Confidence Intervals

PSYC 2020-A01 / PSYC 6022-A01 | 2025-10-17 | Lab 9

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Outline

- Assignment 8 Review
- Confidence Intervals
- One-Sample *t*-test

Learning objectives:

R: CI and *t*-statistics in R

Assignment 8 Review

[placeholder for Assignment 8 review]

Confidence Intervals

Most common: 95% CI

- Interpretation: If you were to take 100 samples, 95 CIs of your 100 samples will contain the true mean

For standard normal,

CI	*z* cutoff	generally
99.7%	[-3, 3]	$[\bar{x} - 3 * SD, \bar{x} + 3 * SD]$
95%	[-2, 2]	$[\bar{x} - 2 * SD, \bar{x} + 2 * SD]$
68%	[-1, 1]	$[\bar{x} - 1 * SD, \bar{x} + 1 * SD]$

Note

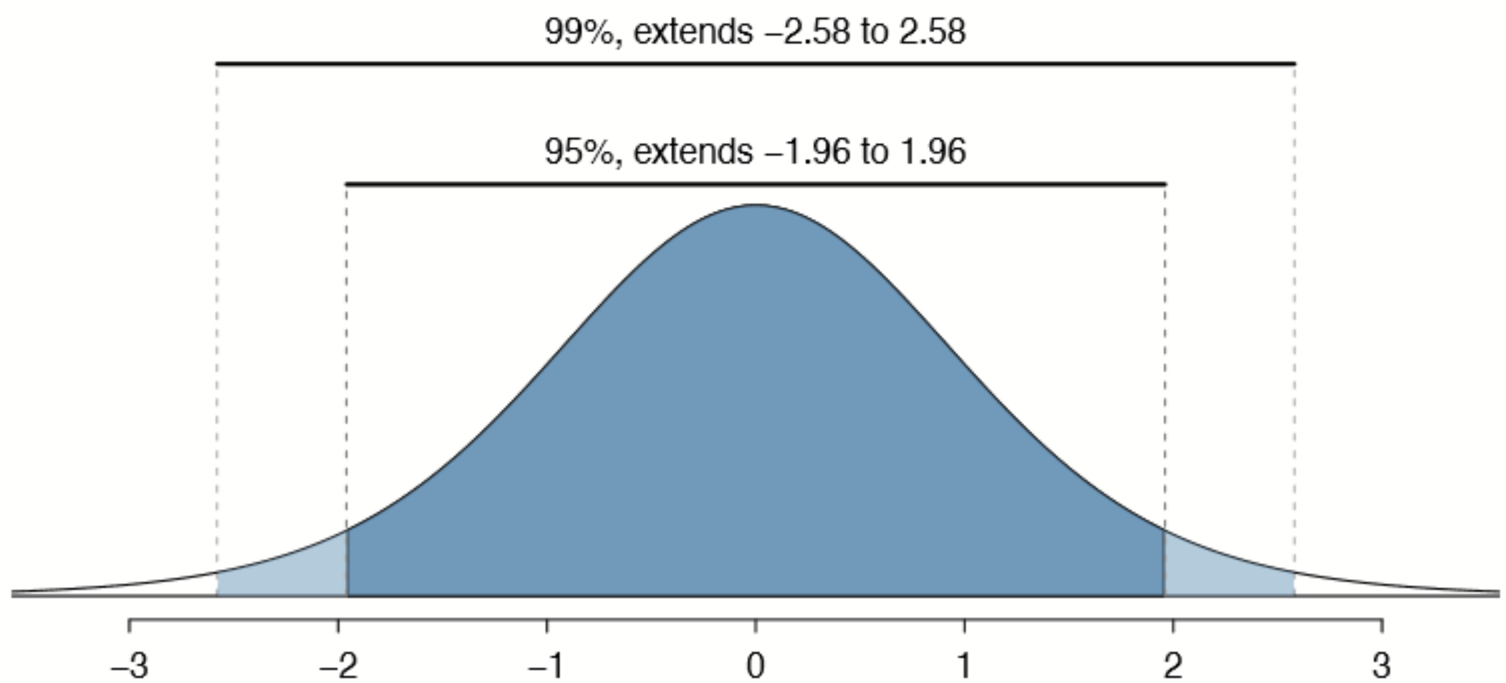
We say 2 here, but what number does the 95% CI really correspond to? 1.96

Confidence Interval and Width

Confidence Level $(1 - \alpha)$ can communicate uncertainty about your results

- Designated proportion of such intervals that will include the true population value
- $\alpha = 0.01$ for 99% CI
- $\alpha = 0.05$ for 95% CI

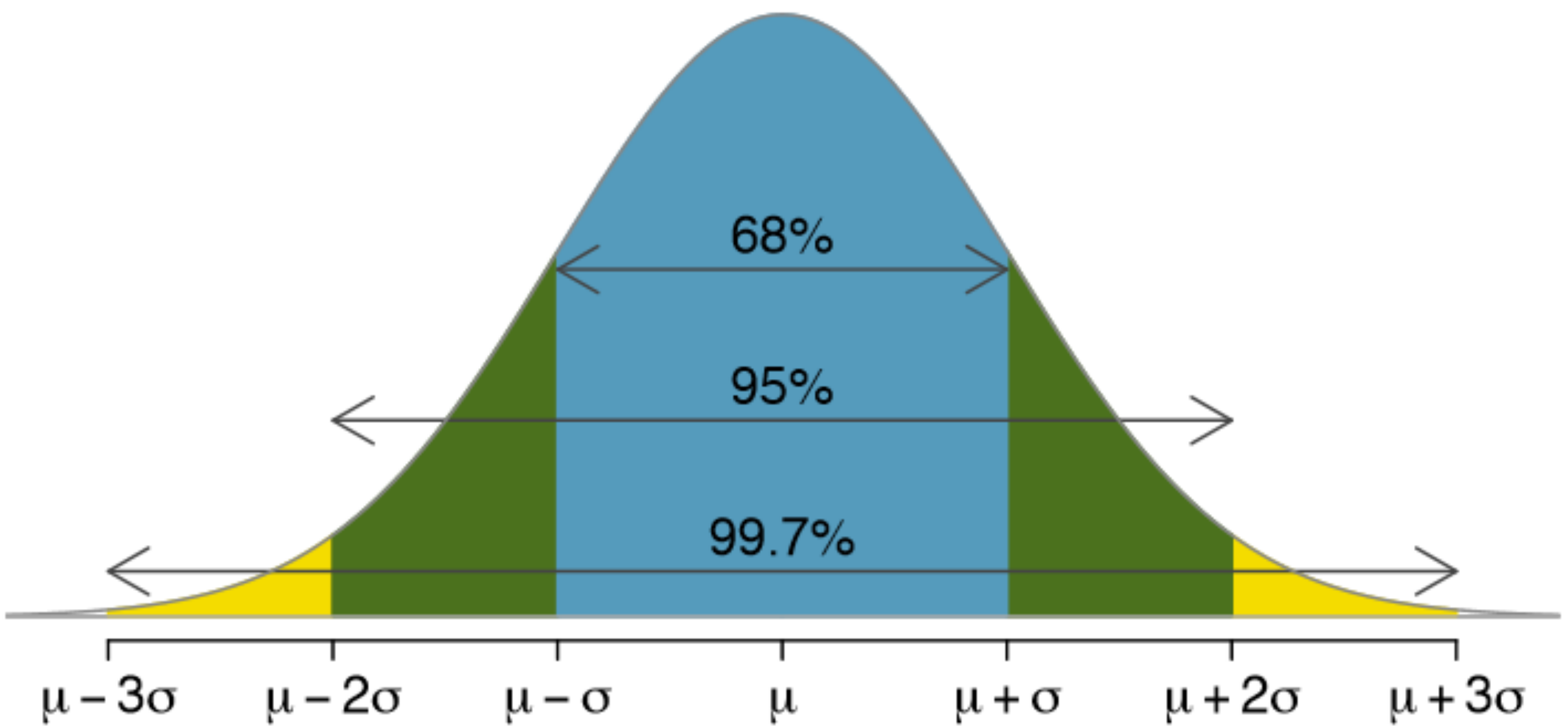
Confidence level proportional to confidence interval width



CIs for Symmetric Distributions

When a distribution is symmetric, CIs for that distribution are also symmetric

- Includes normal (e.g., *z*-) distribution
- *t* distribution



Cutoff *Z*-Values Example

Say you want to find the cutoff *z* values for some confidence interval

Two examples: 95% CI and 97.3% CI (one typical, one as exercise)

We want the $\alpha = 1-$ confidence level piece to be equal on both sides

95% CI $\alpha = 1 - .95 = 5\%$ on both sides

So $.05/2 = .025$ on each side

Need value for $.025$ and $.95 + .025$ ($[.025, .975]$)

```
1  qnorm(c(.025, .975))
```

```
[1] -1.959964  1.959964
```

97.3% CI $\alpha = 1 - .973 = 2.7\%$ on both sides

So $.027/2 = .0135$ on each side

Need value for $.0135$ and $.95 + .0135$ ($[.0135, .9865]$)

```
1  qnorm(c(.0135, 0.9865))
```

```
[1] -2.211518  2.211518
```

Which one has a higher confidence level? Which one has a larger width?

Confidence Interval Generally

Derived with sample mean ($\bar{x}$) and standard error ($\frac{\sigma}{\sqrt{n}}$)

$CI = \bar{x} \pm z\frac{\sigma}{\sqrt{n}}$ or

$CI = [\bar{x} - z\frac{\sigma}{\sqrt{n}}, \bar{x} + z\frac{\sigma}{\sqrt{n}}]$

Food for Thought

With this formula, we would only use the positive version of the *z* cutoff, so that the lower bound ends up lower than the mean and the higher bound ends up higher. You can also think instead as both adding the *z* cutoff—it just ends up becoming a minus sign because the lower bound has a negative *z* cutoff.

Confidence Interval Example

Let’s find a 95% confidence interval of the mean for iris Petal Length

```
head(iris$Petal.Length)
```

```
[1] 1.4 1.4 1.3 1.5 1.4 1.7
```

```
x_bar <- mean(iris$Petal.Length)
x_sd <- sd(iris$Petal.Length)
n <- length(iris$Petal.Length) # although remember to be thinking about missing data

z_cutoff <- qnorm(.975)

Petal.Length.CI <- c(x_bar - z_cutoff * x_sd / sqrt(n), x_bar + z_cutoff * x_sd / sqrt(n))
Petal.Length.CI
```

```
[1] 3.475499 4.040501
```

If we collected samples of petal length many times, we would expect the interval [3.47, 4.04] to contain the true population mean of petal length 95% of the time.

Confidence Interval Example

Let’s find a 80% confidence interval of the mean for iris Sepal Length

```
head(iris$Sepal.Length)
```

```
[1] 5.1 4.9 4.7 4.6 5.0 5.4
```

```
Sepal.Length.CI <- c(mean(iris$Petal.Length) - qnorm(.9) * sd(iris$Petal.Length) /
                       sqrt(sum(!is.na(iris$Sepal.Length))),

                     mean(iris$Petal.Length) + qnorm(.9) * sd(iris$Petal.Length) /
                       sqrt(sum(!is.na(iris$Sepal.Length))))
Sepal.Length.CI
```

```
[1] 3.573282 3.942718
```

If we collected samples of petal length many times, we would expect the interval [3.57, 3.94] to contain the true population mean of petal length 95% of the time.

Confidence Intervals and NHST

If a 95% confidence interval does not contain a value, that is mathematically equivalent to it being “significantly different” from that value.

E.g., if your null hypothesis H_0 was that the mean of petal length is no different from an expected population mean of 3.3, would you reject or accept the null hypothesis?

```
Petal.Length.CI
```

```
[1] 3.475499 4.040501
```

We would reject the null hypothesis because the 95% CI does not include 3.3.

From Z to T: No longer normal

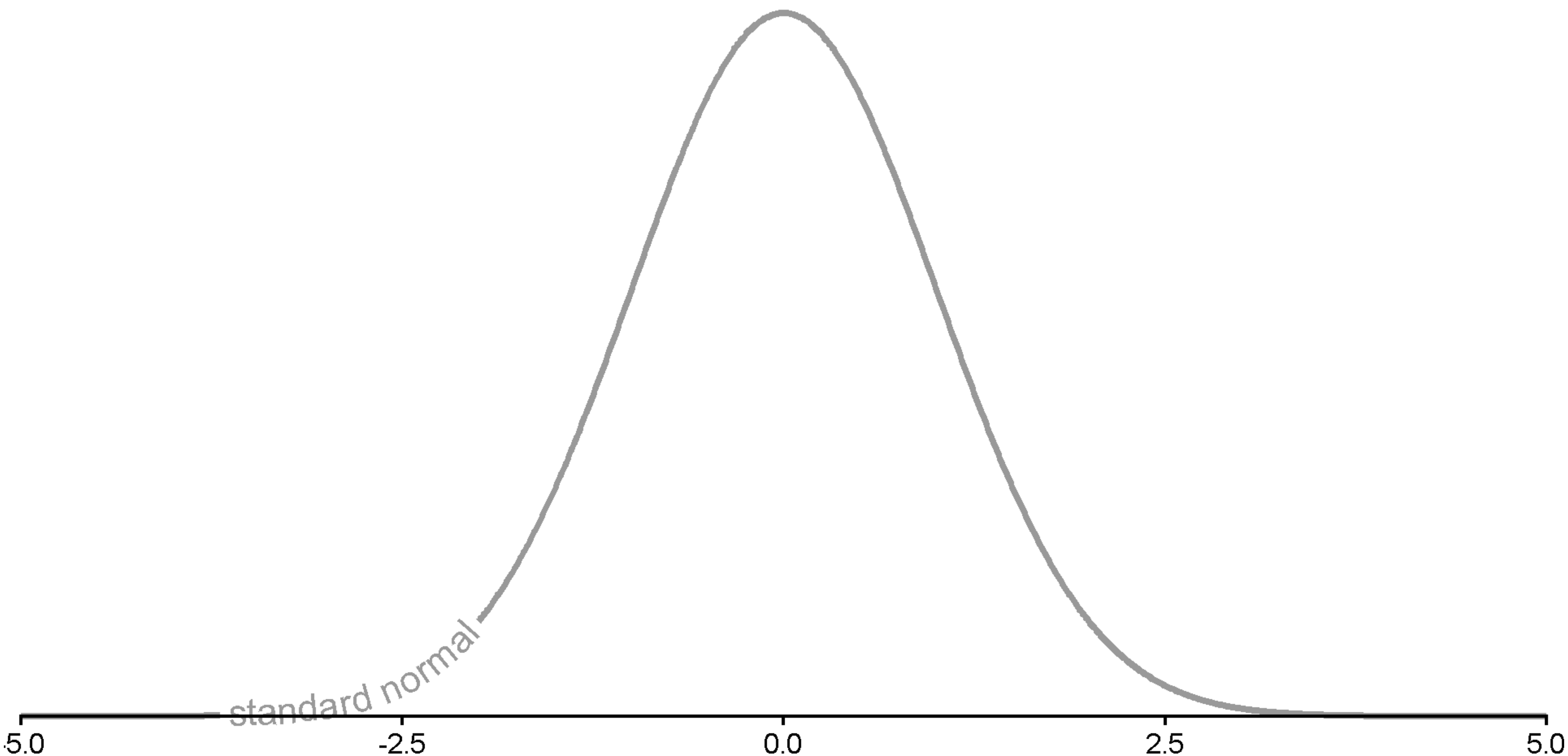
Z- vs. T-Distribution

T-distribution has thicker tails

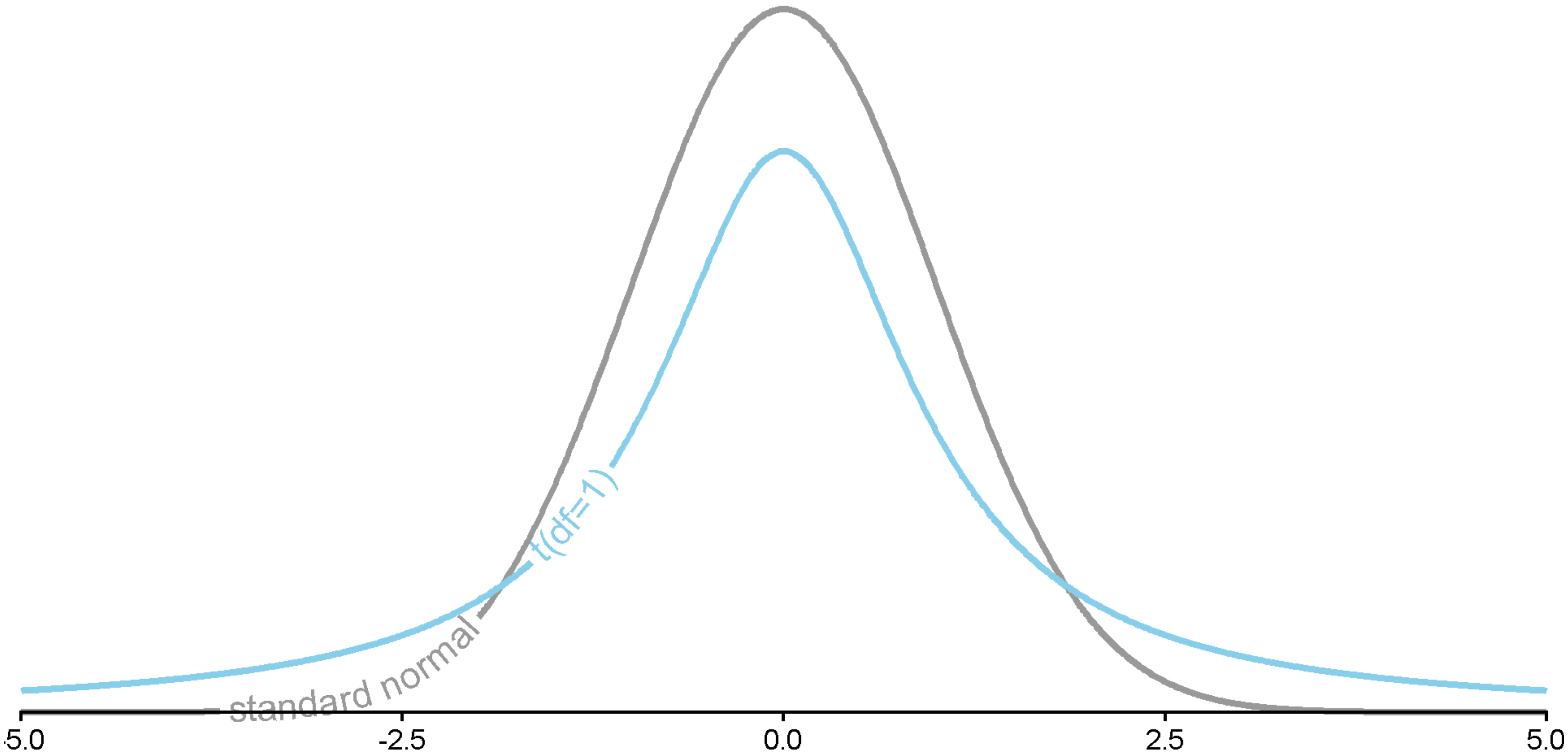
As df increases, it looks more like a standard normal distribution

With df = ∞, exactly follows a normal distribution (so approximates with large df)

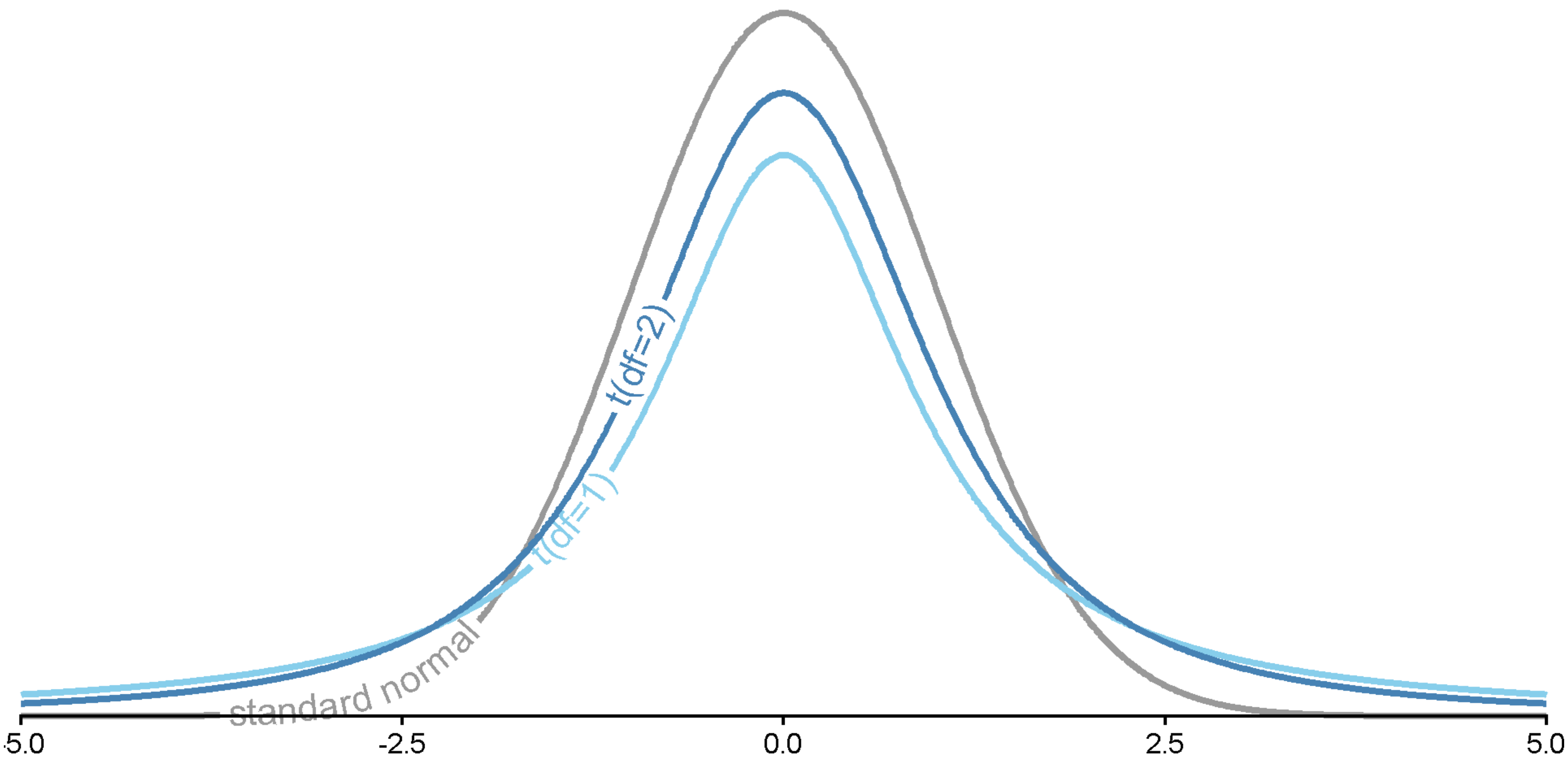
Z- vs. *T*-Distribution



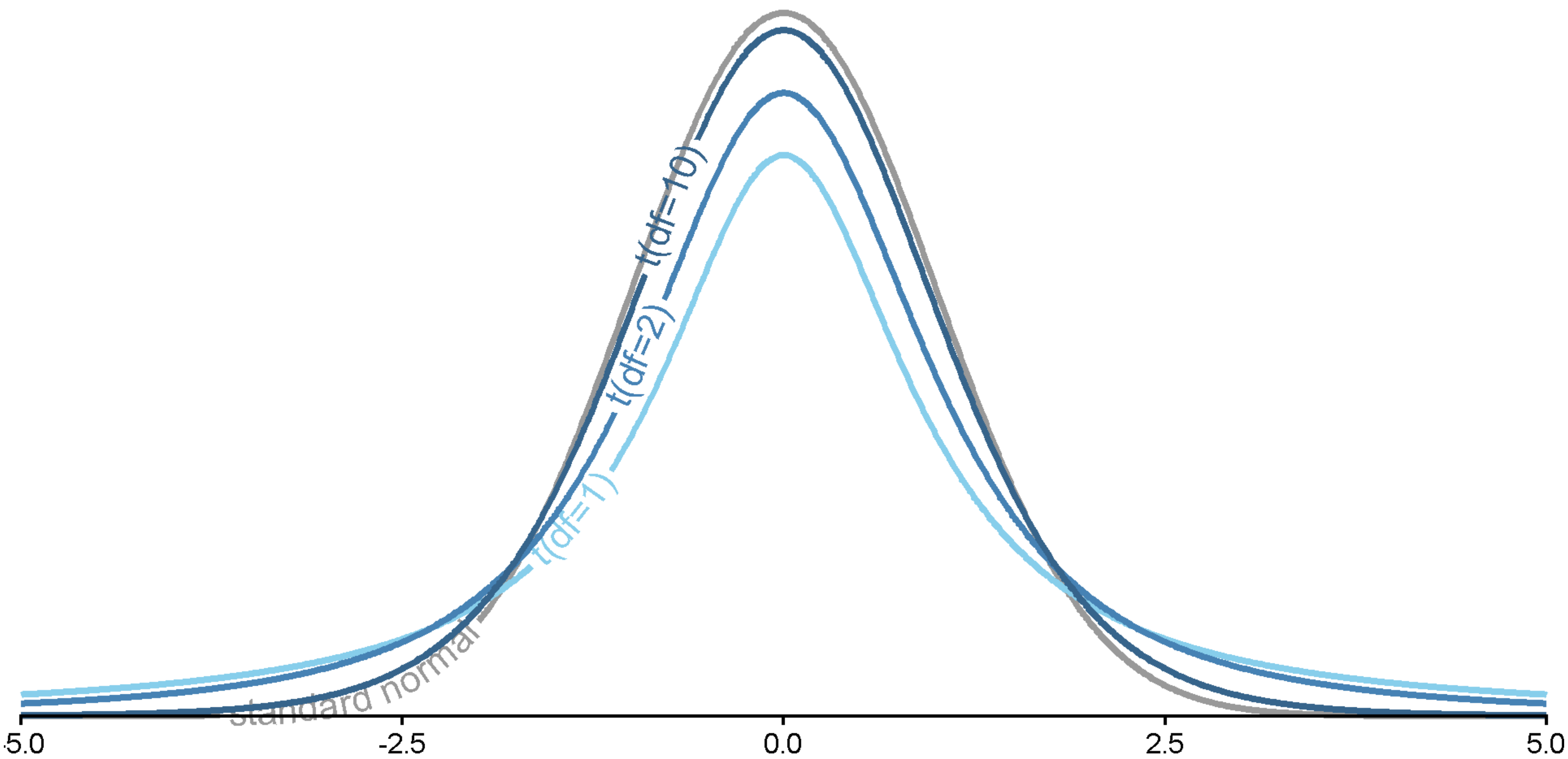
Z- vs. T-Distribution



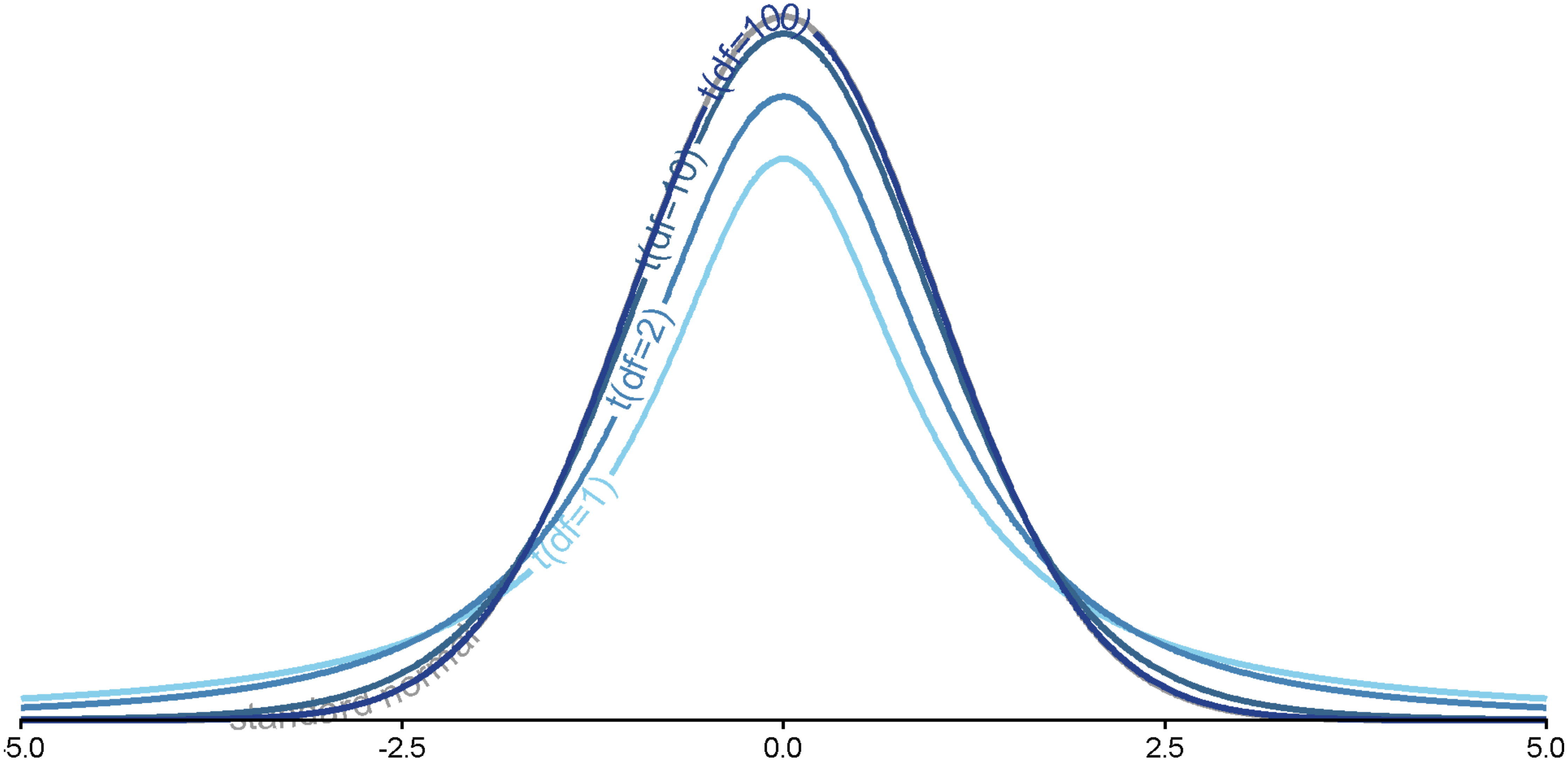
Z- vs. T-Distribution



Z- vs. *T*-Distribution



Z- vs. *T*-Distribution



T-Test: How many tails?

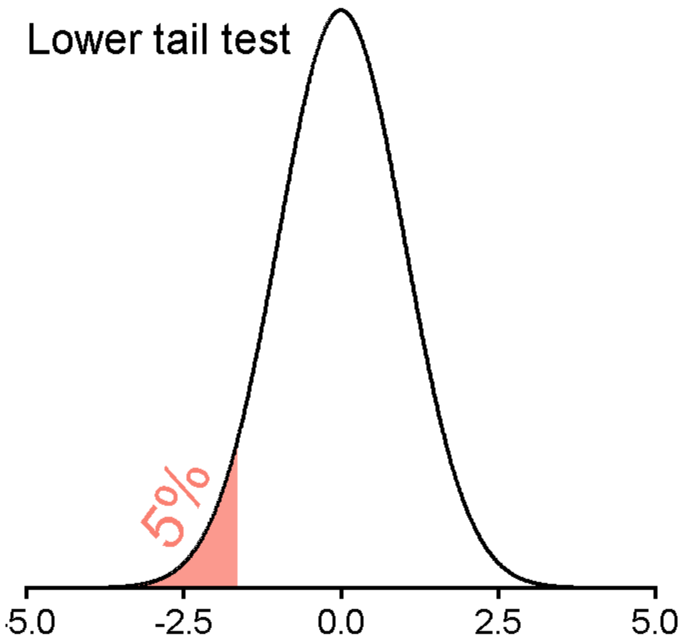
Need to consider whether to use a “one-tail” or “two-tail” *t*-test.

One-Tail (One-Sided)	**Two-Tails (Two-Sided)**
We want to test whether something is lower or higher than a value, but **not both**	We want to test whether something is either lower or higher than a value
Only one limit	Two limits (like how we’ve been doing *z*-tests

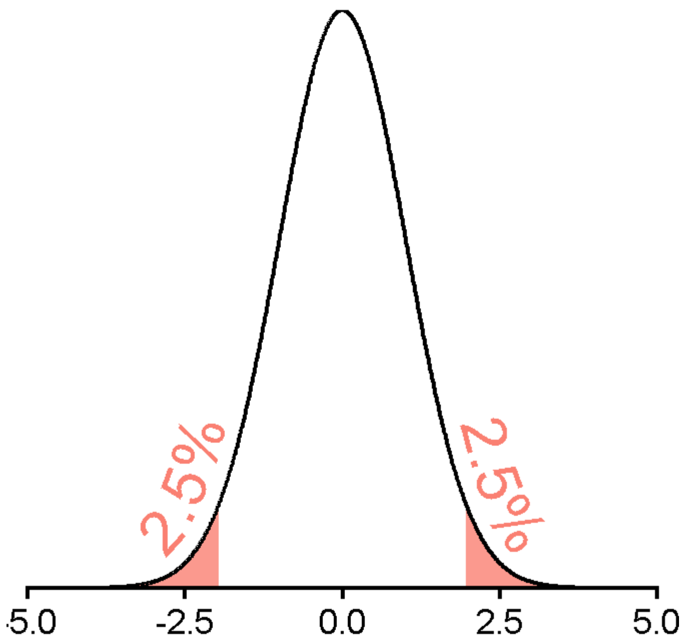
T-Test: How many tails?

Need to consider whether to use a “one-tail” or “two-tail” *t*-test.

One-Tail (One-Sided)

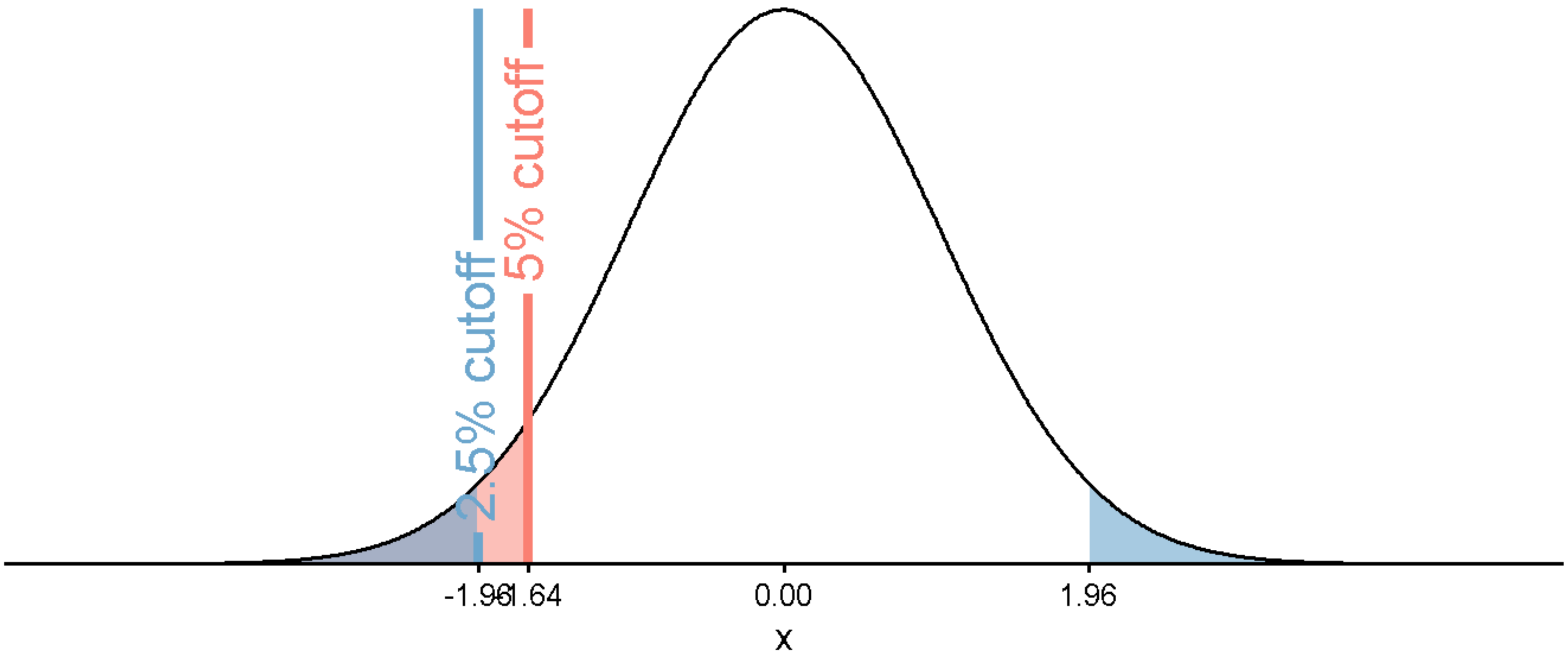


Two-Tails (Two-Sided)



T-Test: How many tails?

Notice that two-tailed tests are harder to “beat.”



Cutoff *T*-Values Example

Say you want to find the cutoff *t* values

Two examples: t(df = 3) and t(df = 37) for $\alpha = .05$

Both upper one-tailed and two-tailed

Which will have the larger magnitude cutoff values?

One-Tailed

All of our $\alpha = .05$ goes on the upper side

Need a cutoff for $.95$

```r
qt(p = .95, df = 3, lower.tail = F)
```

```
[1] -2.353363
```

```r
qt(p = .95, df = 37, lower.tail = F)
```

```
[1] -1.687094
```

$$t_{crit}(3) = -2.35$$

$$t_{crit}(37) = -1.69$$

Two-Tailed

$\alpha = 1 - .95 = 5\%$ on both sides

So $.05/2 = .025$ on each side

Need value for $.025$ and $.95 + .025$ $([.025, .975])$

```r
qt(p = c(.025, .975), df = 3)
```

```
[1] -3.182446  3.182446
```

```r
qt(p = c(.025, .975), df = 37)
```

```
[1] -2.026192  2.026192
```

$$t_{crit}(3) = [-3.18, -3.18]$$

$$t_{crit}(37) = [-2.032.06]$$

Symmetrical cutoffs, so can also just flip sign

One-Sample *T*-Test Generally

Asks “is there a question between our sample and the population?”

Derived with sample mean ($\bar{x}$), population mean (μ), and standard error ($\frac{\bar{\sigma}}{\sqrt{n}}$)

$$t = \frac{\bar{x} - \mu}{\frac{\bar{\sigma}}{\sqrt{n}}}$$

With a *t*-test, we don’t have a known population SD (σ), so we use the SD we observe in our sample $\bar{\sigma}$

Get our *t*-statistic and compare it to a critical *t* cutoff value

T-Test Example

Let's say a researcher claims the average highway miles per gallon across all cars is 30mpg. They collect a sample of 234 cars and would like you to test this. We do not know the population standard deviation.

One- or two-tailed?

```
head(mpg$hwy)
```

```
[1] 29 29 31 30 26 26
```

```
x_bar <- mean(mpg$hwy)
x_sd <- sd(mpg$hwy)
n <- length(mpg$hwy) # although remember to be thinking about missing data
df <- n - 1

t_cutoff <- qt(.975, df)

hwy_t_stat <- (x_bar - 30) / (x_sd / sqrt(n))
hwy_t_stat
```

```
[1] -16.85174
```

Our observed t-statistic exceeds our cutoff t-statistic, so we reject the null.

T-Test Function

Alternatively, we can use `t.test(x)`

- `x` = vector of numeric data
- `mu` = hypothesized population mean (default is 0)
- `alternative` = one of `"two.sided"`, `"less"`, `"greater"` (default is `"two.sided"`)

```
t.test(mpg$hwy, mu = 30, alternative = "two.sided")
```

```
	One Sample t-test

data:  mpg$hwy
t = -16.852, df = 233, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 30
95 percent confidence interval:
 22.67324 24.20710
sample estimates:
mean of x
 23.44017
```

[placeholder for output interpretation]

T-Test Example

Let's say a different researcher claims the average **city** miles per gallon across all cars is 30mpg. They collect a sample of 234 cars You are confident they are wrong—you think it is certainly less than that. We do not know the population standard deviation.

One- or two-tailed?

```r
t.test(mpg$cty, mu = 30, alternative = "less")
```

```
	One Sample t-test

data:  mpg$cty
t = -47.233, df = 233, p-value < 2.2e-16
alternative hypothesis: true mean is less than 30
95 percent confidence interval:
     -Inf 17.31843
sample estimates:
mean of x
```

```
16.85897
```

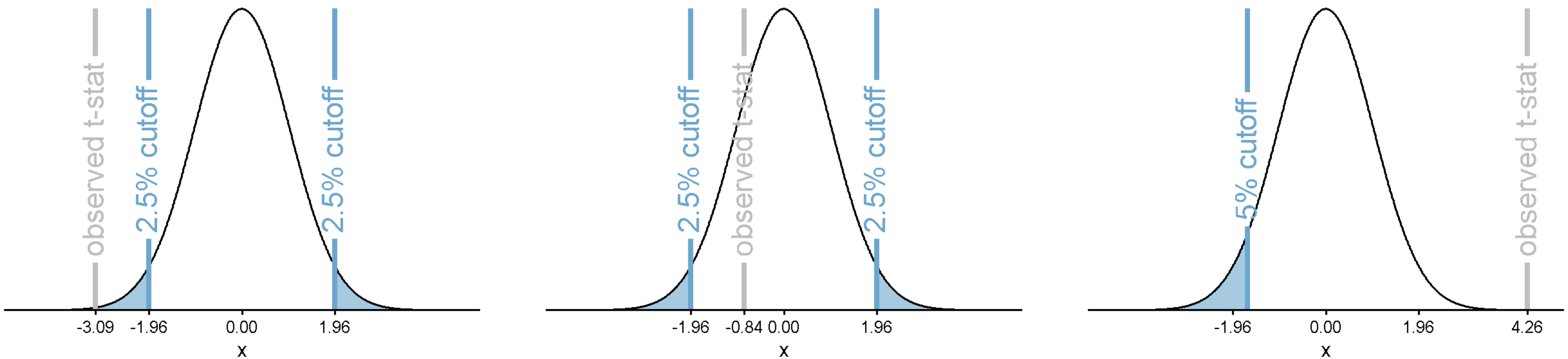
[placeholder for output interpretation]

T-Test and NHST

Remember, even when the statistic is small, for two-tailed tests (because negative), we reject when we exceed the bounds of our critical value

For one-tailed tests, it needs to exceed the bound of that tail's cutoff

Reject or accept null?



Assignment 9