

T-tests:

One sample practice

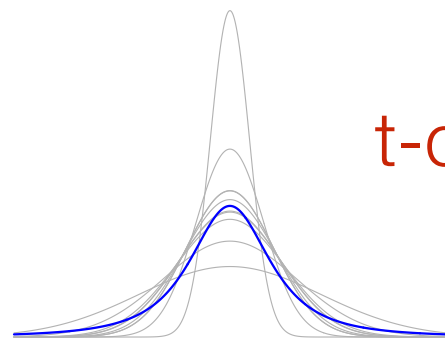
Research Methods for Human Inquiry
Andrew Perfors

So far we've constructed our test...

- 1) A diagnostic test statistic, T

$$t = \frac{\bar{X} - \mu}{\hat{\sigma} / \sqrt{N}}$$

- 2) Sampling distribution of T if the null is true

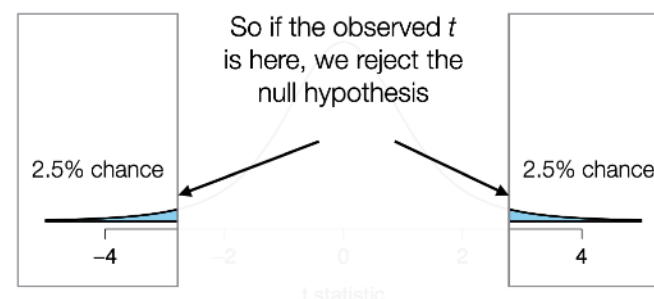


t-distribution with $N-1$ degrees of freedom

- 3) The observed T in your data

6.86

- 4) A rule that maps every value of T onto a decision (accept or reject H_0)



Here's the data

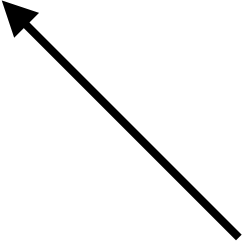
```
> dcr <- read_csv(file=here("crscores.csv"))
> dcr
# A tibble: 34 x 2
  name          cr
  <chr>        <dbl>
1 bunny         70
2 gladly        69
3 flopsy        63
4 doggie        87
5 nosey         67
6 cuddly paws   56
7 shadow        56
8 pink bunny    59
9 purple bunny  68
10 blue bunny   55
# ... with 24 more rows
```

One-sample t-test

```
> t.test( x = dcr$cr, mu = 50 )
```



The variable containing
the raw data



True population mean,
according to the null
hypothesis

One-sample t-test

```
> t.test( x = dcr$cr, mu = 50 )
```

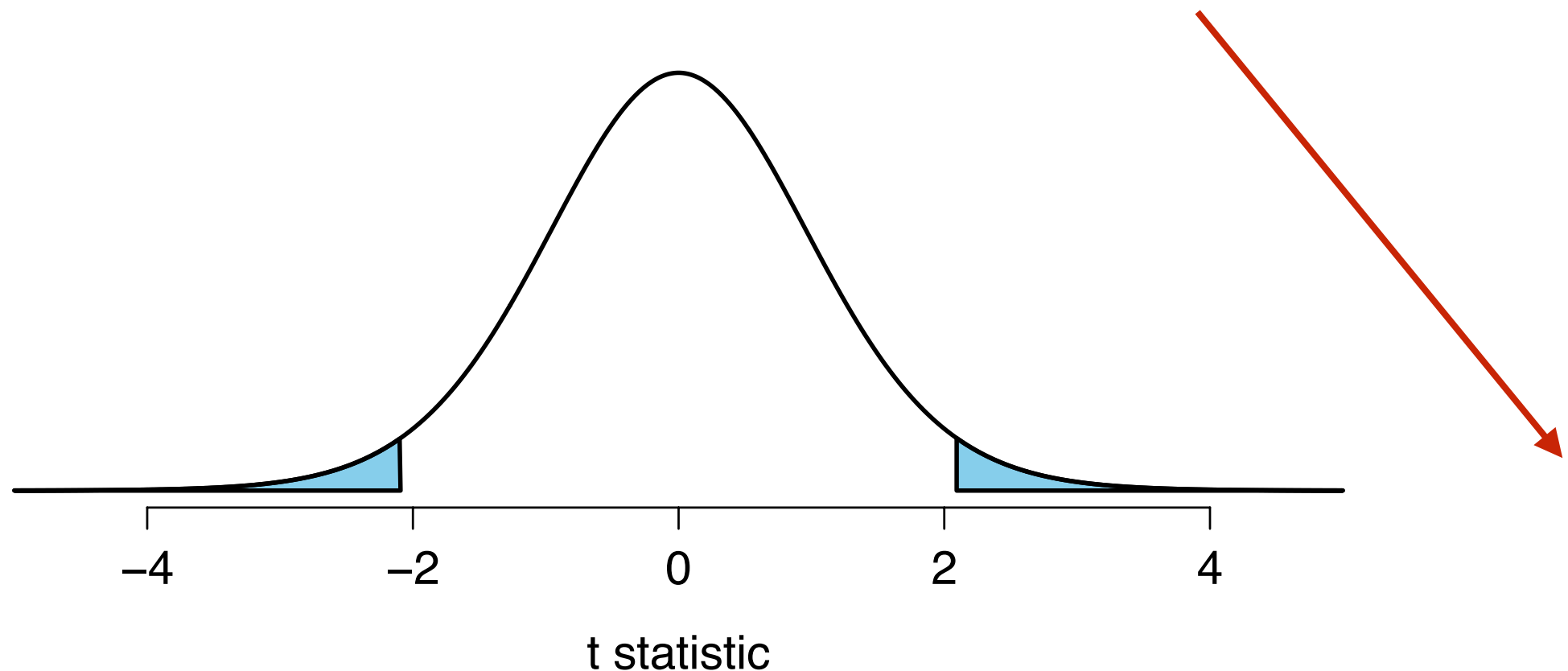
One Sample t-test

data: dcr\$cr

t = 6.862, df = 33, p-value = 7.817e-08

Test statistic, degrees of freedom, and the p-value

The t-statistic falls here so we reject the null



One-sample t-test

```
> t.test( x = dcr$cr, mu = 50 )
```

One Sample t-test

data: dcr\$cr

t = 6.862, df = 33, p-value = 7.817e-08

alternative hypothesis: true mean is not equal to 50

95 percent confidence interval:

59.60087 67.69325

sample estimates:

mean of x

63.64706

Test statistic, degrees of freedom, and the p-value

Confidence interval and estimate for the population mean

Alternative hypothesis

Measuring effect size with Cohen's d

Cohen's d

- “Simple” measure of effect size:

$$d = \frac{\text{“mean 1”} - \text{“mean 2”}}{\text{“std dev”}}$$

- Difference in means divided by an estimate of the standard deviation.

Cohen's d	rough interpretation
0.2	small
0.5	medium
0.8	large

Great visualisation: <http://rpsychologist.com/d3/cohend/>

Calculating Cohen's d in R

```
> library(lsr)
> cohensD( dcr$cr ,mu=50)
[1] 1.17683
```

Note that it takes the raw data and the comparison mu

```
> (mean(dcr$cr)-50)/sd(dcr$cr)
[1] 1.17683
```

Could also do it manually if you want to be masochistic

Writing up the results?

statement of null
hypothesis

descriptive statistics

People in Bunnyland had a mean CR score of 63.6 (SD = 11.6).

To test the null hypothesis that the data came from a population with true mean 50, we ran a one-sample t-test and obtained a significant result, $t(33) = 6.086$, $p < .0001$. This suggests that Bunnyland residents' CR scores were significantly higher than the typical mean on this test.

whether
significant

interpretation

what test was run

Writing up the results?

People in Bunnyland had a mean CR score of 63.6 (SD = 11.6).

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sampling distribution
is a t-distribution



degrees of
freedom

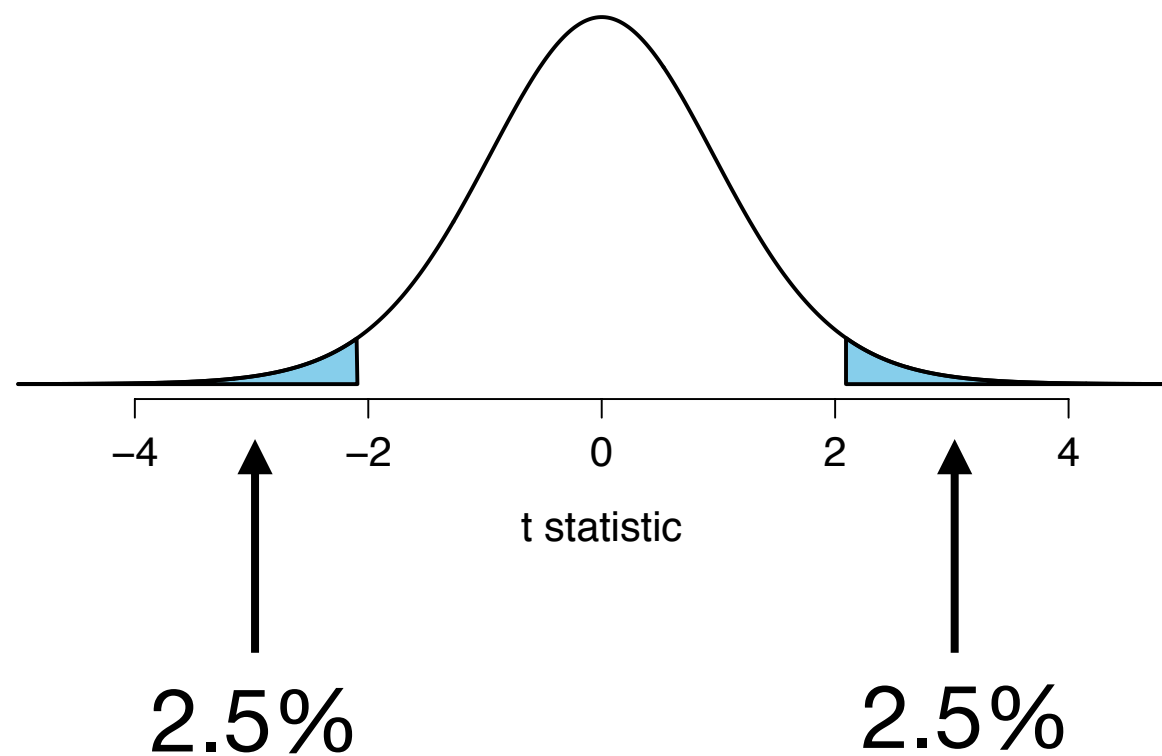
t-statistic

P-value

Two sided test

H0: true mean is 50

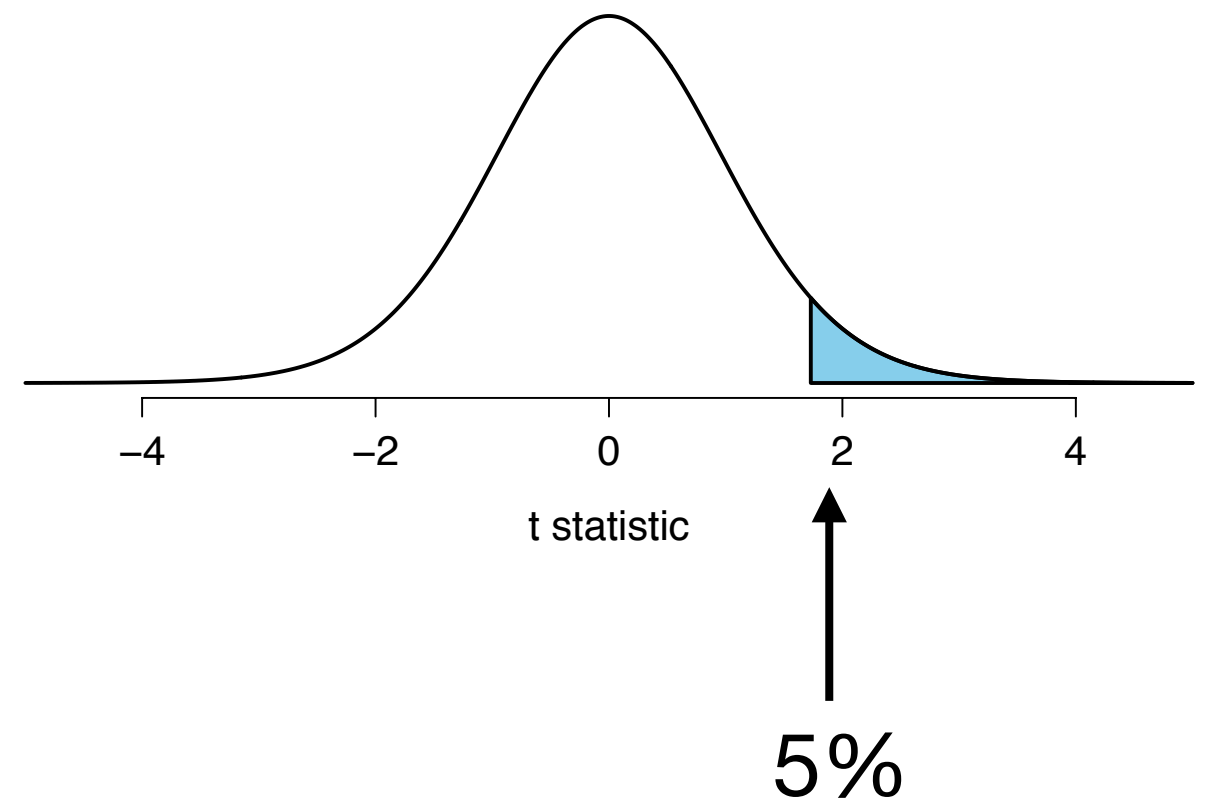
H1: true mean isn't 50



One sided test

H1: true mean is **above*** 50

So we only care about one side of the sampling distribution in making our accept/reject decision



(*or, equivalently, H1 is below 50)

I mention these because people do them and you'll see them, but I think they are a bad idea.

The null hypothesis (and nature of the t distribution) haven't changed and NHST by definition should depend only on H_0

The logic given is usually that you should do it if you genuinely believe you should not see results on one side — but if that's the case, H_0 would be different and so would the sampling distribution

In practice they are a way of sneakily getting “significant” results and IMHO often result in inflated Type I error

One sided test

There is a way of calculating one-sided tests in R using the `t.test()` function with the `alternative` argument but I will not assess this or ask you to ever do it because I don't think we should use them

Exercises are in `w7day1exercises.Rmd`