### Welcome

**NCI Data Science Learning Exchange** 

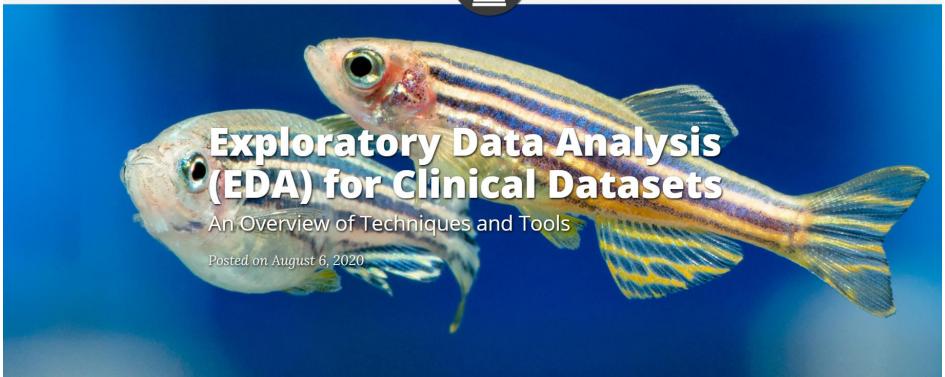


**GETTING STARTED** 

**LEARNING RESOURCES** ▼

COLLABORATION

N EVE



### Today's Presenter





George Zaki, PhD Bioinformatics Manager George.Zaki@nih.gov

Strategic and Data Science Initiatives (SDSI) Team Biomedical Informatics and Data Science (BIDS)



https://tinyurl.com/yxn5nwk9



### Exploratory Data Analysis of Clinical Data using Pandas, Scikit-learn, and Seaborn

George Zaki, Ph.D.

**Biomedical Informatics and Data Science (BIDS)** 

**August 6, 2020** 

The Frederick National Laboratory is a Federally Funded Research and Development Center operated by Leidos Biomedical Research, Inc., for the National Cancer Institute

DEPARTMENT OF HEALTH AND HUMAN SERVICES • National Institutes of Health • National Cancer Institute

### NCI Data Science Learning Exchange





Website: <a href="https://cbiit.github.io/">https://cbiit.github.io/</a>
<a href="p2p-datasci/">p2p-datasci/</a>

- Peer-to-peer community
- Connects NCI staff learning data science with each other
- See Resources & engage!
  - Website
  - Microsoft Teams

### Join the MS Team! General Channel + 17 Topic-specific Channels! Laboratory



https://bit.ly/2VjpFHn

Intro to Data Science

**Biowulf + HPC Systems** 

**Bioinformatics** 

**C-based languages** 

**Command Line & Shell Scripting** 

**Data Pipelines & Workflow Management** 

R

SAS

**Image Analysis** 

Java

**Machine Learning & Al** 

Math for MI

**Python** 

**Database** 

#### In each channel:

- Posts open discussions; Q & A; recommendations; resources
- **Files**
- Wiki

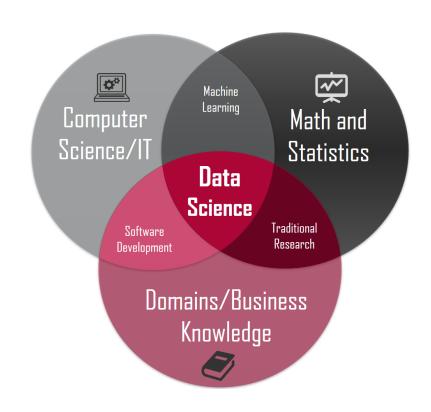


### Data Science Initiative: NCI CBIIT, FNL

Leverage breakthrough advancements in scientific computing and data science to help NCI scientific staff advance basic research, understanding, and treatments in cancer.

Thanks to the team:
Lynn Borkon, Amar Khalsa,
Laurie Morrissey, Carl McCabe,
Ravi Ravichandran, Eric
Stahlberg, Andrew Weisman

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### Know about you

- Have you used exploratory data analysis in your research?
  - If yes, for what?

What would like to get out of this workshop?

### **Exploratory Data Analysis**

- What?
  - Summarize and visualize statistical characteristics of data sets.
- Why?
  - Find outliers and replicates, missing values, cleanup data
  - Understand relationships, suggest hypothesis
- How?
  - Single variable, bivariate and multivariate plots, data imputation, clustering, scaling, correlation, dimensionality reduction, etc.

'Exploratory data analysis' is an attitude, a state of flexibility, a willingness to look for those things that we believe are not there, as well as those we believe to be there.'

**John Tukey** 













SUMMARY STATISTICS



**TRANSFORMATIONS** 



**VISUALIZATION** 



**IMPUTATION** 

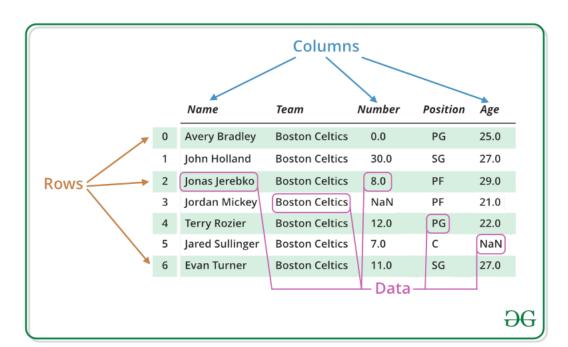


DIMENSIONALITY REDUCTION



### **Data Ingestion**

- Data sources: own experiments, online portal, data repositories.
- Original data might need to be processed/cleaned. Generate gene expression count, remove artifact from processing tools, etc.
- Very important to clearly document/version control what you have done
- Once the data is in a form of: Samples \* features, then in can be loaded in memory as dataframe (e.g. Pandas)

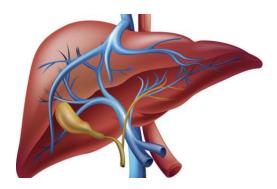


### The clinical data for this workshop

- Breast Cancer Wisconsin (Diagnostic) Data Set
- Cervical cancer (Risk Factors) Data Set
- Hepatitis C Virus (HCV) for Egyptian patients Data Set
- Each one of these datasets would highlight different aspects on the application of EDA to better understand the data.
- Github examples: <a href="https://github.com/georgezakinih/exploratory-data-analysis">https://github.com/georgezakinih/exploratory-data-analysis</a>









### **Summary Statistics**

Pandas' head, describe, summary, and info

```
raw_data.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1385 entries, 0 to 1384
Data columns (total 29 columns):
     Column
                                       Non-Null Count
#
                                                       Dtype
                                       1385 non-null
    Age
                                                       int64
     Gender
                                       1385 non-null
                                                       int64
                                       1385 non-null
     BMI
                                                       int64
                                       1385 non-null
                                                       int64
     Fever
                                       1385 non-null
                                                       int64
    Nausea/Vomting
 5
     Headache
                                       1385 non-null
                                                       int64
                                       1385 non-null
     Diarrhea
                                                       int64
     Fatigue & generalized bone ache 1385 non-null
                                                       int64
     Jaundice
 8
                                       1385 non-null
                                                       int64
                                       1385 non-null
     Epigastric pain
                                                       int64
```



### **Categorical versus Numerical Data**

#### Numerical data:

- Can be positive integer, integer, real, have a specific domain
- Have statistics: mean, median, 25, 75 percentiles, standard deviation, minimum, maximum

#### Encoding of categorical features:

- Usually represented as integer and unique string.
- Might need to be coded for subsequent machine learning tasks

One hot coding: pd.get\_dummies (df['Category'], prefix='Cat')

Original column		New coded columns				
	Category	Cat_A	Cat_B	Cat_C		
	Α	1	0	0		
	В	0	1	0		
	С	0	0	1		
	Α	1	0	0		

### Map, apply functions

- df.apply: Applies any user defined transformation, aggregation, split on a data frame or a series. Can be used row or column wise.
- Series.map: Map every value of a series to another values.

```
699, Uniformity of Cell Shape
699, Marginal Adhesion
699, Single Epithelial Cell Size
683, Bare Nuclei
699, Bland Chromatin
699, Normal Nucleoli
699, Mitoses
699, Class
```

```
def replace_NaN(x, median):
    if np.isnan(x):
        return median
    else:
        return x
```

- Calculate median: median = 1
- Replace NaN (e.g. missing) values with 1

```
data["Bare Nuclei"] =
   data["Bare Nuclei"].map(lambda x: replace_NaN(x,1))
```

When to use df.apply? Here is a good discussion

### **Slicing and Dicing**

#### Subsetting:

```
- raw_data[(raw_data.Age < 40)]]
- raw_data[(raw_data.Age < 40)] & ( raw_data.BMI < 20 ) ]
Returns a subset of the data frame rows that satisfy the condition</pre>
```

- Here is a nice <u>tutorial</u>
- df.groupby: Creates summary statistics per group in the data.

```
raw_data.groupby(["Gender"])['Age '].mean()

Gender
1    46.404526
2    46.230088
Name: Age , dtype: float64
```



### **Boundary checks**

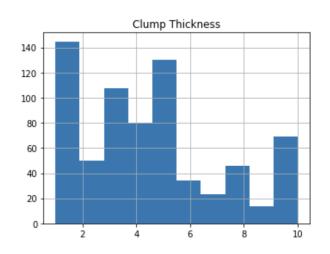
- Sometimes, the values will not fit a meaningful range, the distribution might be not be normal.
- pd.crosstab and df.describe functions can help spot inconsistent data.

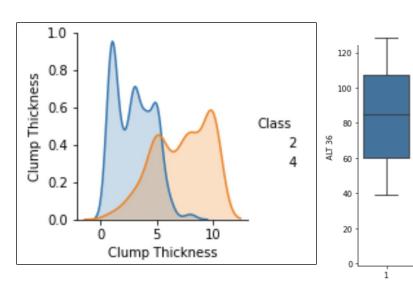
col_0	% observations	
Smokes		
0.0	0.841492	
1.0	0.143357	
?	0.015152	
# of un	ique values	3

	Clump Thickness	Uniformity of Cell Size	Uniformity of Cell Shape	Marginal Adhesion	Single Epithelial Cell Size	
count	699.000000	699.000000	699.000000	699.000000	699.000000	6
mean	4.417740	3.134478	3.207439	2.806867	3.216023	
std	2.815741	3.051459	2.971913	2.855379	2.214300	
min	1.000000	1.000000	1.000000	1.000000	1.000000	
25%	2.000000	1.000000	1.000000	1.000000	2.000000	
50%	4.000000	1.000000	1.000000	1.000000	2.000000	
75%	6.000000	5.000000	5.000000	4.000000	4.000000	
max	10.000000	10.000000	10.000000	10.000000	10.000000	

### **Univariate plots**

- These are methods to show the distribution of a single variable.
- Popular methods are histograms, dot plots, box plots, and kernel density plots: df.hist, seaborn.pairplot, seaborn.catplot



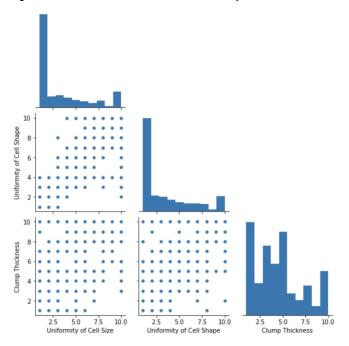


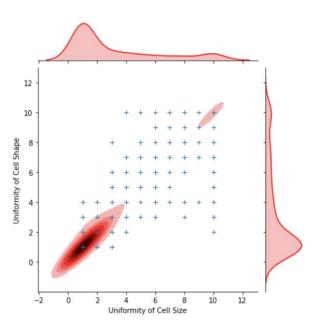
 These plots helps in understanding the assumptions in a model (e.g., normal probability plot) and check the limitations where a model may not fit well the data.

Baselinehistological staging

### **Bivariate plots**

- Scatter plots can highlight the relationship between two variables and possible trends. seaborn.jointplot, seaborn.pairplot
- The components of the trend are: (a) direction (positive or negative), (b) form (linear or curvilinear), and (c) strength (degree of variability around the trend).

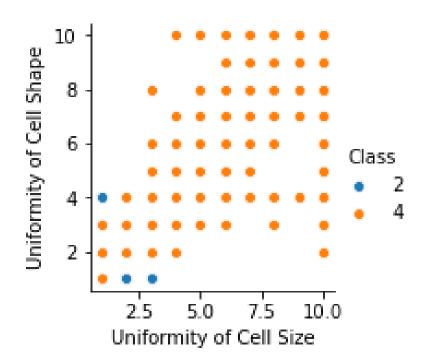




Existence of clusters can also be identified in a scatter plot.

### **Multivariate**

- Exponential number of plots: 3 variables: N<sup>3</sup>, 4 variables: N<sup>4</sup>
- To limit the number of plots, use insights from the bivariate plots and select few candidates for multivariate you will investigate.
- In Seaborn, we can use 2D plots + the semantics of hue, size, and style to add up to three more variables.



Note that in this scatter plot, the dots with same values are *overlapping*. The data is not that imbalanced.

### **Missing Data Imputation**

- Missing features is a typical phenomena in clinical data.
- Techniques to handle missing features are:
  - Detect and quantify, find systematic bias in missing data
    - Can I predict that data is missed based on other features in the sample?
  - Remove this feature from all the samples
    - Might miss important signal
  - Remove samples with missing features
    - Might introduce bias the samples left (e.g. a specific medical test can be done in sever cases)
  - Keep the feature, but impute its value when missing

Sklearn's SimpleImputer, IterativeImputer
MissingIndicator, KNNImputer



### **Missing Data Imputation**

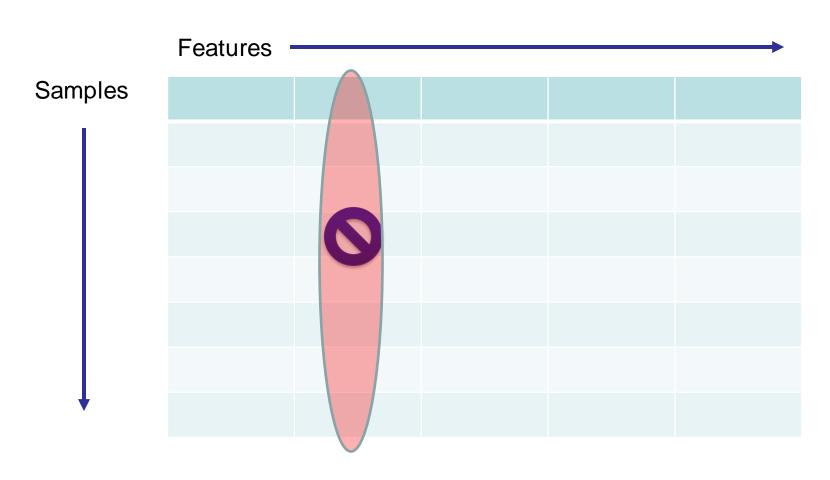
- Keep the feature, but impute its value when missing:
  - Numerical: median, mean, most frequent, constant
  - Categorical: most frequent, create a "missing" category
  - Add extra column indicating when the variable has been imputed
    - Be careful that a ML algorithm can learn this information
  - Impute the value from other features in the same sample
  - Impute the value randomly from the closest set of samples

Sklearn's SimpleImputer, IterativeImputer, MissingIndicator, KNNImputer

 Warning! Imputation might introduce correlation in some samples. Make sure you understand/quantify the implication of the imputation technique you choose.



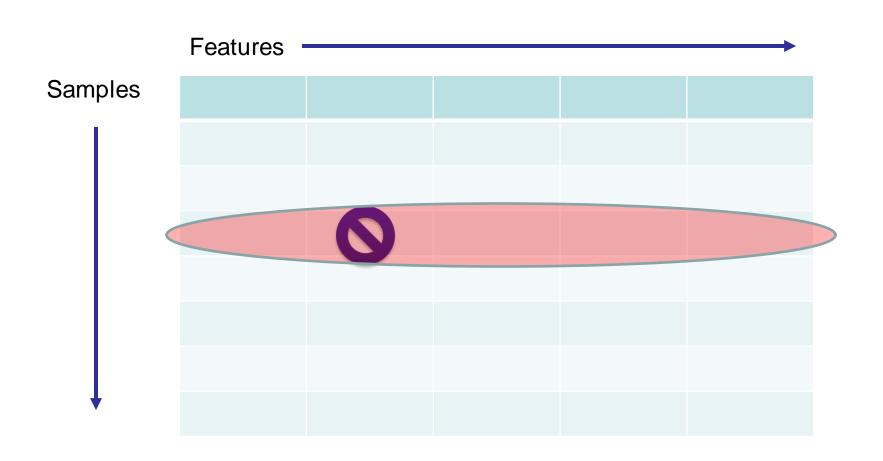




Impute using statistics of the features from other samples: mean, median

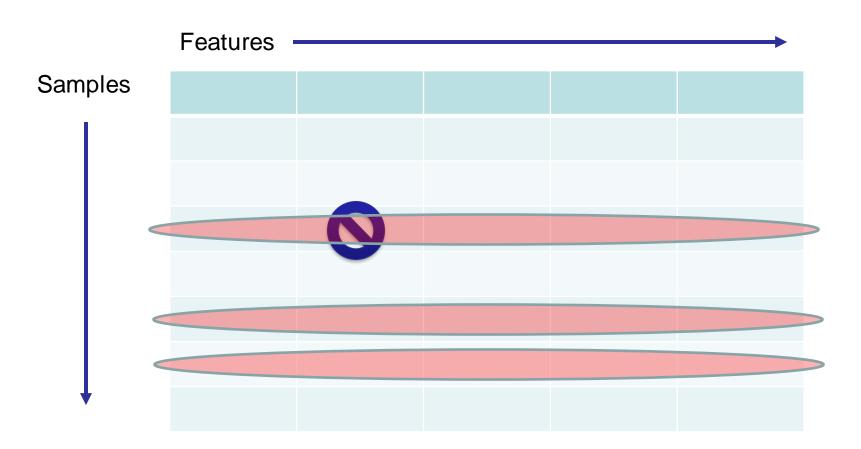








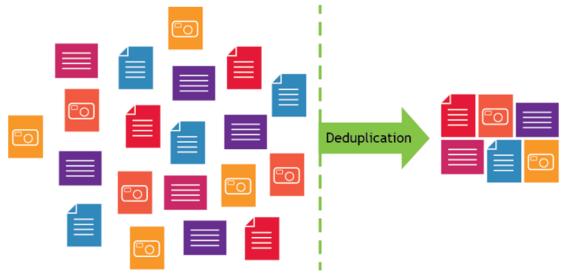
### **Data Imputation**



Infer the missing values from other close samples in the dataset.

### **Data Duplication**

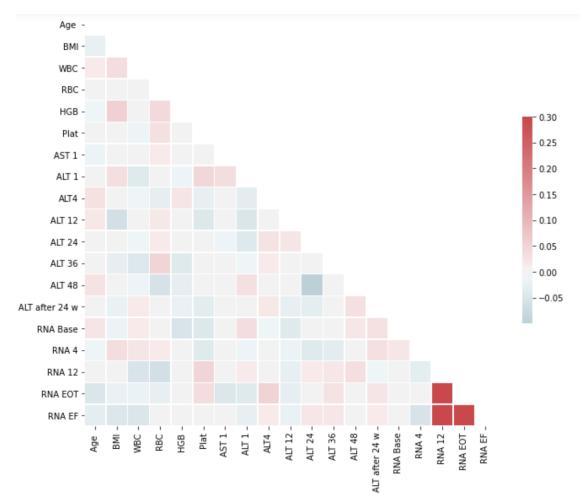
- Duplication of samples can be a result of repeating experiments, or error in the data.
- It is important to identify and quantify duplication specifically if machine learning models will be built later. DataFrame.duplicated
- More importantly, find inconsistency in the data if the features are the same, but the outcomes are different.
  - In this case regression outcomes of duplicate samples can be summarized as mean and variance.



#### Correlation

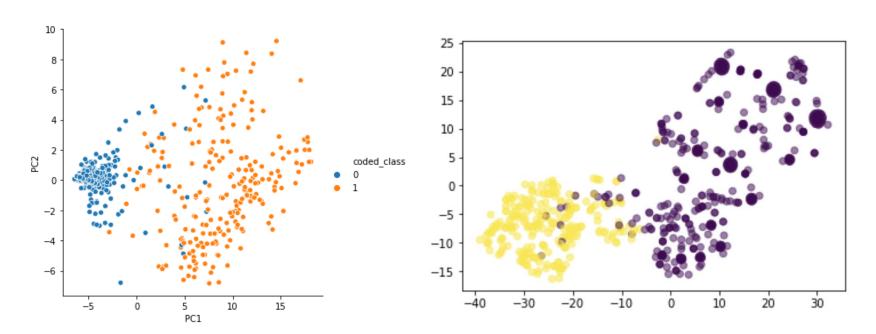
 One common step in feature selection is to remove correlated variables.

 Correlation can be computed using df.corr and visualized using seaborn.diverging\_ palette



### **Dimensionality Reduction**

- To visualize raw numeric data on a 2D plot, we need to reduce the dimensions.
- Two popular techniques: Principal Component Analysis (PCA) (linear), and TSNE (non linear)



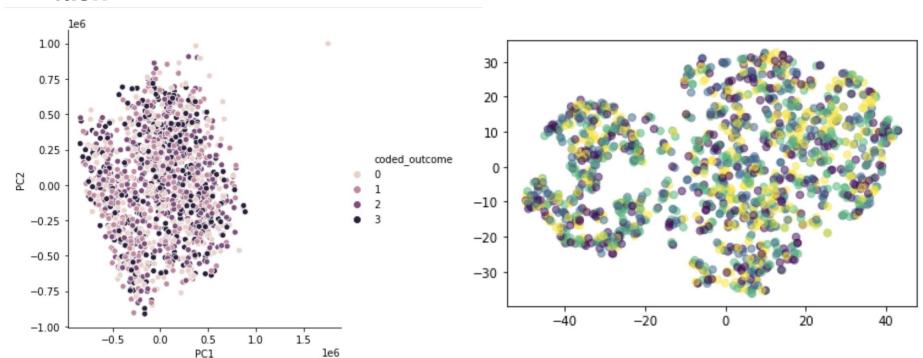
sklearn.decomposition.PCA

sklearn.manifold.TSNE



### **PCA and TSNE**

- In some data, clusters might not always show up.
- Neural network techniques like Autoencoders may help in this task



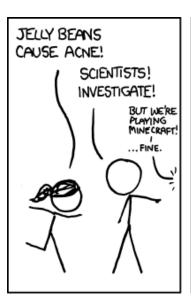


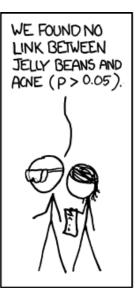
### **Avoid Data Dredging, p-hacking**

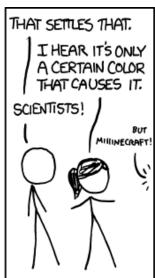
- The purpose of EDA is discovery, whereas the purpose of confirmatory research is validation
- While checking statistical significance between 1000 variables, p value of 5%, with many tests, by chance, 5% will be reported significant.

#### Mitigation:

- Out of sample tests
- Cross validation
- Bonferroni correction







### P-hacking

### Frederick National Laboratory for Cancer Research

WE FOUND NO LINK BETWEEN PURPLE JELLY BEANS AND ACNE (P > 0.05).



WE FOUND NO LINK BETWEEN BROWN JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN PINK JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN BLUE JELLY BEANS AND AGNE (P>0.05).



WE FOUND NO LINK BETWEEN TEAL JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN SALMON JELLY BEANS AND AGNE (P>0.05).



WE FOUND NO LINK BETWEEN RED JELLY BEANS AND AONE (P>0.05).



WE FOUND NO LINK BETWEEN TURQUOISE JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN MAGENTA JELLY BEANS AND AONE (P > 0.05).



WE FOUND NO LINK BETWEEN YELLOW JELLY BEANS AND ACNE (P>0.05)



WE FOUND NO LINK BETWEEN GREY JELLY BEANS AND ACNE (P>0.05)



WE FOUND NO LINK BETWEEN TAN JELLY BEANS AND AONE (P>0.05).



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).



WE FOUND NO LINK BETWEEN MAUVE JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN BEIGE JELLY BEANS AND AONE (P > 0.05)



WE FOUND NO LINK BETWEEN LILAC JELLY BEANS AND ACNE (P>0.05)



WE FOUND NO LINK BETWEEN BLACK JELLY BEANS AND ACNE (P > 0.05)



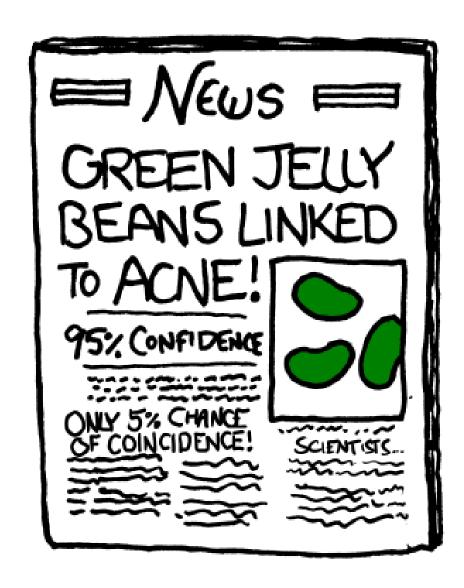
WE FOUND NO LINK BETWEEN PEACH JELLY BEANS AND ACNE (P>0.05).



WE FOUND NO LINK BETWEEN ORANGE JELLY BEANS AND ACNE (P>0.05).



### P-Hacking



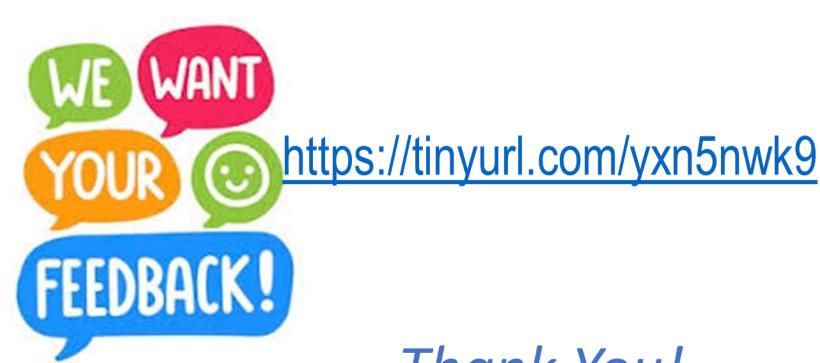


### **Summary**

- It is important to gather facts about the data before applying machine learning.
- EDA tools and analysis techniques help in identifying trends, problems, and possible hypothesis from the data.
- Many python libraries like pandas, sklearn, and seaborn provide very nice tools to conduct EDA.
- It is important not to torture the data and conduct confirmatory data analysis after hypothesis are generated.



### Your feedback is valuable to us!



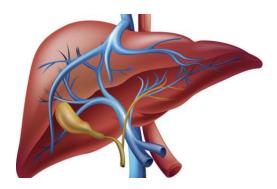
Thank You!

#### Hands On

- Breast Cancer Wisconsin (Diagnostic) Data Set
- Cervical cancer (Risk Factors) Data Set
- Hepatitis C Virus (HCV) for Egyptian patients Data Set
- Each one of these datasets would highlight different aspects on the application of EDA to better understand the data.
- Github examples: <a href="https://github.com/georgezakinih/exploratory-data-analysis">https://github.com/georgezakinih/exploratory-data-analysis</a>









### References & Examples



- Pandas, Seaborn, Matplotlib
- <u>Exploratory Data Analysis</u>, Oxford Bibliographis
- An extensive guide to EDA
- Heart attack risk prediction
- Andrew T. Jebb, Scott Parrigon, Sang Eun Woo, "Exploratory data analysis as a foundation of inductive research", Human Resource Management Review, Volume 27, Issue 2, 2017
- Simmons, J. P., Nelson, L. D., & Simonsohn, U. (2011). "False-Positive Psychology: Undisclosed Flexibility in Data Collection and Analysis Allows Presenting Anything as Significant." Psychological Science, 22(11), 1359–1366.