

**Computer Science**  
**GRADUATE PROGRAMS**

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**2,500+**

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Our PhD students, with very few exceptions, are funded by a research or a teaching assistantship and/or by a fellowship. These provide a stipend and a full tuition waiver. Many of our MS students are also funded. Students may also qualify for fellowships offered by Illinois Computer Science, the College of Engineering at Illinois, the Graduate College, or apply to external funding agencies such as the NSF.

# Computer Science

GRADUATE PROGRAM	ENTRY	APPLICATION DEADLINE(S)
PhD in Computer Science	Fall	December 15
MS in Computer Science	Fall	December 15
MS in Bioinformatics	Fall Spring	January 15 October 15
Professional Master of Computer Science (MCS) <b>In Chicago</b>	Fall Spring	January 15 September 15
Professional MCS and MCS in Data Science Online	Fall Spring Summer	April 15 October 31 May 30 October 15 February 15



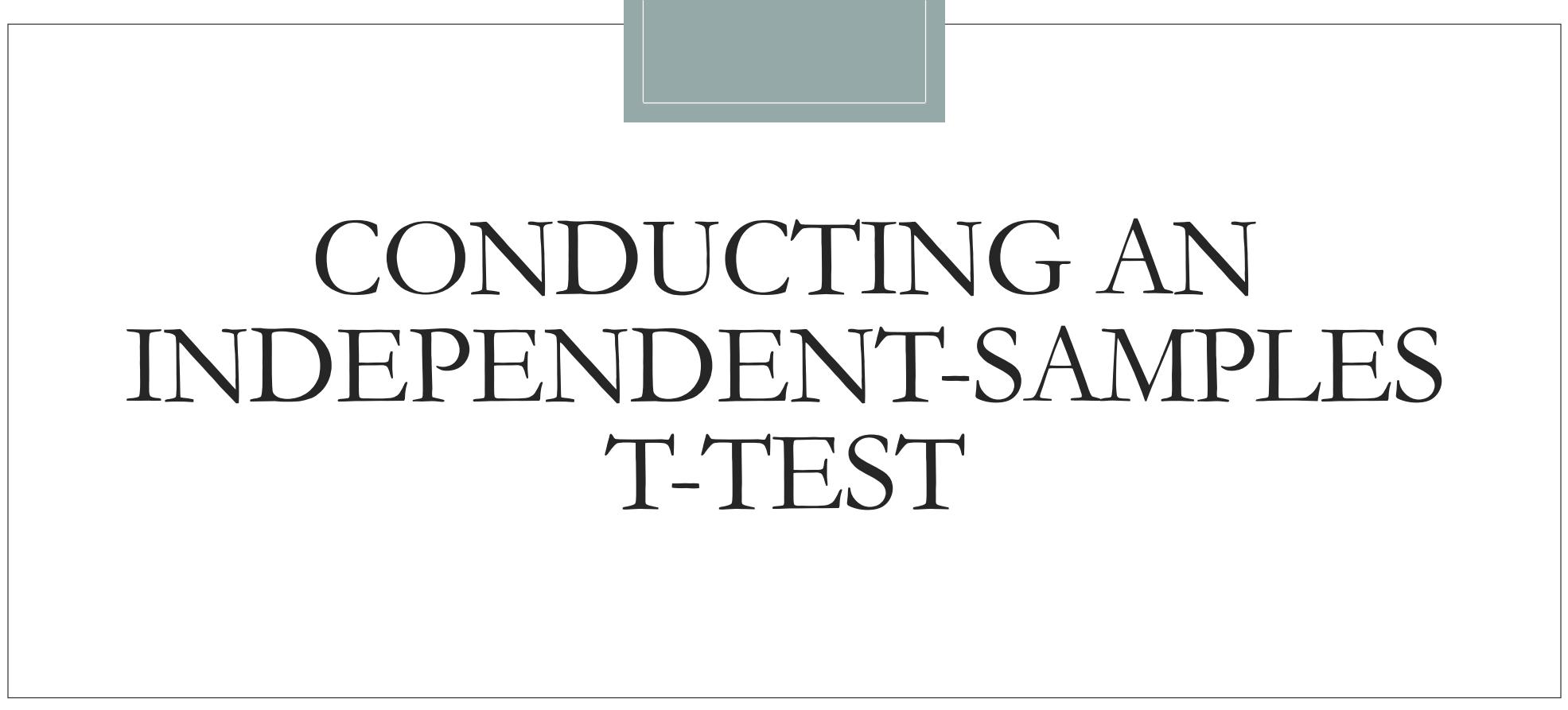
**Thomas M. Siebel Center for Computer Science**  
201 North Goodwin Avenue  
Urbana, IL 61801-2302

**Illinois Computer Science in Chicago**  
200 South Wacker Drive, 7th Floor  
Chicago, IL 60606

## OFFICE OF GRADUATE PROGRAMS

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Online programs - [online-mcs@cs.illinois.edu](mailto:online-mcs@cs.illinois.edu)  
[go.cs.illinois.edu/GradPrograms](http://go.cs.illinois.edu/GradPrograms) 





# CONDUCTING AN INDEPENDENT-SAMPLES T-TEST

# Example: Comparing Attractiveness Ratings

To test our hypothesis, we randomly assign 4 participants to view a filtered photo of someone and 4 participants to view an unfiltered photo of someone.

We then have them rate how attractive they think that person is on a scale from 1 to 10, with 10 being very attractive.



We want to know: Does adding a filter to a photo influence attractiveness ratings?



Filtered Photo Group		Unfiltered Photo Group	
Subject	Attractiveness	Subject	Attractiveness
1	9	5	5
2	8	6	6
3	6	7	5
4	9	8	4

# Step 1: Check Assumptions

- **The distributions for each sample are normal** (no skew/outliers)
- **The samples are independent of one another**
  - The participants in one condition are not the same participants in the other condition (there is no effect of one sample on the other)
- **Homogeneity of variance**
  - The variance of the populations (represented by each sample) **are equal**—this means that the spread or variability in scores around the population mean is the same in both samples



For this: We don't have a lot of data for this example, but in normal circumstances, you would **create a histogram of the data to check for normality**



For this: **We have to know how our sample was collected** and know that we controlled for confounding variables to ensure the two samples are collected from different participants

For this: We need to run a **Levene's Test** (if our data is less or not normally distributed) or a **Barlett's Test** (if our data is close to or normally distributed) to test whether the variances are the same

# Step 1: Check Assumptions

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- Homogeneity of variance

- The variance of the populations (represented by each sample) **are equal**—this means that the spread or variability in scores around the population mean is the same in both samples

Both **Levene's** and **Bartlett's Tests** *are* hypothesis tests. They test the null and alternative hypotheses that the variances are equal or not, respectively. (P.s., always two-tailed!)

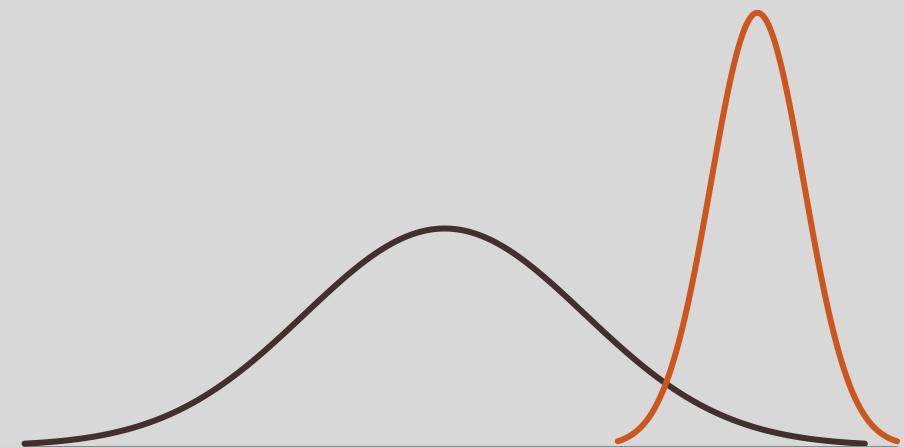
$$H_0: \sigma_1^2 = \sigma_2^2 = \dots \sigma_x^2$$

$$H_a: \sigma_1^2 \neq \sigma_2^2 \neq \dots \sigma_x^2$$

You will test whether you **fail to reject the null hypothesis (homogenous/equal variances)**

or

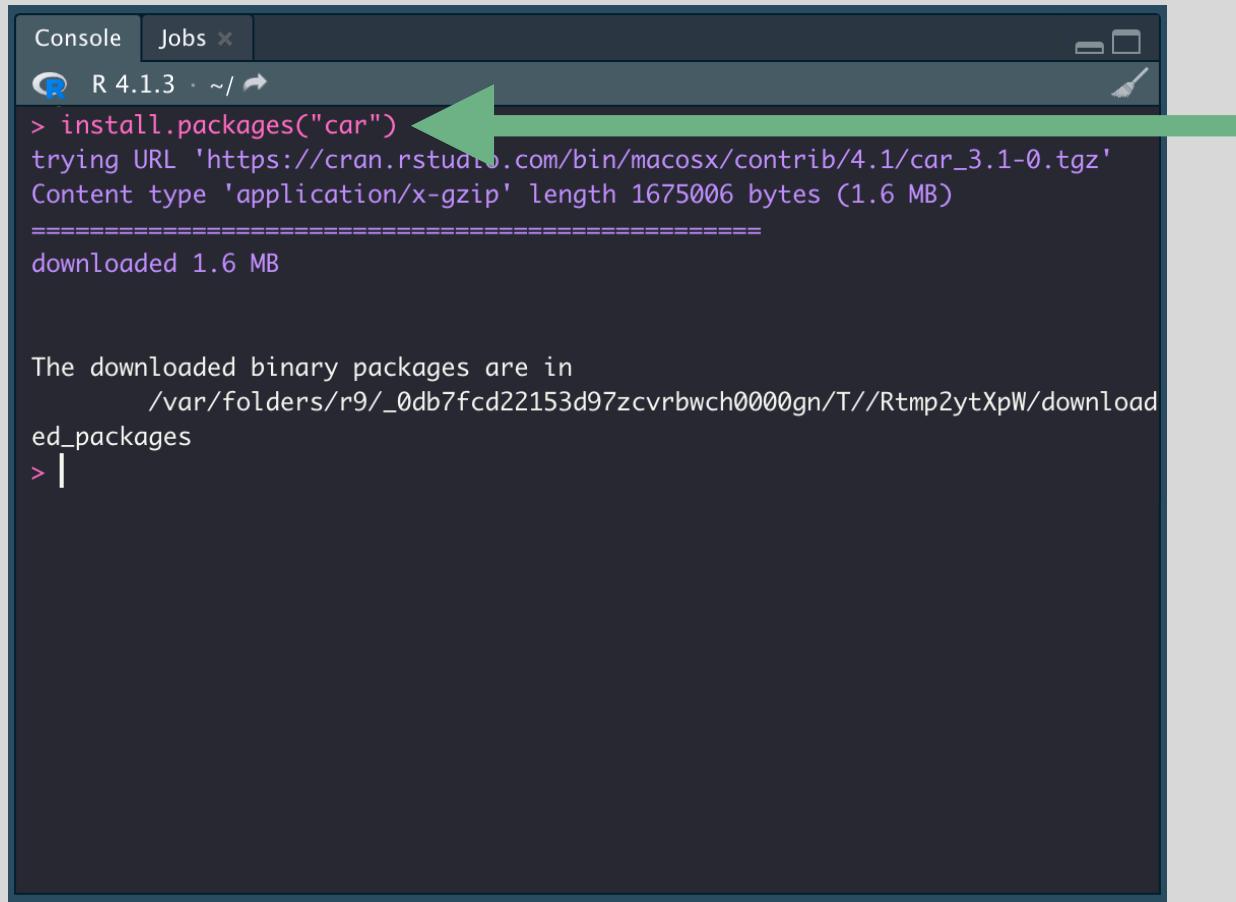
**reject the null hypothesis (heterogeneous/unequal variances)**



The variances of **Group 1** and **Group 2** are not equal if this were actually our distributions.

# Step 1: Check Assumptions

For this: We need to run a **Levene's Test** (if our data is less or not normally distributed) or a **Barlett's Test** (if our data is close to or normally distributed) to test whether the variances are the same



The screenshot shows the RStudio interface with the 'Console' tab selected. The command `> install.packages("car")` is entered, followed by its output: trying URL from CRAN, content type 'application/x-gzip', length 1675006 bytes (1.6 MB), and a message indicating it was downloaded 1.6 MB. Below this, a message states the downloaded binary packages are in a specific directory, and the command `ed_packages` is partially visible.

```
Console Jobs ×
R 4.1.3 · ~/ ↻
> install.packages("car")
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.1/car_3.1-0.tgz'
Content type 'application/x-gzip' length 1675006 bytes (1.6 MB)
=====
downloaded 1.6 MB

The downloaded binary packages are in
  /var/folders/r9/_0db7fcd22153d97zcvrbwch0000gn/T//Rtmp2ytXpW/download
ed_packages
> |
```

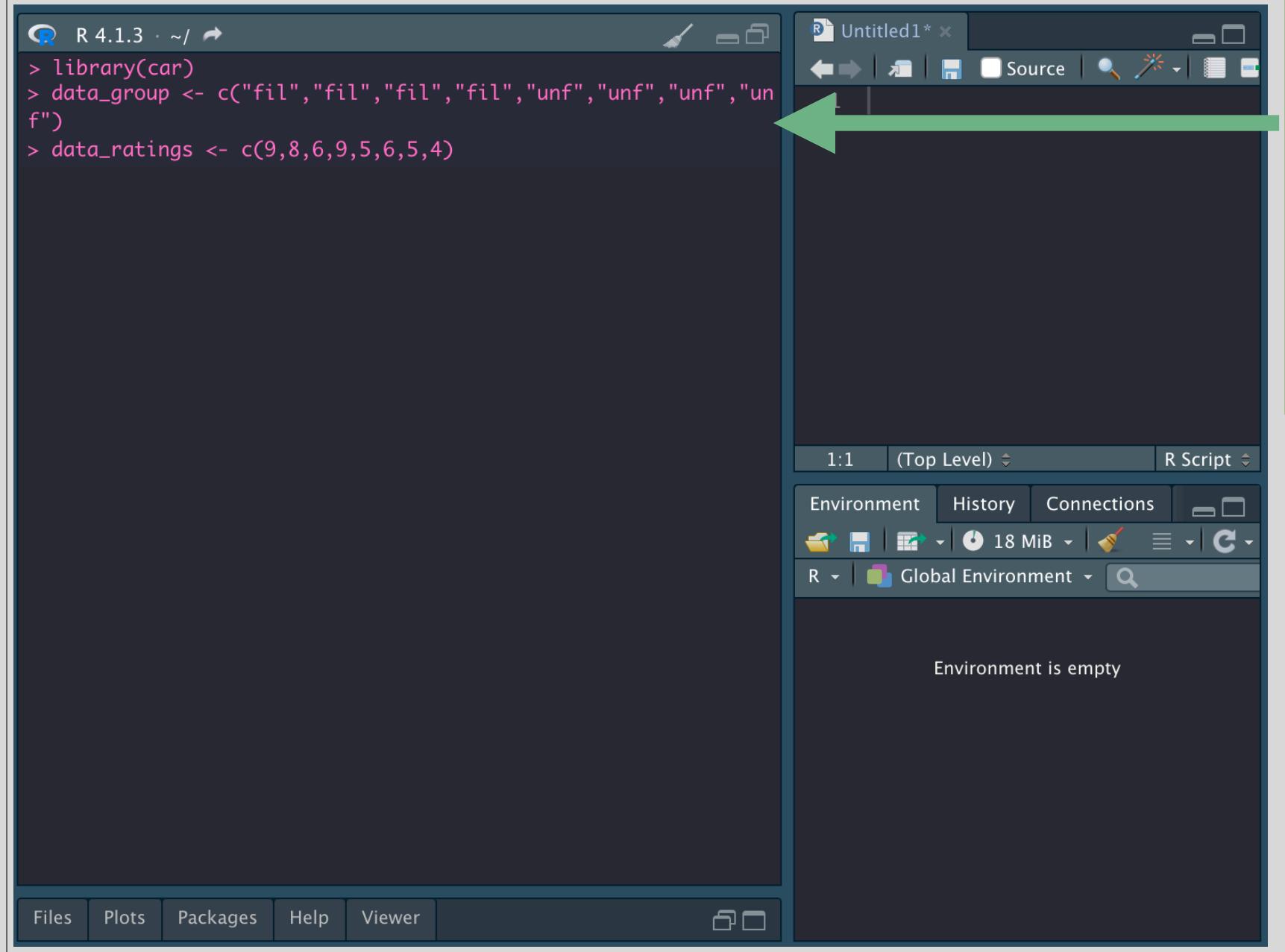
Install the **car** package in R.  
Remember: You only ever need to install a package *once*.

A screenshot of the RStudio interface. The top-left corner shows the R logo and "R 4.1.3 · ~/". Below it is the console window with the command "> library(car)" entered. A large green arrow points from the text "Load the car package" to this command. To the right of the console is the script editor window titled "Untitled1 \*". At the bottom of the screen is the navigation bar with tabs: Files, Plots, Packages, Help, and Viewer.

```
R 4.1.3 · ~/ 
> library(car)
> |
```

Load the **car** package from your **library** in R. Remember: You need to do this *every* time you open RStudio and start coding a new script.

## Create your dataset in R.



- You will do this just the same way as before using a name, assignment operator, and **c()**.
- **NOTE:** R analyzes data in *long* format. This means that instead of having a column for each dataset (or condition), you need to have one column for your dependent variable (across datasets) and one column for your independent variable.

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## A note about **Wide** versus **Long** format for data files

Let's say we wanted to conduct a study on how happiness is affected by the weather/season. So, on four selected days over the course of one year, we asked people to rate their happiness on a scale from 1 (*really unhappy*) to 10 (*really happy*).

Wide Format: A column for each level of the independent variable

Long Format: Multiple rows for each level of the independent variable

### Wide Format

Rainy & Fresh Spring Day	Warm & Sunny Summer Day	Chilly & Risk Fall Day	Cold & Snowy Winter Day
5	7	6	2
6	8	2	1
4	9	5	3
3	10	7	4

### Long Format

Season	Happiness Rating
Spring	5
	6
	4
	3
Summer	7
Summer	8
Summer	9
Summer	10
Fall	6
Fall	2
Fall	5
Fall	7
Winter	2
Winter	1
Winter	3
Winter	4

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### Long Format

Season	Happiness Rating
Spring	5
Spring	6
Spring	4
Spring	3
Summer	7
Summer	8
Summer	9
Summer	10
Fall	6
Fall	2
Fall	5
Fall	7
Winter	2
Winter	1
Winter	3
Winter	4

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3	10	7	4

### Long Format

Season	Happiness Rating
Spring	5
Spring	6
Spring	4
Spring	3
Summer	7
Summer	8
Summer	9
Summer	10
Fall	6
Fall	2
Fall	5
Fall	7
Winter	2
Winter	1
Winter	3
Winter	4

## Create your dataset in R.

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- **NOTE:** R analyzes data in *long* format. This means that instead of having a column for each dataset (or condition), you need to have one column for your dependent variable (across datasets) and one column for your independent variable.

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Wide Format: A column for each level of the independent variable

Long Format: Multiple rows for each level of the independent variable

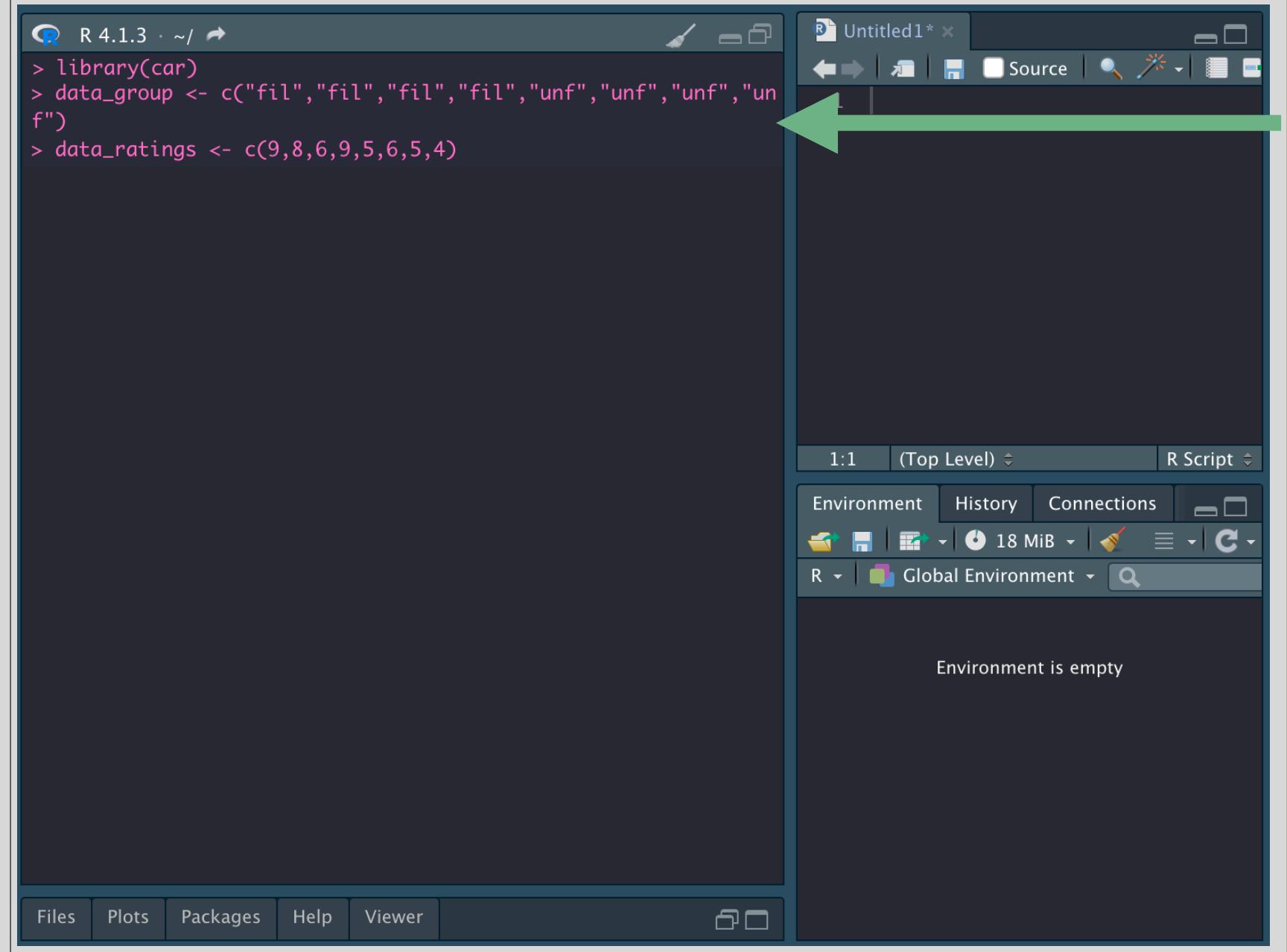
### Wide Format

Rainy & Fresh Spring Day	Warm & Sunny Summer Day	Chilly & Brisk Fall Day	Cold & Snowy Winter Day
5	7	6	2
6	8	2	1
4	9	5	3
3	10	7	4

### Long Format

Season	Happiness Rating
Spring	5
Spring	6
Spring	4
Spring	3
Summer	7
Summer	8
Summer	9
Summer	10
Fall	6
Fall	2
Fall	5
Fall	7
Winter	2
Winter	1
Winter	3
Winter	4

## Create your dataset in R.



A screenshot of the RStudio interface. On the left, the 'Console' tab shows R code being run:

```
R 4.1.3 · ~/ 
> library(car)
> data_group <- c("fil","fil","fil","fil","unf","unf","unf")
> data_ratings <- c(9,8,6,9,5,6,5,4)
```

The 'Source' tab is open, containing an empty script. A large green arrow points from the 'Source' tab towards the 'Environment' tab. The 'Environment' tab shows:

- 1:1 (Top Level) R Script
- Environment History Connections
- 18 MiB
- Global Environment
- Environment is empty

The bottom navigation bar includes 'Files', 'Plots', 'Packages', 'Help', 'Viewer'.

- You will do this just the same way as before using a name, assignment operator, and **c()**.
- **NOTE:** R analyzes data in *long* format. This means that instead of having a column for each dataset (or condition), you need to have one column for your dependent variable (across datasets) and one column for your independent variable.
- Be careful about writing your code because you need to line up your values for your IV and DV.



unfiltered	filter
5	9
6	8
5	6
4	9

## Create your dataset in R.

The screenshot shows the RStudio interface. In the top-left pane, R code is written:

```
R 4.1.3 · ~/ 
> library(car)
> data_group <- c("fil","fil","fil","fil" "unf","unf","unf","unf")
> data_ratings <- c(9,8,6,9 5,6,5,4)
```

A blue box highlights the assignment operator `<-` and the values `c("fil", "fil", "fil", "fil", "unf", "unf", "unf", "unf")`. A green arrow points from this box to the **Unfiltered Photo Group** data frame below.

In the bottom-left pane, there are two data frames:

Filtered Photo Group	
Subject	Attractiveness
1	9
2	8
3	6
4	9

Unfiltered Photo Group	
Subject	Attractiveness
5	5
6	6
7	5
8	4

The bottom-right pane shows the message **Environment is empty**.

Bottom navigation bar: Files, Plots, Packages, Help, Viewer.

- You will do this just the same way as before using a name, assignment operator, and `c()`.
  - **NOTE:** R analyzes data in *long* format. This means that instead of having a column for each dataset (or condition), you need to have one column for your dependent variable (across datasets) and one column for your independent variable.
  - Be careful about writing your code because you need to line up your values for your IV and DV.
- 
- A large red hand-drawn style X is drawn over a small data frame. The frame has the text **unfiltered filter** at the top and contains the following data:
- |   |   |
|---|---|
| 5 | 9 |
| 6 | 8 |
| 5 | 6 |
| 4 | 9 |

## Create your dataset in R.

The screenshot shows the RStudio interface. On the left, the 'Source' tab contains R code:

```
R 4.1.3 · ~/ ↻
> library(car)
> data_group <- c("fil","fil","fil","fil","unf","unf","unf")
> data_ratings <- c(9,8,6,9,5,6,5,4)
```

A green arrow points from the 'Source' tab to the 'Environment' tab on the right. The 'Environment' tab shows the global environment with two objects:

data_group	chr [1:8]	"fil" "fil" ...
data_ratings	num [1:8]	9 8 6 9 5 6 ...

A green box contains the text: "Your data will appear in your Environment after running the two lines of code."

Below the tabs, the menu bar includes: Files, Plots, Packages, Help, Viewer.

- You will do this just the same way as before using a name, assignment operator, and **c()**.
- **NOTE:** R analyzes data in *long* format. This means that instead of having a column for each dataset (or condition), you need to have one column for your dependent variable (across datasets) and one column for your independent variable.
- Be careful about writing your code because you need to line up your values for your IV and DV.

	unfiltered	filtered
5		9
6		8
5		6
4		9

- I decided to assign values for the **Filtered group = "fil"** and values for the **Unfiltered group = "unf"**. The first four values listed are attractiveness ratings for Filtered and then Unfiltered.

The screenshot shows the RStudio interface. On the left, the R Console window displays the following R code:

```
R 4.1.3 · ~/ 
> library(car)
> data_group <- c("fil","fil","fil","fil","unf","unf","unf")
> data_ratings <- c(9,8,6,9,5,6,5,4)
> ex.data <- data.frame(data_group, data_ratings)
>
```

A large green arrow points from the line of code `ex.data <- data.frame(data_group, data_ratings)` to the right pane. The right pane is the Environment browser, which shows the following environment structure:

- 1:1 (Top Level) R Script
- Environment
- History
- Connections
- 18 MiB
- Global Environment
- Data
  - ex.data 8 obs. of 2 variables
- Values
  - data\_group chr [1:8] "fil" "fil" ...
  - data\_ratings num [1:8] 9 8 6 9 5 6 ...

Use **data.frame()** to create your combined data matrix.

- Type the names you assigned for your data in the parentheses in no particular order.

Your data matrix will appear in your Environment after running the line of code.

```
R 4.1.3 · ~/ ↻
> library(car)
> data_group <- c("fil","fil","fil","fil","unf","unf","unf")
> data_ratings <- c(9,8,6,9,5,6,5,4)
> ex.data <- data.frame(data_group, data_ratings)
> View(ex.data)
> |
```

The screenshot shows the RStudio interface. On the left is the R console window displaying R code and its output. On the right is a data viewer window titled "Untitled1\* ex.data". The data viewer displays a table with two columns: "data\_group" and "data\_ratings". The data is as follows:

	data_group	data_ratings
1	fil	9
2	fil	8
3	fil	6
4	fil	9
5	unf	5
6	unf	6
7	unf	5
8	unf	4

Below the table, it says "Showing 1 to 8 of 8 entries, 2 total columns". At the bottom of the RStudio interface, there's a "Global Environment" pane showing the "ex.data" object.

You can see now how the data is encoded into R (i.e., *long* format).

The **data\_group** column corresponds to whether the score in **data\_ratings** is from the filtered or unfiltered group.

Use **View()** to see your data matrix.

- Type the name you assigned your data matrix in the parentheses.

The screenshot shows the RStudio interface. The left pane is the R console, displaying R code and its output. A green arrow points from the text "Levene's Test for Homogeneity of Variance (center = median)" to the output table. A green box highlights the first row of the table, which contains the column headers "Df", "F value", and "Pr(>F)". The right pane is the Environment browser, showing a list of objects: "data", "fil", "unf", "ex.data", "group", "values", "data\_group", and "data\_ratings".

```
R 4.1.3 · ~/ 
> library(car)
> data_group <- c("fil","fil","fil","fil","unf","unf","unf")
> data_ratings <- c(9,8,6,9,5,6,5,4)
> ex.data <- data.frame(data_group, data_ratings)
> View(ex.data)
> leveneTest(data_ratings ~ data_group, ex.data)
Levene's Test for Homogeneity of Variance (center = median)
    Df F value Pr(>F)
group  1   0.7  0.4198
      6
Warning message:
In leveneTest.default(y = y, group = group, ...) : group coerce
d to factor.
> |
```

## Use `leveneTest()` from the `car` package to run Levene's test for homogeneity of variance.

- For your code, the first thing you will type in the parentheses is your dependent variable by (~) your independent variable: `data_ratings ~ data_group`. You will then use a comma and type the name of your data matrix to indicate to the function which data to run the code.
- Levene's Test is similar to a t-test in that you have a null hypothesis [that the variances for each of your samples are the same] and an alternative hypothesis [that the variances for each of your samples is different].
- To meet the assumption criteria, you need to fail to reject the null—stating that there are no differences.
- For your output, you will pay attention to the value for `Pr(>F)` otherwise known as a *p*-value.
- If your *p*-value is greater than 0.05, then you fail to reject the null meaning the variances for each of your samples are statistically equivalent (good!). If your *p*-value is less than 0.05, you reject the null meaning the variances for each of your samples are statistically different (bad!).

```
R 4.1.3 · ~/ ↻
> library(car)
> data_group <- c("fil","fil","fil","fil","unf","unf","unf")
> data_ratings <- c(9,8,6,9,5,6,5,4)
> ex.data <- data.frame(data_group, data_ratings)
> View(ex.data)
> leveneTest(data_ratings ~ data_group, ex.data)
Levene's Test for Homogeneity of Variance (center = median)
  Df F value Pr(>F)
group  1   0.75 0.4198
      6
Warning message:
In leveneTest.default(y = y, group = group, ...) : group coerce
d to factor.
> library(stats)
> bartlett.test(data_ratings ~ data_group, ex.data)

Bartlett test of homogeneity of variances

data: data_ratings by data_group
Bartlett's K-squared = 0.73975, df = 1, p-value =
0.3897
> |
```

	data_group	data_ratings
1	fil	9
2	fil	
3	fil	
4	fil	
5	unf	
6	unf	
7	unf	5
8	unf	4

Load the **stats** library. This is a base library meaning you do not need to install it like some of the others we have used.

Use **bartlett.test()** from the **stats** package to run Bartlett's test for homogeneity of variance.

- **NOTE:** You only need to run *either* Levene's or Bartlett's test depending upon the normality of your data. More normal = use Bartlett's; less normal = use Levene's.
- Your code, output, and interpretation is the same at Levene's Test. You will use the IV ~ DV, dataset code, read the *p*-value, and [hopefully] fail to reject the null hypothesis.

# Step 2: State Hypotheses

There is **no significant difference** in means between the two samples.

Implies the samples represent the **same population** of scores.

$$\left. \begin{array}{l} H_0: \mu_1 = \mu_2 \\ H_0: \mu_1 - \mu_2 = 0 \end{array} \right\}$$

$$\left. \begin{array}{l} H_a: \mu_1 \neq \mu_2 \\ H_a: \mu_1 - \mu_2 \neq 0 \end{array} \right\}$$

There is a **significant difference** between the two sample means. Implies the means from each sample represent **different populations** of scores

## Step 3: Degrees of Freedom and T-Critical

- We are still going to use our T-Table to determine our  $t$ -critical values.
- Formula for the degrees of freedom is a bit different for an independent-samples  $t$ -test because we now take into consideration **two samples**.

$$df = (N_1 - 1) + (N_2 - 1)$$

$$df = (4 - 1) + (4 - 1)$$

$$df = (3) + (3) = 6$$

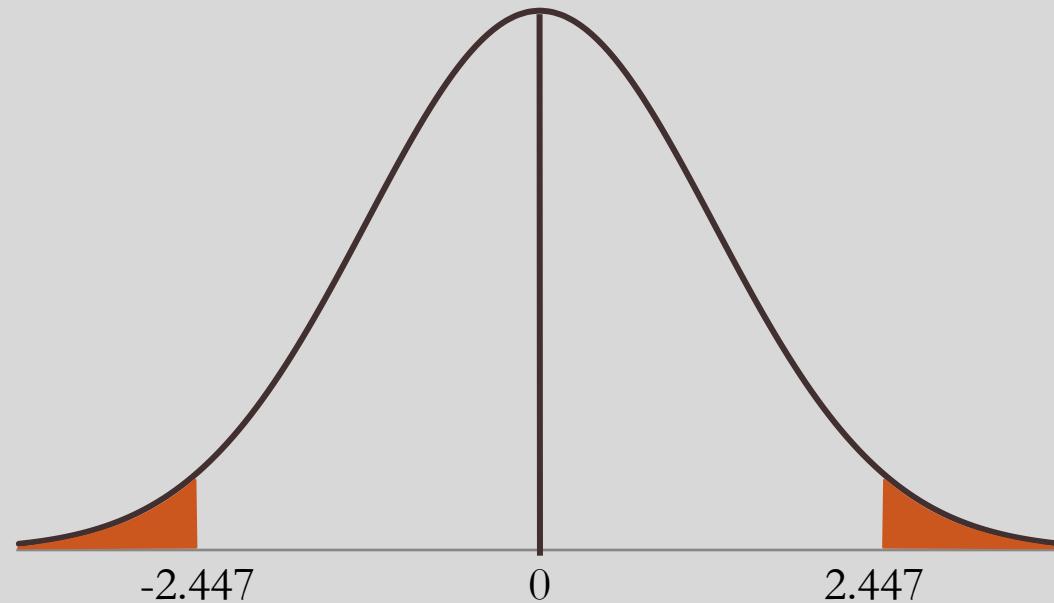
# Step 3: Degrees of Freedom and T Critical

*total df = 6*

*t*-critical (two-tailed test at  $\alpha = .05$ ) =  $\pm 2.447$

cum. prob	$t_{.50}$	$t_{.75}$	$t_{.80}$	$t_{.85}$	$t_{.90}$	$t_{.95}$	$t_{.975}$	$t_{.99}$	$t_{.995}$	$t_{.999}$	$t_{.9995}$
one-tail	<b>0.50</b>	<b>0.25</b>	<b>0.20</b>	<b>0.15</b>	<b>0.10</b>	<b>0.05</b>	<b>0.025</b>	<b>0.01</b>	<b>0.005</b>	<b>0.001</b>	<b>0.0005</b>
two-tails	<b>1.00</b>	<b>0.50</b>	<b>0.40</b>	<b>0.30</b>	<b>0.20</b>	<b>0.10</b>	<b>0.05</b>	<b>0.02</b>	<b>0.01</b>	<b>0.002</b>	<b>0.001</b>
df											
1	0.000	1.000	1.376	1.963	3.078	6.314	<b>12.71</b>	31.82	63.66	318.31	636.62
2	0.000	0.816	1.061	1.386	1.886	2.920	<b>4.303</b>	6.965	9.925	22.327	31.599
3	0.000	0.765	0.978	1.250	1.638	2.353	<b>3.182</b>	4.541	5.841	10.215	12.924
4	0.000	0.741	0.941	1.190	1.533	2.132	<b>2.776</b>	3.747	4.604	7.173	8.610
5	0.000	0.727	0.920	1.156	1.476	2.015	<b>2.571</b>	3.365	4.032	5.893	6.869
6	<b>0.000</b>	<b>0.718</b>	<b>0.906</b>	<b>1.134</b>	<b>1.440</b>	<b>1.943</b>	<b>2.447</b>	3.143	3.707	5.208	5.959
7	0.000	0.711	0.896	1.119	1.415	1.895	2.365	2.998	3.499	4.785	5.408
8	0.000	0.706	0.889	1.108	1.397	1.860	2.306	2.896	3.355	4.501	5.041
9	0.000	0.703	0.883	1.100	1.383	1.833	2.262	2.821	3.250	4.297	4.781
10	0.000	0.700	0.879	1.093	1.372	1.812	2.228	2.764	3.169	4.144	4.587
11	0.000	0.697	0.876	1.088	1.363	1.796	2.201	2.718	3.106	4.025	4.437
12	0.000	0.695	0.873	1.083	1.356	1.782	2.179	2.681	3.055	3.930	4.318
13	0.000	0.694	0.870	1.079	1.350	1.771	2.160	2.650	3.012	3.852	4.221
14	0.000	0.692	0.868	1.076	1.345	1.761	2.145	2.624	2.977	3.787	4.140
15	0.000	0.691	0.866	1.074	1.341	1.753	2.131	2.602	2.947	3.733	4.073

## Step 3: Degrees of Freedom and T-Critical



# Step 4: Calculate T-Statistic

- **Calculate the mean as usual** (sum all scores and then divide by sample size)

Filtered Photo Group	
Subject	Attractiveness
1	9
2	8
3	6
4	9
<hr/>	
8.00	
<hr/>	

Unfiltered Photo Group	
Subject	Attractiveness
5	5
6	6
7	5
8	4
<hr/>	
5.00	
<hr/>	

# Step 4: Calculate T-Statistic

Then use the raw scores for each sample to calculate an **estimated population variance** for each group.

- If you remember from earlier in the semester, the variance formula is basically the same thing as the SD formula.
  - The only difference is that the variance is **missing** the square root sign.

$$\hat{\sigma}^2 = \frac{\sum X^2 - \frac{(\sum X)^2}{N}}{N - 1}$$

# Calculating the Estimated Population Variance

Filtered Photo Group	
Subject	Attractiveness
1	9
2	8
3	6
4	9
	8.00

Unfiltered Photo Group	
Subject	Attractiveness
1	5
2	6
3	4
4	4
	5.00

$$\hat{\sigma}_{filter}^2 = \frac{262 - \frac{(32)^2}{4}}{4 - 1}$$

$$\hat{\sigma}_{filter}^2 = 2.00$$

$$\hat{\sigma}_{unfiltered}^2 = \frac{102 - \frac{(20)^2}{4}}{4 - 1}$$

$$\hat{\sigma}_{unfiltered}^2 = .6667$$

# Pooling the Variances

When we “pool” the variances, we are basically just adding them together and finding the average between them.

$$\sigma_{pool}^2 = \frac{(df_1)\hat{\sigma}_1^2 + (df_2)\hat{\sigma}_2^2}{(df_1) + (df_2)}$$

## Pooling the Variances

$$\sigma_{pool}^2 = \frac{(df_1)\hat{\sigma}_1^2 + (df_2)\hat{\sigma}_2^2}{(df_1) + (df_2)}$$

$$\sigma_{pool}^2 = \frac{(3)2.00 + (3).6667}{(3) + (3)} \rightarrow \sigma_{pool}^2 = \frac{8.0001}{6} = 1.3334$$

# Step 4: Calculate T-Statistic

- After calculating the two sample means and the estimated population variance, we can plug those values into our  $t$ -statistic formula.

$\bar{X}_1$  = sample 1 mean

$\bar{X}_2$  = sample 2 mean

$\sigma_{pool}^2$  = pooled estimated population variance

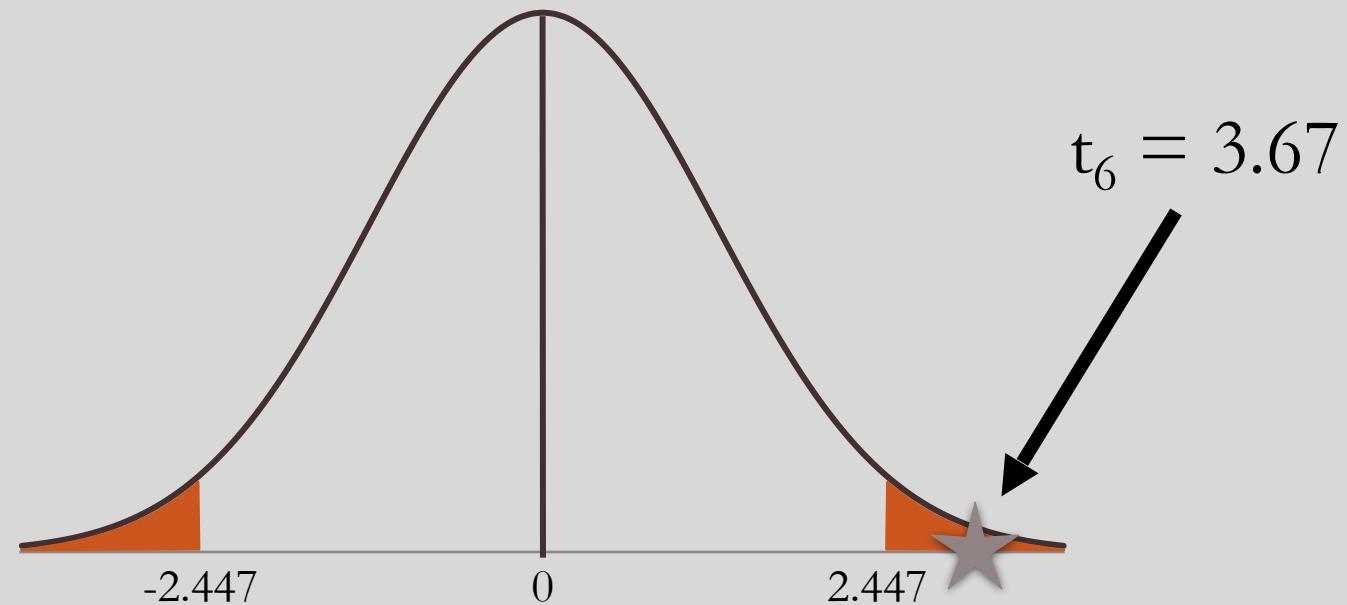
$N$  = sample size (for each sample 1 and 2)

$$t_{df} = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{\sigma_{pool}^2}{N_1} + \frac{\sigma_{pool}^2}{N_2}}}$$

## Step 4: Calculate T-Statistic

$$t_{df} = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\frac{\sigma_{pool}^2}{N_1} + \frac{\sigma_{pool}^2}{N_2}}} \rightarrow t_6 = \frac{8 - 5}{\sqrt{\frac{1.3334}{4} + \frac{1.3334}{4}}} \rightarrow t_6 = 3.674$$

## Step 5: Compare T-Statistic to Rejection Region



## Step 6: Calculate 95% Confidence Interval

- For a two-tailed test, we are going to want to calculate both an upper and lower confidence interval limit.

$$CI_{\text{upper}} = t \text{ critical} \left( \sqrt{\frac{\sigma_{\text{pool}}^2}{N_1} + \frac{\sigma_{\text{pool}}^2}{N_2}} \right) + (\bar{X}_1 - \bar{X}_2)$$

$$CI_{\text{lower}} = -t \text{ critical} \left( \sqrt{\frac{\sigma_{\text{pool}}^2}{N_1} + \frac{\sigma_{\text{pool}}^2}{N_2}} \right) + (\bar{X}_1 - \bar{X}_2)$$

# Step 6: Calculate 95% Confidence Interval

## Upper Confidence Interval Limit

$$CI_{upper} = 2.447 \left( \sqrt{\frac{1.3334}{4} + \frac{1.3334}{4}} \right) + (8 - 5)$$

$$CI_{upper} = 2.447 \left( \sqrt{.6667} \right) + (3)$$

$$CI_{upper} = 1.9980 + 3$$

$$CI_{upper} = 4.9980$$

## Lower Confidence Interval Limit

$$CI_{lower} = -2.447 \left( \sqrt{\frac{1.3334}{4} + \frac{1.3334}{4}} \right) + (8 - 5)$$

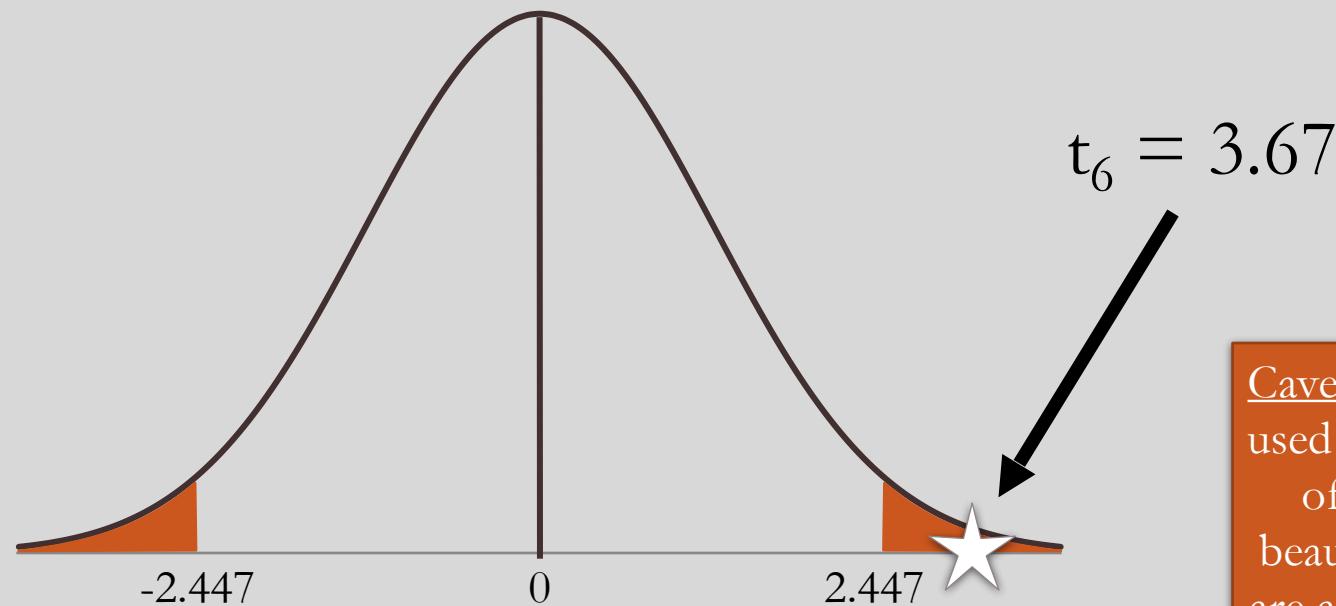
$$CI_{lower} = -2.447 \left( \sqrt{.6667} \right) + (3)$$

$$CI_{lower} = -1.9980 + 3$$

$$CI_{lower} = 1.0020$$

# Step 7: Interpretation/Conclusion

Reject the null hypothesis:  
Participants who viewed filtered photos ( $\bar{X} = 8$ ) differed significantly in their attractiveness rating compared to participants who saw unfiltered photos ( $\bar{X} = 5$ ),  $t(6) = 3.67, p < .05$ . Participants who saw filtered photos rated them as more attractive. We can be confident the true mean difference in attractiveness rating between filtered and unfiltered photos is between 1.00 and 5.00.



Caveat: This is FAKE data used only for the purposes of this class. You are beautiful just the way you are and you do NOT need a filter to be a 10 out of 10 holy hot! level of attractiveness.

# Independent-Samples T-Test in R (two-tailed)

```
Console Jobs x
R 4.1.3 · ~/ →
> t.test(data_ratings ~ data_group, data = ex.data, var.equal =
TRUE, na.rm = TRUE)

Two Sample t-test ←

data: data_ratings by data_group
t = 3.6742, df = 6, p-value = 0.0104
alternative hypothesis: true difference in means between group
fil and group unf is not equal to 0
95 percent confidence interval:
1.002105 4.997895
sample estimates:
mean in group fil mean in group unf
8 5

> |
```

## Use **t.test()** to conduct your analysis.

- The first thing you will write in your parentheses is the formula: **dependent variable ~ independent variable**.
- Then, you will include a comma and type in the name of your dataset. You will write **data =** and then the name of your data.
- Then, you will include another comma and fill in the argument **var.equal =** with either a **TRUE** (if you met the homogeneity of variance assumption) or **FALSE** (if you did NOT meet the assumption).
- Then, you will include a final comma and fill in the argument **na.rm =** with either a **TRUE** or **FALSE**. When na.rm is **TRUE**, the function skips over any NA values (not applicable; this means there is a missing data point). However, when na.rm is **FALSE**, then it returns NA from the calculation being done on the entire row or column.

REMEMBER: If you are doing a one-tailed test, you need to include the **alternative =** argument (!!!!!!!)

# Independent-Samples T-Test in R (two-tailed)

```
Console Jobs ×
R 4.1.3 · ~/ →
> t.test(data_ratings ~ data_group, data = ex.data, var.equal =
TRUE, na.rm = TRUE)

Two Sample t-test

data: data_ratings by data_group
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1.002105 4.997895
sample estimates:
mean in group fil mean in group unf
8 5

> |
```

$t = t$ -statistic that we calculate to compare to the  $t$ -critical value

# Independent-Samples T-Test in R (two-tailed)

```
Console Jobs ×
R 4.1.3 · ~/ →
> t.test(data_ratings ~ data_group, data = ex.data, var.equal =
TRUE, na.rm = TRUE)

Two Sample t-test

data: data_ratings by data_group
t = 3.6742, df = 6, p-value = 0.0104
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95 percent confidence interval:
1.002105 4.997895
sample estimates:
mean in group fil mean in group unf
8 5

> |
```

**t** =  $t$ -statistic that we calculate to compare to the  $t$ -critical value

**df** = degrees of freedom for an independent-samples  $t$ -test

# Independent-Samples T-Test in R (two-tailed)

```
Console | Jobs x
R 4.1.3 · ~/ →
> t.test(data_ratings ~ data_group, data = ex.data, var.equal =
TRUE, na.rm = TRUE)

Two Sample t-test

data: data_ratings by data_group
t = 3.6742, df = 6, p-value = 0.0104
alternative hypothesis: true difference in means between group
fil and group unf is not equal to 0
95 percent confidence interval:
1.002105 4.997895
sample estimates:
mean in group fil mean in group unf
8 5
> |
```

**t** =  $t$ -statistic that we calculate to compare to the  $t$ -critical value

**df** = degrees of freedom for an independent-samples  $t$ -test

**p-value** =  $p$ -value that we compare to 0.05; if our  $p$ -value is less than 0.05, we reject the null hypothesis; if our  $p$ -value is greater than or equal to 0.05, we fail to reject the null hypothesis

# Independent-Samples T-Test in R (two-tailed)

```
Console Jobs ×
R 4.1.3 · ~/ →
> t.test(data_ratings ~ data_group, data = ex.data, var.equal =
TRUE, na.rm = TRUE)

Two Sample t-test

data: data_ratings by data_group
t = 3.6742, df = 6, p-value = 0.0104
alternative hypothesis: true difference in means between group
fil and group unf is not equal to 0
95 percent confidence interval:
1.002105 4.997895
sample estimates:
mean in group fil mean in group unf
8 5
> |
```

**t** =  $t$ -statistic that we calculate to compare to the  $t$ -critical value

**df** = degrees of freedom for an independent-samples  $t$ -test

**p-value** =  $p$ -value that we compare to 0.05; if our  $p$ -value is less than 0.05, we reject the null hypothesis; if our  $p$ -value is greater than or equal to 0.05, we fail to reject the null hypothesis

**95% confidence interval** = if our CI includes 0 (zero), then we fail to reject the null hypothesis; if our CI does not include zero, we reject the null hypothesis