

# Introduction to R

## Lecture 2

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Dr. Kristin Eccles

kristin.eccles@utoronto.ca

 @kristineccles

[https://github.com/kristineccles/Introduction\\_to\\_R](https://github.com/kristineccles/Introduction_to_R)

# Overview

## —Crash course in statistics

- Probability distribution and the p-value
- Descriptive statistics
- Parametric Tests
  - Difference of means: T-Test and ANOVA
  - Relational Statistics: correlations, linear regression
  - PCA

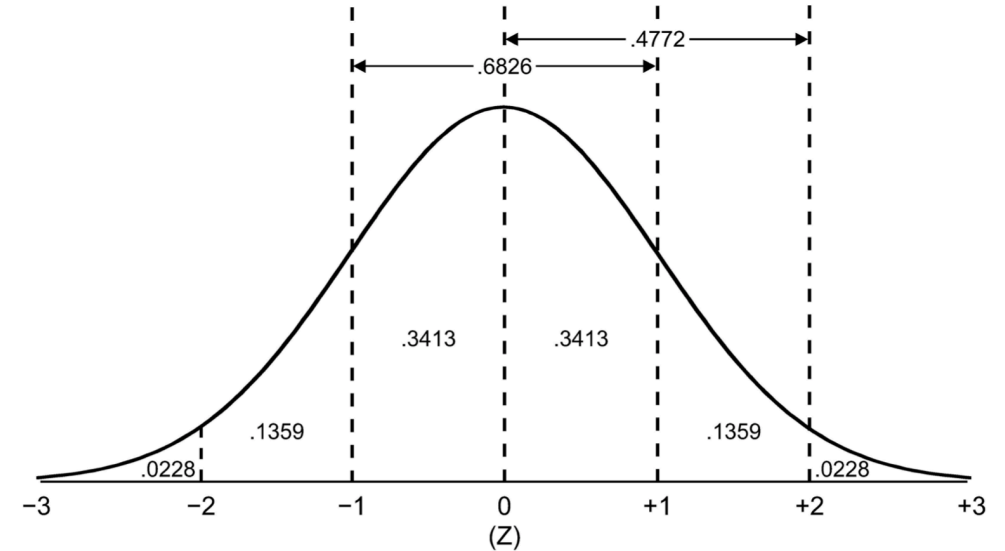
# Steps of Statistical Analysis

Step 1	State the null and alternative hypothesis
Step 2	Select the appropriate statistical test
Step 3	Select level of significance
Step 4	Delineate regions of rejection and non-rejection of the null ( $\alpha$ )
Step 5	Calculate test statistic
Step 6	Make decision regarding null and alternative hypothesis

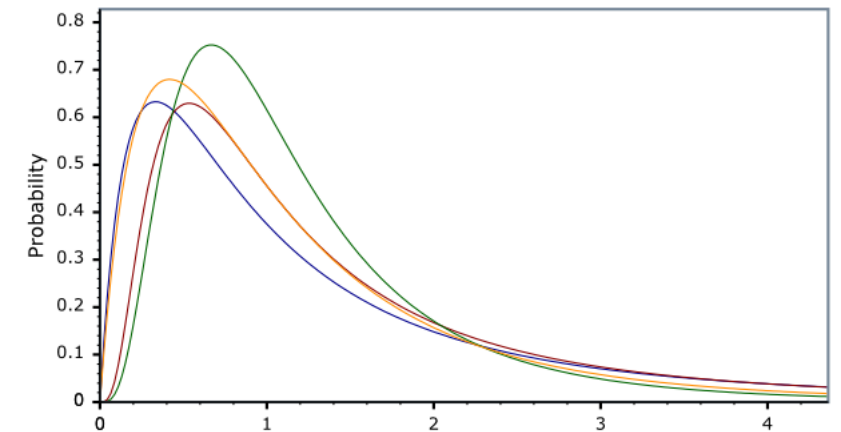
# Statistics

- **Descriptive** statistics uses the data to provide descriptions of the population, either through numerical calculations, graphs, or tables.
- **Inferential** statistics makes inferences **and** predictions about a population based on a sample of data taken from the population in question.
  - Based on probability distributions
  - Probability theory deals with random events
    - Random/probabilistic independent sample(s)

T/z-distribution



F-distribution



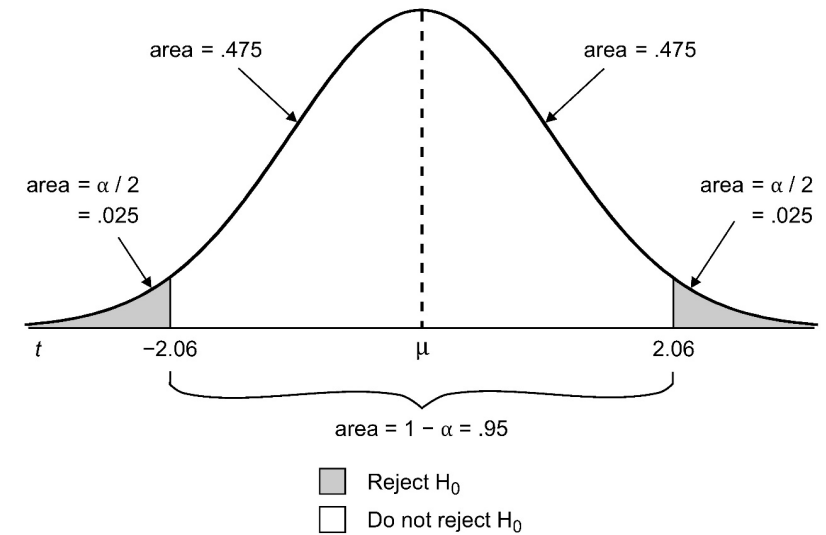
# Probability Distributions

- The area under the curve gives the probability of finding a given value in that range
- Total area under the curve is = 1 (probability is 1)
- The normal distribution
  - What the probability is of getting an extreme value (the tail)
    - 68% of the values are within 1 s.d. of the mean
    - Or, there is a probability of 0.68 that a given value is within 1 s.d. of the mean
    - **95% of the area under the curve is within 1.96 s.d. of the mean**
    - 99.7% of the area is within 3 standard deviations of the mean
- Empirical probability relies on the **law of large numbers**: the relative frequency will eventually converge on the true probability



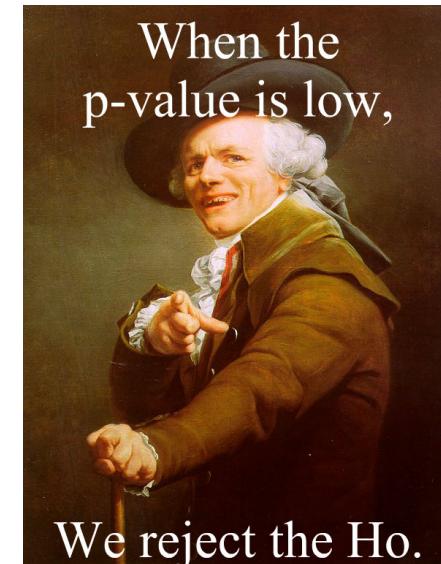
# P-value

- Evaluates the validity of our prediction using a statistical test
  - This will say if the result is statistically significant or not
- Two hypotheses:
  - $H_0$  – the null hypothesis
    - Status quo, no change, nothing special going on, conservative
  - $H_A$  (aka  $H_1$ ) – the alternate hypothesis
    - Your hypothesis – there is a difference/change.
- They are mutually exclusive and exhaustive



**FIGURE 9.2**

Normal Distribution Values Associated with a Significance Level ( $\alpha$ ) = .05: Two-Tailed Case



# Descriptive Statistics

- Characteristics of a normal (Gaussian) distribution:
  - Mean, median, mode are all the same & in the middle of the distribution
- Symmetrical, smooth, continuous distribution
- Is my data normal?
  - Make a histogram
  - Look at mean, median, and modal values
  - Check the shape of the distribution:
    - Skewness and Kurtosis

**summary(df)**

- no st.dev in summary
- sd(df)

**library(psych)**

- **describe(df)**

# Unpaired T-Test

- Objective: Test if there is a difference between the **mean** of two groups
  - Boxplots show the median
- Data type: one continuous and one categorical variable
- Assumptions: variable normality, equal variance between the groups
  - For unequal variance use Welch's T-Test



# ANOVA

- Test: If there is a difference between the **mean** of 3 or more groups
  - This only tells you if there is a difference NOT where the difference is
- Data: Three or more groups and a continuous variable
- Assumptions (F-test): variable normality, equal variance between the groups (ish)

# ANOVA Post-hoc test (Tukey)

- Test: Multiple comparison to determine the differences in means after an ANOVA
- Data: Three or more groups and a continuous variable
- Assumptions (t-test): variable normality, equal variance between the groups
- Note the p adj: This p-value is adjusted for multiple comparison
  - By default R uses Bonferroni ( $\alpha / n$ ), where  $n$  = number of comparisons

# Correlation (Pearson Product-Moment)

- Test: Association between variables
  - correlation coefficient  $\rho$  (Greek letter rho)
- Data: Two continuous variables
  - Pearson product-moment correlation
  - Spearman rank and Kendall Tau are the non-parametric version
  - Contingency analysis (categorical data)
- Assumptions (t-test): variable normality, linear association between variables

# Linear Regression (Univariate)

- Test: the slope coefficient is significant
- Data: two continuous variables
  - Generalized linear model is used for non-parametric (e.g. logit)
- Assumptions ( $t$ -test): , Test statistic:  $t$ , Assumptions: Variable normality , Random/probabilistic sample of paired variables, Variables have a linear association
- Test: Goodness of fit ( $R^2$ )
  - test that the model predicts a significant amount of the variance in  $y$
  - Coefficient of determination (not the same as  $p$  )
- Assumptions (  $F$ -test): Variable normality ,Random/probabilistic sample of paired variables, Variables have a linear association

# Assumptions of the residuals

- $e = y - \hat{Y}$
- In linear regression we have assumptions on the residuals too
  - Normality (Shapiro-Wilk)
  - Linearity (RESET test)
  - Lack of serial autocorrelation (Durbin-Watson test)
  - Homogeneity (Breusch-Pagan test)
- Can use individual test or `plot(lm1)`

# Readings a Regression Output

Call:

```
lm(formula = y ~ x, data = dataset)
```

Residuals:

Min	1Q	Median	3Q	Max
-212.04	-62.52	30.87	86.77	121.88

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	28.149	180.756	0.156	0.88010
x	39.057	9.172	4.258	0.00277 **

---

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

Residual standard error: 121.8 on 8 deg. of freedom

Multiple R-squared: 0.69, Adjusted R-squared: 0.65

F-statistic: 18.13 on 1 and 8 DF, p-value: 0.002767

- What you asked for:
  - the formula here says predict 'y' from 'x' with data from 'dataset'
- Residuals:
  - 5 number summary of the residuals



# Reading a Regression Output

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## Model coefficients (aka parameters)

- cols are the coefficient **estimates**, the **standard error** of the coefficient, the **t value** for the coefficient & the **p-value** for this **t value**
- y-intercept (intercept)
- slope (Estimate)
- legend explaining level of significance codes ( $\alpha=0.05$ )

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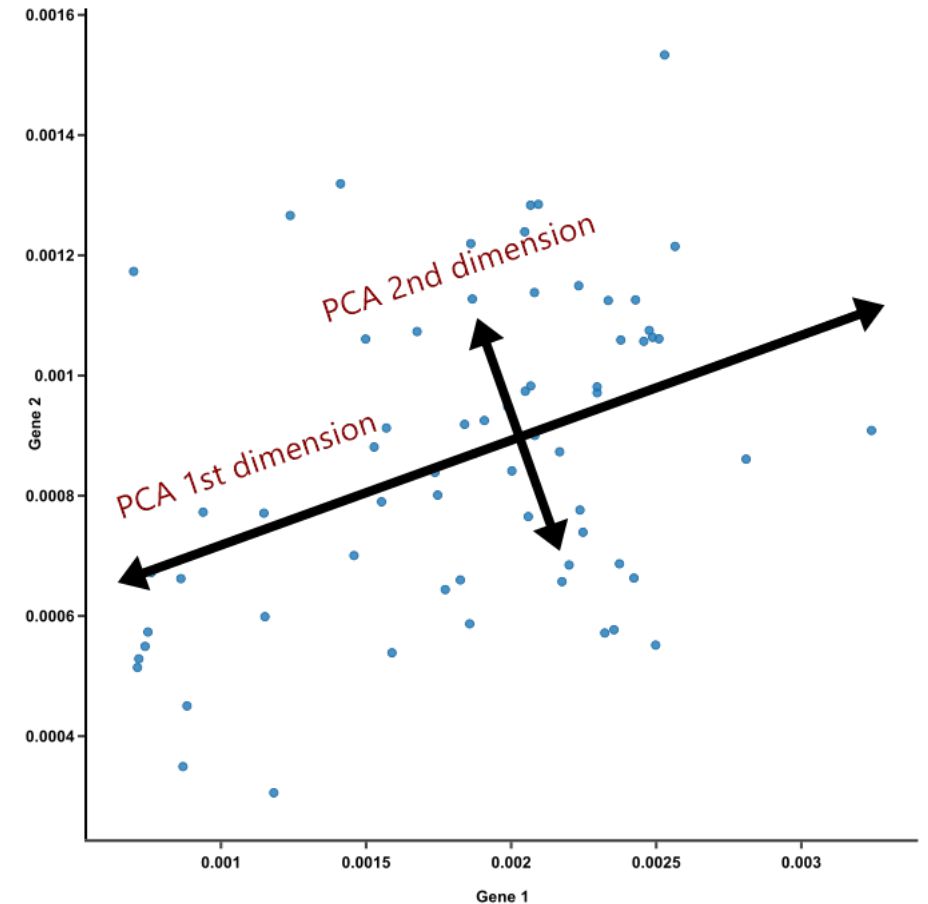
- Overall model performance
- Standard error of the residuals (SSE)
- $R^2$  and the adjusted  $R^2$
- Use the adj.  $R^2$  since it is more conservative
- F statistic and the p-value (prob. of getting a bigger F)

# Multivariate

- $\text{lm}(y \sim v1 + v2 + v3\dots)$
- Assumptions and test the same as univariate linear regression
- One additional
  - Multicollinearity
    - Cannot have a high correlation between independent variables
    - $> +/- 0.70$  it typically the threshold
    - Correlation matrices are helpful
  - Can test this using a variance inflation factor (VIF)
    - $>5$

# Principal Component Analysis (PCA)

- Test:
  - Clustering
    - A way to summarize complex real-valued data with a single categorical variable
  - Dimensionality reduction
    - A way to simplify complex high-dimensional data
- Data: ratio of 5 cases: 1 variable, variables must be of similar magnitude, and must not have outliers
  - Scale and center
- In R **prcomp** and **princomp** are used



# PCA Outputs

- Variance explained

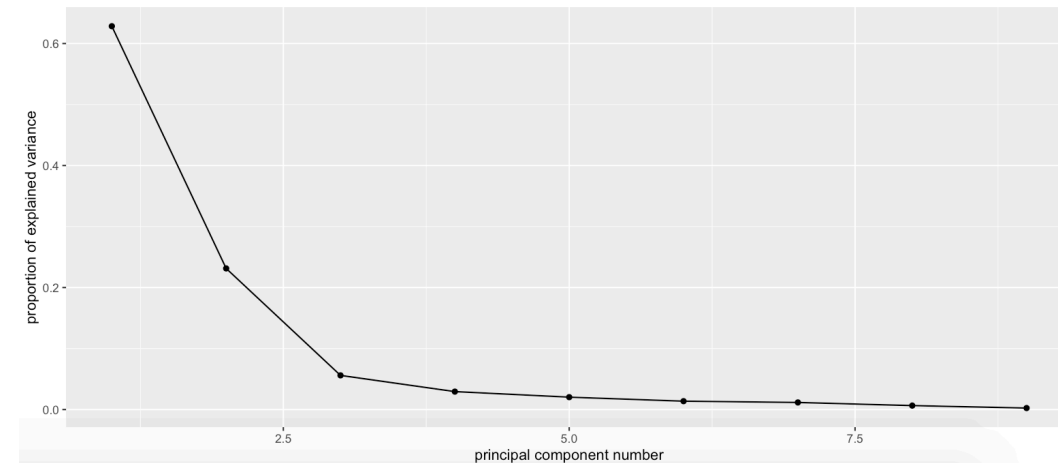
- Summary(pca1)
- # of variables = # of PCs

Importance of components:

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Standard deviation	2.3782	1.4429	0.71008	0.51481	0.42797	0.35184	0.32413	0.2419
Proportion of Variance	0.6284	0.2313	0.05602	0.02945	0.02035	0.01375	0.01167	0.0065
Cumulative Proportion	0.6284	0.8598	0.91581	0.94525	0.96560	0.97936	0.99103	0.9975

- Scree plot

- Displays how much variation each principal component captures from the data
- Used to determine the number of factors to retain components in an analysis



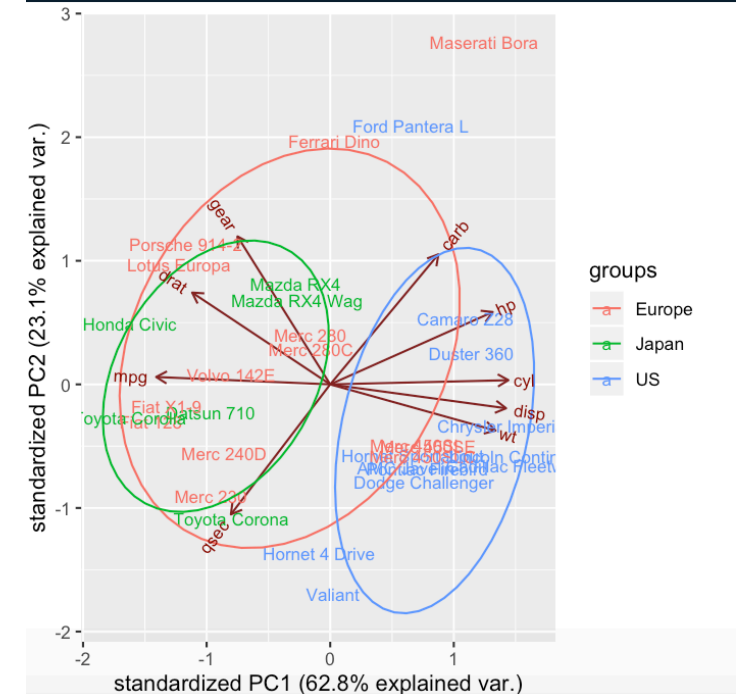
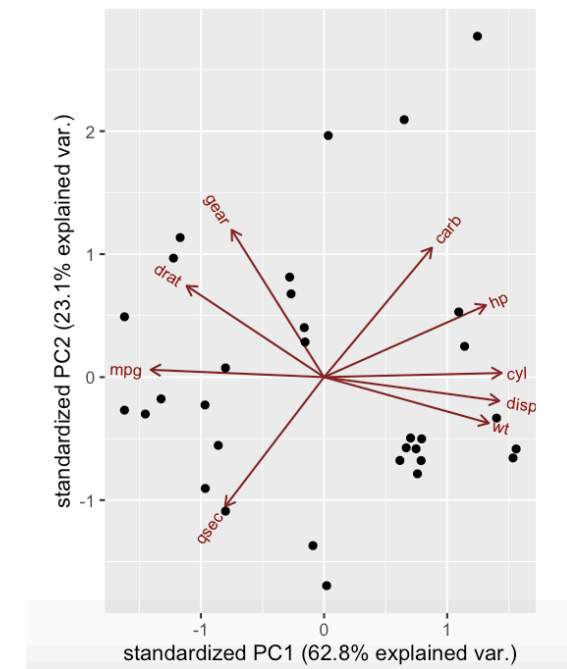
# PCA Outputs

## ■ Biplot

- PCA biplot = PCA score plot (points) + loading plot (arrows)
- Biplots are a type of exploratory **graph** used in statistics, a generalization of the simple two-variable scatterplot.
- A loading plot shows how strongly each characteristic influences a principal component.
- Shows how samples cluster based on their similarity

## ■ Eigenvalues (scores)

## ■ Eigenvectors (loadings)





- Loadings (eigenvectors)

	PC1	PC2	PC3	PC4	PC5	PC6
length	0.3832508	0.03786529	-0.5932799	-0.089331673	0.040512600	0.699651086
diameter	0.3835732	0.06532324	-0.5853661	-0.008285814	0.008517628	-0.711025627
height	0.3481438	0.86683603	0.3148764	-0.165564868	-0.027110424	0.009841283
whole_weight	0.3906735	-0.23327117	0.2308252	0.052280164	-0.110183954	-0.021653298
shucked_weight	0.3781883	-0.34801069	0.2315678	-0.496179039	-0.545339050	-0.011030516
gut_weight	0.3815134	-0.25290295	0.2702527	-0.140972073	0.809328460	-0.023996063
shell_weight	0.3789217	-0.05837478	0.1621047	0.834110000	-0.181668556	0.060561675

- Scores (eigenvalues)
- Scores can be mapped (to look for spatial clustering) and can be used in linear regression
  - Can be difficult to interpret

# What is reproducible analysis?

- One particular form:
  - code transforms raw data and meta-data into processed data,
  - code runs analyses on the data, and
  - code incorporates analyses into a report
- Ideally, the process involves a one-click build
  - Knitr: an engine for dynamic report generation with R.
- Public sharing of document, code, and data is optional, but forms part of gold standard of scientific openness
  - Journals are now requiring this

# intro\_to\_r\_lecture2\_excercise.R

kristineccles

2020-01-12

```
#####  
# Introduction to R  
# Lecture 2- Statistics  
# By: Kristin Eccles  
# Written in R 3.6.2  
#####  
  
# Install Libraries  
# only need to run this once  
#install.packages(c("psych", "car", "stats", "corrplot", "factoextra", "lmtest", "devtools"))  
  
# Load Libraries  
library(ggplot2)  
library(psych) # describe and mutli.hist  
  
##  
## Attaching package: 'psych'  
  
## The following objects are masked from 'package:ggplot2':  
##  
##    %+%, alpha  
library(car) #stats  
  
## Loading required package: carData  
  
##  
## Attaching package: 'car'  
  
## The following object is masked from 'package:psych':  
##
```


# Reproducible analysis in R

- Combine R and plain text file format to produce documents (e.g., pdfs, HTML documents, etc.)

## Rmarkdown

- General workflow
  - Create an RMarkdown File
    - either use Rstudio File – New File – RMarkdown or just create a file with an empty text file with the .rmd extension
  - Optionally add a header
    - Options to specify output format (see RMarkdown cheat sheet)
  - Write the main document in Markdown
  - Embed R code chunks
  - R code chunks can be customised to control output

**3. Markdown** Next, write your report in plain text. Use markdown syntax to describe how to format text in the final report.

syntax	becomes
Plain text End a line with two spaces to start a new paragraph. *italics* and _italics_ **bold** and __bold__ superscript^2^ --strikethrough-- [link] (www.rstudio.com)	Plain text End a line with two spaces to start a new paragraph. <i>italics</i> and <i>italics</i> <b>bold</b> and <b>bold</b> superscript <sup>2</sup> <del>strikethrough</del> <a href="#">link</a>
# Header 1	Header 1
## Header 2	Header 2
### Header 3	Header 3
#### Header 4	Header 4
##### Header 5	Header 5
##### Header 6	Header 6
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> block quote * unordered list * item 2 + sub-item 1 + sub-item 2  1. ordered list 2. item 2 + sub-item 1 + sub-item 2	> block quote • unordered list • item 2 ◦ sub-item 1 ◦ sub-item 2  1. ordered list 2. item 2 ◦ sub-item 1 ◦ sub-item 2
Table Header   Second Header ----- Table Cell   Cell 2 Cell 3   Cell 4	Table Header   Second Header ----- Table Cell   Cell 2 Cell 3   Cell 4

See RMarkdown Cheat Sheet for more info

## Reproducible Science is good. Replicated Science is better.

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