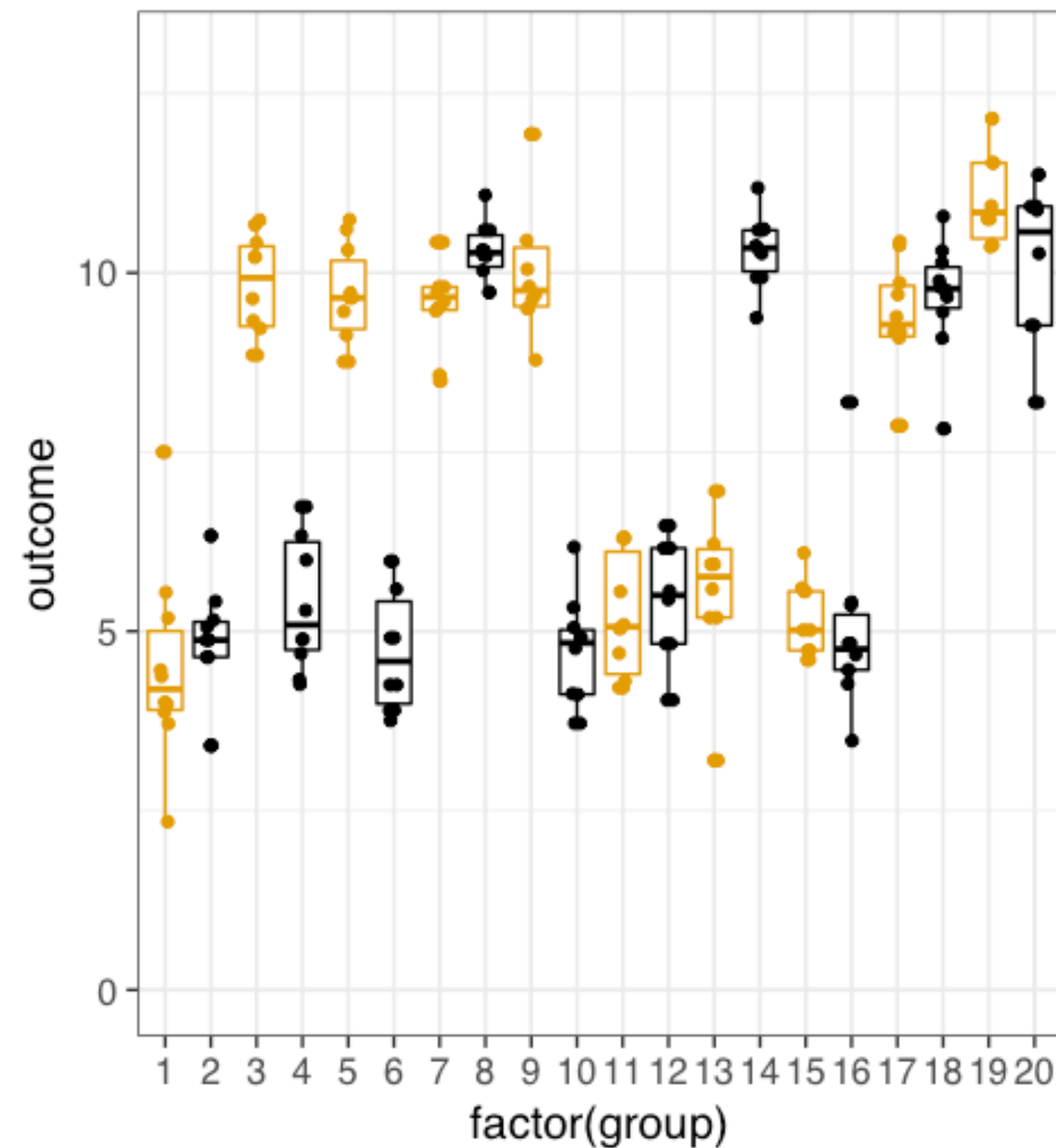
Residual standard error: 1.138 on 18 degrees of freedom
Multiple R-squared: 0.8037, Adjusted R-squared: 0.7928
F-statistic: 73.7 on 1 and 18 DF, p-value: 8.845e-08

Simulated 50x: mean treatment effect: 0.59

Simulating Group Randomization

(examples in R at simulated-cluster-randomization-example.R)

Comparing Outcomes Between Groups
20 groups, 10 observations per group



Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.0362	0.2629	26.766	<2e-16 ***
group%%2	0.9522	0.3718	2.561	0.0112 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

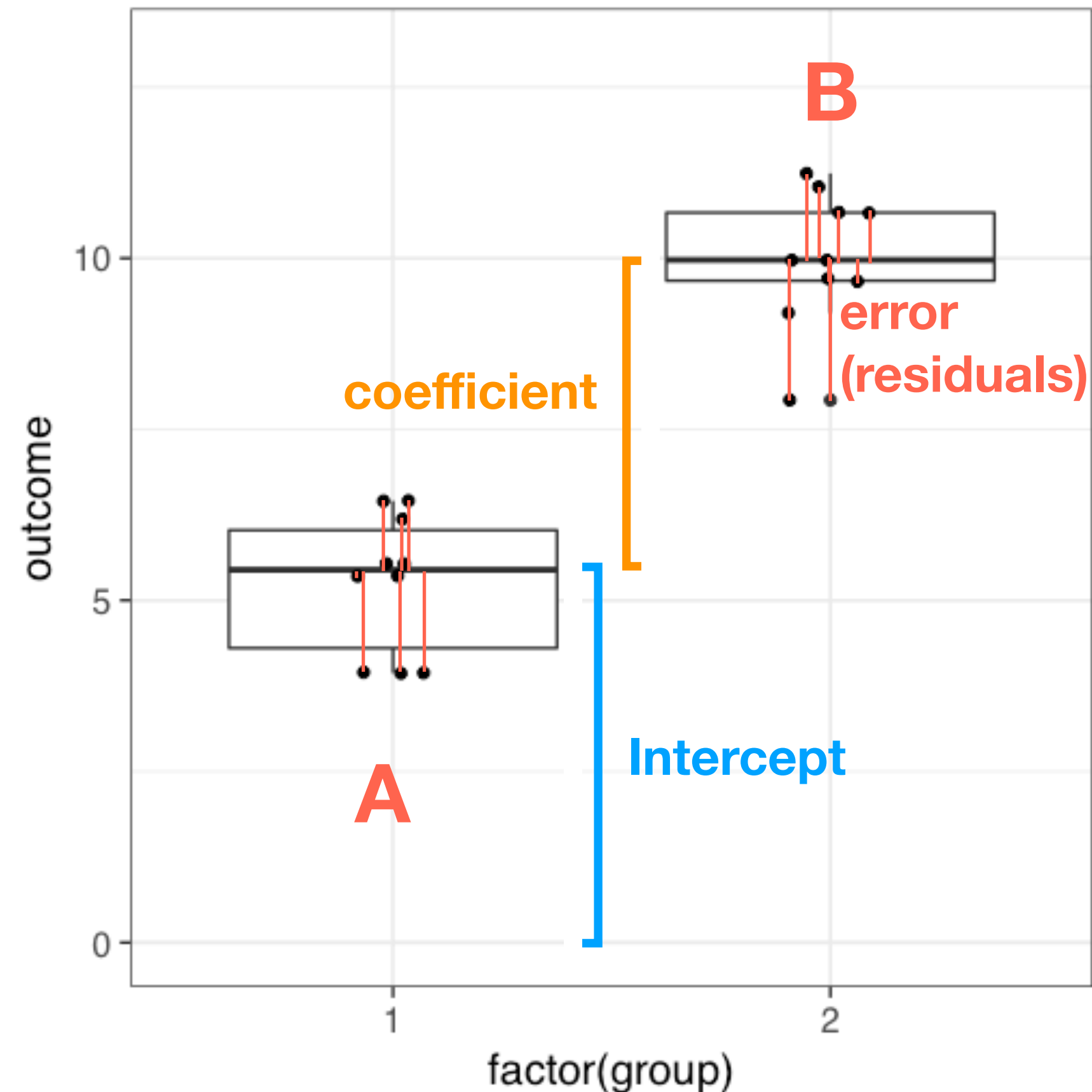
Residual standard error: 2.629 on 198 degrees of freedom
Multiple R-squared: 0.03207, Adjusted R-squared: 0.02718
F-statistic: 6.56 on 1 and 198 DF, p-value: 0.01117

Simulated 50x: mean treatment effect: 0.13

Estimating ATE for Group Randomization

Random Intercepts Models and Clustered Standard Errors

Comparing Outcomes Between Groups
2 groups, 10 observations per group



Strategies

- Random Intercepts model
 - Especially useful for comparing individuals ***and*** groups
- Clustered standard errors (useful for getting point estimates)
 - Without specifying groups
 - With specifying groups

Random Intercepts Model

Random Intercepts Models

- Very specific assumptions
- Useful when comparing blocked randomization in a cluster randomized design (such as different kinds of posts or schools)
- Multilevel & hierarchical modeling could be its own entire semester. As always, take the time to familiarize yourself with a modeling approach before using it regularly

Example R code:

```
library(lme4)
```

```
library(lmerTest)
```

```
summary(glmer(outcome ~ group.treat + (1|group), data=posts))
```


Clustered Standard Errors

Huber White Standard Errors

- Useful when you want a single point estimate & standard errors
- Ongoing discussion about the best methods to cluster standard errors (Green's lab now uses Bell & McCaffrey clustered SEs)
- Here we will use Huber White

Example code:

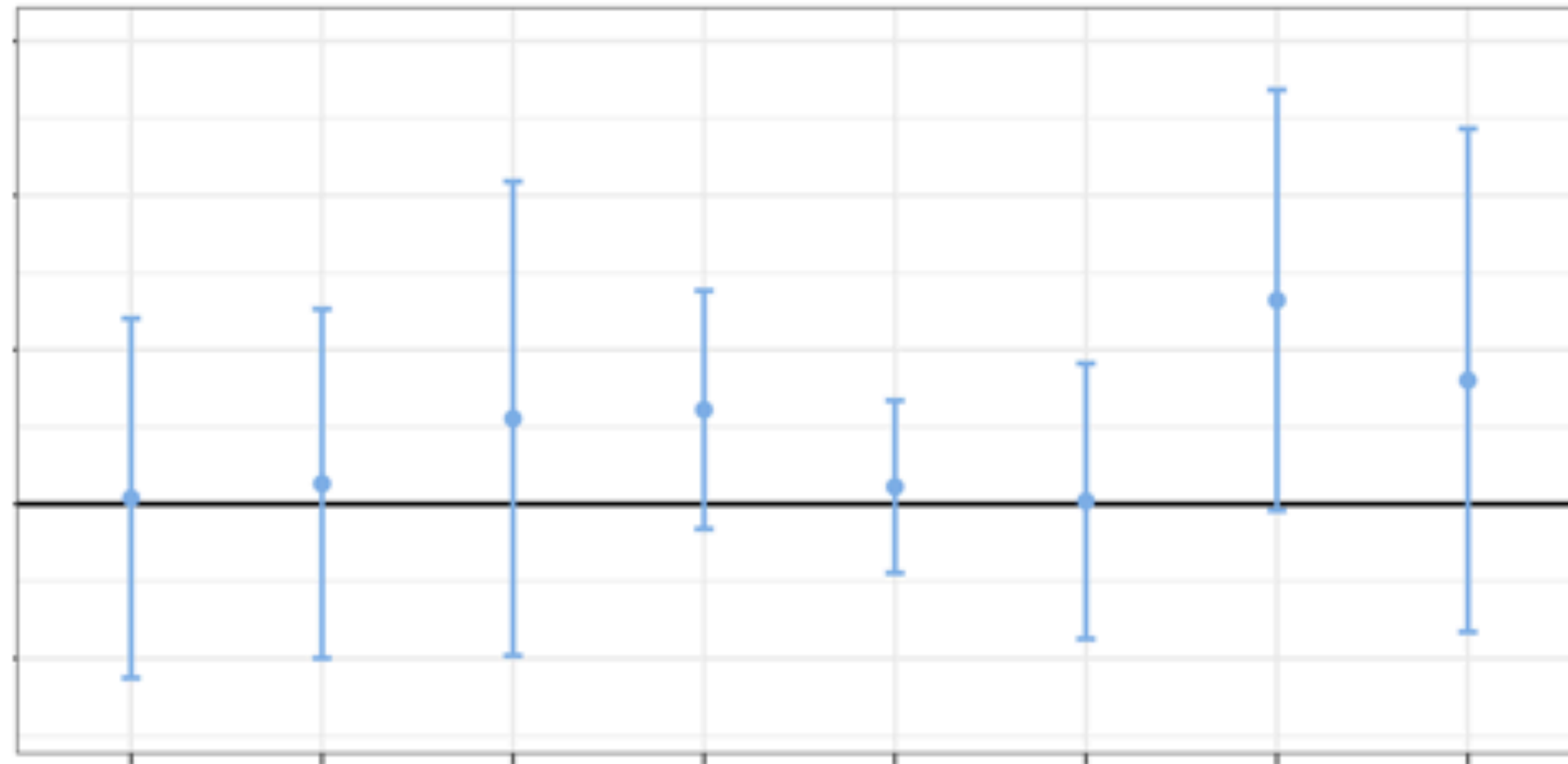
```
library(rms)
r1 = ols(outcome ~ group.treat, data=posts, x=TRUE)
r1.adjusted <- robcov(r1, cluster=factor(posts$group), method='huber')
screenreg(list(r1))
```

<https://www.rdocumentation.org/packages/rms/versions/5.1-2/topics/robcov>

Regression Adjustment

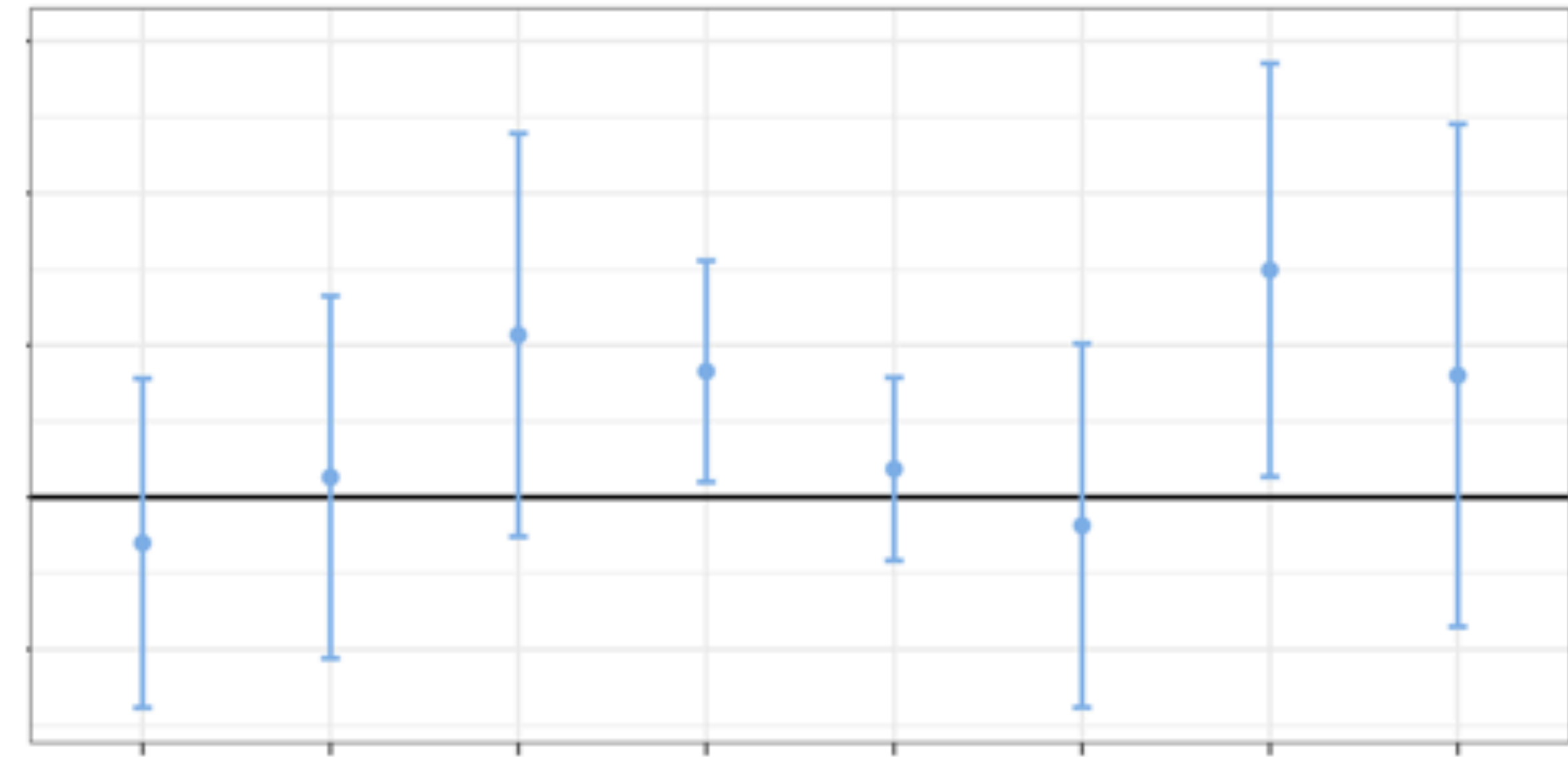
Improving the precision of standard errors

$$\ln \text{Interactions} = \beta_0 + \beta_1 \text{TREAT} + \epsilon$$



(n=8 experiments conducted on Facebook)
Linear models estimating effect on log-transformed interactions.
Experiment by SOC 412: github.com/natematias/SOC412

$$\ln \text{Interactions} = \beta_0 + \beta_1 \text{TREAT} + \beta_2 \text{Weekend} + \epsilon$$



(n=8 experiments conducted on Facebook)
Linear models estimating effect on log-transformed interactions, adjusted by weekend. Experiment by SOC 412: github.com/natematias/SOC412

Regression Adjustment

Avoid conditioning on post-treatment variables

scholars often unwittingly distort
treatment effect estimates by
conditioning on variables that
could be **affected by their**
experimental manipulation.

Montgomery, J. M., Nyhan, B., & Torres, M. (2016, November). **How conditioning on post-treatment variables can ruin your experiment and what to do about it.** In Annual meeting of the Midwest Political Science Association, Chicago, IL, April.

Block Randomization

Preventing Problems From Introducing Selection Bias

Bonferroni Adjustment

Adjusting p-values for multiple comparison

Note: Bonferroni is the most conservative, so you may choose others

```
num.comparisons <- 2
m1 <- lm(outcome ~ group.treat, data=posts)
p.adjust(summary(m1)$coefficients['(Intercept)',][['Pr(>|t|)']],
          method="bonferroni",
          n=num.comparisons)
```