

# Introduction to Machine Learning for Life Sciences



**Barcelona  
Supercomputing  
Center**

*Centro Nacional de Supercomputación*

# Course Outline

Day 1

Day 2

Day 3

Day 4

## Data Processing & Feature Engineering

- Python refresher: NumPy, pandas, scikit-learn
- Data exploration & preprocessing
- Feature extraction & selection techniques

## Supervised & Unsupervised Deep Learning Learning

- Linear & logistic regression, decision trees
- Ensemble methods: Random Forest, XGBoost
- Clustering: K-means, DBSCAN
- Hands-on model training in Google Colab

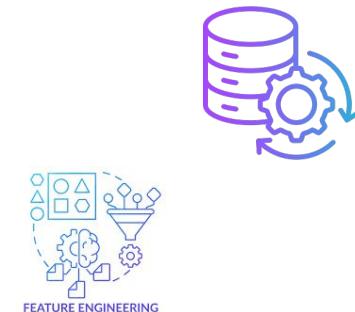
Day 3

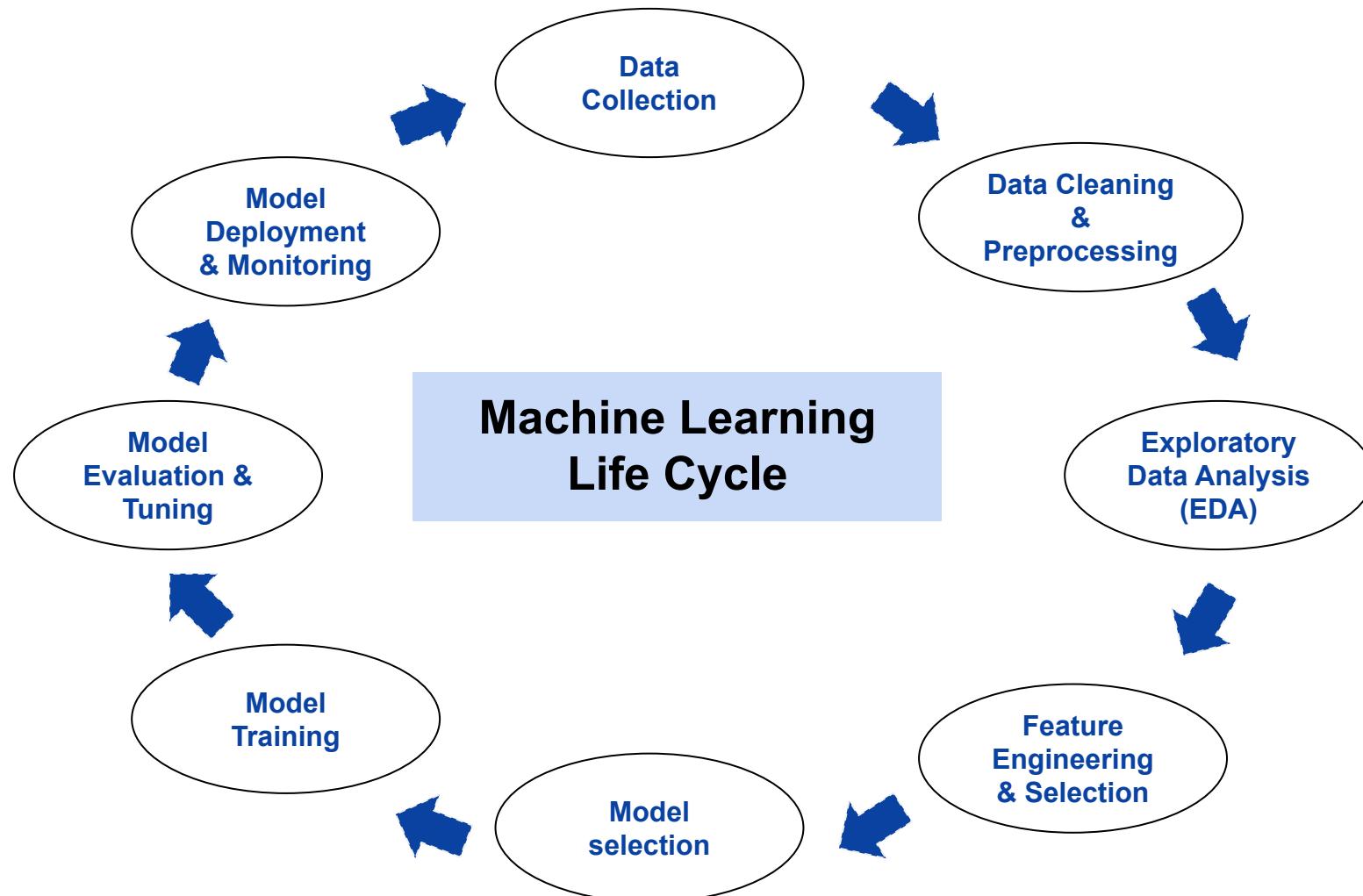
## Large Language Models (LLMs)

- Neural networks & CNNs explained
- PyTorch for image & tabular data classification
- Model interpretability with SHAP
- Transformer architecture & attention mechanisms
- Practical demo with Hugging Face Transformers
- Fine-tuning LLMs

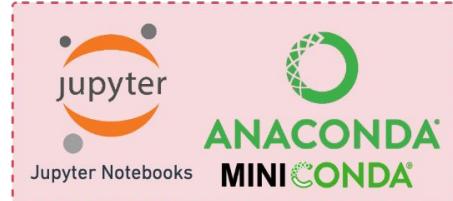
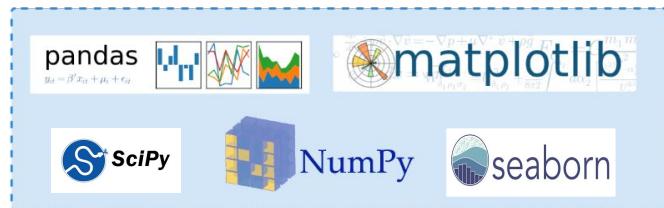
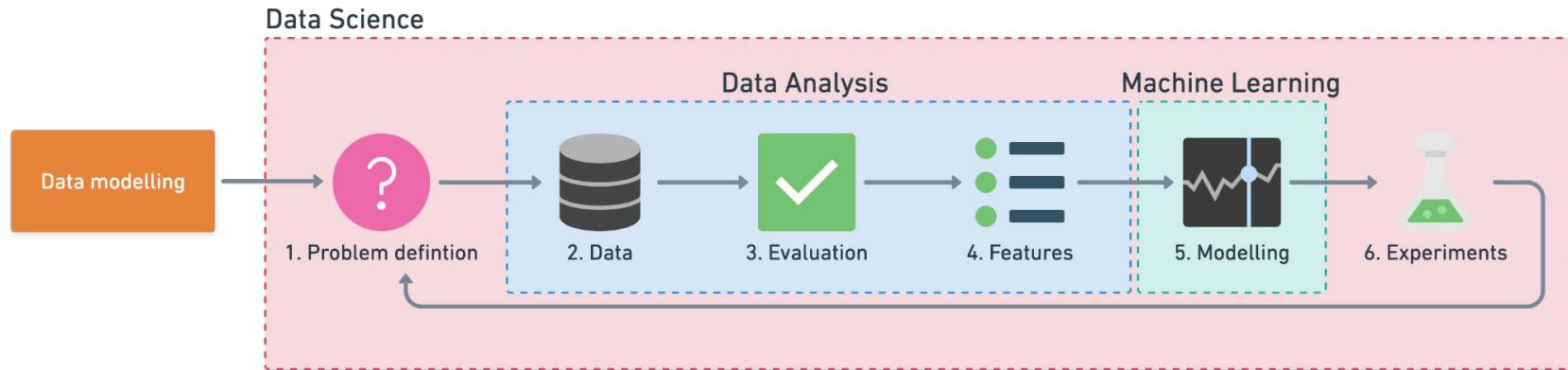
**Day 1– *Introduction to Machine Learning for Life Sciences***

# Data Processing & Feature Engineering





# Tools you can use



# Jupyter Notebooks



- Interactive coding tool, mostly for Python
- Combine code + text + math + visuals
- Great for data science and analysis
- Runs locally

The screenshot shows a Jupyter Notebook interface with the following details:

- Header:** Welcome To Colab, File, Edit, View, Insert, Runtime, Tools, Help.
- Toolbar:** Share, Gemini, B.
- Search Bar:** q, Commands, + Code, + Text, Copy to Drive.
- Section Header:** Data science.
- Notebook Content:**
  - A warning message: "With Colab you can harness the full power of popular Python libraries to analyze and visualize data. The code cell below uses numpy to generate some random data, and uses matplotlib to visualize it. To edit the code, just click the cell and start editing."
  - An error message: "You can import your own data into Colab notebooks from your Google Drive account, including from spreadsheets, as well as from Github and many other sources. To learn more about importing data, and how Colab can be used for data science, see the links below under Working with Data."
  - A code cell (Cell 1) containing Python code to generate a scatter plot:

```
import numpy as np
import IPython.display as display
from matplotlib import pyplot as plt
import io
import base64

ys = 200 + np.random.randn(100)
x = [x for x in range(len(ys))]

fig = plt.figure(figsize=(4, 3), facecolor='w')
plt.plot(x, ys, 'r')
plt.fill_between(x, ys, 195, where=(ys > 195), facecolor='g', alpha=0.6)
plt.title("Sample Visualization", fontsize=16)

data = io.BytesIO()
plt.savefig(data)
image = Image.open(BytesIO(base64.b64decode(data.getvalue())))
alt = "Sample visualization"
display.display(display.Markdown(f'![[{alt}]({image})'))
```
  - A plot area showing a scatter plot with green points above a red line, titled "Sample Visualization".
- Footer:** Colab notebooks execute code on Google's cloud servers, meaning you can leverage the power of Google hardware, including GPUs and TPUs, regardless of the power of your machine. All you need is a browser.

# Google Colab



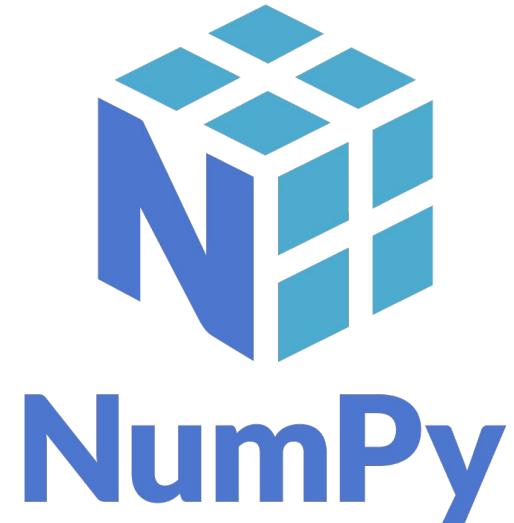
- Google's online version of Jupyter Notebook
- Runs in the cloud (no setup needed)
- Free GPU/TPU access
- Google Drive integration
- Real-time collaboration like Google Docs

<https://github.com/bsc-life/ml4br-ml-course/>

# NumPy :

## *Numerical Python*

1. What is Numpy ? why?
2. ndarray object
3. Creating, indexing & slicing
4. Reshaping
5. Iterating
6. Filtering



# What is NumPy?

NumPy (Numerical Python) is a powerful library for numerical computing in Python.

## Why Use NumPy over Lists?

- **Element Overhead:** Lists store extra metadata per element, increasing memory usage.
- **Datatype:** Mixed data types reduce efficiency.
- **Memory Fragmentation:** Non-contiguous storage can cause fragmentation.
- **Performance:** lists are Slower for numerical tasks due to lack of optimization.
- **Functionality:** Lacks specialized tools for numerical operations.

## Install NumPy using:

```
pip install numpy
```

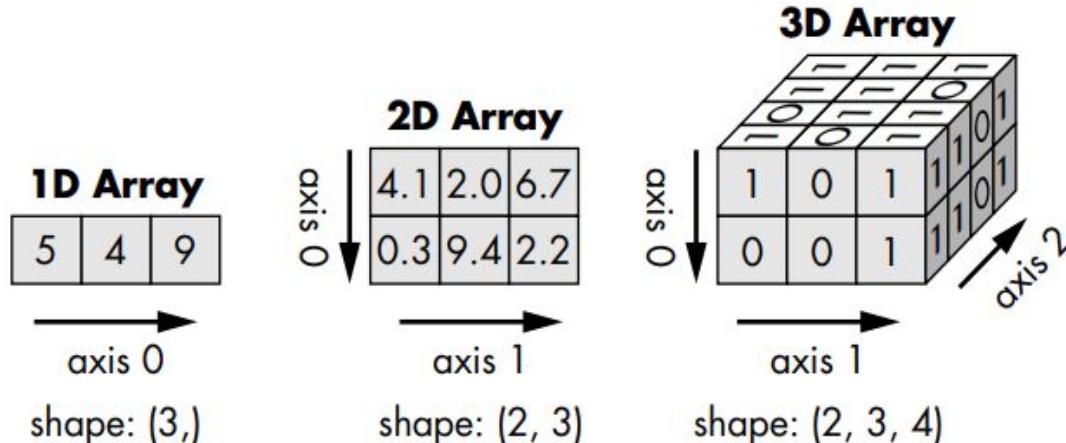
## Importing NumPy :

```
import numpy as np
```



# NumPy Arrays

- NumPy's main object is the ndarray (N-dimensional array)
- Stores data in a grid-like structure (rows, columns, etc.)
- Can have any number of dimensions (1D, 2D, 3D, ...) with any length

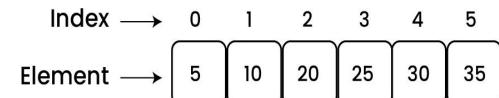


# NumPy Arrays :Creating Array

We can create a NumPy **ndarray** object by using the **array()** function.

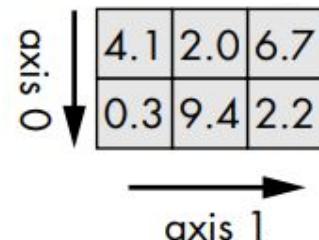
## Creating 1D arrays from lists:

```
my_list= [5,10,20,25,30,35]  
array= np.array(my_list)
```



## Creating 2D arrays from lists:

```
my_list_of_list=[[4.1 , 2.0 , 6.7],[0.3 , 9.4 , 2.2]]  
array2= np.array(my_list_of_list)
```



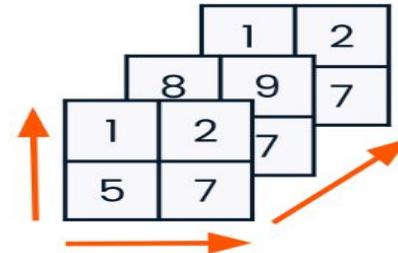
*Remember : Numpy Array can contain only a single data type !!!*

# NumPy Arrays :Creating Array

## Creating 3D arrays from lists:

we can create a 3D array by creating a list of lists of lists.

```
my_list= [[[1,2],[5,7]],[[8,9],[6,7]],[[1,2],[3,7]]]  
array= np.array(my_list)
```



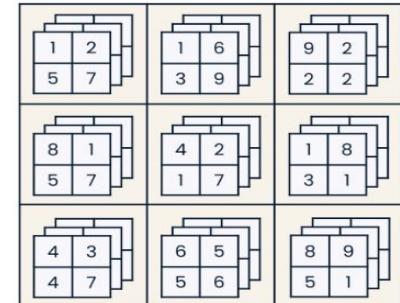
## Creating 4D arrays from lists:

we can create a 4D array by creating an array of 3D arrays..

## How to check dimension ?

The `ndim` attribute returns an integer that tells us how many dimensions the array have.

```
print(array2.ndim)
```



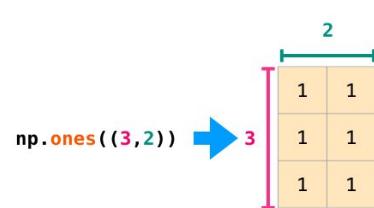
# NumPy Arrays :Creating Array

There are many Numpy functions to create array, including :

## 1. np.zeros ()

the function name  
`np.zeros(shape = (1, 3), type = float )`

A tuple of values specifying the shape  
the data type



## 2 .np.random.randint ( )

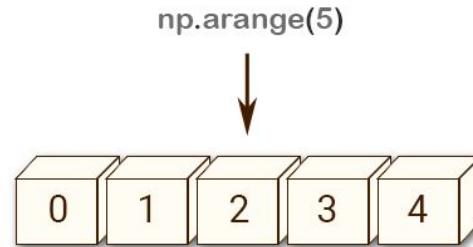
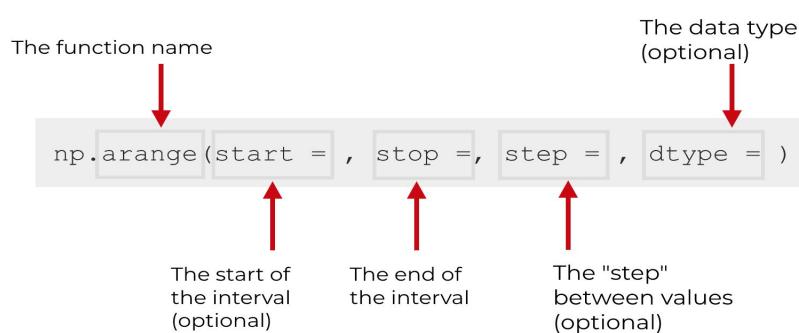
The function name  
`np.random.randint(low ,high= ,size= ,dtype=)`

The shape of the output  
The lowest possible integer  
The highest possible integer  
The datatype of the output



# NumPy Arrays :Creating Array

## 3. np.arange( )



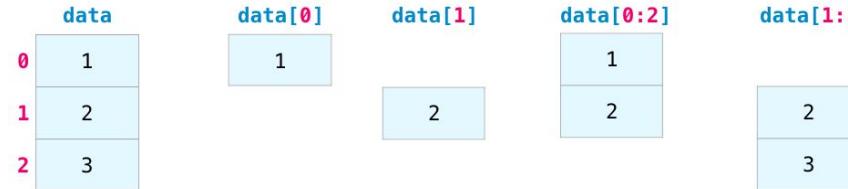
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# NumPy Arrays : Indexing

Indexing is an order-based method for accessing data.

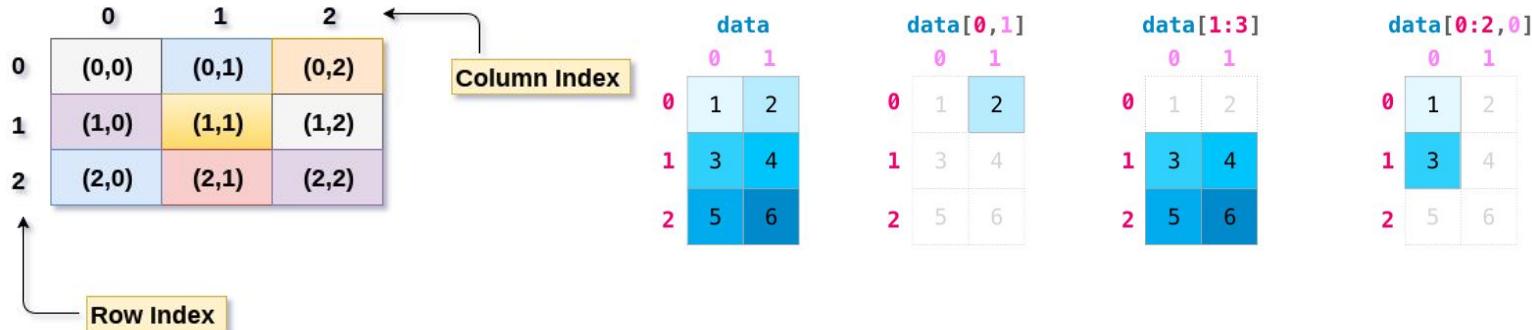
## Indexing 1D:

1	3	5	7	9
index → 0	1	2	3	4
negative index → -5	-4	-3	-2	-1



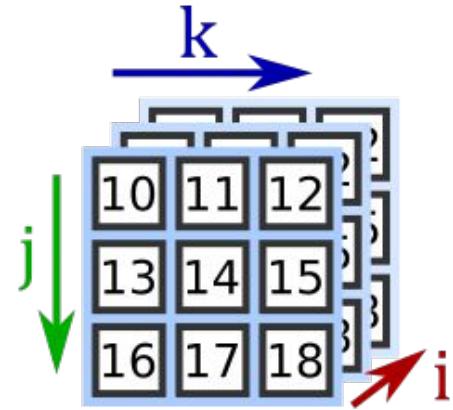
## Indexing 2D:

use comma separated integers representing the dimension and the index of the element.



# NumPy Arrays : Indexing

## Indexing 3D:



## Negative Indexing:

Use negative indexing to access an array from the end.

Positive indexing				
	0	1	2	3
0	1	2	3	4
1	5	6	7	8
2	9	10	11	12

Negative indexing				
	-4	-3	-2	-1
-3	1	2	3	4
-2	5	6	7	8
-1	9	10	11	12

# NumPy Arrays : Slicing

Extracts a subset of data based on given indices from one array and creates a new array with the sliced data.

We pass slice instead of index like this: `[start:end]`

1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	16

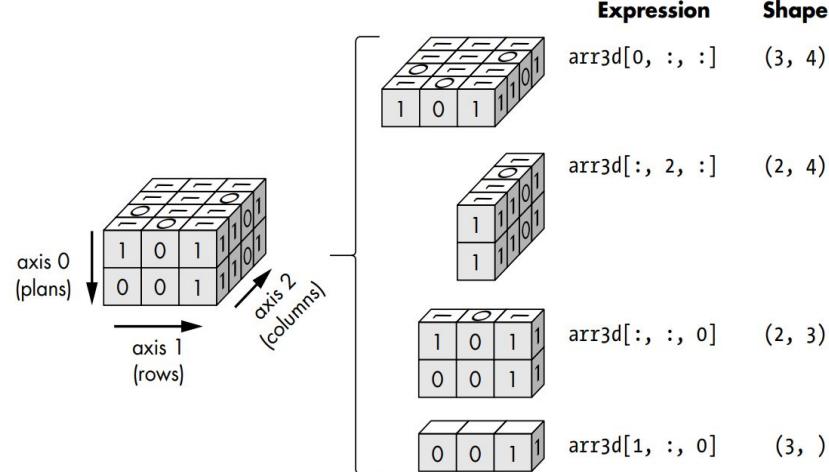
Row one, columns two to four

1	2	3	4
5	6	7	8
9	10	11	12
13	14	15	16

All rows in column one

```
>>> arr[1, 2:4]  
array([7, 8])
```

```
>>> arr[:, 1]  
array([2, 6, 10, 14])
```



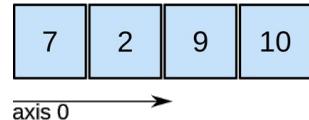
# NumPy Arrays : Shape

Number of elements in each dimension

```
np.shape(input_array)
```

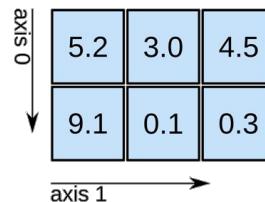
The function name  
↓  
The array from which you want to retrieve the shape  
↑

1D array



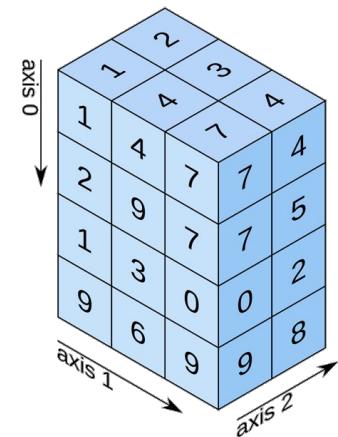
shape: (4,)

2D array



shape: (2, 3)

3D array



shape: (4, 3, 2)

## NumPy Arrays : Reshaping

Changing the shape of an array by adding or removing dimensions or change number of elements in each dimension.

```
name of the new array           name of the original NumPy array           a tuple of values specifying the new shape  
new_array = old_array.reshape((2, 6))  
  
the reshape() method, called with "dot" notation
```

data
1
2
3
4
5
6

data.reshape(2,3)
1 2 3
4 5 6

data.reshape(3,2)
1 2
3 4
5 6

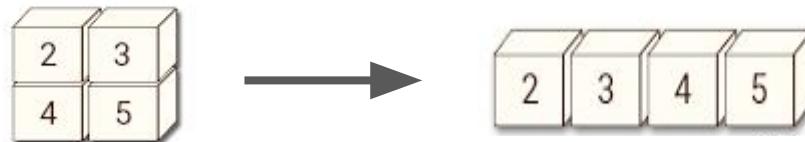
!!!! Only one unknown dimension is allowed & we pass -1 as the value for that dimension.



## NumPy : Flattening Array

converting a multidimensional array into a 1D array. We can use:

1. **np.reshape (-1)**
2. **np.flatten ( )**



# Numpy : Array Iterating

Iterating means going through elements one by one.

## 1. Using Basic For Loops

```
1D array:  
for x in arr:  
    print(x)
```

```
2D array:  
for x in arr:  
    for y in x:  
        print(y)
```

```
3D array:  
for x in arr:  
    for y in x:  
        for z in y:  
            print(z)
```

## 2. Using np.nditer ( )

We can define order of iteration (row-major order 'C' or column-major order 'F')

## 2. Using np.nditer ( )

To access both the index and value during iteration.

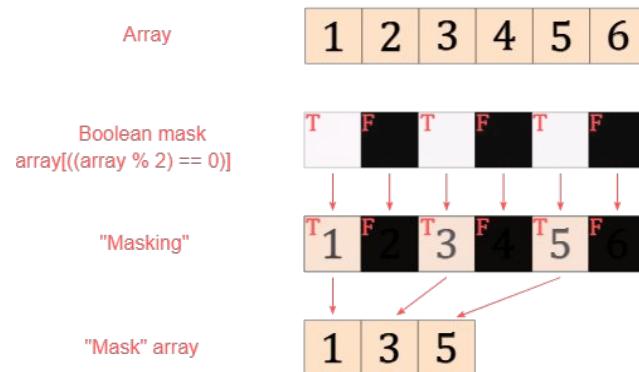


# Numpy : Filtering Arrays

Getting some elements out of an existing array and creating a new array out of them

## 1. Masks & indexing

Using condition for filtering the array & Create a new array with that filtering function



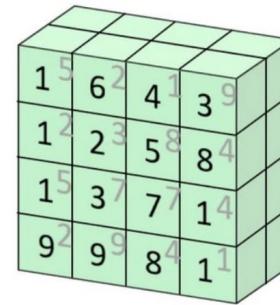
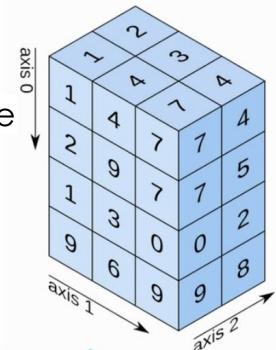
## 2. `np.where` (condition)

search an array for a certain value, and return the indexes that get a match

# PyTorch vs NumPy

## NumPy :

- Array Based (ndarray)
- used in typical machine learning algorithms
- Run on CPUs



## Pytorch :

- n-dimensional array called Tensor
- Run on GPUs
- used in deep learning for **heavy matrix computation.**
- Automatic differentiation for building and training neural networks





## NumPy

`import numpy as np`

```
>>> np.array([7, 2, 9, 10])
```

```
np.array([5.2, 3.0, 4.5], [9.1, 0.1, 0.3])
```

1D array

```
[7 2 9 10]
```

2D array

```
[[5.2, 3.0, 4.5], [9.1, 0.1, 0.3]]
```

3D array

```
[[[1, 2, 3, 4], [1, 4, 7, 5], [1, 9, 7, 5], [1, 3, 0, 2]], [[9, 6, 8, 7], [4, 5, 6, 8], [2, 3, 4, 5], [8, 9, 0, 1]]], [[[1, 2, 3, 4, 5], [1, 2, 3, 4, 5], [1, 2, 3, 4, 5], [1, 2, 3, 4, 5], [1, 2, 3, 4, 5]]]]
```

shape: (4,)

shape: (2, 3)

shape: (4, 3, 2)

## Creating Arrays

```
>>> a = np.array([1,2,3])
>>> b = np.array([(1,5,2,3), (4,5,6)], dtype = float)
>>> c = np.array([(1,[1,5,2,3), ([4,5,6), [(3,2,1), (4,5,6)]], dtype = float)
```

## Initial Placeholders

```
>>> np.zeros((3,4))
>>> np.ones((2,3,4), dtype=np.int16)
>>> d = np.arange(10,25)
>>> np.linspace(0,2,9)
>>> e = np.full((2,2),7)
>>> f = np.eye(2)
>>> np.random.random((2,2))
>>> np.empty((3,2))
```

Create an array of zeros  
Create an array of ones  
Create an array of evenly spaced values (step value)  
Create an array of evenly spaced values (number of samples)  
Create a constant array  
Create a 2x2 identity matrix  
Create an array with random values  
Create an empty array

## I/O

### Saving & Loading On Disk

```
>>> np.savetxt('my_array', a)
>>> np.savetxt('array.hpz', a, b)
>>> np.load('my_array.npy')
```

### Saving & Loading Text Files

```
>>> np.loadtxt("myfile.txt")
>>> np.genfromtxt("my_file.csv", delimiter=',')
>>> np.savetxt("myarray.txt", a, delimiter=" ")
```

## Data Types

```
>>> np.int64
Signed 64-bit integer types
>>> np.float32
Standard double-precision floating point
Complex numbers represented by 128 floats
>>> np.bool_
Boolean type storing TRUE and FALSE values
>>> np.object_
Python object type
>>> np.string_
Fixed-length string type
>>> np.unicode_
Fixed-length unicode type
```

## Inspecting Your Array

<code>&gt;&gt;&gt; a.shape</code>	Array dimensions
<code>&gt;&gt;&gt; len(a)</code>	Length of array
<code>&gt;&gt;&gt; a.ndim</code>	Number of array dimensions
<code>&gt;&gt;&gt; a.size</code>	Number of array elements
<code>&gt;&gt;&gt; a.dtype</code>	Data type of array elements
<code>&gt;&gt;&gt; a.dtype.name</code>	Name of data type
<code>&gt;&gt;&gt; a.astype(int)</code>	Convert an array to a different type

## Asking For Help

```
>>> np.info(np.ndarray.dtype)
```

## Array Mathematics

### Arithmetic Operations

```
>>> g = a - b
array([[-0.5, 0., 0., 1.],
       [-3., -3., -3., 1.]])
>>> np.subtract(a,b)
>>> b + a
array([[ 2.5,  4.,  6.1],
       [ 5.,  7.,  9.1]])
>>> np.add(b,a)
>>> a / b
array([[ 0.66666667,  1. ,
       0.25,  0.4 ,  1. ,
       0.5 ,  1. ]])
>>> np.divide(a,b)
>>> a * b
array([[ 1.5,  4.,  9. ],
       [ 4., 10., 18. ]])
>>> np.multiply(a,b)
>>> np.exp(b)
>>> np.sqrt(b)
>>> np.sin(a)
Print sines of an array
>>> np.cos(b)
Element-wise cosine
>>> np.log(a)
Element-wise natural logarithm
>>> e.dot(f)
Dot product
```

### Subtraction

### Addition

### Division

### Multiplication

### Exponentiation

### Square root

### Print sines of an array

### Element-wise cosine

### Element-wise natural logarithm

### Dot product

## Comparison

```
>>> a == b
array([[ True,  True,  True],
       [False, False, False]], dtype=bool)
>>> a < 2
array([[ True, False, False], dtype=bool)
>>> np.array_equal(a, b)
```

### Element-wise comparison

### Element-wise comparison

### Array-wise comparison

## Aggregate Functions

```
>>> a.sum()
>>> a.min()
>>> b.max(axis=0)
>>> b.cumsum(axis=1)
>>> a.mean()
>>> b.median()
>>> a.correlcoef()
>>> np.std(b)
```

### Array-wise sum

### Array-wise minimum value

### Maximum value of an array row

### Cumulative sum of the elements

### Mean

### Median

### Correlation coefficient

### Standard deviation

## Copying Arrays

```
>>> h = a.view()
Create a view of the array with the same data
>>> np.copy(a)
Create a copy of the array
>>> h = np.copy(a)
Create a deep copy of the array
```

## Sorting Arrays

```
>>> a.sort()
Sort an array
>>> c.sort(axis=0)
Sort the elements of an array's axis
```

## Subsetting, Slicing, Indexing

### Also see Lists

### Subsetting

```
>>> a[2]
3
>>> b[1,2]
6.0
>>> a[0:2]
array([1, 2, 3])
>>> b[0:2,1]
array([ 2.,  5.])
>>> b[:1]
array([1.5, 2., 3.])
>>> c[1,:,:]
array([[ 3.,  2.,  1.],
       [ 4.,  5.,  6.]])
```

Select the element at the 2nd index  
Select the element at row 1 column 2 (equivalent to `b[1][2]`)  
Select items at index 0 and 1  
Select items at rows 0 and 1 in column 1

```
>>> a[0:2]
array([1, 2, 3])
>>> b[0:2,1]
array([ 2.,  5.])
>>> b[:1]
array([1.5, 2., 3.])
>>> c[1,:,:]
array([[ 3.,  2.,  1.],
       [ 4.,  5.,  6.]])
```

Reversed array `a`  
Select elements from `a` less than 2

```
>>> b[1, 0, 1, 0]
array([ 1.,  2.,  6., 1.5])
>>> b[1, 0, 1, 0][1][0,2,0]
array([ 1.,  2.,  6., 1.5])
array([ 4.,  5.,  6., 4.5],
      [ 4.,  5.,  6., 4.5],
      [ 4.,  5.,  6., 4.5],
      [ 4.,  5.,  6., 4.5])
```

Select elements `(1,0), (0,1), (1,2) and (0,0)`  
Select a subset of the matrix's rows and columns

## Array Manipulation

### Transposing Array

```
>>> i = np.transpose(b)
>>> i.T
```

Permute array dimensions  
Permute array dimensions

### Changing Array Shape

```
>>> b.ravel()
>>> g.reshape(3,-2)
```

Flatten the array  
Reshape, but don't change data

### Adding/Removing Elements

```
>>> h.resize((2,6))
>>> np.append(h,g)
>>> np.insert(a, 1, 5)
>>> np.delete(a, [1])
```

Return a new array with shape (2,6)  
Append items to an array  
Insert items in an array  
Delete items from an array

### Combining Arrays

```
>>> np.concatenate((a,d),axis=0)
array([[ 1.,  2.,  3., 10., 15., 20.])
>>> np.vstack((a,b))
array([[ 1.,  2.,  3., 10., 15., 20.],
       [ 1.,  2.,  3., 10., 15., 20.]])
>>> np.r_[e,f]
>>> np.hstack((e,f))
array([[ 7.,  7.,  1.,  0.,  1.],
       [ 7.,  7.,  0.,  1.,  1.]])
>>> np.column_stack((a,d))
array([[ 1.,  10.],
       [ 2.,  15.],
       [ 3.,  20.]])
>>> np.c_[a,d]
```

Concatenate arrays  
Stack arrays vertically (row-wise)  
Stack arrays vertically (row-wise)  
Stack arrays horizontally (column-wise)  
Create stacked column-wise arrays  
Create stacked column-wise arrays

### Splitting Arrays

```
>>> np.hsplit(a,(3))
[array([1],array([2]),array([3]))]
>>> np.vsplit(c,2)
[array([[ 1.5,  2.,  1.], [ 4.,  5.,  6.]]),
 array([[ 3.,  2.,  1.], [ 4.,  5.,  6.]]])
```

Split the array horizontally at the 3rd index  
Split the array vertically at the 2nd index

# Pandas :

## Python Data Analysis

1. What is pandas? why?
2. Pandas series & DataFrame
3. Loading and viewing Data
4. Cleaning DataFrames
5. Correlation



Pandas



# Pandas

"Panel Data", and "Python Data Analysis" is a Python library used for working with data sets.

## Why Use Pandas?

1. Including functions for analyzing, cleaning, exploring, and manipulating data.
2. Allow to analyze big data and make conclusions based on statistical theories.
3. clean messy data sets, and make them readable and relevant.

### Install

```
pip install pandas
```

### Import

```
Import pandas as pd
```



# Panda Series

The **Series** object represents one-dimensional data structures in Pandas.

A series consists of two components.

- One-dimensional data (Values)
- Index

## Series

Index Value

Index	Value

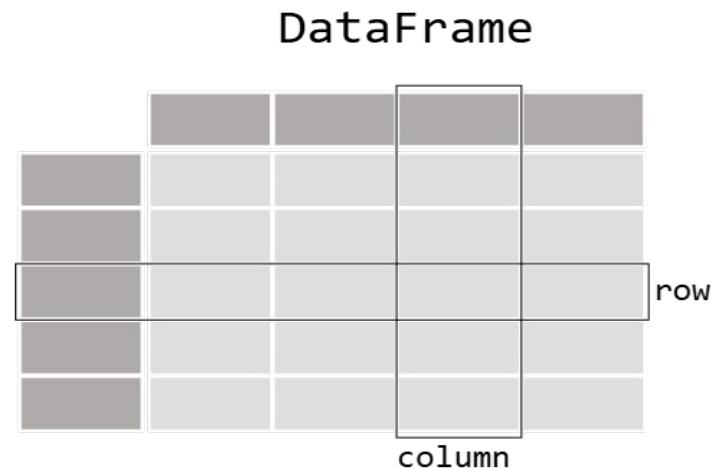
# DataFrames

Datasets in Pandas are multi-dimensional tables called **DataFrames**.

Each **Series** is a column in Data Frames.

## Creating DataFrames

```
data = {'col1': [1, 2], 'col2': [3, 4]}\ndf = pd.DataFrame(data=data)
```



# Load Files Into a DataFrame

```
df = pd.read_csv('data.csv')    #To read .CSV files
```

```
df = pd.read_json('data.json')  #To read .json Files
```

Pandas by default will only return the first 5 rows, and the last 5 rows.

To print the entire DataFrame:

```
pd.options.display.max_rows
```

```
df.to_string()
```

# Viewing Data

1. **.head( )**: returns the headers and a specified number of rows, starting from the top.
2. **.tail( )**: returns the headers and a specified number of rows, starting from the bottom.
3. **.shape** : returns a tuple containing the shape of the DataFrame. (No. rows, No. columns )
4. **.describe( )**: summary statistics for numerical columns, like mean and median.
5. **.info ( )**: Information about the dataset
6. **.isnull.sum( )**: to count the number of nulls in each column.
7. **.isnull.sum.sum ( )**: to count the number of nulls in DataFrame

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 169 entries, 0 to 168
Data columns (total 4 columns):
 #   Column      Non-Null Count  Dtype  
---  --          --          --      
 0   Duration    169 non-null    int64  
 1   Pulse       169 non-null    int64  
 2   Maxpulse    169 non-null    int64  
 3   Calories    164 non-null    float64 
dtypes: float64(1), int64(3)
memory usage: 5.4 KB
None
```

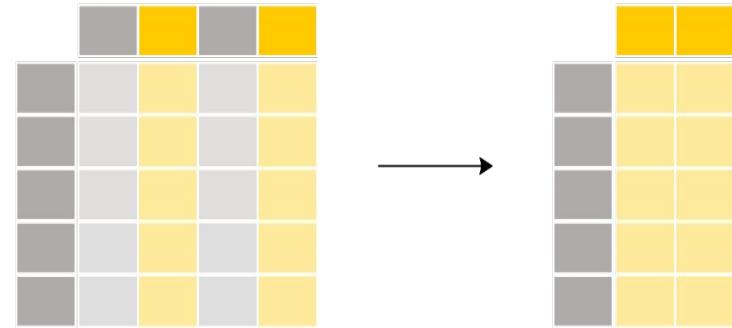
# Subsetting Column

Subsetting the column:

```
df ["my_column1"]
```

Subsetting **multiple** column:

```
df [["my_column1","my_column1"]]
```



# Subsetting Rows

- **Index based** : Row/s can be fetched by passing in a boolean series with one/multiple **True**

```
df[df.index== value]
```

```
df[df.index.isin(range(start_index,last_index))]
```

- **Conditional Expression:** To select rows based on a conditional expression, use a condition inside the selection brackets **[ ]**.

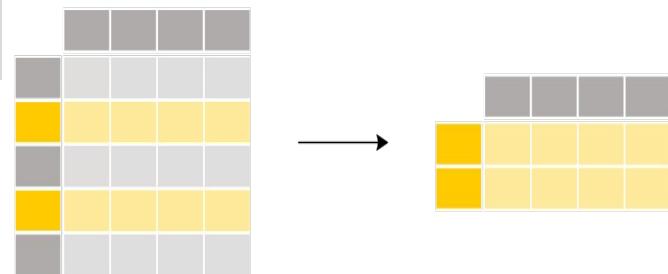
```
df[df [“my_column1”] > condition ]
```

- **.isin( ) method:** returns a **True** for each row the values are in the provided list.

```
df[df [“my_column1”].isin([2,3])]
```

- **.notna( ) method :** returns a **True** for each row the values are not a **Null** value.

```
df[df [“my_column1”].notna()]
```



# Subsetting Rows & Columns

- **.iloc[ ] method:** when using the positions in the table.

```
df.iloc[start_row:end_row,start_column:end_column]
```

- **.loc[ ] method:** Select specific rows and/or columns using loc when using the row and column names.

```
df.loc[condition for selecting rows, column_name]
```



# Cleaning DataFrame

Data cleaning means fixing bad data in your data set.

Bad data could be:

- Missing values (Empty Cells)
- Wrong data
- Duplicates
- Column Renaming

# Missing values

- **.dropna( ) to remove Rows:** removing rows with Nan values.

```
new_df = df.dropna( )
```

dropna( ) returns a *new* DataFrame, and will not change the original

To change the original DataFrame, use the **inplace = True** argument:

```
df.dropna(inplace= True )
```

To remove the columns with one or more NaN values, use the **axis = 1** argument:

```
df.dropna(inplace= True, axis = 1 )
```

# Missing Values

- **.fillna( ) to replace values:** replace empty cells with a value.

1. Fill all nan values with a certain value

```
df.fillna(value, inplace=True )
```

2. Specific column with a certain value

```
df.fillna({“column_name”: value}, inplace=True )
```

3. Mean, Median or Mode value of the specified column

```
x = df[“column_name”].mean()
```

```
df.fillna(x, inplace=True )
```

# Duplicates

- **.duplicated method:** returns a True Boolean values for every row that is duplicated.

```
df.duplicated ()
```

- **.drop\_duplicates () :** To remove duplicates.

```
df.drop_duplicates (inplace = True)
```

# Wrong Values and Typos

It does not have to be "empty cells" or "wrong format", it can just be wrong, like if someone registered "199" instead of "1.99".

- **Replacing values:** set boundaries for values and replace it with a certain value if a cell falls out of boundary.

```
for x in df.index:  
    if df.loc[x, "Duration"] > 120:  
        df.loc[x, "Duration"] = 120
```

- **Removing Rows:** remove the rows that contains wrong data and not include in the analysis.

```
for x in df.index:  
    if df.loc[x, "Duration"] > 120:  
        df.drop(x, inplace = True)
```

# Column Renaming

**.rename()** : you can use columns as an argument to rename specific columns.

```
df.rename(columns={"old_column1": "new_renamed_column"},inplace =True)
```

# Data Correlation

**.corr( ) Method:** Compute pairwise correlation of columns, excluding NA/null values.

```
df.corr()
```

## Method of correlation:

- **pearson** : standard correlation coefficient

*The linear relationship between two variables*

- **kendall** : Kendall Tau correlation coefficient

*Non-parametric test procedure when the data is not normally distributed and the two variables only have an ordinal scale level.*

- **spearman** : Spearman rank correlation

*The non-parametric counterpart of Pearson's correlation.*

## Data Wrangling

with pandas Cheat Sheet  
<http://pandas.pydata.org>

Pandas API Reference Pandas User Guide

## Creating DataFrames

	a	b	c
1	4	7	10
2	5	8	11
3	6	9	12

```
df = pd.DataFrame([{"a": [4, 5, 6], "b": [7, 8, 9], "c": [10, 11, 12]}, index=[1, 2, 3])
```

Specify values for each column.

```
df = pd.DataFrame([{"a": [4, 7, 10], [5, 8, 11], [6, 9, 12]}, index=[1, 2, 3], columns=['a', 'b', 'c'])
```

Specify values for each row.

	a	b	c
d	1	4	7
e	2	5	8
f	3	6	9
g	4	7	10
h	5	8	11
i	6	9	12

```
df = pd.DataFrame([{"a": [4, 5, 6], "b": [7, 8, 9], "c": [10, 11, 12]}, index = pd.MultiIndex.from_tuples([(4, 1), (4, 2), (4, 3)], names=['n', 'v']))
```

Create DataFrame with a MultiIndex

## Method Chaining

Most pandas methods return a DataFrame so that another pandas method can be applied to the result. This improves readability of code.

```
df = (pd.melt(df)
      .rename(columns={'variable': 'var',
                       'value': 'val'},
      .query('val > 200'))
```

)

**Tidy Data – A foundation for wrangling in pandas**

In a tidy data set:

- Each variable is saved in its own column
- Each observation is saved in its own row

**Reshaping Data – Change layout, sorting, reindexing, renaming**

**Subset Observations - rows**

**Subset Variables - columns**

**Subset - rows and columns**

**Using query**

query() allows Boolean expressions for filtering rows.

```
df.query("Length > 7")
df.query("Length > 7 and Width < 8")
df.query("Name.str.startswith('abc')", engine="python")
```

**Logic in Python (and pandas)**

<	Less than	!=	Not equal to
>	Greater than	df.column.isin(values)	Group membership
==	Equals	pd.isnull(obj)	Is NaN
<=	Less or equal	pd.notnull(obj)	Is not NaN
>=	Greater or equal	~(df...&#38;)   df.all()	Logical and, or, not, xor, any, all

**regex (Regular Expressions) Examples**

```
'\.' Matches strings containing a period .
'^Length$' Matches string ending with word 'length'
'^Sepal' Matches string beginning with the word 'Sepal'
'^[a-z]*$' Matches string beginning with 'a' and ending with 1,2,3,4,5
'^(?i)Species.*' Matches strings except the string 'Species'
```

Cheatheet for pandas (<http://pandas.pydata.org>) originally written by Luis M. Rodriguez, inspired by RStudio Data Wrangling Cheatheet

**Summarize Data**

**Handling Missing Data**

**Make New Columns**

**Group Data**

The examples below can also be applied to groups. In this case, the function is applied on a per-group basis, and the returned vectors are of the length of the original data frame.

**Windows**

**Plotting**

**Combine Data Sets**

**Standard Joins**

**Join Operations**

**Filtering Joins**

**Set-like Operations**

**Cheatheet for pandas (<http://pandas.pydata.org>) originally written by Luis M. Rodriguez, inspired by RStudio Data Wrangling Cheatheet**



# Matplotlib:

## Matlab, Plot, and Library

1. What is Matplotlib? why?
2. Axes interface
3. Pyplot interface
4. Creating subplots



# What is Matplotlib?

Matplotlib is a graph plotting library in python that serves as a visualization utility.

Matplotlib has two interfaces:

## 1. Axes interface (object-based, explicit)

create a **Figure** and one or more **Axes** objects, then *explicitly* use methods on these objects to add data, configure limits, set labels etc.

## 2. pyplot interface (function-based, implicit)

consists of functions in the **pyplot** module. Figure and Axes are manipulated through these functions and are only *implicitly* present in the background.

# Axes Interface

Install :

```
pip install matplotlib
```

Axes allow placement of plots at any location in the figure. A given figure can contain many axes.

API:

- **Figure**: for figure-level method
- **axes**: add data, limits, labels etc.
- **subplots**: create Figure and Axes

Import:

```
import matplotlib
```

```
fig= plt.figure()  
ax1 =fig.add_subplot(1,1,1)  
ax.plot()  
plt.show()
```

# .axes cheatsheet

- **plot(x, y)** : Generate y vs x graph
- **set\_xlabel()** : Label for the X-axis
- **set\_ylabel()** : Label for the Y-axis
- **set\_title()** : Title of the plot
- **legend()** : Generate legend for the graph
- **hist()** : Generate histogram plot
- **scatter()**: Generate scatter plot

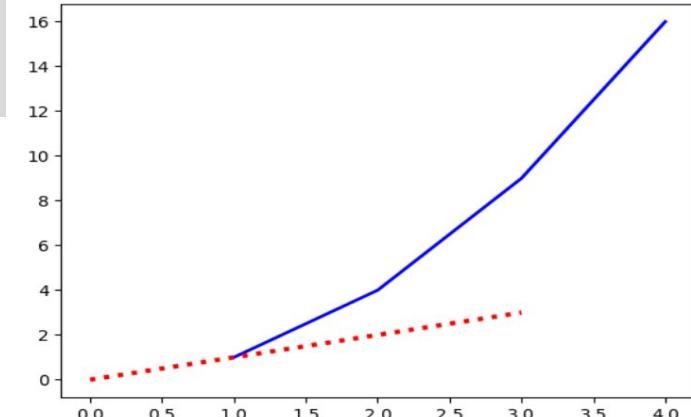
# Pyplot Interface

```
import matplotlib.pyplot as plt
```

**plt.plot() method** : create a line plot where the 1st argument is the **x** variable and the 2nd argument is the **y** variable.

```
plt.plot([1, 2, 3, 4], [1, 4, 9, 16],ls= “-”,color=“Blue”,lw=2)  
plt.plot(np.arange(4),ls= “:”,color=“red”,lw=3)  
plt.savefig(“myfigure”)  
plt.show()
```

**Linestyle or ls** : string argument  
**Color or c** : string argument  
**Linewidth or lw** : float argument  
**marker** : string argument to mark points



# .plt cheatsheet

Add <b>title</b> to figure :	<code>plt.title()</code>
Add <b>label</b> to <b>x_axis</b> :	<code>plt.xlabel()</code>
Add <b>label</b> to <b>y_axis</b> :	<code>plt.ylabel()</code>
Add <b>Text</b> to the figure :	<code>plt.text ()</code>
Define <b>axis limits</b> :	<code>plt.axis() or plt.xlim() &amp; plt.ylim()</code>
Add <b>grid</b> :	<code>plt.grid(True)</code>
<b>Annotate</b> figure :	<code>plt.annotate()</code>
<b>Axis scale</b> :	
<i>Logarithmic</i>	<code>plt.yscale("log")</code>
<i>Linear</i>	<code>plt.yscale("linear")</code>
<i>Symmetric log</i>	<code>plt.yscale("symlog")</code>
<i>Logit</i>	<code>plt.yscale("logit")</code>
Add <b>legend</b> :	<code>plt.legend( )</code>

# Creating subplots

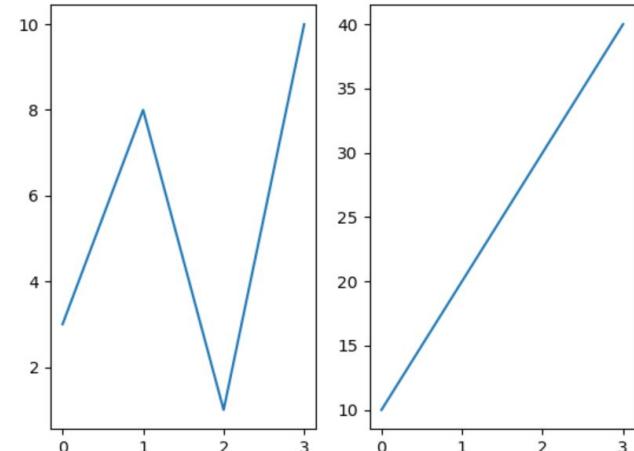
With the **`plt.subplot()`** function we can draw multiple plots in one figure.

3 arguments that describes the layout of the figure :

- **1st** argument as the number of **rows**
- **2nd** argument as the number of **columns**
- **3rd** argument as **index of current plot**

```
plt.subplots(1, 2, 1)
```

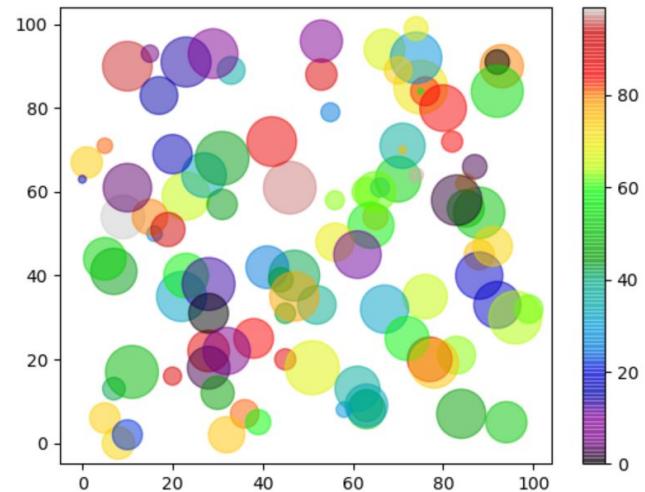
*#the figure has 1 row, 2 columns, and this plot is the first plot.*



# `plt.scatter`

`scatter()` function to draw a scatter plot as one dot for each observation. It needs two arrays of the same length, one for the values of the x-axis, and one for values on the y-axis.

- multiple scatter plot in one figure by calling before `plt.show()`
- define the color for each point by setting **c argument**
- define the size for each point by setting **s argument**
- Define transparency of dots by setting **alpha argument**
- Using a colormap by setting the **cmp argument** and include in the plot by calling `plt.colorbar()`



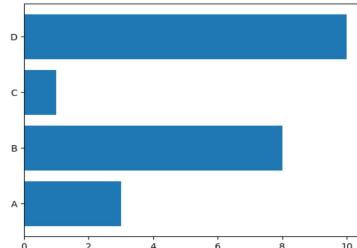
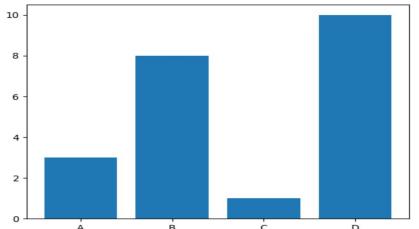
## plt.bar

the **bar()** function to draw bar graphs for categorical data.

1. **X-axis** as the 1st arguments : **categories**
2. **Y-axis** as the second categories: **values**

use the **barh()** function for horizontal bars.

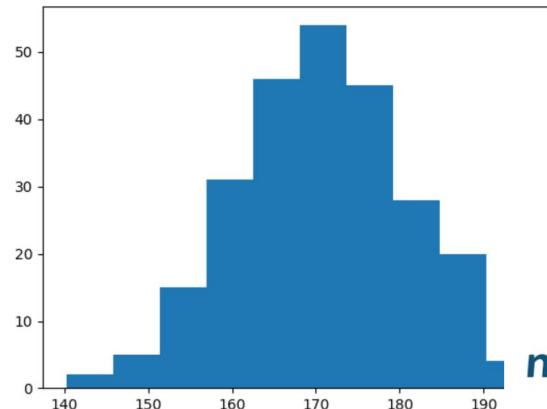
- **Color keyword** to define colors as strings or Hexadecimal color values
- For bar() : **width** to set width of the bars
- For barh(): **height** to set height of the bars



## plt.hist

The **hist()** create a histogram graph showing frequency distributions.

It is a graph showing the number of observations within each given interval.



matplotlib



Basic plots

`plot([X], Y, [fmt], ...)``scatter(X, Y, ...)``bar[h](x, height, ...)``imshow(Z, ...)``contour(f)([X], [Y], Z, ...)``colormesh([X], [Y], Z, ...)``quiver([X], [Y], U, V, ...)``pie(X, ...)``text(x, y, text, ...)``fill[_between][x](...)`

Scales

`ax.set_[x|yscale](scale, ...)``symlog``logit`

Projections

`subplot(..., projection=p)``p='polar'``p=ccrs.Orthographic()`

Lines

`linestyle or ls``capstyle or dash_capstyle`

Markers

`marker``markerface``markeredge``markeredgecolor``markeredgewidth``markerfacecolor``markerfacecoloralt``markerhatch``markeroffset``markerpath``markerpath_effects``markerstyle`

Advanced plots

`step(X, Y, [fmt], ...)``boxplot(X, ...)``errorbar(X, yerr, yerr, ...)`

Histograms

`hist(..., bins, ...)``violinplot(D, ...)``barbs([X], [Y], U, V, ...)``eventplot(positions, ...)``hexbin(X, Y, C, ...)`

Tick locators

`from matplotlib import ticker``ax.[x|y].set_[minor|major].locator(locator)``ticker.IndexLocator()``ticker.MultipleLocator(s,5)``ticker.FixedLocator([0,1,5])``ticker.LinearLocator(numticks=3)``ticker.MaxNLocator(n=4)``ticker.LogLocator(base=10, numticks=15)``ticker.AutoLocator()``ticker.IndexLocator(base=0.5, offset=0.25)``ticker.MaxNLocator(n=4)``ticker.LogLocator(base=10, numticks=15)``ticker.AutoLocator()``ticker.IndexLocator(base=0.5, offset=0.25)``Event handling``fig, ax = plt.subplots()``def on_click(event):` `print(event)` `fig.canvas.mpl_connect('button_press_event', on_click)` `1. Know your audience` `2. Identify your message` `3. Adapt the figure` `4. Captions are not optional` `5. Do not trust the defaults` `6. Use color effectively` `7. Do not mislead the reader` `8. Avoid "chartjunk"` `9. Message trumps beauty` `10. Get the right tool` `11. Know your audience`

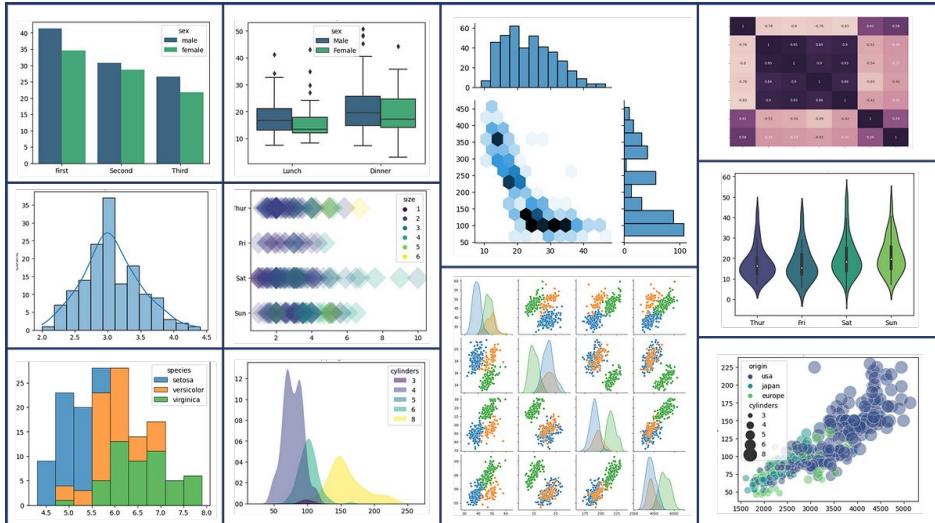
# Seaborn:

## Statistical data visualization

1. What is Seaborn
2. Seaborn vs. Matplotlib
3. Seaborn functions (relashional plots , Categorical Plot, Distribution plots)



# seaborn



# Seaborn

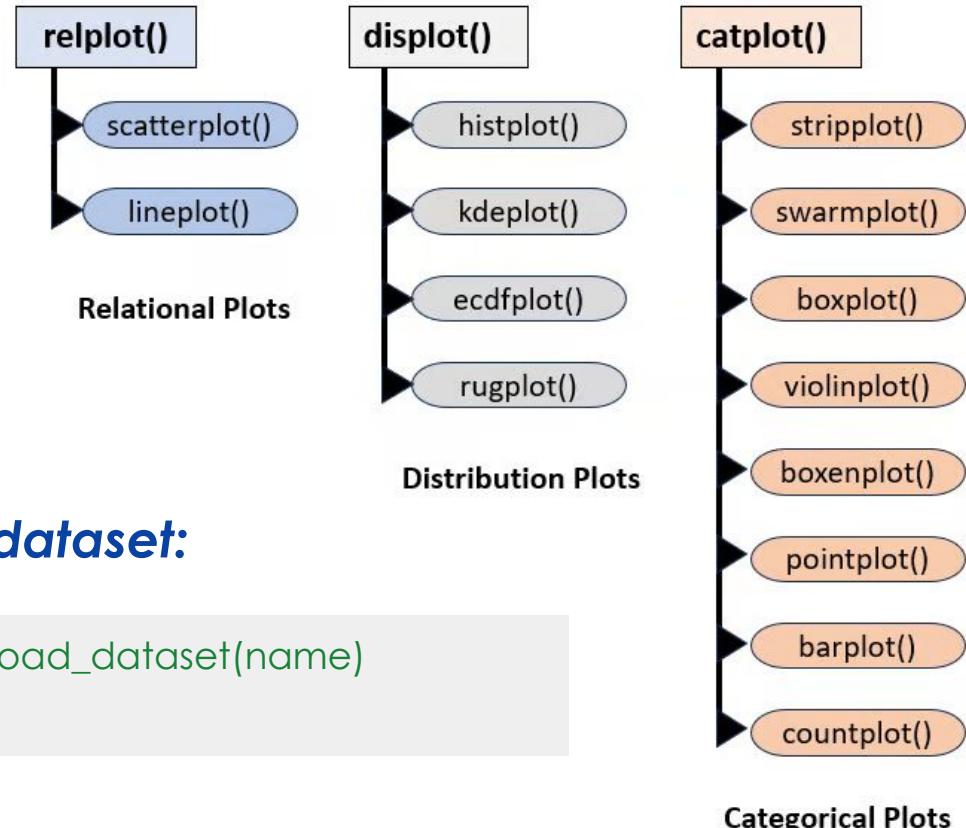
Python data visualization library  
based on matplotlib.

- Easy to use
- Works well with **pandas**
- Built on top of **matplotlib**

## Import :

```
Import seaborn as sns  
Import pandas as pd
```

## Seaborn Function Classifications



# Seaborn vs matplotlib

Aspect	Matplotlib	Seaborn
Type	Low-level plotting library	High-level interface for statistical graphics
Flexibility	Highly flexible, create almost any plot	Simplified interface for common statistical plots
Ease of Use	Steeper learning curve, more verbose code	Easier to use, minimal code
Data Handling	General data structures	Designed to work with Pandas DataFrames
Statistical Features	No built-in statistical functions	Includes built-in statistical functions
Default Styles	Limited default styles and color palettes	Offers a range of default styles and optimized color palettes
Customization	Requires manual customization for visual appeal	Visually appealing by default
Best Suited For	Highly customizable plots for presentations and publications	Statistical graphics and exploratory data analysis
Integration	Standalone library	Built on top of Matplotlib; can be used together

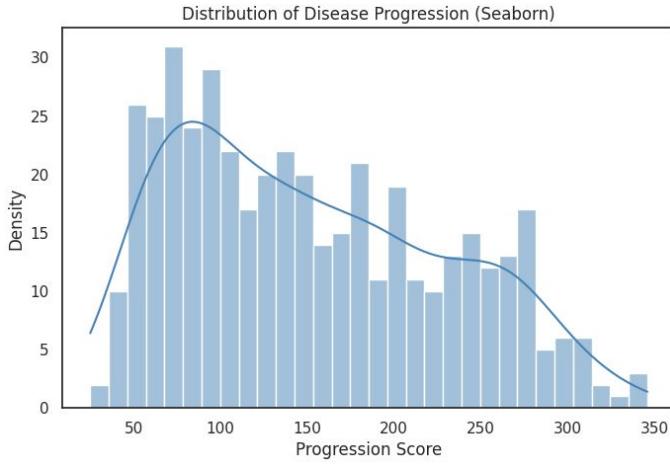
# Seaborn vs matplotlib

```
import seaborn as sns
import pandas as pd
from sklearn.datasets import load_diabetes

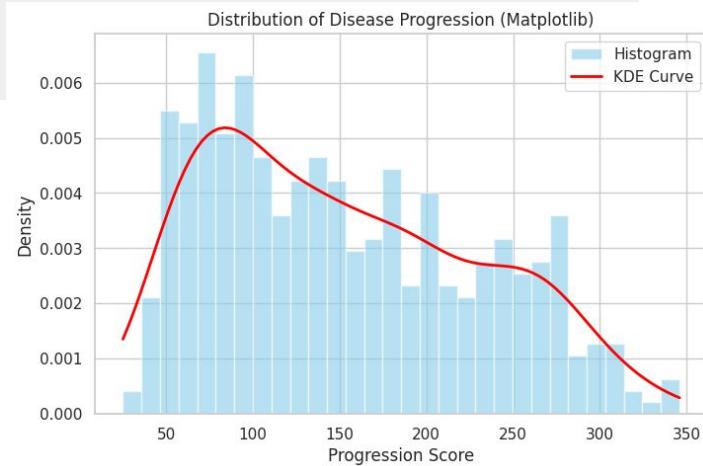
# Load data
diabetes = load_diabetes()
df = pd.DataFrame(data=diabetes.data, columns=diabetes.feature_names)
df['progression'] = diabetes.target

# Plot
sns.set(style="whitegrid")
plt.figure(figsize=(8, 5))
sns.histplot(df['progression'], kde=True, bins=30, color='steelblue')

plt.title("Distribution of Disease Progression (Seaborn)")
plt.xlabel("Progression Score")
plt.ylabel("Density")
plt.show()
```



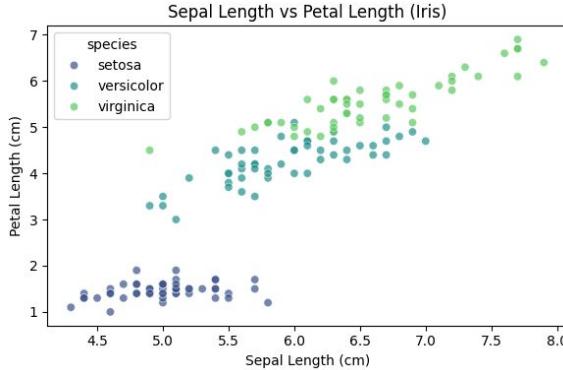
```
import matplotlib.pyplot as plt
from sklearn.datasets import load_diabetes
import numpy as np
from scipy.stats import gaussian_kde
diabetes = load_diabetes() # Load data
y = diabetes.target
kde = gaussian_kde(y) # KDE estimation
x_vals = np.linspace(min(y), max(y), 100)
# Plot
plt.figure(figsize=(8, 5))
plt.hist(y, bins=30, density=True, alpha=0.6, color='skyblue',
label='Histogram')
plt.plot(x_vals, kde(x_vals), color='red', linewidth=2, label='KDE
Curve')
plt.title("Distribution of Disease Progression (Matplotlib)")
plt.xlabel("Progression Score")
plt.ylabel("Density")
plt.legend()
plt.grid(True)
plt.show()
```



# Relational Plot (relplot)

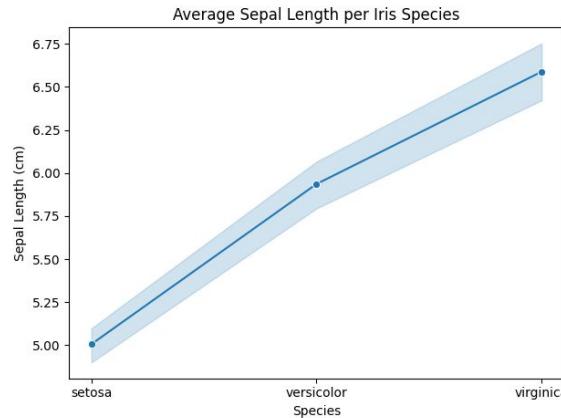
## 1. Scatterplot

Shows the relationship between two numeric variables. Helps you see correlation, clusters, outliers, or trends.



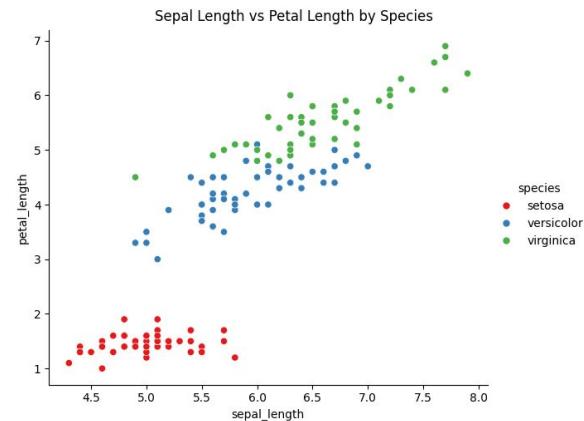
## 2. LinePlot

Displays a continuous trend over time or order.



## 3. relplot

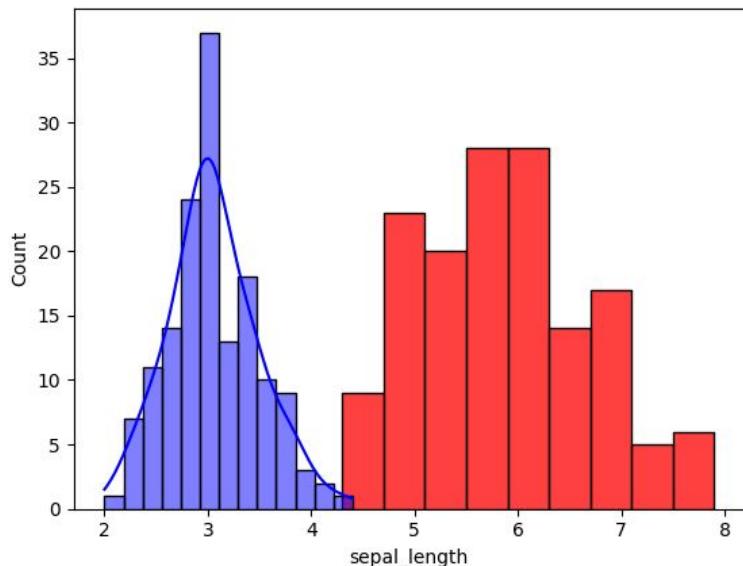
Show the relationship between two continuous variables.



# Distribution Plot (displot)

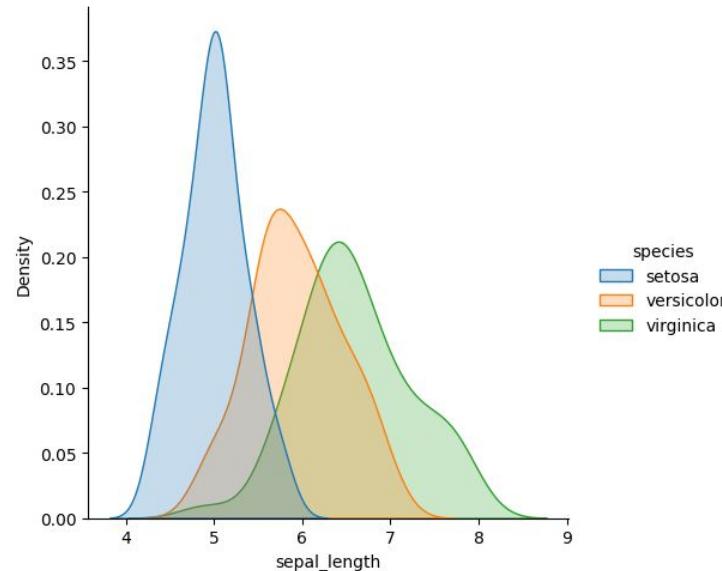
## 1. histplot

- Histograms visualize the distribution of a continuous variable.



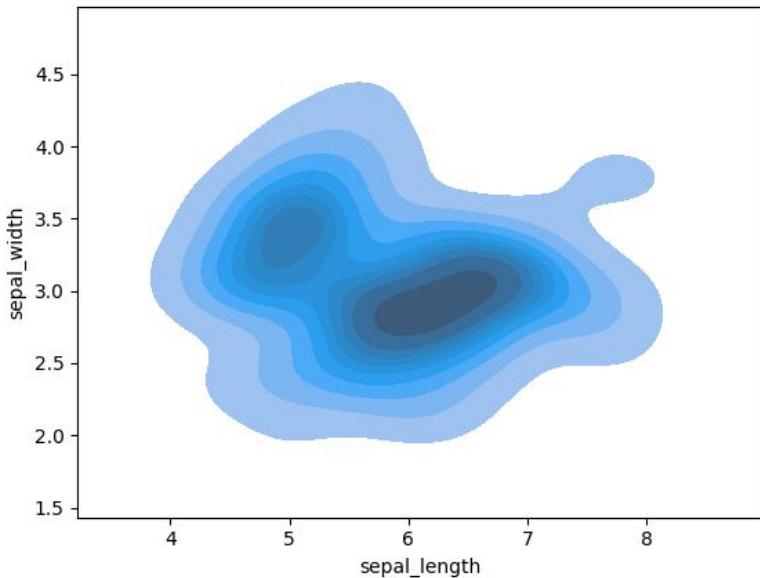
## 2. Displot

- Displays a continuous trend over time or order.



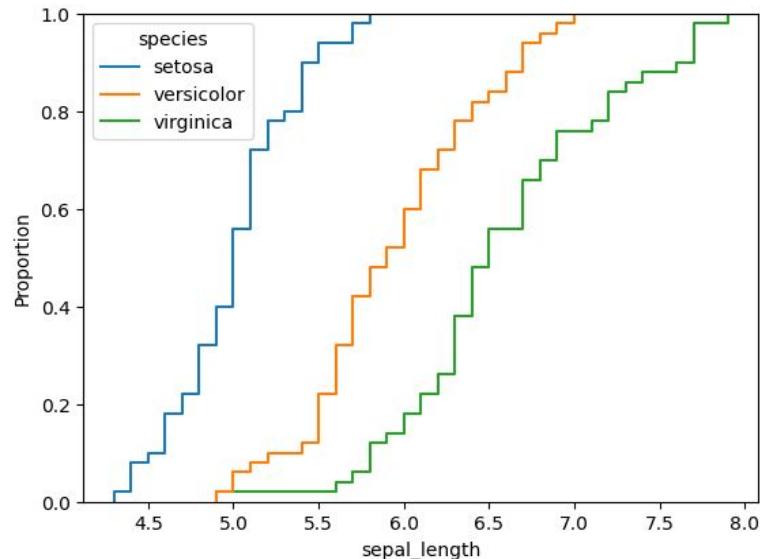
# Distribution Plot (displot)

## 3. KDE Plot



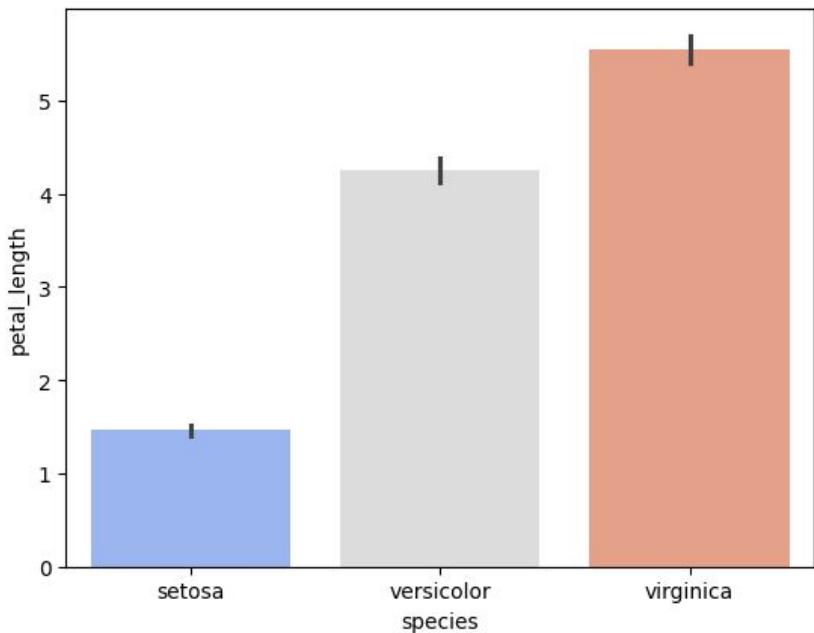
## 4. ECDF Plot

➤ Cumulative distribution



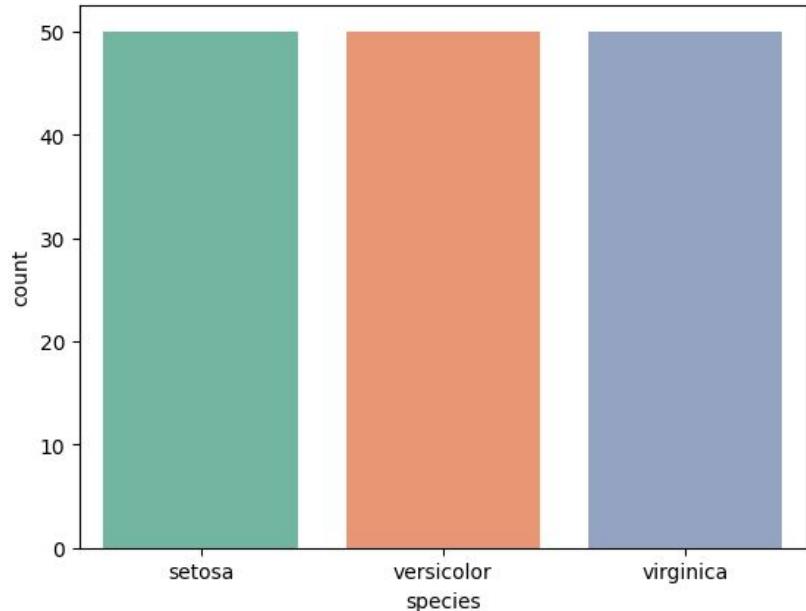
# Categorical Plot (catplot)

## 1. Barplot



## 2. count plot

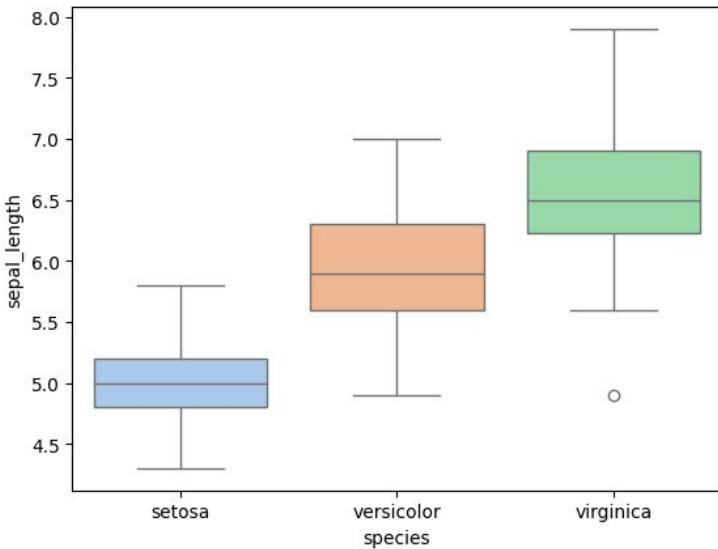
Count plots take in a categorical list and return bars that represent the number of list entries per category.



# Categorical Plot (catplot)

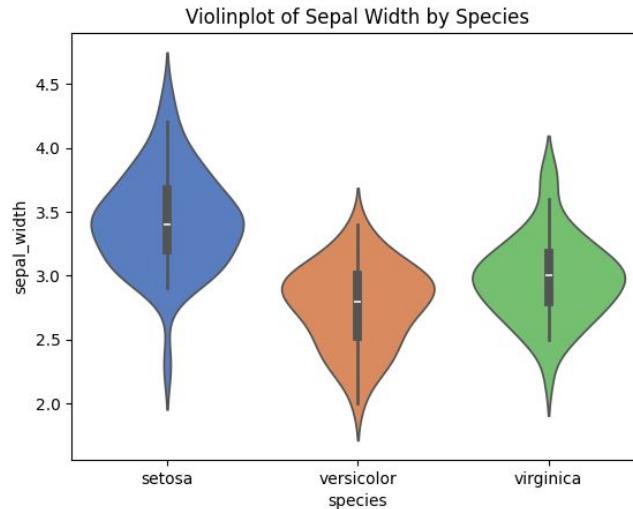
## 3. Box plot

commonly used to compare the distribution of one or more variables across different categories.



## 4. Violin plot

- combines aspects of both box plots and density plots.
- displays a density estimate of the data, smoothed by kernel density estimator, along with the interquartile range (IQR) and median in a box plot-like form.



# matrix plots

**Correlation** : "How strongly are two variables connected?"

- **Detect multicollinearity**

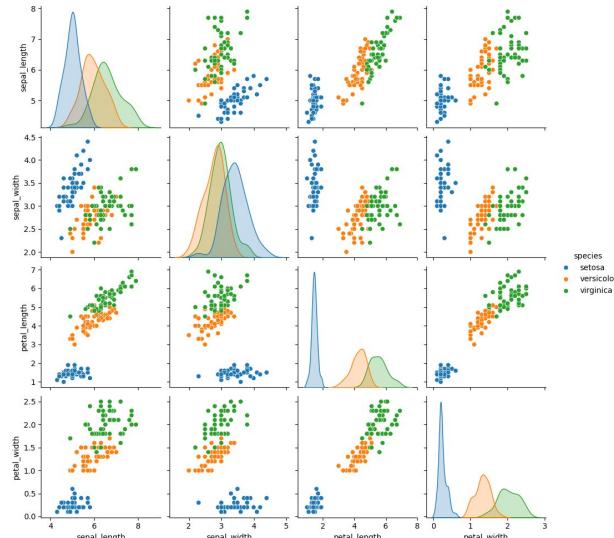
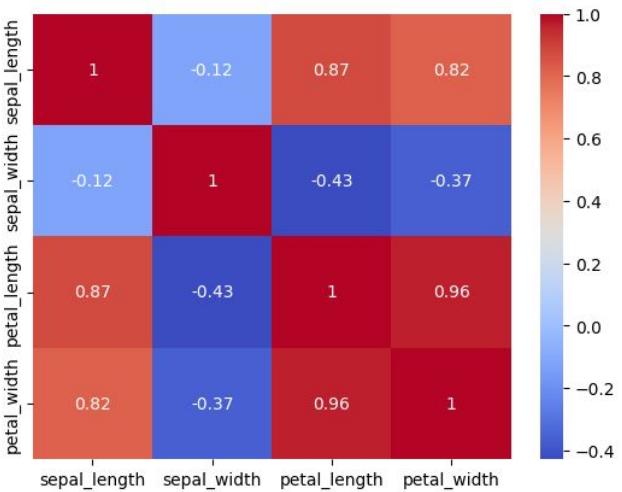
Useful for identifying pairs of features with high correlation, which can negatively affect certain models (e.g., linear regression).

- **Feature relevance**

Helps highlight variables that are strongly correlated with the target, assisting in feature selection.

- **Exploratory overview**

Provides a compact visual summary of relationships among variables, guiding deeper analysis and model design.





COFFEE BREAK

# Scikit Learn:

**S**cientific *toolkit* for Machine **L**earning

What is Scikit-learn?

Overview of the Scikit-learn API

Loading Example Datasets and  
preprocessing

Hands-on Practical



# Scikit-Learn

- Built on **NumPy**, **SciPy**, and **matplotlib**
- Open Source , Provides extensive documentation on its website <https://scikit-learn.org>

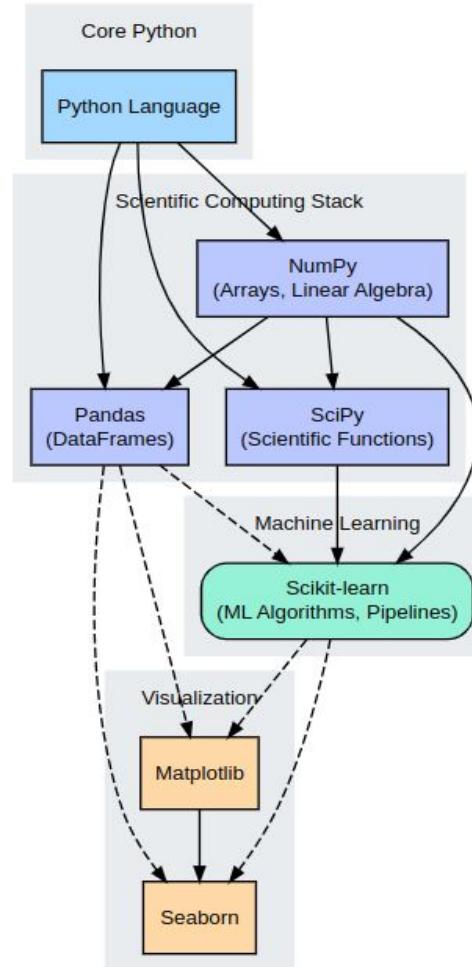
## Scikit-Learn datasets

- Iris plants dataset
- Diabetes dataset

## Installation

```
pip install scikit-learn
```

```
Import sklearn
```



# Scikit-Learn

- Simple and efficient tools for predictive data analysis

data preprocessing

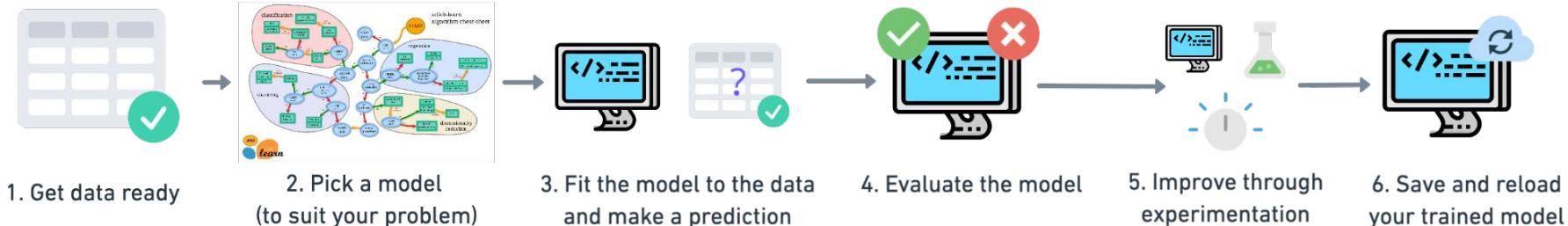
supervised and unsupervised learning (clustering, regression & classification)

model fitting

model selection

model evaluation

## A Scikit-Learn Workflow



# Scikit-Learn

- **Clean and Consistent API**

**The Estimator: The Base Object:** with a `fit(X, y)` method that learns from data and stores results in attributes.

**The Transformer:** Learns from data using `fit(X, y)` and modifies it with `transform(X)` or combined `fit_transform(X, y)`.

**The Predictor:** Fits data with `fit(X, y)`, predicts new results using `predict(X)`, and evaluates performance via `score(X, y)`

# Data Representation in Scikit-learn

## Features Matrix (X)

The input data, often called features, samples, or instances, is typically represented as a two-dimensional array-like structure.

**Shape:** The expected shape of X is `(n_samples, n_features)`.

## Target Variable (y)

- Shape:** The target variable is typically represented as a one-dimensional array (a vector). Its expected shape is `(n_samples,)`.

Component	Convention	Typical Structure	Shape	Data Type (Common)
Features	X	2D Array/Dat aFrame	<code>(n_samples , n_features)</code>	<code>float64</code>
Target Variable	y	1D Array/Serie s	<code>(n_samples ,)</code>	<code>float64</code> <code>(Regression) int or object</code> <code>(Classification)</code>

# Scikit-Learn

Essential step in any machine learning project to prepare data ready for modeling including:

## Step 1: Data Cleaning

- Removing duplicates
- Correcting inconsistent formats
- Handling missing values

## Step 2: Data splitting

```
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,random_state=42)
```

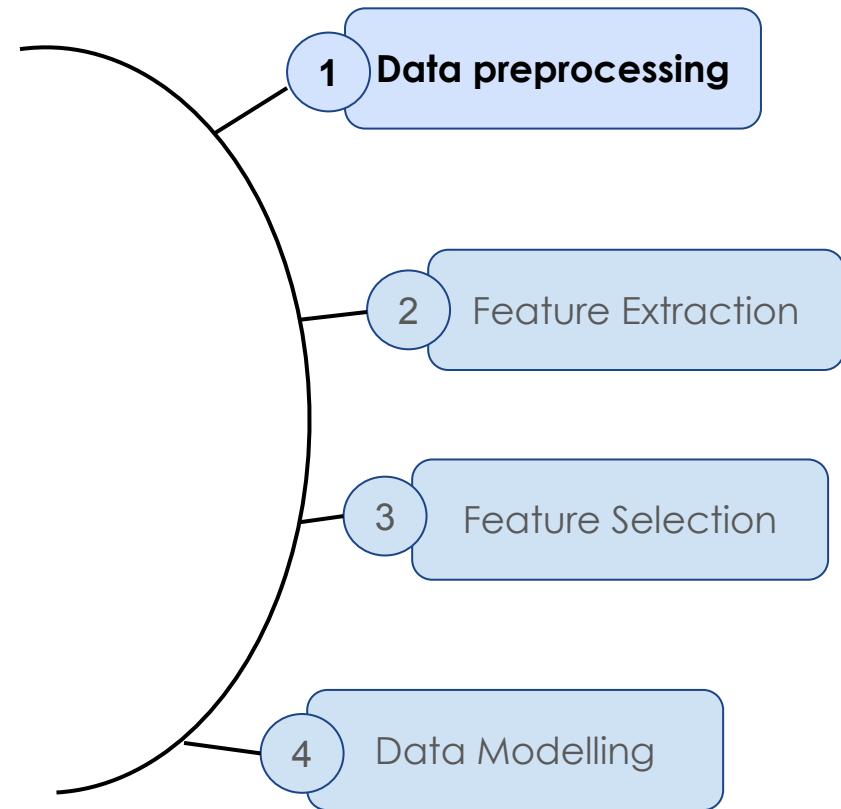
## Step 3: Data Transformation

- Scaling and normalization
- Encoding categorical variables
- Feature engineering and extraction (Dimensionality reduction, kernel approximation , ect.. )

## Step 4 : Model Training & Evaluation

# 1. Data Preprocessing

Steps for  
Machine Learning



# Missing data

## **MCAR** (Missing Completely At Random)

- The missingness has no relation to any variable.
- Safest to handle via deletion or simple imputation.

## **MAR** (Missing At Random)

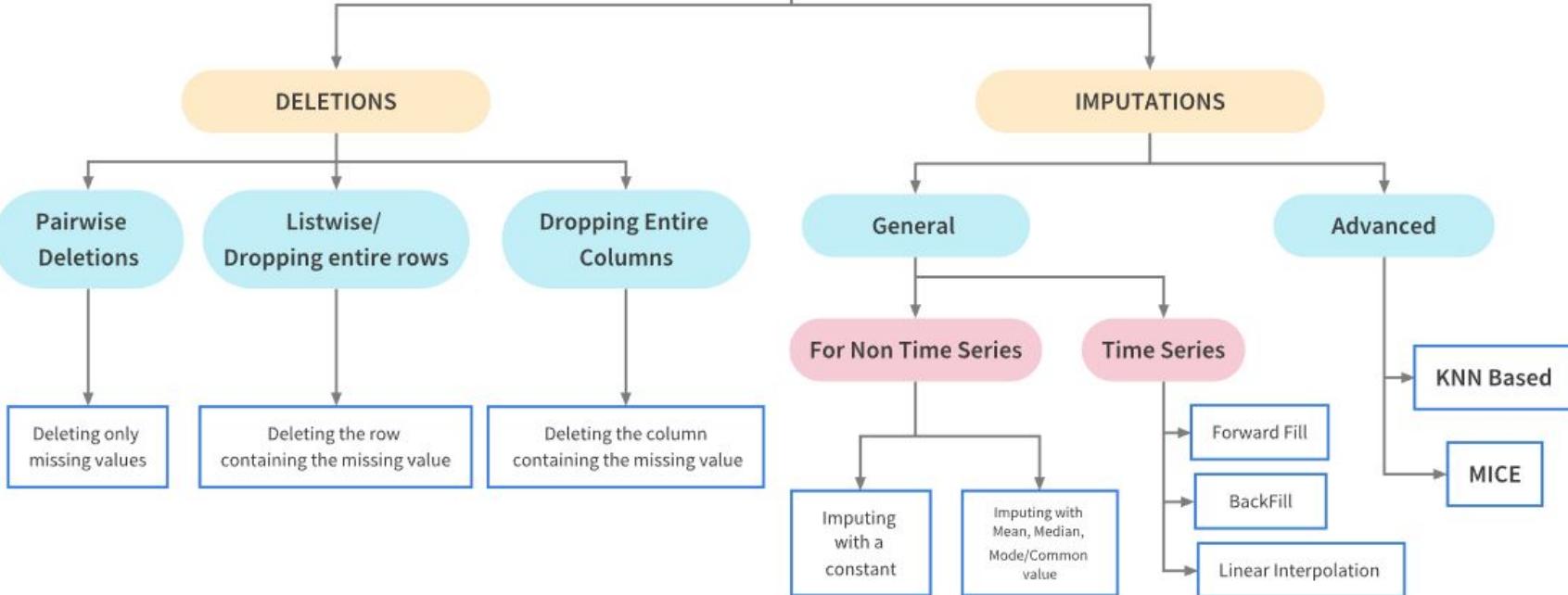
- The missingness is related to other observed data.
- Can be handled with imputation models using other variables.

## **MNAR** (Missing Not At Random)

- The missingness depends on unobserved data (e.g., income missing more often for high earners).
- Most challenging. Requires domain expertise or advanced models.



## Missing values Treatment



Pandas dropna( ), Pandas dropna( axis=1 )

Panda Fillna( ).mean fillna( ).median() fillna( ).mode()

Panda Fillna ( method="bfill") Fillna ( method="ffill")

imputer = SimpleImputer(missing\_values=np.nan,  
strategy= ['mean', 'median', 'most\_frequent', 'constant'])

Panda interpolate (method='linear', 'polynomial'  
'cubic', 'limit\_direction='forward', 'backward', 'both',  
'axis=0')

# Missing data - Imputation

## Iterative Imputer

- For datasets where imputing each feature independently would lose important correlations.
- Predicts missing values by modeling each feature as a function of others (uses regression).

```
imputer = sklearn.IterativeImputer(random_state=0)
```

## KNN Imputer

- Fills missing values with the average of the k closest rows (neighbors) based on similarity.

```
imputer = KNNImputer(n_neighbors=2)
```

**fit() or .fit\_transform()**

# Data Transformation

Converting the data from one form to another to make it more suitable for analysis.

1. Scaling
  - Normalization
  - standardization
2. Encoding categorical Data

# Normalization

The process of adjusting values measured on different scales to a common scale.  
shifts and scales a distribution; it does not change its shape.

Common methods include:

- Min-Max normalization
- Abs-Max normalization
- Long normalization
- Decimal scaling

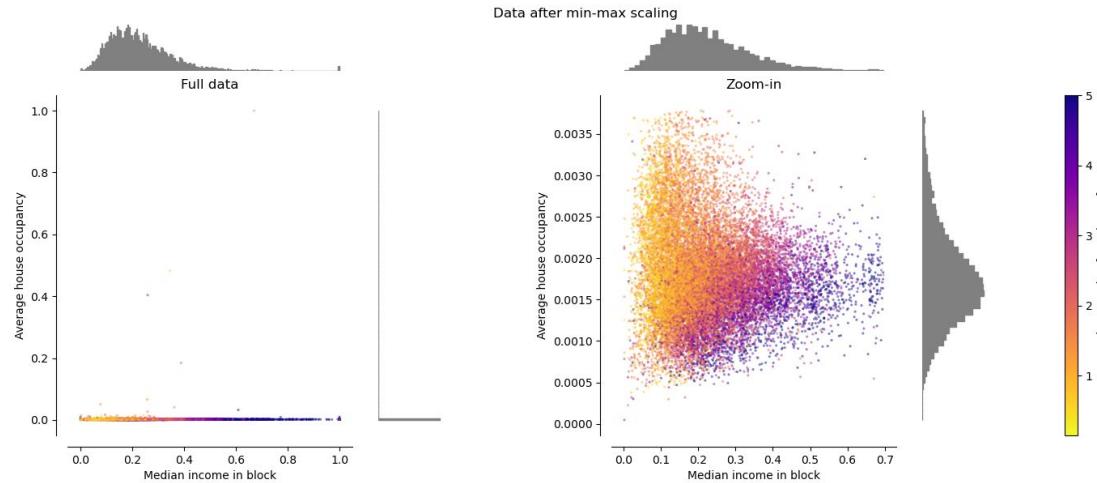


## Normalization (Min-Max Scaling):

- Scales the values to a specified range, typically **[0,1]**.
- preserves the original distribution.

```
from sklearn.preprocessing import MinMaxScaler  
scaler = MinMaxScaler()  
data[['scaled_column']] = scaler.fit_transform(data[['numeric_column']])
```

$$X_{scaled} = \frac{X - X_{min}}{X_{max} - X_{min}}$$

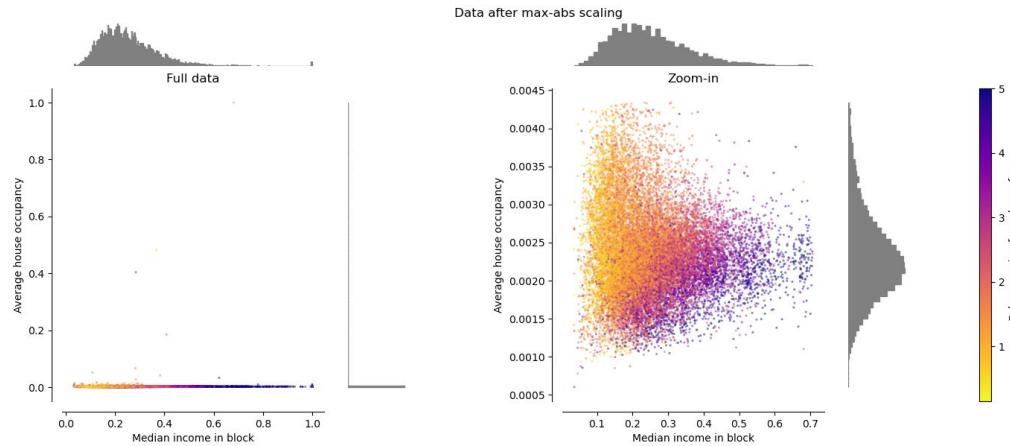


## Normalization (MaxAbsScaler):

- scales in a way that the data lies within the **range [-1, 1]** .
- Suitable for data that is already centered at zero or sparse data.
- doesn't reduce the effect of outliers; linearly scales them down.

```
from sklearn.preprocessing import MinAbsScaler  
scaler = MinAbsScaler()  
data[['scaled_column']] = scaler.fit_transform(data[['numeric_column']])
```

$$x_{scaled} = \frac{x}{\max(x)}$$

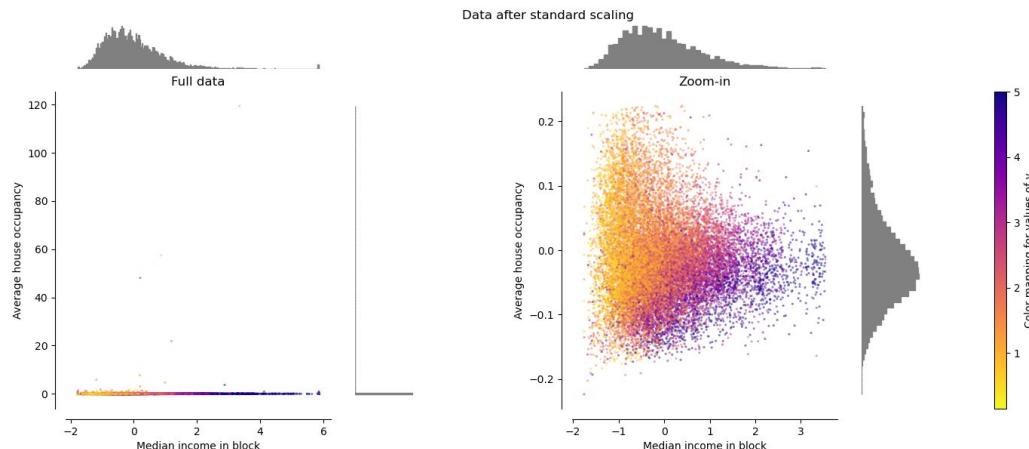


## Standardization (StandardScaler):

- Removes the mean and scales the data to unit variance.
- Help to reduce outliers impact but have an influence when computing the empirical mean and standard deviation.
- cannot guarantee balanced feature scales in the presence of extreme outliers.

```
from sklearn.preprocessing import StandardScaler  
scaler = StandardScaler()  
data[['standardized_column']] = scaler.fit_transform(data[['numeric_column']])
```

$$X'_i = \frac{X_i - \mu}{\sigma} = \frac{X_i - X_{\text{mean}}}{X_{\text{std}}}$$

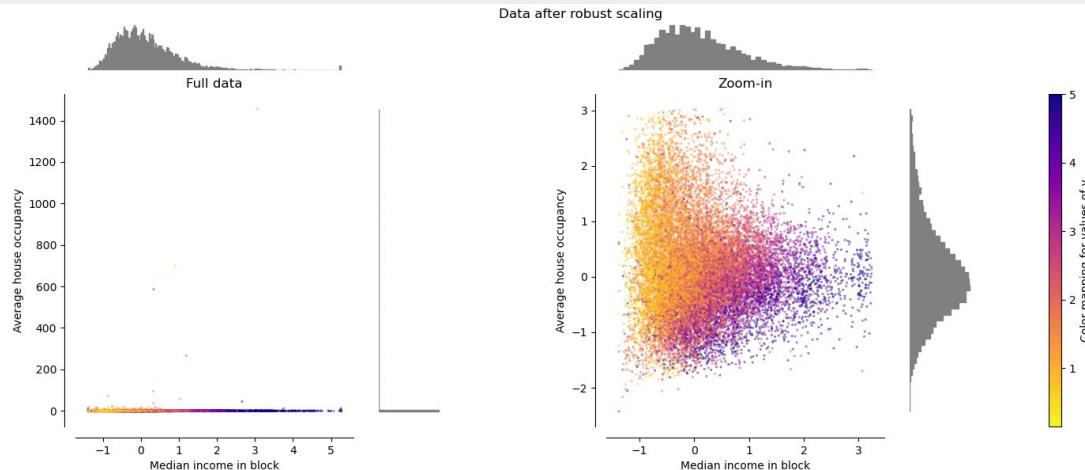


## RobustScaler:

- The centering and scaling statistics are based on percentiles
- Not influenced by a small number of very large marginal outliers

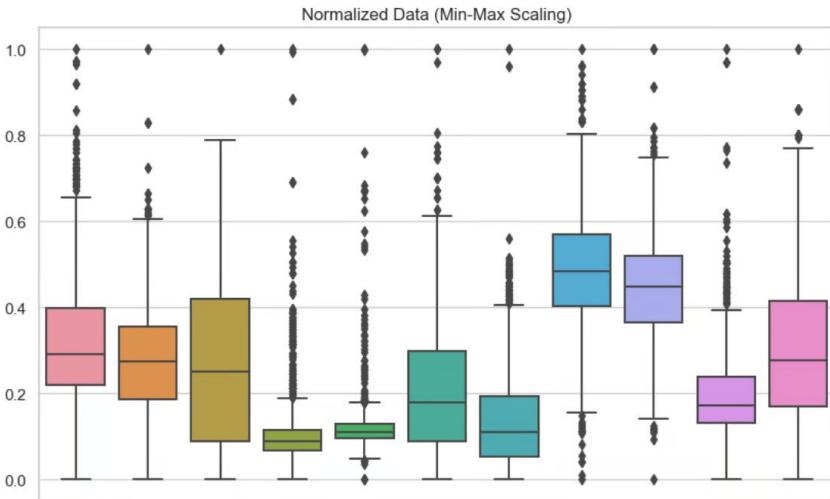
```
from sklearn.preprocessing import RobustScaler  
scaler = RobustScaler()  
data[['standardized_column']] = scaler.fit_transform(data[['numeric_column']])
```

$$\frac{x_i - Q_1(x)}{Q_3(x) - Q_1(x)}$$

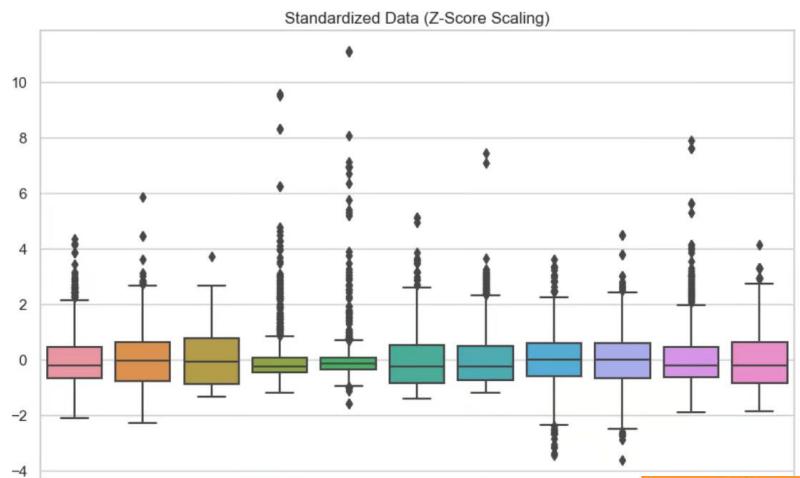


# Normalization vs. Standardization

- Scale data to a range based on min & max values
- Can help adjust for outliers depending on the technique
- Applied in KNN and neural network that require data to be on a consistent scale



- Centers around 0 mean and scales by standard deviation 1.
- More consistent to fix outlier
- Best for algorithms that requires features to have common scale such as PCA, SVM, and logistic regression



# Encoding Categorical data

Categorical data need to be encoded into numerical values before they can be used in machine learning algorithms. We can use :

## 1. Label Encoder

*Encode target labels with value between 0 and n\_classes-1.*

```
from sklearn.preprocessing import LabelEncoder  
le = LabelEncoder()  
data['encoded_column'] = le.fit_transform(data['categorical_column'])
```

Original Data:

Color	Size	Price
Blue	L	100
Green	M	150
Red	S	200
Green	XL	120
Red	M	180

Label Encoding  


Label Encoded Data:

Color	Size	Price
0	0	100
1	1	150
2	2	200
1	3	120
2	1	180

*!! Label Encoder can introduce an unintended ordinal relationship between categories if they don't have a natural order*

# Encoding Categorical data

## 2. One-Hot Encoder

Encode categorical features as a one-hot numeric array.

```
from sklearn.preprocessing import OnehotEncoder  
encoder= OnehotEncoder()  
data['encoded_column'] = encoder.fit_transform(data['categorical_column'])
```

id	color
1	red
2	blue
3	green
4	blue

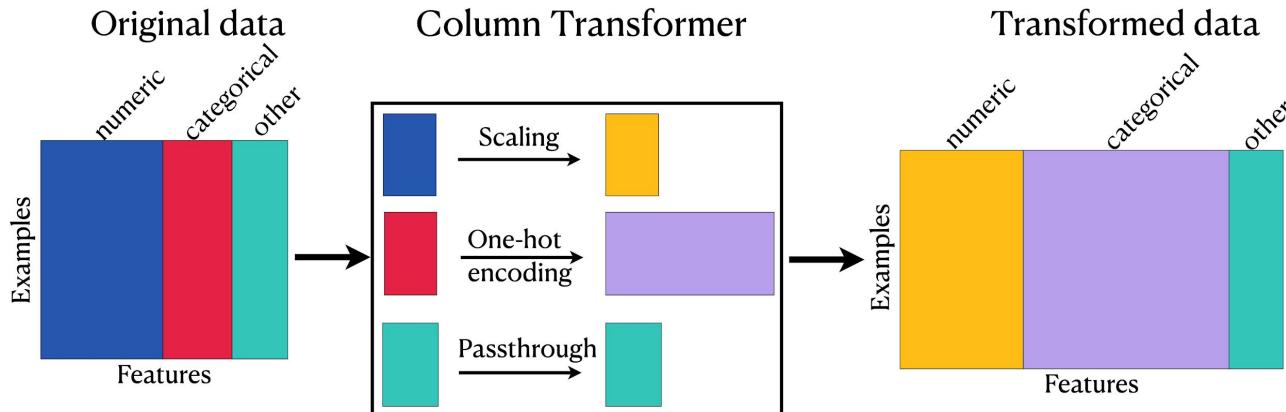


# Encoding Categorical data

## 3. Column Transformer

Applies transformers only to a group of columns .

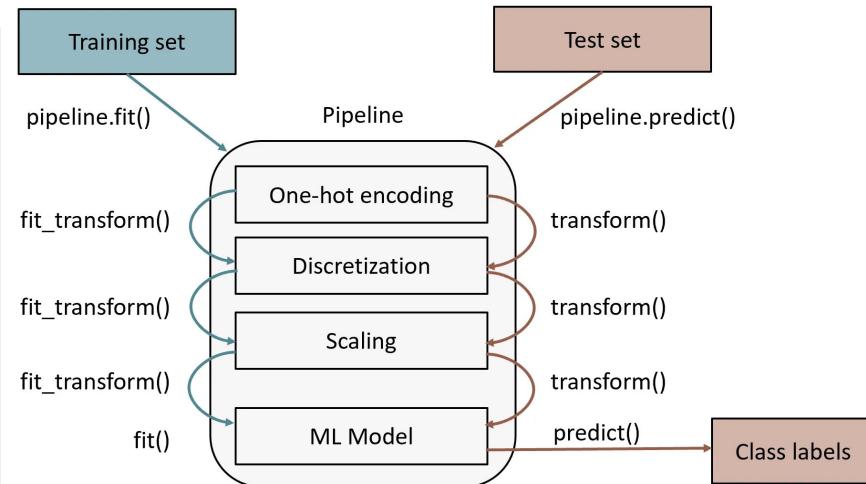
```
from sklearn.compose import ColumnTransformer
preprocessor = ColumnTransformer( [ ("categorical", categorical_preprocessor, ["catg", "catag"]),
("numerical", numeric_preprocessor, ["num", "num"]), ] )
```



# Scikit-learn Pipeline

- Combine all the preprocessing in one step

```
from sklearn.pipeline import pipeline , make_pipeline  
  
pipe= Pipeline([('scaler', StandardScaler()), ('clf', LogisticRegression())])  
  
pipe = make_pipeline(StandardScaler(),  
OneHotEncoder(), LogisticRegression())  
  
pipeline.fit(X_train, y_train)  
  
y_pred = pipeline.predict(X_test)  
  
accuracy = accuracy_score(y_test, y_pred)
```



# Best Practices for Data Preprocessing

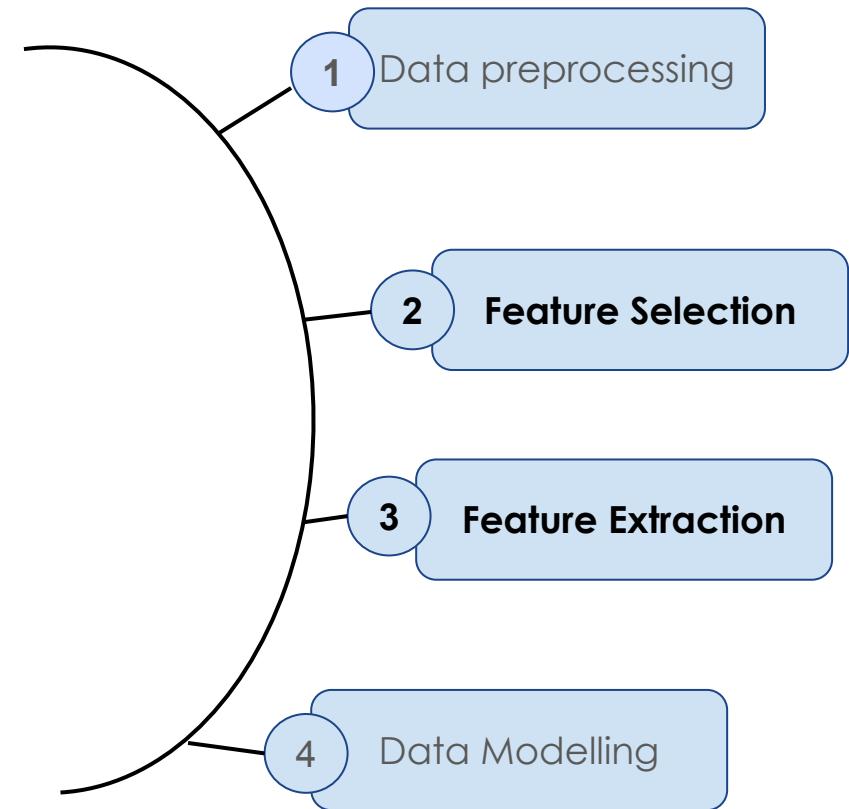
- **Understand the data**
  - **Key features:** Identify the most relevant variables for your task.
  - **Potential anomalies:** Look for outliers or inconsistencies that may distort the analysis.
  - **Relationships:** Explore correlations and dependencies between variables to inform transformations or feature engineering.
- **Automate repetitive steps**
  - Use tools like `sklearn Pipeline()` to build repeatable, structured workflows.
- **Document every preprocessing step**
  - Makes it easier to revisit your process later — for yourself or other team members.
- **Iterate and improve over time**
  - Let model feedback guide adjustments to your pipeline.
  - Example: Feature engineering might reveal valuable new inputs, or fine-tuning how outliers are handled can boost performance.



COFFEE BREAK

## 2. Feature Engineering

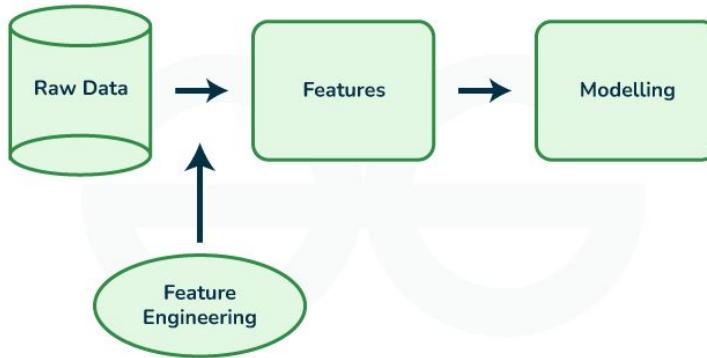
Steps for  
Machine Learning



# Feature Engineering

The process of **transforming raw data into features** that are suitable for machine learning models

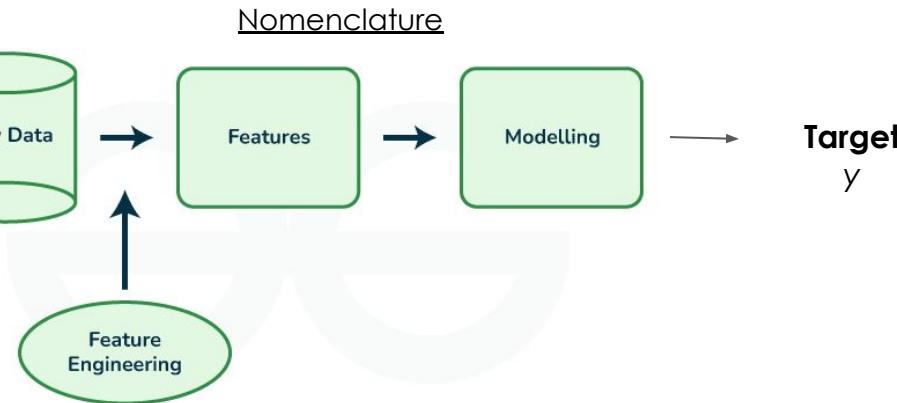
that better represent the underlying patterns to machine learning models, leading to **improved performance**.



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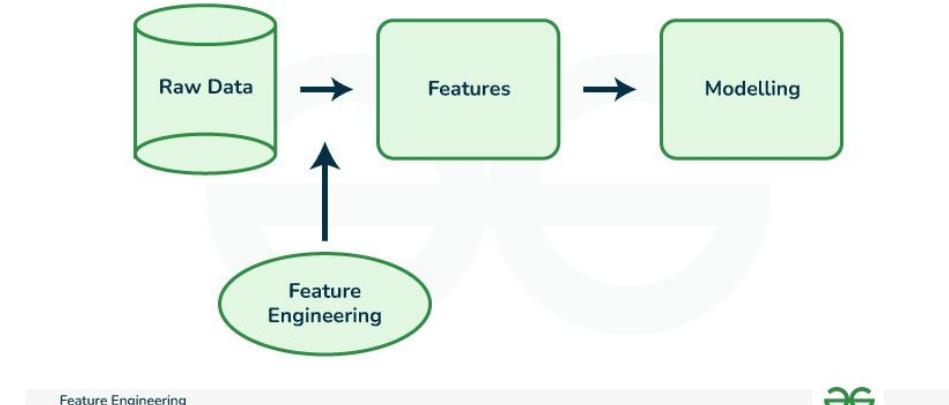


# Feature Engineering

Feature engineering is the process of **transforming** raw **data** into features that better represent the underlying patterns to machine learning models, leading to **improved performance**.

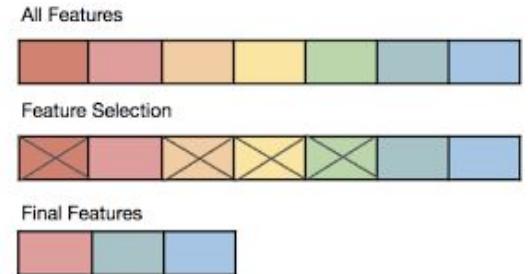
It includes:

- Creating new features
- Transforming or encoding features
- Selecting the most useful features
- Extracting new representations of the data



# Feature Selection

**Reduce** the number of features by keeping only the most informative ones.

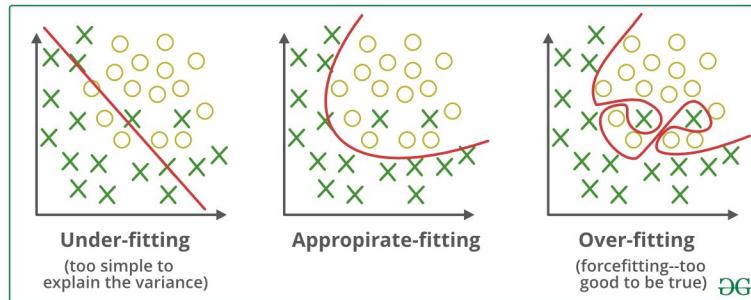
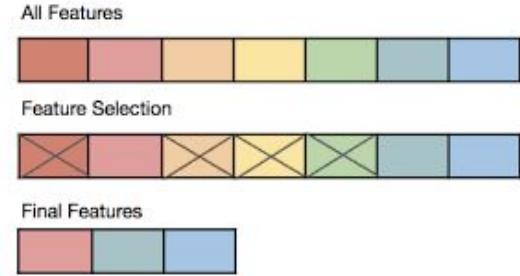


# Feature Selection

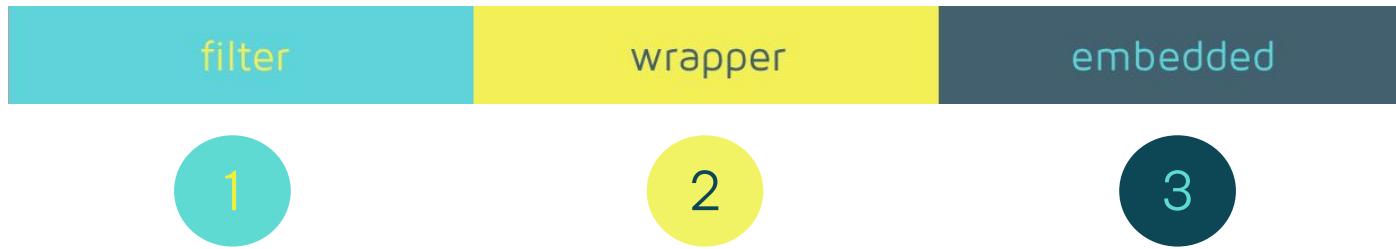
**Reduce** the number of features by keeping only the most informative ones.

This helps:

- **Improve** model **accuracy** (removing noisy or irrelevant features)
- **Reduce overfitting** (better generalization to new / unseen data)
- **Speed up training and inference** (specially critical for real-time systems or large-scale models)
- **Increase** model **interpretability** (simpler models tend to be easier to interpret)

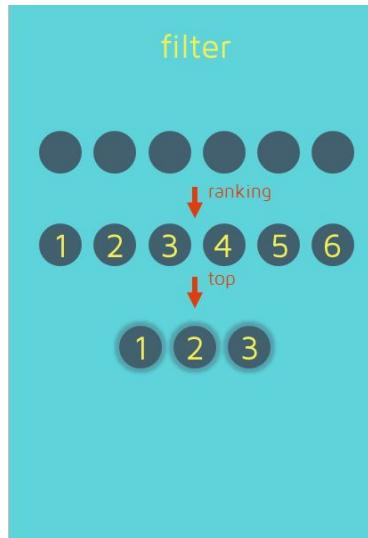


# Feature Selection



# Feature Selection - Filter methods

Use **statistical tests** to rank or score each feature, independent of the model (**model-independent**).



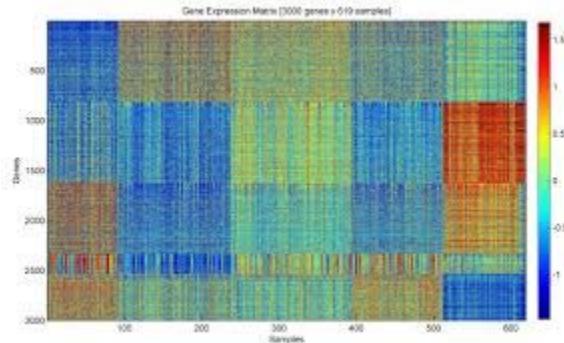
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Examples:

- **Variance Threshold** – remove features with little variability.
- **Chi-squared test** – for categorical targets.
- **Mutual Information** – measures mutual dependency between features and target.

E.g. Gene expression Matrix



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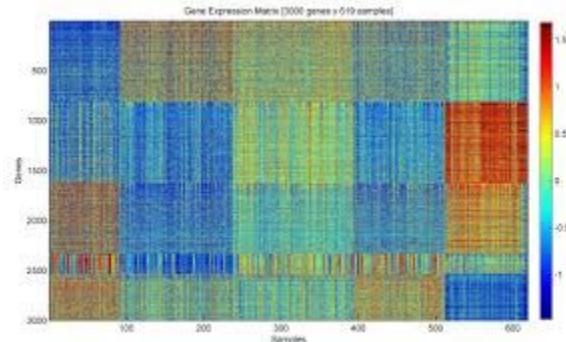
Examples:

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Use when:

- You want a quick, **model-agnostic** selection
- For high-dimensional data (e.g., genomics, text)

E.g. Gene expression Matrix



# Feature Selection - Filter methods

**Chi-squared test** - statistical test to **assess if two categorical variables are independent.**

Output:  $\chi^2$  statistic (higher, more dependence) and p-value

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

- $O$  = observed frequency
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**Feature selection:** Assess the **independence** between **each feature** and the **target variable**

Features are sorted by their  $\chi^2$  or p-value and then **top-k or top-percentile** of features are selected.

E.g. Classification based on genomic mutation data (presence/absence of variants)

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Use when:

- Your **features are categorical** or can be discretized (e.g. using binning)
- The **target** variable is **categorical (classification)**
- Simple, fast way to rank feature relevance

Limitations:

- Requires **non-negative**, discrete inputs (not ideal for continuous values)
- Not suitable for regression (target must be categorical)
- **Assumes independence between features** (evaluates one at a time) and doesn't capture interactions or complex relationships.

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**Mutual Information** - measures the **dependency** between two variables. It quantifies how much knowing one variable reduces uncertainty about the other. (0, Inf)

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Feature selection: How much **information** does this **feature** give me about the **target**?

Compute MI between each feature and the target. Then, rank features based on the score. (Higher MI, greater dependency)

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Feature selection: How much **information** does this **feature** give me about the **target**?

Compute MI between each feature and the target. Then, rank features based on the score. (Higher MI, greater dependency)

Use when:

- **Features can be continuous or discrete**  
(encode categorical as integers)
- Compatible with **classification** and **regression**
- Captures **nonlinear relationships** and it does not assume independence between features (non-parametric).

Limitations:

- Doesn't consider feature interactions (evaluates one at a time)
- Could yield redundant features

E.g. Regression/Classification based on continuous/discrete/categorical values with non-linear relationships to target

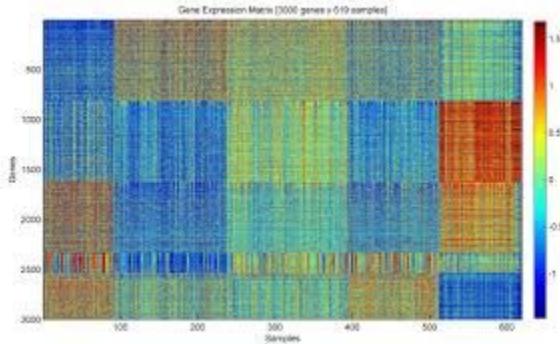
# Feature Selection - Filter methods

Use **statistical tests** to rank or score each feature, independent of the model (**model-independent**).

## Other:

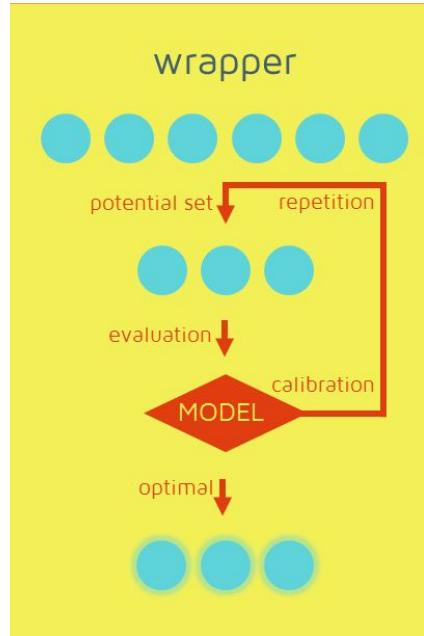
- **Biological priors:** sDEGs, mutated genes, ...
- **Low count** filtering (removing genes with low read counts in transcriptomics)
- Remove **highly correlated features** (using a correlation threshold or mrmr)

E.g. Gene expression Matrix



# Feature Selection - Wrapper methods

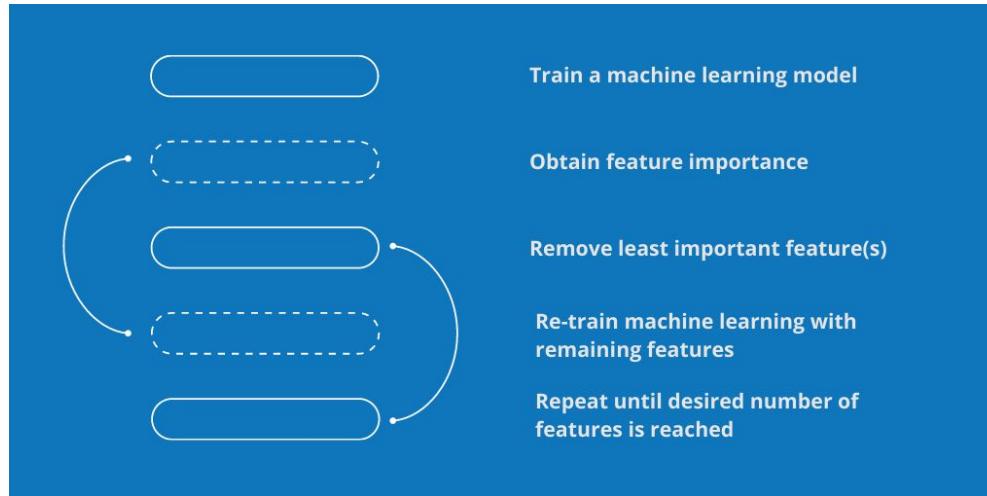
Wrapper methods train a model on different feature subsets and select the one that performs best (**model-based**).



# Feature Selection – [Wrapper methods](#)

Wrapper methods train a model on different feature subsets and select the one that performs best (**model-based**).

**Recursive Feature Elimination (RFE)** – removes the least important feature(s) recursively



# Feature Selection – Wrapper methods

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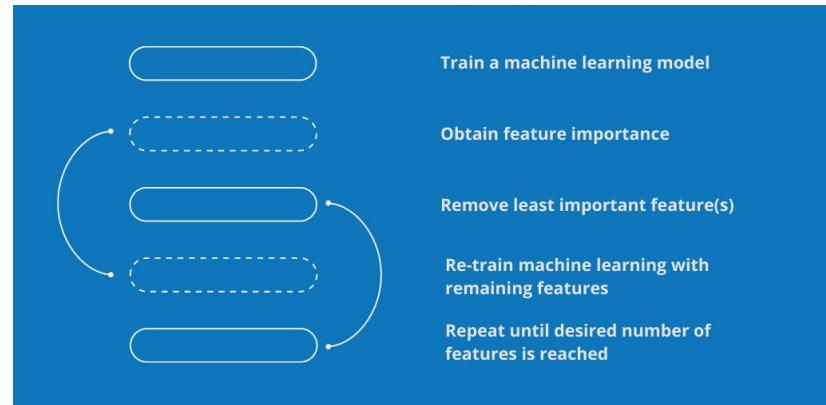
**Recursive Feature Elimination (RFE)** – removes the least important feature(s) recursively

Use when:

- You want **high accuracy**
- Okay with high computational cost
- Consider feature interactions
- Model-aware selection

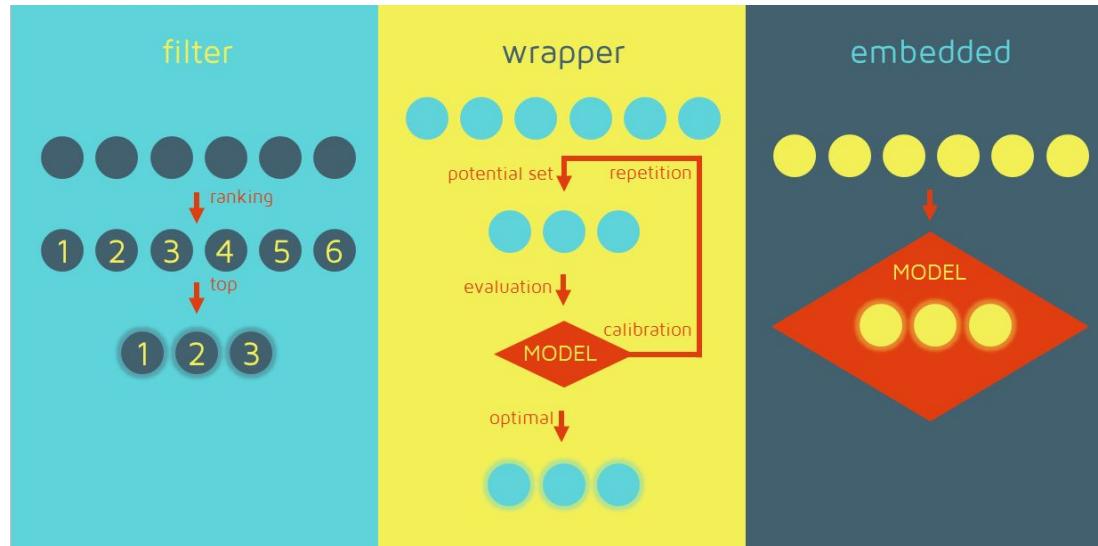
Limitations:

- **Computationally expensive**
- Slow or impractical with very large data sets (does not scale well)
- Risk of overfitting (specially on small datasets if not cross-validated)



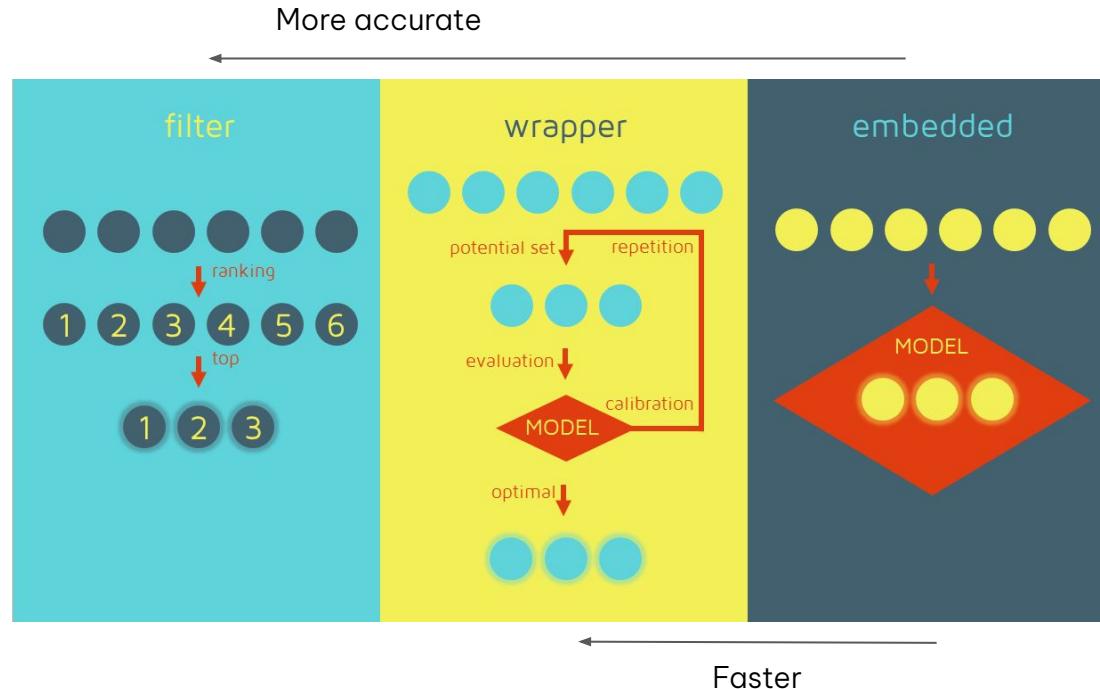
# Feature Selection - Embedded methods

Embedded methods perform feature selection **during training (Built-in to Model)**.



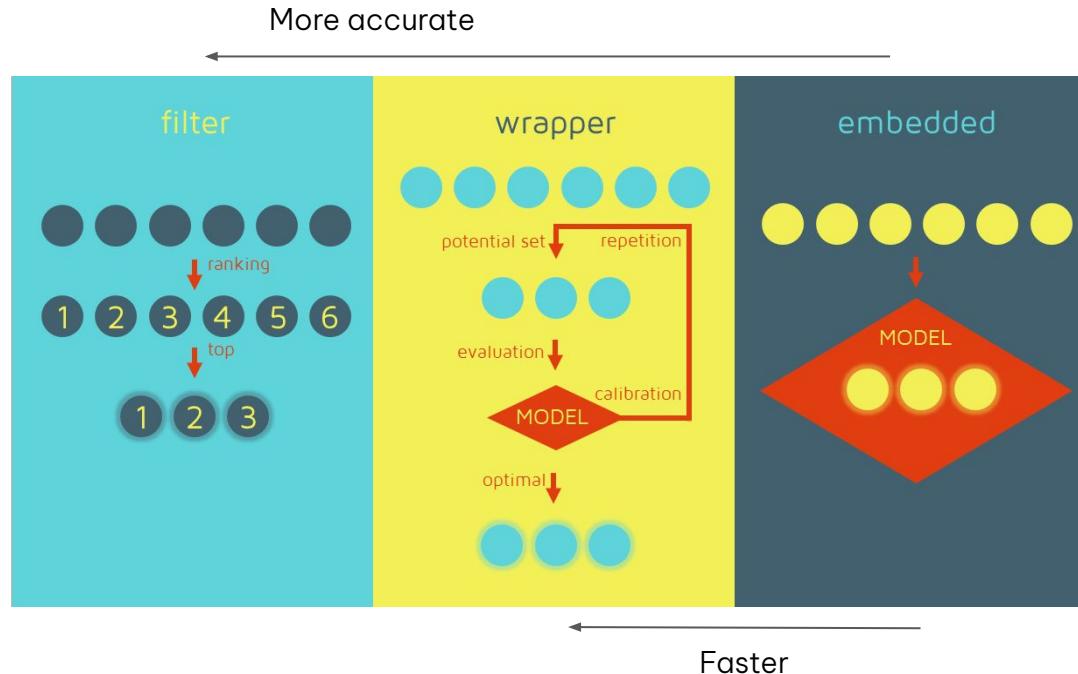
# Feature Selection - Embedded methods

Embedded methods perform feature selection **during training (Built-in to Model)**.



# Feature Selection - Embedded methods

Embedded methods perform feature selection **during training (Built-in to Model)**.



Internal mechanisms to determine:

- Which features **to keep**
- Which features **to drop** by assigning low or zero importance

# Feature Selection - Embedded methods

Embedded methods perform feature selection **during training (Built-in to Model)**.

Examples:

## Lasso Regression (L1 Regularization)

**L1 penalty:** forces some coefficients  
to become zero.

All Features



Feature Selection



Final Features



# Feature Selection – Embedded methods

Embedded methods perform feature selection **during training (Built-in to Model)**.

Examples:

## Lasso Regression (L1 Regularization)

**L1 penalty:** forces some coefficients to become zero.

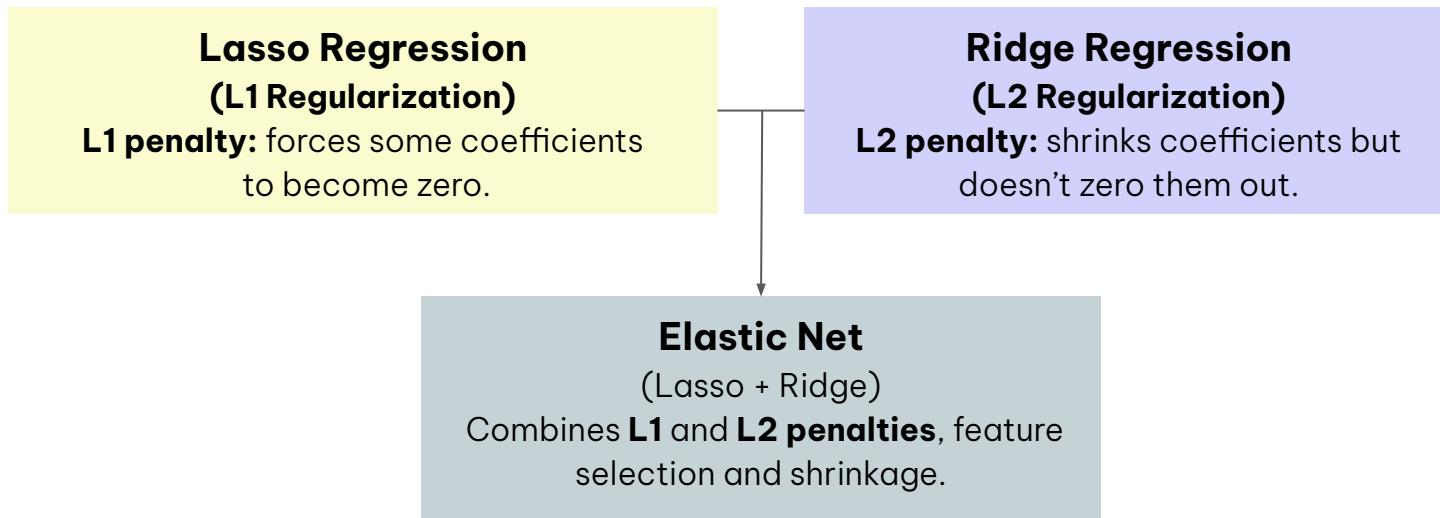
## Ridge Regression (L2 Regularization)

**L2 penalty:** shrinks coefficients but doesn't zero them out.

# Feature Selection - Embedded methods

Embedded methods perform feature selection **during training (Built-in to Model)**.

Examples:



# Feature Selection – Embedded methods

	Lasso Regression	Ridge Regression	Elastic Net
Type of penalty	L1 (absolute value)	L2 (squared magnitude)	L1 + L2
Feature selection	Yes	No	Yes (via L1)
When to use	Many features and want to remove irrelevant ones	Many small effects, all features matter	Best for many correlated features, balance of shrinkage & selection
Hyperparameters	Alpha (controls the strength of regularization)	Alpha	Alpha and L1_ratio (adjusts the balance between Lasso and Ridge)

\*A higher alpha means more shrinkage.

# Feature Selection - Embedded methods

## Lasso Regression

```
from sklearn.linear_model import Lasso  
  
lasso = Lasso(alpha=0.1)  
lasso.fit(X_train, y_train)
```

## Ridge Regression

```
from sklearn.linear_model import Ridge  
  
ridge = Ridge(alpha=1.0)  
ridge.fit(X_train, y_train)
```

## Elastic Net

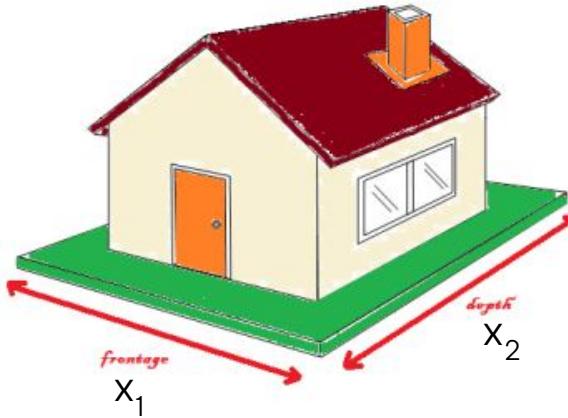
```
from sklearn.linear_model import ElasticNet  
  
enet = ElasticNet(alpha=0.1, l1_ratio=0.5)  
enet.fit(X_train, y_train)
```

50% L1, 50% L2

# Feature Extraction

Transform the **feature space** by combining or projecting features into a new set of variables.

Instead of removing features, **you create new ones** that summarize or better represent the data.



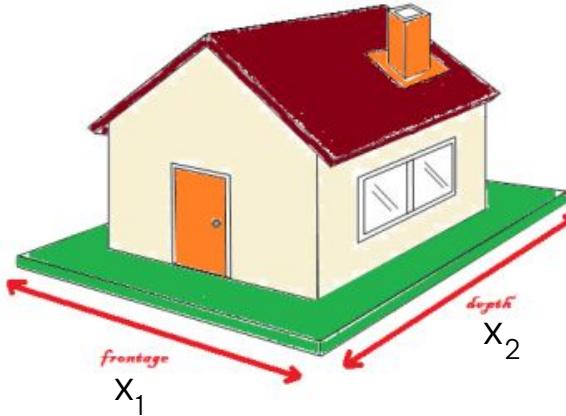
# Feature Extraction

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Price

$$y = ax_1 + bx_2 + c$$



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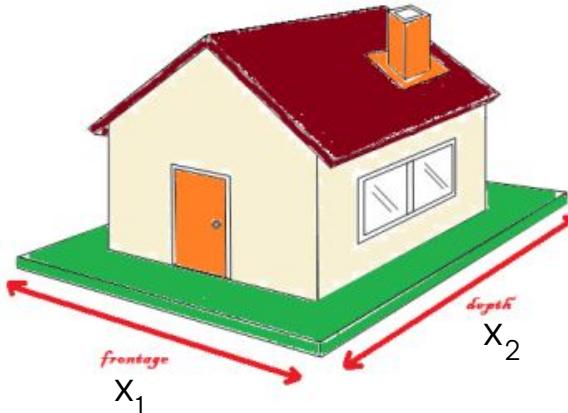
Price       $y = ax_1 + bx_2 + c$

Area = frontage x depth

$$x_3 = x_1 x_2$$

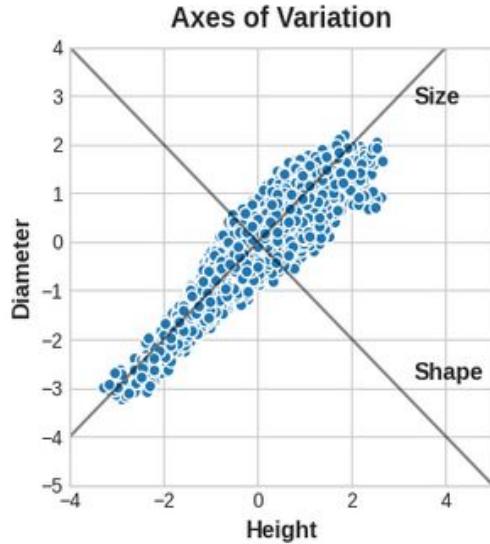
new feature

Price       $y = ax_1 + bx_2 + cx_3 + c$



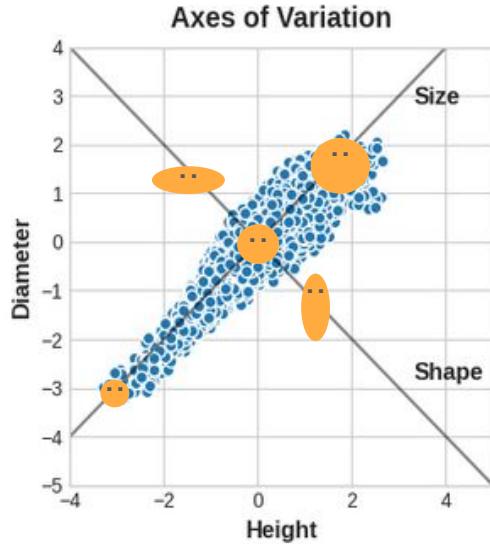
# Feature Extraction - Principal Component Analysis (PCA)

PCA is a **dimensionality reduction** technique used to transform high-dimensional data into fewer dimensions (called **principal components**) while preserving as much variability as possible.



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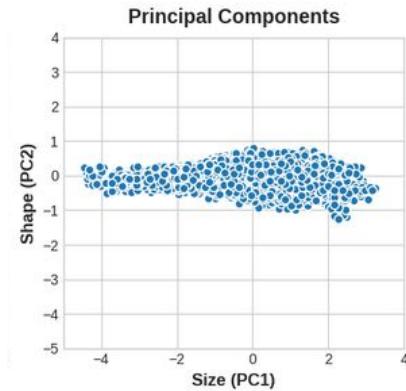
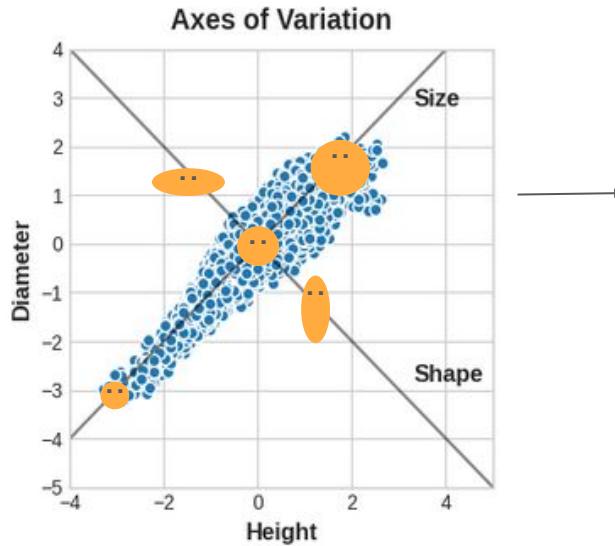


Abalone



# Feature Extraction - Principal Component Analysis (PCA)

PCA is a **dimensionality reduction** technique used to transform high-dimensional data into fewer dimensions (called **principal components**) while preserving as much variability as possible.

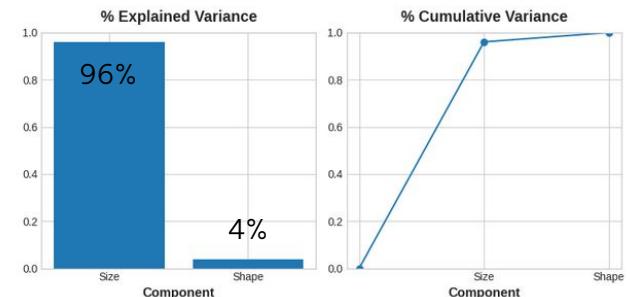


**Principal components** (linear combinations of the original features)

**Loadings** (weights)

$$\text{PC1 (Size)} = 0.707 * \text{Height} + 0.707 * \text{Diameter}$$

$$\text{PC2 (Shape)} = 0.707 * \text{Height} - 0.707 * \text{Diameter}$$



# Feature Extraction – Principal Component Analysis (PCA)

PCA projects data into a **lower-dimensional space** that **maximizes variance**.

- **Unsupervised** method
- New components are **linear combinations** of original features
- First components capture most of the variance

Use when:

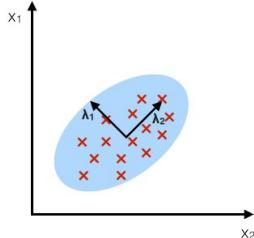
- Features are **correlated**
- PCA for preprocessing, UMAP/t-SNE for visualization
- You don't care about preserving interpretability of original features

# Feature Extraction – Linear Discriminant Analysis (LDA)

LDA is a **supervised dimensionality reduction** technique that **maximizes class separability**.  
Finds a linear combination of features that separate two or more classes.

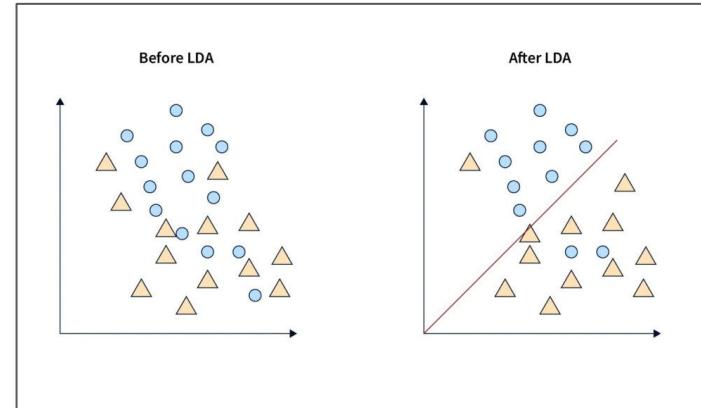
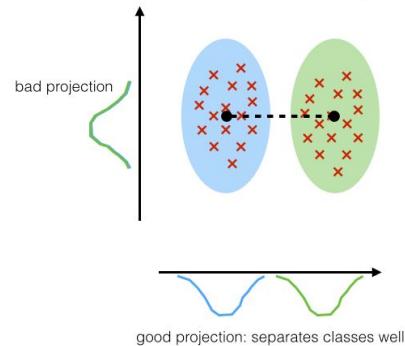
## PCA:

component axes that maximize the variance



## LDA:

maximizing the component axes for class-separation



Use when:

- Your data has labels
- You want features that help classification of linearly separable classes

# Feature Engineering

## Final notes

- In deep learning (especially vision, NLP), raw data is often used directly.
- Neural networks learn features automatically, making manual engineering less critical.
- However, structured/tabular data still benefits heavily from thoughtful feature engineering.
- Domain knowledge & data exploration and visualization.

Thanks!