Gov 50: 22. More Hypothesis testing

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Roadmap

1. Reviewing hypothesis testing
2. Issues with hypothesis testing
3. Power Analyses

1/ Reviewing hypothesis testing

Difference-in-means

```
library(gov50data)
trains <- trains |>
  mutate(treated = if_else(treatment == 1, "Treated", "Untreated"))
trains
```

```
## # A tibble: 115 x 15
##      age  male income white college usborn treatment ideol~1
##    <dbl> <dbl>  <dbl> <dbl>   <dbl>  <dbl>     <dbl>   <dbl>
##  1    31     0 135000     1       1      1         1       3
##  2    34     0 105000     1       1      0         1       4
##  3    63     1 135000     1       1      1         1       2
##  4    45     1 300000     1       1      1         1       4
##  5    55     1 135000     1       1      1         0       2
##  6    37     0  87500     1       1      1         1       5
##  7    53     0  87500     1       0      1         0       5
##  8    36     1 135000     1       1      1         1       4
##  9    54     0 105000     1       0      1         0       3
## 10    42     1 135000     1       1      1         1       4
## # ... with 105 more rows, 7 more variables:
## #   numberim.pre <dbl>, numberim.post <dbl>,
## #   remain.pre <dbl>, remain.post <dbl>, english.pre <dbl>,
## #   english.post <dbl>, treated <chr>, and abbreviated
```

Calculating the ATE

```
library(infer)
ate <- trains |>
  specify(numberim.post ~ treated) |>
  calculate(stat = "diff in means",
            order = c("Treated", "Untreated"))
ate
```

```
## Response: numberim.post (numeric)
## Explanatory: treated (factor)
## # A tibble: 1 x 1
##    stat
##   <dbl>
## 1 0.383
```

Difference in means hypotheses

Hypotheses:

$$H_0 : \mu_T - \mu_C = 0$$
$$H_1 : \mu_T - \mu_c \neq 0$$

Observed difference in means:

$$\widehat{ATE} = \overline{Y}_T - \overline{Y}_C$$

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How can we approximate the **null distribution**? **Permute** the outcome/treatment variables.

Permuting the treatment

Let's do 2 permutations to see how things vary:

```
set.seed(02138)
perm <- trains |>
  specify(numberim.post ~ treated) |>
  hypothesize(null = "independence") |>
  generate(reps = 1000,
           type = "permute")
```

`generate(type = "permute")` shuffles to the outcomes, keeping treatment the same:

```
perm |> filter(replicate == 1)
```

```
## # A tibble: 115 x 3
## # Groups:   replicate [1]
##   numberim.post treated   replicate
##           <dbl> <fct>         <int>
##  1            3 Treated           1
##  2            2 Treated           1
##  3            5 Treated           1
##  4            3 Treated           1
##  5            3 Untreated         1
##  6            3 Treated           1
##  7            2 Untreated         1
##  8            2 Treated           1
##  9            3 Untreated         1
## 10            3 Treated           1
## # ... with 105 more rows
```

```
perm |> filter(replicate == 2)
```

```
## # A tibble: 115 x 3
## # Groups:   replicate [1]
##   numberim.post treated   replicate
##           <dbl> <fct>         <int>
##  1            2 Treated           2
##  2            3 Treated           2
##  3            3 Treated           2
##  4            3 Treated           2
##  5            3 Untreated         2
##  6            4 Treated           2
##  7            2 Untreated         2
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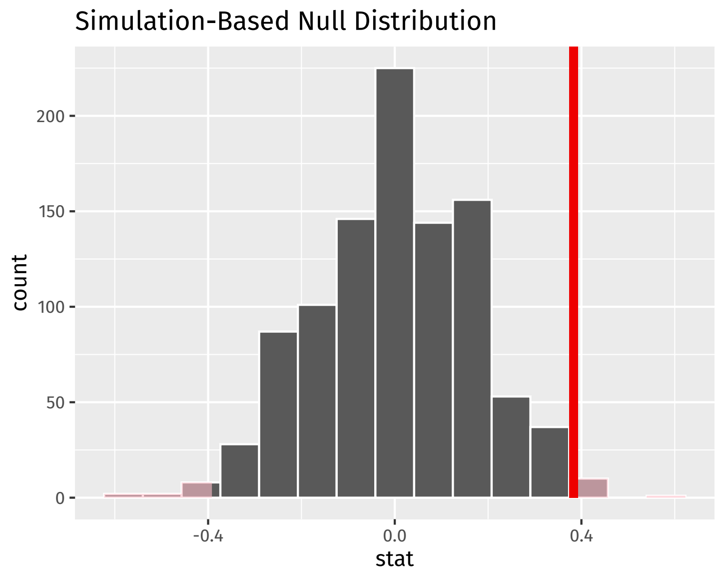
Null distribution

The distribution of the differences-in-means under permutation will be mean 0 because shuffling the outcomes means that the outcomes in each permutation's treated and control group are coming from the same distribution.

```
null_dist <- trains |>
  specify(numberim.post ~ treated) |>
  hypothesize(null = "independence") |>
  generate(reps = 1000,
           type = "permute") |>
  calculate(stat = "diff in means", order = c("Treated", "Untreated"))
```

```r
null_dist |>
  visualize() +
  shade_p_value(obs_stat = ate, direction = "both")
```



Interpreting p-values

```
get_p_value(null_dist, obs_stat = ate, direction = "both")
```

```
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##   p_value
##     <dbl>
## 1   0.022
```

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p-value: probability of an estimated ATE as big as $|\widehat{ATE}|$ by random chance if there is no treatment effect.

Rejecting the null

Decision rule: “reject the null if the p-value is below the **test level** α”

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Test level α controls the amount of false positives:

	Null False (True difference)	Null True (No true difference)
Reject Null	True Positive	False Positive (Type I error)
Retain Null	False Negative (Type II error)	True Negative

Tests and confidence intervals

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    - 95% CI for social pressure experiment: $[0.016, 0.124]$
    - $\rightsquigarrow$ p-value for $H_0 : \mu_T - \mu_C = 0$ less than 0.05.
- Confidence intervals are all of the null hypotheses we **can't reject** with a test.

CI in the trains example

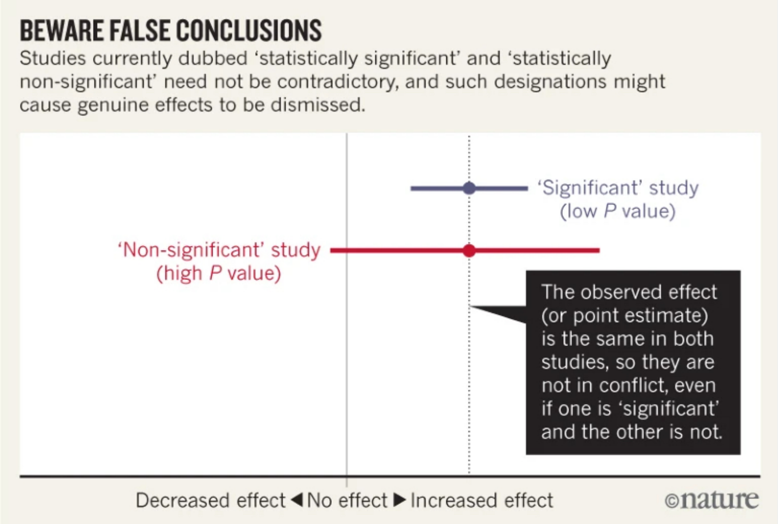
```
trains |>
  specify(numberim.post ~ treated) |>
  generate(reps = 1000, type = "bootstrap") |>
  calculate(stat = "diff in means",
            order = c("Treated", "Untreated")) |>
  get_ci(level = 0.95)
```

```
## # A tibble: 1 x 2
##   lower_ci upper_ci
##      <dbl>    <dbl>
## 1   0.0893    0.698
```

2/ Issues with hypothesis testing

Significant vs not significant

The difference between statistically significant and not statistically significant is itself not statistically significant:



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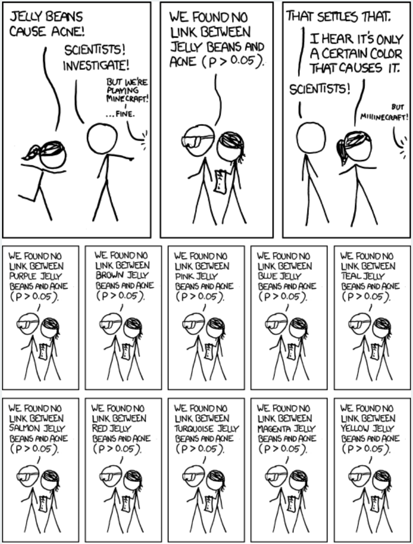
There are different types of significance that don't all have to be true together:

1. **Statistical significance:** we can reject the null of no effect.
2. **Causal significance**: we can interpret our estimated difference in means as a causal effect.
3. **Practical significance**: the estimated effect is meaningfully large.

p-hacking


JELLY BEANS CAUSE ACNE!
SCIENTISTS! INVESTIGATE!
BUT WE'RE PLAYING MINECRAFT!
...FINE.
WE FOUND NO LINK BETWEEN JELLY BEANS AND ACNE (P > 0.05).
THAT SETTLES THAT.
I HEAR IT'S ONLY A CERTAIN COLOR THAT CAUSES IT.
SCIENTISTS!
BUT MINECRAFT!
WE FOUND NO LINK BETWEEN PURPLE JELLY BEANS AND ACNE (P > 0.05).
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WE FOUND NO LINK BETWEEN BLUE JELLY BEANS AND ACNE (P > 0.05).
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WE FOUND NO LINK BETWEEN MAGENTA JELLY BEANS AND ACNE (P > 0.05).
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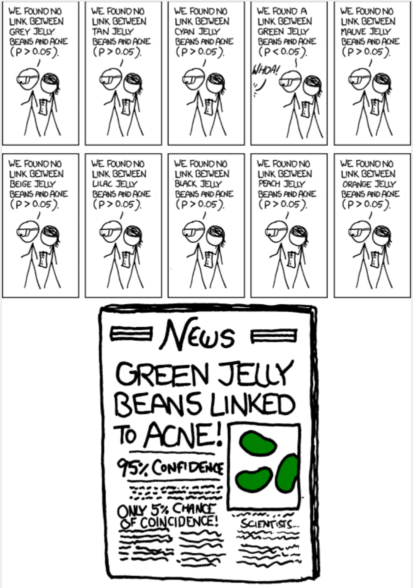
WE FOUND NO LINK BETWEEN GREY JELLY BEANS AND ACNE (P > 0.05).
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WE FOUND NO LINK BETWEEN CYAN JELLY BEANS AND ACNE (P > 0.05).
WE FOUND A LINK BETWEEN GREEN JELLY BEANS AND ACNE (P < 0.05).
WHOA!
WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND ACNE (P > 0.05).
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WE FOUND NO LINK BETWEEN LILAC JELLY BEANS AND ACNE (P > 0.05).
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NEWS
GREEN JELLY BEANS LINKED TO ACNE!
95% CONFIDENCE
ONLY 5% CHANCE OF COINCIDENCE!
SCIENTISTS...

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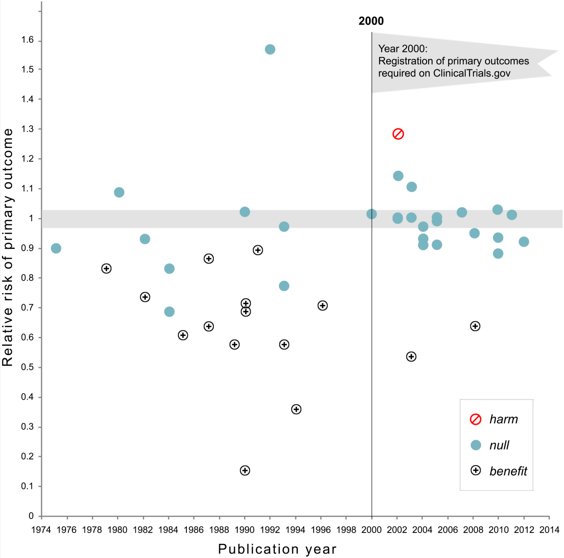

2000
Year 2000:
Registration of primary outcomes
required on ClinicalTrials.gov
Relative risk of primary outcome
1.6
1.5
1.4
1.3
1.2
1.1
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
1974 1976 1978 1980 1982 1984 1986 1988 1990 1992 1994 1996 1998 2000 2002 2004 2006 2008 2010 2012 2014
Publication year
harm
null
benefit

3/ Power Analyses

Effect sizes

TABLE 2. Effects of Four Mail Treatments on Voter Turnout in the August 2006 Primary Election

	Experimental Group				
	Control	Civic Duty	Hawthorne	Self	Neighbors
Percentage Voting	29.7%	31.5%	32.2%	34.5%	37.8%
N of Individuals	191,243	38,218	38,204	38,218	38,201

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- **Detect** here means "reject the null of no effect"

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- If we fail to reject a null hypothesis, two possible states of the world:
    - Null is true (no treatment effect)
    - Null is false (there is a treatment effect), but test had low power.

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    - You sample 10 hiring records of each race, conduct hypothesis test and fail to reject null.
- Say to judge, “look we don’t have any racial discrimination”! What’s the problem?

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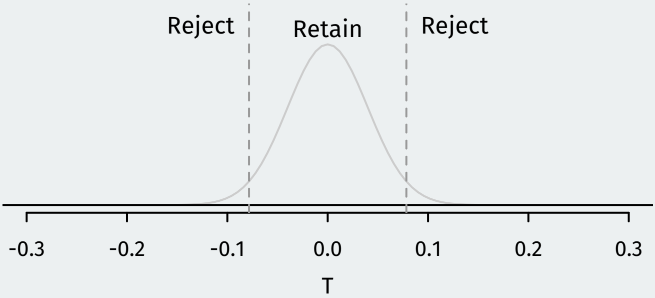
  - Repeat for different effect sizes.

Power graph



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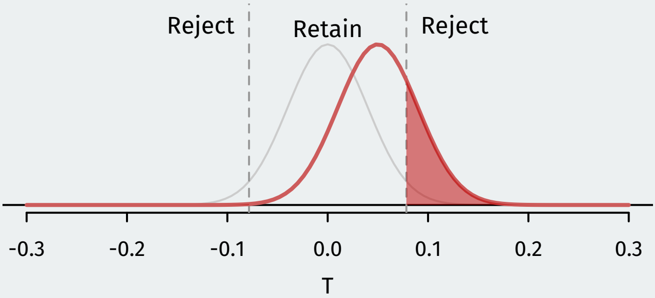

Assumed treatment effect = 0.05 and power = 0.24.

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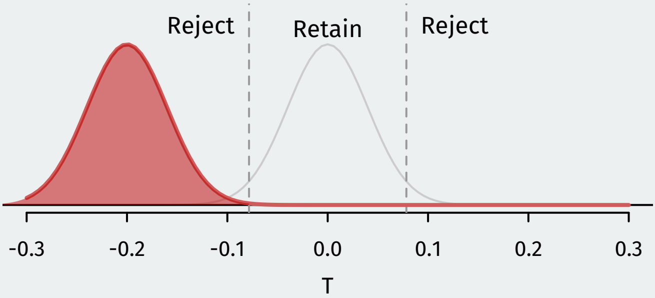
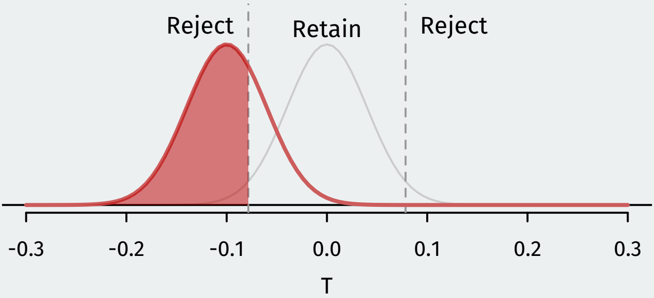


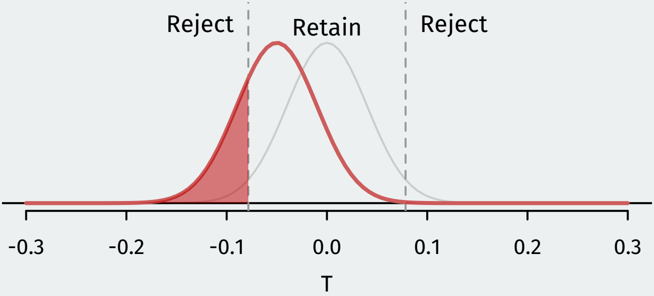
Assumed treatment effect = -0.2 and power = 0.999.

Power graph



Assumed treatment effect = -0.1 and power = 0.705.

Power graph



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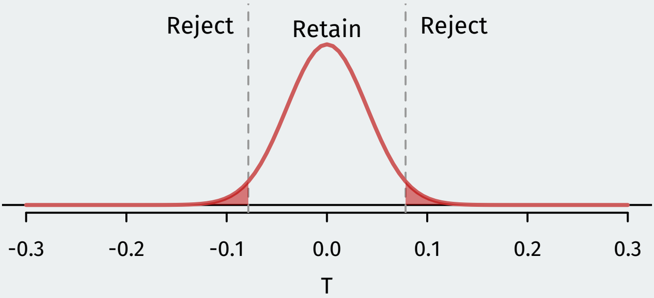
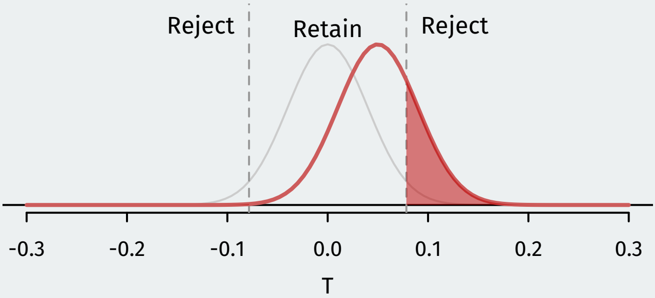


Assumed treatment effect $= 0$ and power $= 0.05$.

Power graph



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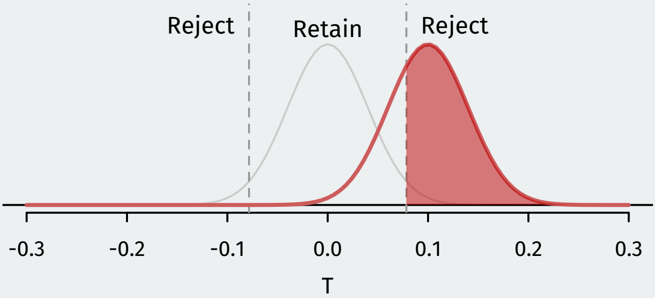

Assumed treatment effect = 0.1 and power = 0.705.

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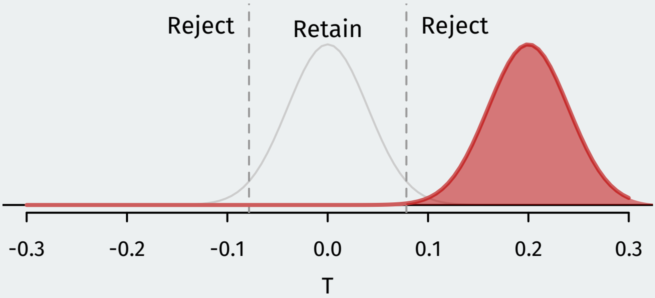

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