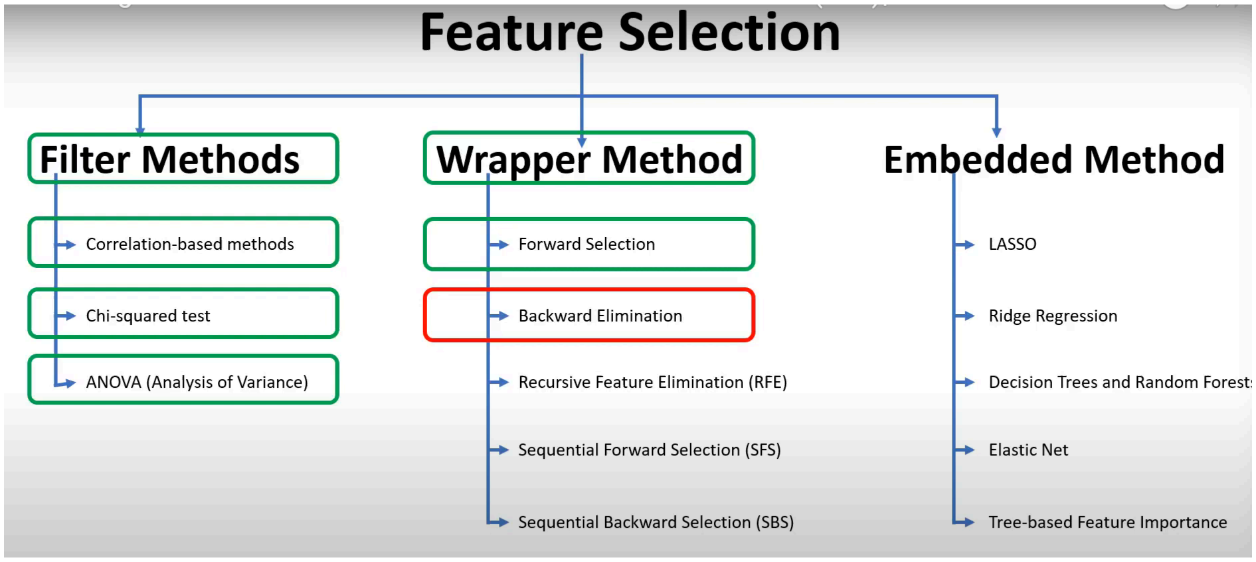
Feature Selection (Filter Methods) (VVIMP-Interview)


Feature Selection
Filter Methods
Correlation-based methods
Chi-squared test
ANOVA (Analysis of Variance)
Wrapper Method
Forward Selection
Backward Elimination
Recursive Feature Elimination (RFE)
Sequential Forward Selection (SFS)
Sequential Backward Selection (SBS)
Embedded Method
LASSO
Ridge Regression
Decision Trees and Random Forests
Elastic Net
Tree-based Feature Importance

- **Feature selection** is the process of choosing a subset of relevant features (variables) for use in a model.
- This is important because not all features contribute to the model's performance, and irrelevant or redundant features can lead to overfitting, increased complexity, and slower computation.
- If your data has 10-15 columns, there's not much need do the feature selection.

Why Feature Selection?

- **Improve Model Performance**: Focuses the model on meaningful patterns.
- **Reduce Overfitting**: Minimizes noise from irrelevant features.
- **Speed Up Training**: Fewer features mean faster computations.
- **Enhance Interpretability**: Simplifies understanding of model decisions.

- **Curse of dimensionality:** As the dimensions increase, the distance between points also increase and therefore it is not reliable if there are too many dimensions.

Types of Feature Selection Methods

1. **Filter Methods**
2. **Wrapper Methods**
3. **Embedded Methods**
4. Hybrid

▼

a. Filter Methods

- **Approach**: Use statistical measures to score feature relevance.
- **Pros**: Fast and model-agnostic.
- **Cons**: Ignores feature interactions.
- **Techniques**:
    - **Correlation**: Pearson's, Spearman's.
    - **Variance Thresholding**: Remove low-variance features.
    - **Chi-Squared Test**: For categorical data.
    - **Mutual Information**: Measures dependency.

b. Wrapper Methods

- **Approach**: Evaluate feature subsets based on model performance.
- **Pros**: Considers feature interactions.
- **Cons**: Computationally expensive.
- **Techniques**:
    - **Forward Selection**: Add features one by one.

  - **Backward Elimination**: Remove features one by one.
  - **Recursive Feature Elimination (RFE)**: Iteratively removes the least important features.

c. Embedded Methods

- **Approach**: Feature selection during model training.
- **Pros**: Balances efficiency and accuracy.
- **Techniques**:
  - **Lasso (L1 Regularization)**: Shrinks less important coefficients to zero.
  - **Tree-Based Models**: Use feature importance (e.g., Random Forest, XGBoost).

1. Filter Methods

- Individually studies each feature with statistical techniques like correlation or variance and decides if to keep it or not.
- Focuses on 1 feature at a time

- **Pros**: Fast and model-agnostic.
- **Cons**: Ignores feature interactions.

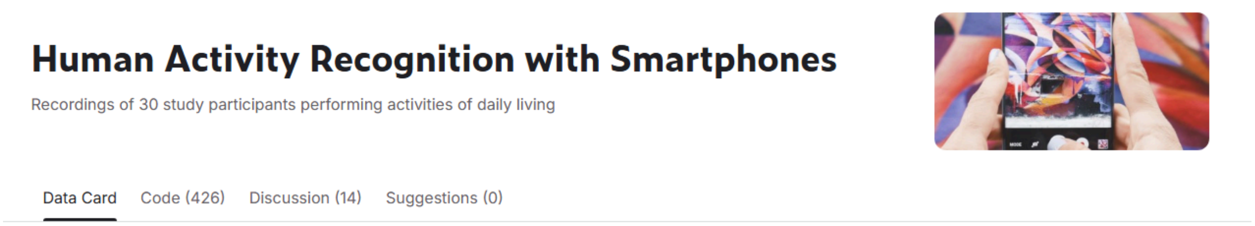
Common techniques:

- **Correlation Matrix**: Select features that are **not highly correlated** with each other.
- **Chi-Square Test**: Tests the independence between features and the target variable (used for categorical data).
- **Variance Threshold**: Removes features with low variance, assuming low variance means little to no information.
- **ANOVA**

- **Mutual Info**

Dataset Used:

- https://www.kaggle.com/datasets/uciml/human-activity-recognition-with-smartphones



Human Activity Recognition with Smartphones

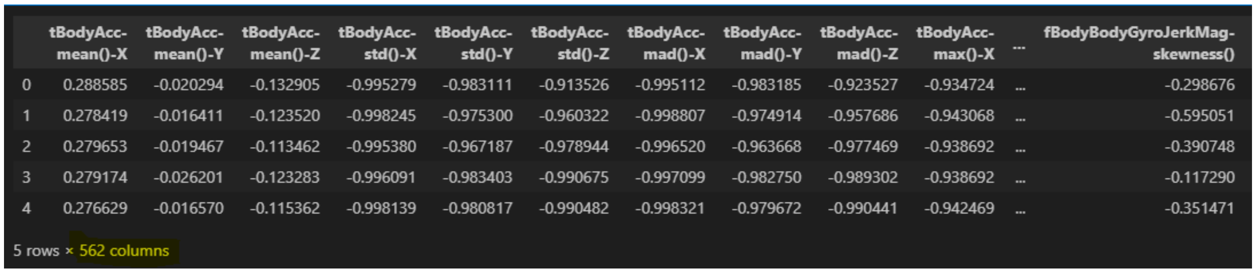
Recordings of 30 study participants performing activities of daily living

Columns → 563

AIM : Reduce 563 → 100 without losing the results

No linear regression → Because output is classification (we'll use logistic regression)

```
df = pd.read_csv(r'Human_Activity\train.csv').drop(columns='subject')
df.head()
```

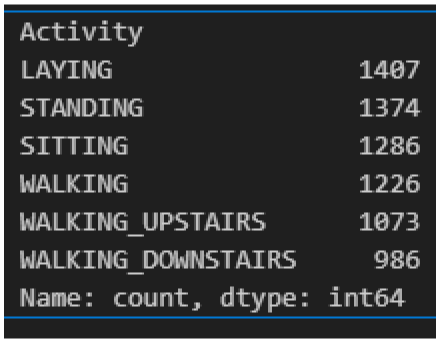


	tBodyAcc-mean()-X	tBodyAcc-mean()-Y	tBodyAcc-mean()-Z	tBodyAcc-std()-X	tBodyAcc-std()-Y	tBodyAcc-std()-Z	tBodyAcc-mad()-X	tBodyAcc-mad()-Y	tBodyAcc-mad()-Z	tBodyAcc-max()-X	...	fBodyBodyGyroJerkMag-skewness()
0	0.288585	-0.020294	-0.132905	-0.995279	-0.983111	-0.913526	-0.995112	-0.983185	-0.923527	-0.934724	...	-0.298676
1	0.278419	-0.016411	-0.123520	-0.998245	-0.975300	-0.960322	-0.998807	-0.974914	-0.957686	-0.943068	...	-0.595051
2	0.279653	-0.019467	-0.113462	-0.995380	-0.967187	-0.978944	-0.996520	-0.963668	-0.977469	-0.938692	...	-0.390748
3	0.279174	-0.026201	-0.123283	-0.996091	-0.983403	-0.990675	-0.997099	-0.982750	-0.989302	-0.938692	...	-0.117290
4	0.276629	-0.016570	-0.115362	-0.998139	-0.980817	-0.990482	-0.998321	-0.979672	-0.990441	-0.942469	...	-0.351471

5 rows × 562 columns

- We dropped 'Subject' as we're dealing with categorical variables
- All these values are **scaled (-1 to +1)**
- **Output → Activity**

```
df['Activity'].value_counts()
```



```
Activity
LAYING                1407
STANDING              1374
SITTING               1286
WALKING               1226
WALKING_UPSTAIRS      1073
WALKING_DOWNSTAIRS     986
Name: count, dtype: int64
```

```
print(df.shape)

Output: (7352, 562)
```

First, apply logistic regression

```
from sklearn.preprocessing import LabelEncoder #CAT → Numeric
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score

# Separate features and target
X = df.drop('Activity', axis=1)
y = df['Activity']

# Encode target labels
le = LabelEncoder()
y = le.fit_transform(y)

# Split data into training and testing sets
```

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

`LabelEncoder` : This is used to **convert categorical labels** (like 'cat', 'dog', 'fish') into numerical values (e.g., 0, 1, 2) so that they can be used in machine learning models that require numerical inputs.

```
print(X_train.shape)
print(X_test.shape)

Output:
(5881, 561)
(1471, 561)
```

Apply Logistic Regression:

```
# Initialize and train logistic regression model
log_reg = LogisticRegression(max_iter=1000)  # Increase max_iter if it doesn't
converge
log_reg.fit(X_train, y_train)

# Make predictions on the test set
y_pred = log_reg.predict(X_test)

# Calculate and print accuracy score
accuracy = accuracy_score(y_test, y_pred)
print("Test accuracy:", accuracy)

Output:
Test accuracy: 0.9809653297076818
```

- **Accuracy score** is used here because the problem is a **classification task**, where the goal is to predict **categories** (e.g., 'yes' or 'no').
- Accuracy measures how many predictions match the true labels.
- On the other hand, **R² (R-squared)** is used for **regression tasks**, where the goal is to predict continuous values.

Delete Duplicate Columns

```
def get_duplicate_columns(df):

    duplicate_columns = {}
    seen_columns = {}

    for column in df.columns:
        current_column = df[column]

        # Convert column data to bytes
        try:
            current_column_hash = current_column.values.tobytes()
        except AttributeError:
            current_column_hash = current_column.to_string().encode()

        if current_column_hash in seen_columns:
            if seen_columns[current_column_hash] in duplicate_columns:
                duplicate_columns[seen_columns[current_column_hash]].append(co
lumn)
            else:
                duplicate_columns[seen_columns[current_column_hash]] = [colum
n]
        else:
            seen_columns[current_column_hash] = column

    return duplicate_columns
```

Simpler Code to delete Duplicates

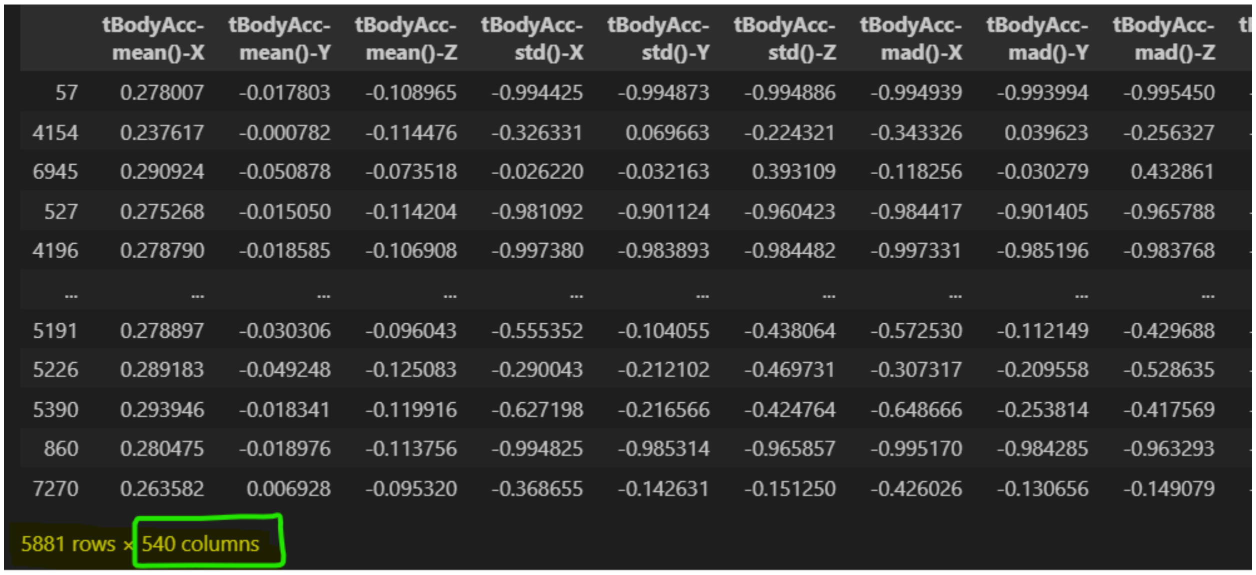
```
def remove_duplicate_columns(df):
    # Transpose the DataFrame to compare columns as rows
    transposed_df = df.T

    # Find duplicate rows (which are the original columns)
    duplicate_columns = transposed_df[transposed_df.duplicated()].index.tolist
()

    # Drop duplicate columns from the original DataFrame
    df_cleaned = df.drop(columns=duplicate_columns)

    return df_cleaned
```

`.index`: In Pandas, every DataFrame or Series has an `index` property, which stores the row labels. In the case of a transposed DataFrame (`df.T`), the `index` represents the column names from the original DataFrame.

`.tolist()`: This method converts the Pandas Index object (which holds column names) into a standard Python list.

So when we call `transposed_df[transposed_df.duplicated()].index.tolist()`, it identifies the index labels (which are the original column names) of the rows that are duplicated. These column names are returned as a list.

```
X_train=remove_duplicate_columns(X_train)
```

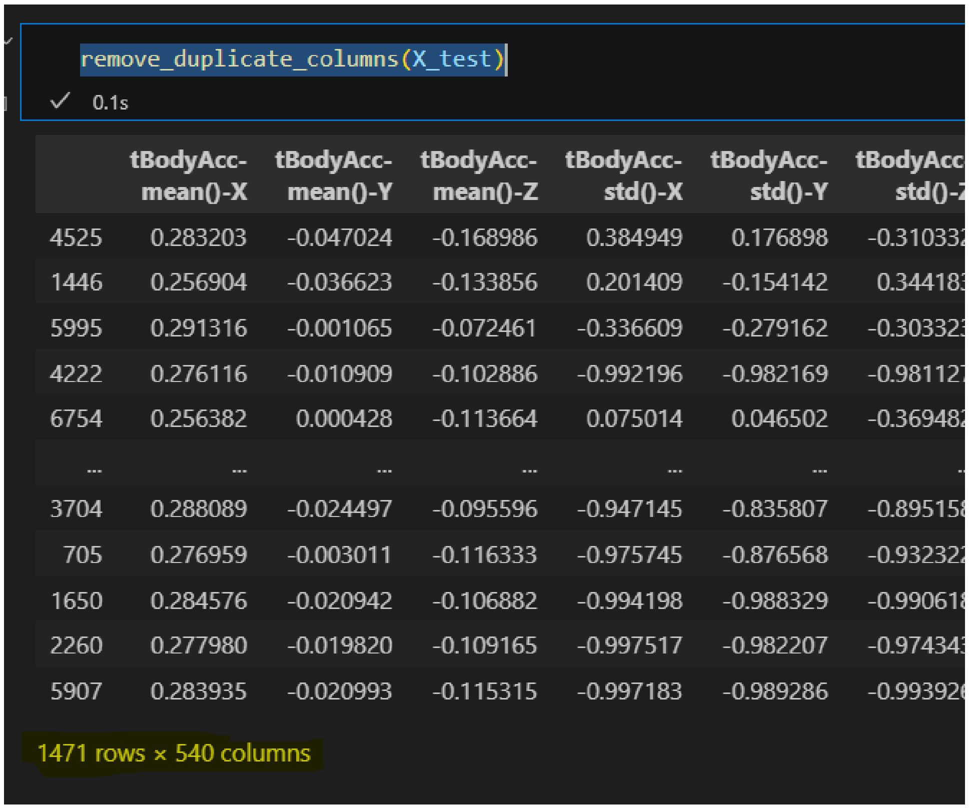


	tBodyAcc-mean()-X	tBodyAcc-mean()-Y	tBodyAcc-mean()-Z	tBodyAcc-std()-X	tBodyAcc-std()-Y	tBodyAcc-std()-Z	tBodyAcc-mad()-X	tBodyAcc-mad()-Y	tBodyAcc-mad()-Z
57	0.278007	-0.017803	-0.108965	-0.994425	-0.994873	-0.994886	-0.994939	-0.993994	-0.995450
4154	0.237617	-0.000782	-0.114476	-0.326331	0.069663	-0.224321	-0.343326	0.039623	-0.256327
6945	0.290924	-0.050878	-0.073518	-0.026220	-0.032163	0.393109	-0.118256	-0.030279	0.432861
527	0.275268	-0.015050	-0.114204	-0.981092	-0.901124	-0.960423	-0.984417	-0.901405	-0.965788
4196	0.278790	-0.018585	-0.106908	-0.997380	-0.983893	-0.984482	-0.997331	-0.985196	-0.983768
...	...	...	...	...	...	...	...	...	...
5191	0.278897	-0.030306	-0.096043	-0.555352	-0.104055	-0.438064	-0.572530	-0.112149	-0.429688
5226	0.289183	-0.049248	-0.125083	-0.290043	-0.212102	-0.469731	-0.307317	-0.209558	-0.528635
5390	0.293946	-0.018341	-0.119916	-0.627198	-0.216566	-0.424764	-0.648666	-0.253814	-0.417569
860	0.280475	-0.018976	-0.113756	-0.994825	-0.985314	-0.965857	-0.995170	-0.984285	-0.963293
7270	0.263582	0.006928	-0.095320	-0.368655	-0.142631	-0.151250	-0.426026	-0.130656	-0.149079

5881 rows × 540 columns

do the same for X_test

```
X_test= remove_duplicate_columns(X_test)
```



```
remove_duplicate_columns(X_test)
```

✓ 0.1s

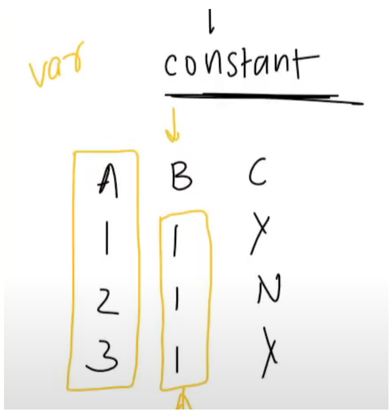
	tBodyAcc-mean()-X	tBodyAcc-mean()-Y	tBodyAcc-mean()-Z	tBodyAcc-std()-X	tBodyAcc-std()-Y	tBodyAcc std()-
4525	0.283203	-0.047024	-0.168986	0.384949	0.176898	-0.31033
1446	0.256904	-0.036623	-0.133856	0.201409	-0.154142	0.34418
5995	0.291316	-0.001065	-0.072461	-0.336609	-0.279162	-0.30332
4222	0.276116	-0.010909	-0.102886	-0.992196	-0.982169	-0.98112
6754	0.256382	0.000428	-0.113664	0.075014	0.046502	-0.36948
...	...	...	...	...	...	.
3704	0.288089	-0.024497	-0.095596	-0.947145	-0.835807	-0.89515
705	0.276959	-0.003011	-0.116333	-0.975745	-0.876568	-0.93232
1650	0.284576	-0.020942	-0.106882	-0.994198	-0.988329	-0.99061
2260	0.277980	-0.019820	-0.109165	-0.997517	-0.982207	-0.97434
5907	0.283935	-0.020993	-0.115315	-0.997183	-0.989286	-0.99392

1471 rows × 540 columns

Variance Threshold

`from sklearn.` `feature_selection` `import` `VarianceThreshold`

- Removes features with low variance, assuming low variance means little to no information.



- Here, B is **constant**
- It doesn't play any role in prediction
- We can drop such columns
- If values of 95% columns is 1 and remaining 5% is → It's **Quasi Constant column**
  - Its variance is close to 0

Steps

- *Normalize data*

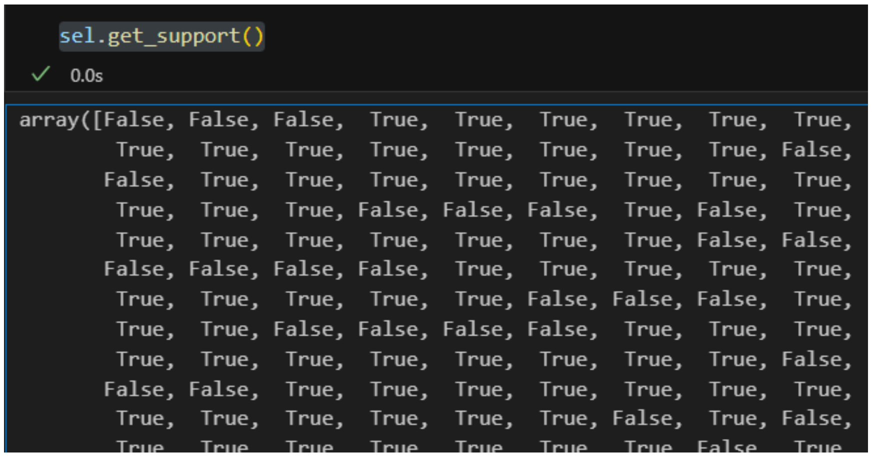
1. Decide a **threshold (eg. 0.1)**
   - ***0.01 to 0.1***
2. Calculate **variance** for every column
3. **Check** which columns' threshold is **less than our decided threshold**
4. Drop em👆

```
from sklearn.feature_selection import VarianceThreshold
sel = VarianceThreshold(threshold=0.05)
sel.fit(X_train)
```

Check which columns' threshold is **more**:

```
sum(sel.get_support())

Output: 349
```

- `sel.get_support()` → returns boolean values: True/False

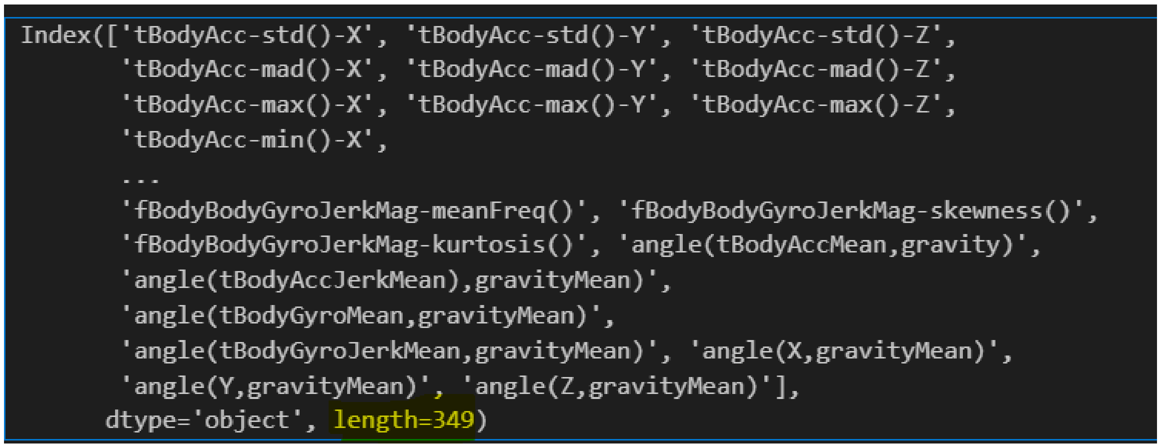


```
sel.get_support()
✓ 0.0s
array([False, False, False,  True,  True,  True,  True,  True,  True,
        True,  True,  True,  True,  True,  True,  True,  True, False,
       False,  True,  True,  True,  True,  True,  True,  True,  True,
        True,  True,  True, False, False, False,  True, False,  True,
        True,  True,  True,  True,  True,  True,  True, False, False,
       False, False, False, False,  True,  True,  True,  True,  True,
        True,  True,  True,  True,  True, False, False, False,  True,
        True,  True, False, False, False, False,  True,  True,  True,
        True,  True,  True,  True,  True,  True,  True,  True, False,
       False, False,  True,  True,  True,  True,  True,  True,  True,
        True,  True,  True,  True,  True,  True, False,  True, False,
        True,  True,  True,  True,  True,  True,  True, False,  True
```

False = columns' threshold is less than our decided one

To see the column names:

```
columns = X_train.columns[sel.get_support()]
columns
```


```
Index(['tBodyAcc-std()-X', 'tBodyAcc-std()-Y', 'tBodyAcc-std()-Z',
       'tBodyAcc-mad()-X', 'tBodyAcc-mad()-Y', 'tBodyAcc-mad()-Z',
       'tBodyAcc-max()-X', 'tBodyAcc-max()-Y', 'tBodyAcc-max()-Z',
       'tBodyAcc-min()-X',
       ...
       'fBodyBodyGyroJerkMag-meanFreq()', 'fBodyBodyGyroJerkMag-skewness()',
       'fBodyBodyGyroJerkMag-kurtosis()', 'angle(tBodyAccMean,gravity)',
       'angle(tBodyAccJerkMean),gravityMean)',
       'angle(tBodyGyroMean,gravityMean)',
       'angle(tBodyGyroJerkMean,gravityMean)', 'angle(X,gravityMean)',
       'angle(Y,gravityMean)', 'angle(Z,gravityMean)'],
      dtype='object', length=349)
```

Let's insert these columns in X_train & X_test:

```
X_train = sel.transform(X_train)
X_test = sel.transform(X_test)

X_train = pd.DataFrame(X_train, columns=columns)
X_test = pd.DataFrame(X_test, columns=columns)
```

X_train = sel.transform(X_train) : This is where the actual feature selection happens for your training data.

- The sel.transform(X_train) → It deletes all columns except the above ones
- But it returns a (**NumPy array**) containing only the *selected* features (columns) - those that had a variance greater than 0.05.

Why we used pd. DataFrame (X_train, columns=columns) ?

- **NumPy arrays → Pandas DataFrames**
- After sel.transform(X_train) and sel.transform(X_test) , X_train and X_test are no longer Pandas DataFrames. They become NumPy arrays.
- To convert them back into Pandas DataFrames (which are often easier to work with, especially if you want to keep column names), you use

`pd.DataFrame()` .

💡 **New sklearn: `.set_output()` → Get the output as DataFrame**

`fit` vs `transform` vs `fit_transform`

- `fit` is used on the **training data** to avoid any potential data leakage.
- `transform` is then used on both the training and test data to ensure the same features are selected in both.
- Using `fit_transform` on the test set would improperly use test data during training, which violates the principles of machine learning and can lead to biased results.

```
print(X_train.shape)
print(X_test.shape)

Output:
(5881, 349)
(1471, 349)
```

Points to Consider whiles using variance threshold:

It:

- Ignores Target Variable
- Ignores Feature Interactions
- Sensitive to Data Scaling
- Arbitrary Threshold Value

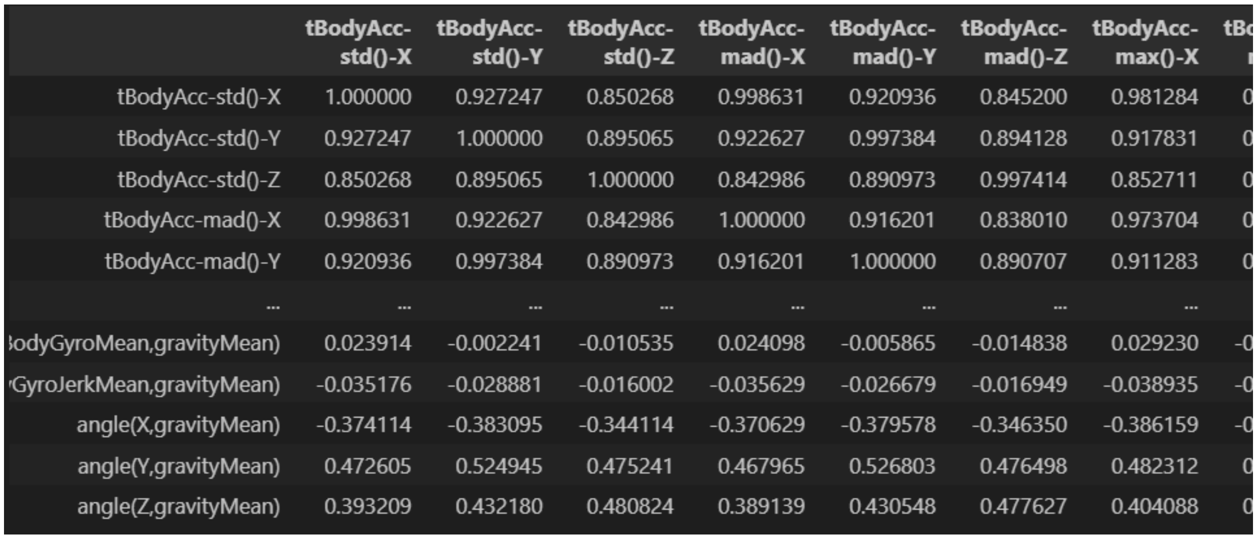
Correlation

- Pearson

Disadvantages of Correlation:

1. **Linearity Assumption**: Only measures **linear** relationships, not non-linear ones.
2. **Limited to Two Variables**: Doesn't capture **complex relationships** involving more than two variables.
3. **Threshold Determination**: Defining what's considered a **"high"** correlation is **subjective**.
4. **Sensitive to Outliers**: A few extreme values can **skew** the correlation coefficient.

```
X_train.corr()
```



	tBodyAcc-std()-X	tBodyAcc-std()-Y	tBodyAcc-std()-Z	tBodyAcc-mad()-X	tBodyAcc-mad()-Y	tBodyAcc-mad()-Z	tBodyAcc-max()-X	tBo
tBodyAcc-std()-X	1.000000	0.927247	0.850268	0.998631	0.920936	0.845200	0.981284	0
tBodyAcc-std()-Y	0.927247	1.000000	0.895065	0.922627	0.997384	0.894128	0.917831	0
tBodyAcc-std()-Z	0.850268	0.895065	1.000000	0.842986	0.890973	0.997414	0.852711	0
tBodyAcc-mad()-X	0.998631	0.922627	0.842986	1.000000	0.916201	0.838010	0.973704	0
tBodyAcc-mad()-Y	0.920936	0.997384	0.890973	0.916201	1.000000	0.890707	0.911283	0
...	...	...	...	...	...	...	...	
odyGyroMean,gravityMean)	0.023914	-0.002241	-0.010535	0.024098	-0.005865	-0.014838	0.029230	-0
GyroJerkMean,gravityMean)	-0.035176	-0.028881	-0.016002	-0.035629	-0.026679	-0.016949	-0.038935	-0
angle(X,gravityMean)	-0.374114	-0.383095	-0.344114	-0.370629	-0.379578	-0.346350	-0.386159	-0
angle(Y,gravityMean)	0.472605	0.524945	0.475241	0.467965	0.526803	0.476498	0.482312	0
angle(Z,gravityMean)	0.393209	0.432180	0.480824	0.389139	0.430548	0.477627	0.404088	0

Here, we can take 2 approaches:

1. Find out corr with y

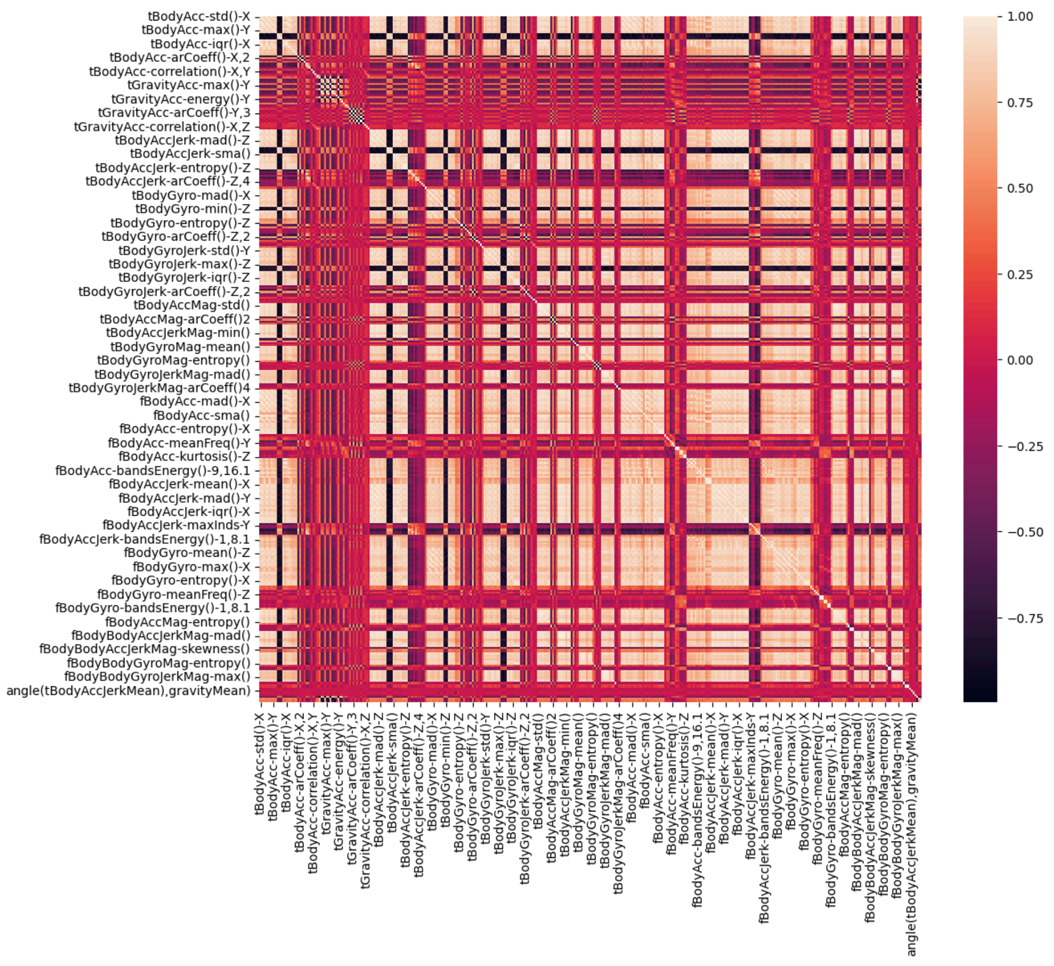
- Decide a range - eg. -0.3 to +0.3
- If it’s below -0.3 or above 0.3, keep the column

2. Find corr **between columns**
    - Select a threshold
    - If Corr is above absolute value, drop that column
    - This is to check **multicollinearity**
    - This is mostly used approach

What’s our approach?

- Find out corr between columns
- If it’s more than 0.95 → drop 1 of the columns

```
import matplotlib.pyplot as plt
plt.figure(figsize=(12,10))
sns.heatmap(X_train.corr())
```



```
corr_matrix = X_train.corr()
```

```
# Get the column names of the DataFrame
columns = corr_matrix.columns

# Create an empty list to keep track of columns to drop
columns_to_drop = []

# Loop over the columns
for i in range(len(columns)):
    for j in range(i + 1, len(columns)):
        # Access the cell of the DataFrame
        if corr_matrix.loc[columns[i], columns[j]] > 0.95:
            columns_to_drop.append(columns[j])

print(len(columns_to_drop))
```

`columns = corr_matrix.columns`: This line extracts the column names

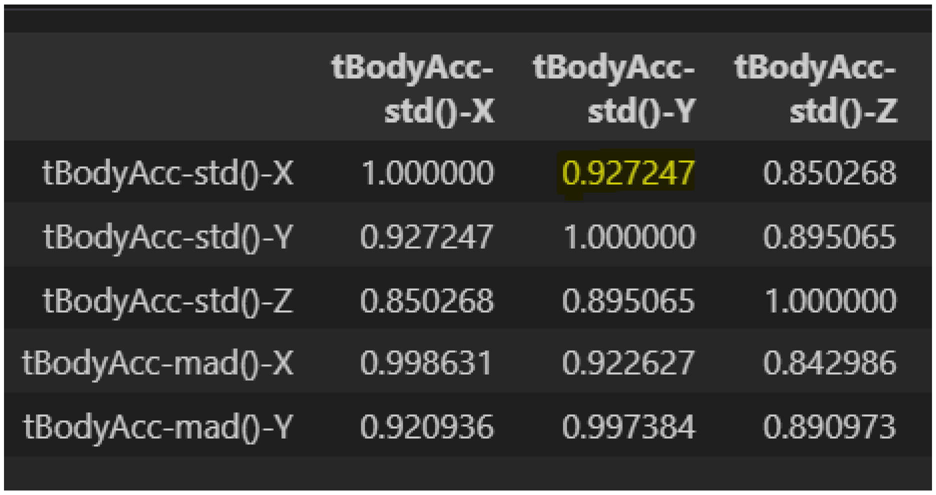
`for i in range(len(columns)):`
`for j in range(i + 1, len(columns)):`

Starting
`j` from `i + 1` ensures we only iterate through the *upper triangle* of the correlation matrix (excluding the diagonal and the lower triangle), thus avoiding redundant comparisons and also avoiding comparing a column with itself.

Remember

```
corr_matrix.loc[columns[0],columns[1]]
```

This will access this value:



	tBodyAcc-std()-X	tBodyAcc-std()-Y	tBodyAcc-std()-Z
tBodyAcc-std()-X	1.000000	0.927247	0.850268
tBodyAcc-std()-Y	0.927247	1.000000	0.895065
tBodyAcc-std()-Z	0.850268	0.895065	1.000000
tBodyAcc-mad()-X	0.998631	0.922627	0.842986
tBodyAcc-mad()-Y	0.920936	0.997384	0.890973

- `columns[0]` which is `'tBodyAcc-std()-X'` is used as the **row label**.
- `columns[1]` which is `'tBodyAcc-std()-Y'` is used as the **column label**.

How It Avoids Duplicate Checking:

- The key part is `for j in range(i + 1, len(columns))`.
    - When `i = 0`, `j` will start from **1**, so it compares column 0 with column 1, column 2, and so on.
    - When `i = 1`, `j` will start from **2**, so it compares column 1 with column 2, column 3, and so on.
    - When `i = 2`, `j` will start from **3**, so it compares column 2 with column 3, column 4, and so on.

> 💡 **It will go through the upper triangle.**

```
if corr_matrix.loc[columns[i], columns[j]] > 0.95:
  columns_to_drop.append(
columns[j] )
```

- If two features have a correlation **greater than 0.95**, the second feature (`columns[j]`) is marked for removal.

```
columns_to_drop = set(columns_to_drop)
len(columns_to_drop)

Output: 197 #columns to drop
```

- We converted the list in set to avoid duplicates

Drop all these columns:

```
X_train.drop(columns = columns_to_drop, axis = 1, inplace=True)
X_test.drop(columns = columns_to_drop, axis = 1, inplace=True)
```

```
print(X_train.shape)
print(X_test.shape)

Output:
(5881, 152)
(1471, 152)
```

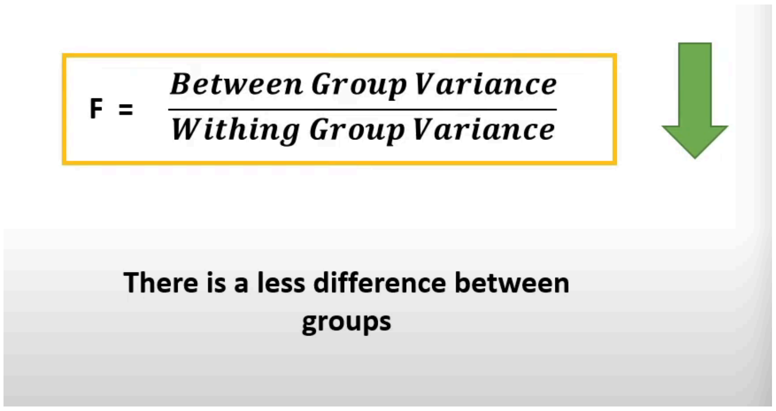
- Now we have 152 columns left.

ANOVA

- ANOVA is used when:
    - Input: Numeric
    - Output: Categorical (Usually 2+)
- Can also be used when output is numeric

How does ANOVA work?

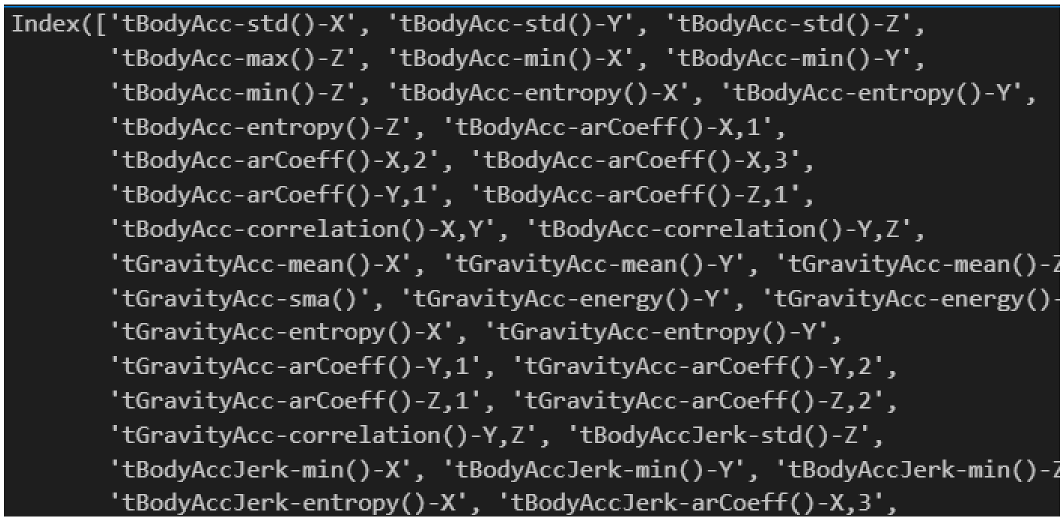
- You take 1 column & study its relationship with output column
- You calculate F-stats/F-ratio



$$F = \frac{\textit{Between Group Variance}}{\textit{Withing Group Variance}}$$

ANOVA using sklearn Python:

```
from sklearn.feature_selection import f_classif
from sklearn.feature_selection import SelectKBest

sel = SelectKBest(f_classif, k=100).fit(X_train, y_train)

# display selected feature names
X_train.columns[sel.get_support()]
```



```
Index(['tBodyAcc-std()-X', 'tBodyAcc-std()-Y', 'tBodyAcc-std()-Z',
       'tBodyAcc-max()-Z', 'tBodyAcc-min()-X', 'tBodyAcc-min()-Y',
       'tBodyAcc-min()-Z', 'tBodyAcc-entropy()-X', 'tBodyAcc-entropy()-Y',
       'tBodyAcc-entropy()-Z', 'tBodyAcc-arCoeff()-X,1',
       'tBodyAcc-arCoeff()-X,2', 'tBodyAcc-arCoeff()-X,3',
       'tBodyAcc-arCoeff()-Y,1', 'tBodyAcc-arCoeff()-Z,1',
       'tBodyAcc-correlation()-X,Y', 'tBodyAcc-correlation()-Y,Z',
       'tGravityAcc-mean()-X', 'tGravityAcc-mean()-Y', 'tGravityAcc-mean()-Z
       'tGravityAcc-sma()', 'tGravityAcc-energy()-Y', 'tGravityAcc-energy()-
       'tGravityAcc-entropy()-X', 'tGravityAcc-entropy()-Y',
       'tGravityAcc-arCoeff()-Y,1', 'tGravityAcc-arCoeff()-Y,2',
       'tGravityAcc-arCoeff()-Z,1', 'tGravityAcc-arCoeff()-Z,2',
       'tGravityAcc-correlation()-Y,Z', 'tBodyAccJerk-std()-Z',
       'tBodyAccJerk-min()-X', 'tBodyAccJerk-min()-Y', 'tBodyAccJerk-min()-Z
       'tBodyAccJerk-entropy()-X', 'tBodyAccJerk-arCoeff()-X,3',
```

`f_classif` → f classification

- calculates the **ANOVA F-value** for each feature

`SelectKBest` → Select the best features (in this case, 100 based on a scoring function (here, f_classif).

- Here, **we'll calculate ANOVA for all 152 columns & select best 100**

```
columns = X_train.columns[sel.get_support()]
```

- Now, transform the data

```
X_train = sel.transform(X_train)
X_test = sel.transform(X_test)
```

```
X_train = pd.DataFrame(X_train, columns=columns)
X_test = pd.DataFrame(X_test, columns=columns)
```

```
print(X_train.shape)
print(X_test.shape)

Output:
(5881, 100)
(1471, 100)
```

Disadvantages of ANOVA

- Assumption of Normality
- Assumption of Homogeneity of Variance
- Independence of Observations
- Effect of Outliers
- Doesn't Account for Interactions

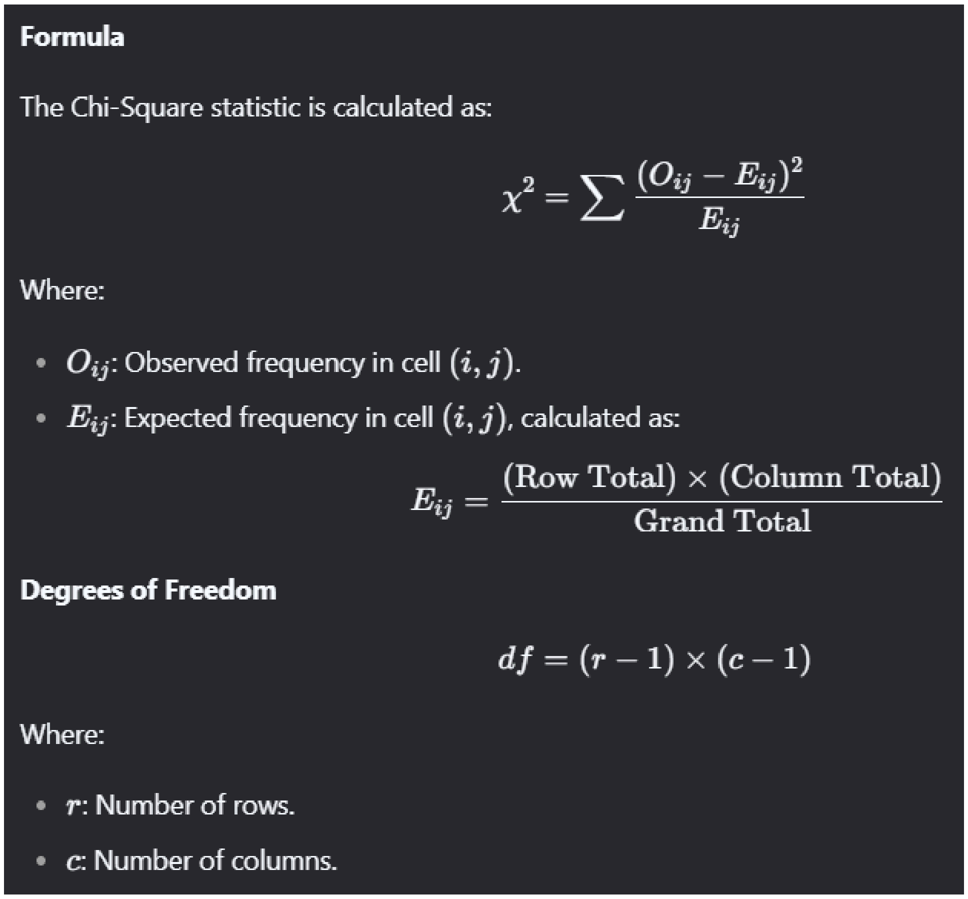
NOW, APPLY LOGISTIC REGRESSION AGAIN WITH NEW DATA

```
# Initialize and train logistic regression model
log_reg = LogisticRegression(max_iter=1000)  # Increase max_iter if it doesn't converge
log_reg.fit(X_train, y_train)

# Make predictions on the test set
y_pred = log_reg.predict(X_test)

# Calculate and print accuracy score
```

```
accuracy = accuracy_score(y_test, y_pred)
print("Test accuracy:", accuracy)
```

Output: Test accuracy: 0.9694085656016316

Chi-square Test



Formula

The Chi-Square statistic is calculated as:

$$\chi^2 = \sum \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

Where:

- O_{ij}: Observed frequency in cell (i, j).
- E_{ij}: Expected frequency in cell (i, j), calculated as:

$$E_{ij} = \frac{(\text{Row Total}) \times (\text{Column Total})}{\text{Grand Total}}$$

Degrees of Freedom

$$df = (r - 1) \times (c - 1)$$

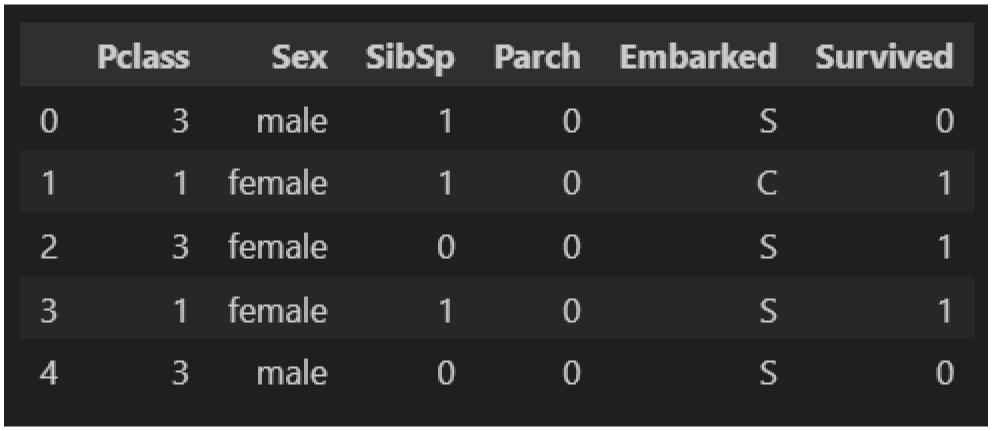
Where:

- r: Number of rows.
- c: Number of columns.

Chi Square

- Used when **both input & output** columns are **categorical**
- We'll use Titanic dataset

```
titanic = pd.read_csv('titanic/train.csv')[['Pclass','Sex','SibSp','Parch','Embarke
d','Survived']]
titanic.head()
```

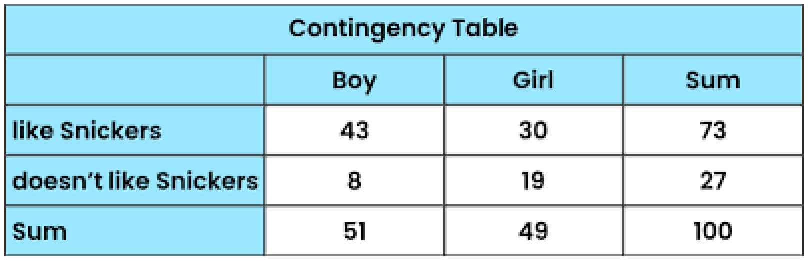


	Pclass	Sex	SibSp	Parch	Embarked	Survived
0	3	male	1	0	S	0
1	1	female	1	0	C	1
2	3	female	0	0	S	1
3	1	female	1	0	S	1
4	3	male	0	0	S	0

- Survived ll be output

How Chi Square works

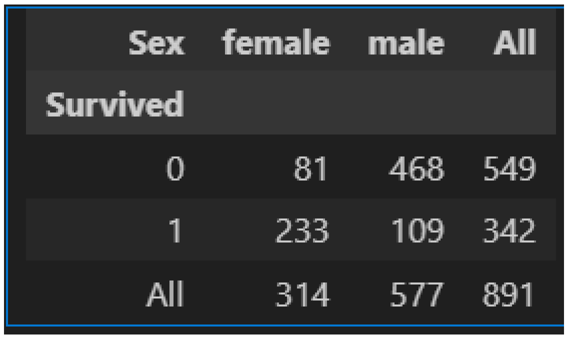
- We'll ask question: Is there any relationship betweent the columns sex & survived?
    - If no → we'll drop the sex column
- You form a contingency table like: 👇



Contingency Table			
	Boy	Girl	Sum
like Snickers	43	30	73
doesn't like Snickers	8	19	27
Sum	51	49	100

- We can do the same in python with `pd.crosstab()`

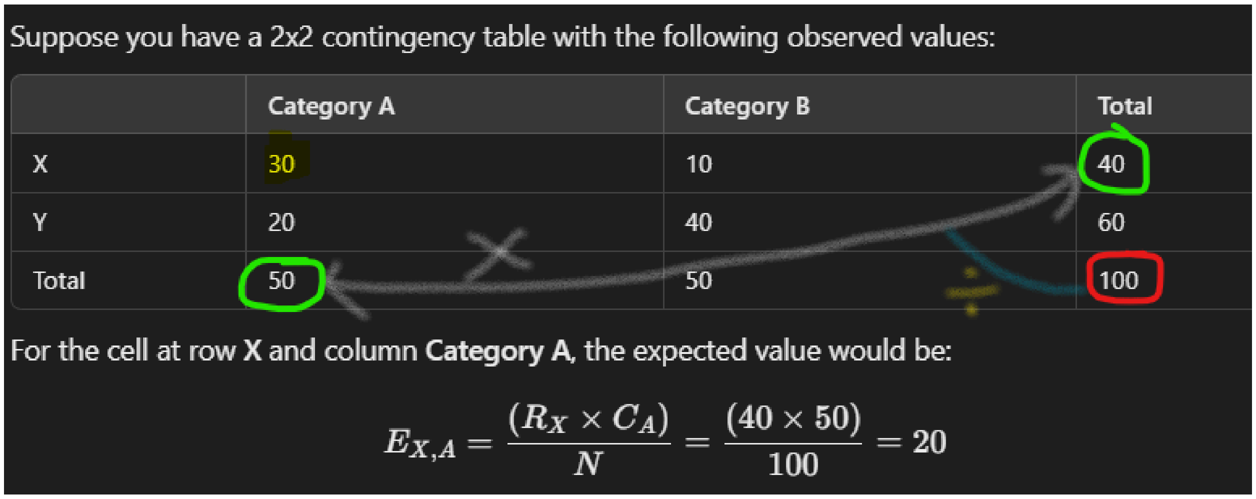
```
ct = pd.crosstab(titanic['Survived'],titanic['Sex'],margins=True)
ct
```



Sex	female	male	All
Survived			
0	81	468	549
1	233	109	342
All	314	577	891

- You can this👆 observed value

- You make one more table “**Expected**” with ideal data



Suppose you have a 2x2 contingency table with the following observed values:

	Category A	Category B	Total
X	30	10	40
Y	20	40	60
Total	50	50	100

For the cell at row **X** and column **Category A**, the expected value would be:

$$E_{X,A} = \frac{(R_X \times C_A)}{N} = \frac{(40 \times 50)}{100} = 20$$

```
ct2= pd.crosstab(titanic['Survived'],titanic['Sex'])
ct2

from scipy.stats import chi2_contingency
chi2_contingency(ct2)

Output:
Chi2ContingencyResult(statistic=260.71702016732104, pvalue=1.1973570627
755645e-58, dof=1, expected_freq=array([[193.47474747, 355.52525253],
       [120.52525253, 221.47474747]]))
```

- We used ct2 **without the all column because the all column interferes with results**

- Run a loop and calculate `chi2_contingency` for each column

```
score = []

for feature in titanic.columns[:-1]:

    # create contingency table
    ct = pd.crosstab(titanic['Survived'], titanic[feature])

    # chi_test
    p_value = chi2_contingency(ct)[1]
    score.append(p_value)
```

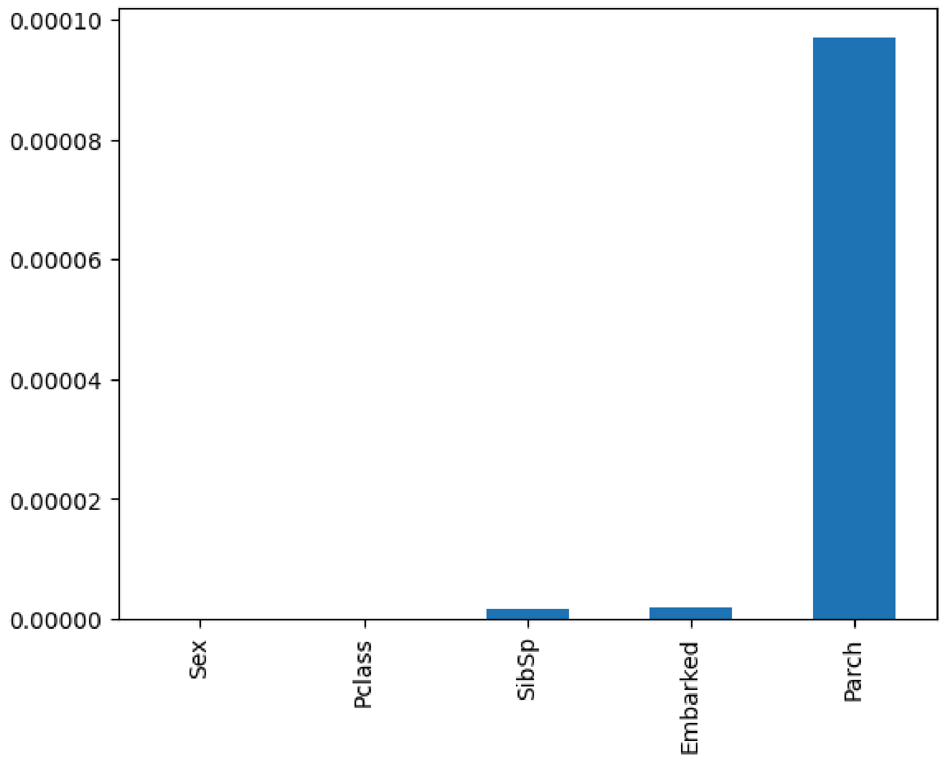
`titanic.columns[:-1]` → All columns except last one i.e. "Survived"

`chi2_contingency(ct)[1]` → p-value

```
score

Output:
[4.549251711298793e-23,
 1.1973570627755645e-58,
 1.5585810465902118e-06,
 9.703526421039996e-05,
 1.769922284120912e-06]
```

- Plot these on graph

```
pd.Series(score, index=titanic.columns[:-1]).sort_values(ascending=True).plot
(kind='bar')
```

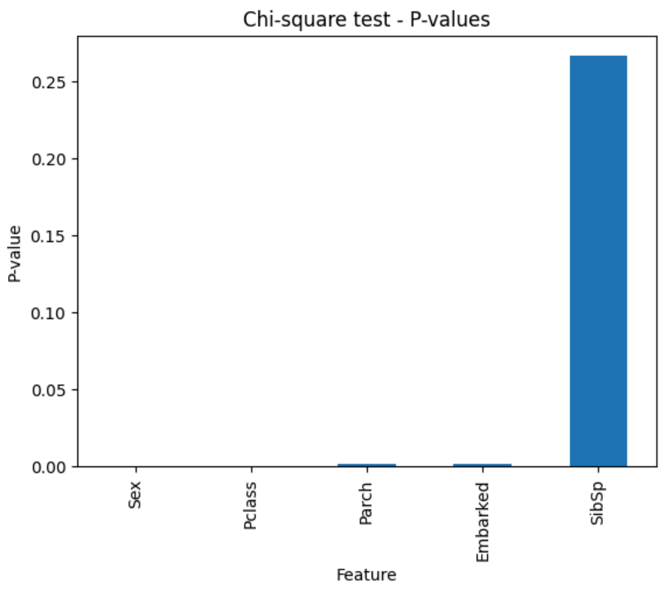


- More the p-value, less the importance of the feature.

Alternate code with `sklearn`

```
from sklearn.preprocessing import LabelEncoder
from sklearn.feature_selection import chi2
import matplotlib.pyplot as plt

# assuming titanic is your DataFrame and 'Survived' is the target column

# Encode categorical variables
le = LabelEncoder()
titanic_encoded = titanic.apply(le.fit_transform)
```

```
X = titanic_encoded.drop('Survived', axis=1)
y = titanic_encoded['Survived']

# Calculate chi-squared stats
chi_scores = chi2(X, y)

# chi_scores[1] are the p-values of each feature.
p_values = pd.Series(chi_scores[1], index = X.columns)
p_values.sort_values(inplace = True)

# Plotting the p-values
p_values.plot.bar()

plt.title('Chi-square test - P-values')
plt.xlabel('Feature')
plt.ylabel('P-value')

plt.show()
```



`le = LabelEncoder()`
`titanic_encoded = titanic.apply(le.fit_transform)`

- In this method, you have to convert the variables into Category
- This above code works with `SelectKBest`

`.apply(...)`: This is a Pandas DataFrame method that applies a function to each column (or row, depending on the `axis` argument, which defaults to columns if not specified) of the DataFrame.

`chi2(X, y)` returns→ ***Chi2 statistics & p_values***

Advantages and Disadvantages of Filter Methods

Advantages

- Simplicity
- Speed
- Scalability
- Pre-processing Step:
    - They can serve as a pre-processing step for other feature selection methods.
    - For instance, you could use a filter method to remove irrelevant features before applying a more computationally expensive method, such as a wrapper method.

Disadvantages

- Lack of Feature Interaction
- Model Agnostic:
    - This means that the selected features might not necessarily contribute to the accuracy of the specific model you want to use.

    - Can work well for one model & might not give that accurate results for another model.
- Statistical Measures Limitation:
    - For example, correlation is a measure of linear relationship and might not capture non-linear relationships effectively.
    - Similarly, variance-based methods might keep features with high variance but low predictive power.
- Threshold Determination

Mutual Information (MI)

`mutual_info_classif` → When Output column in Binary (Yes/No)

`mutual_info_regression` → When Output is Numerical

How Mutual Information Works in Feature Selection

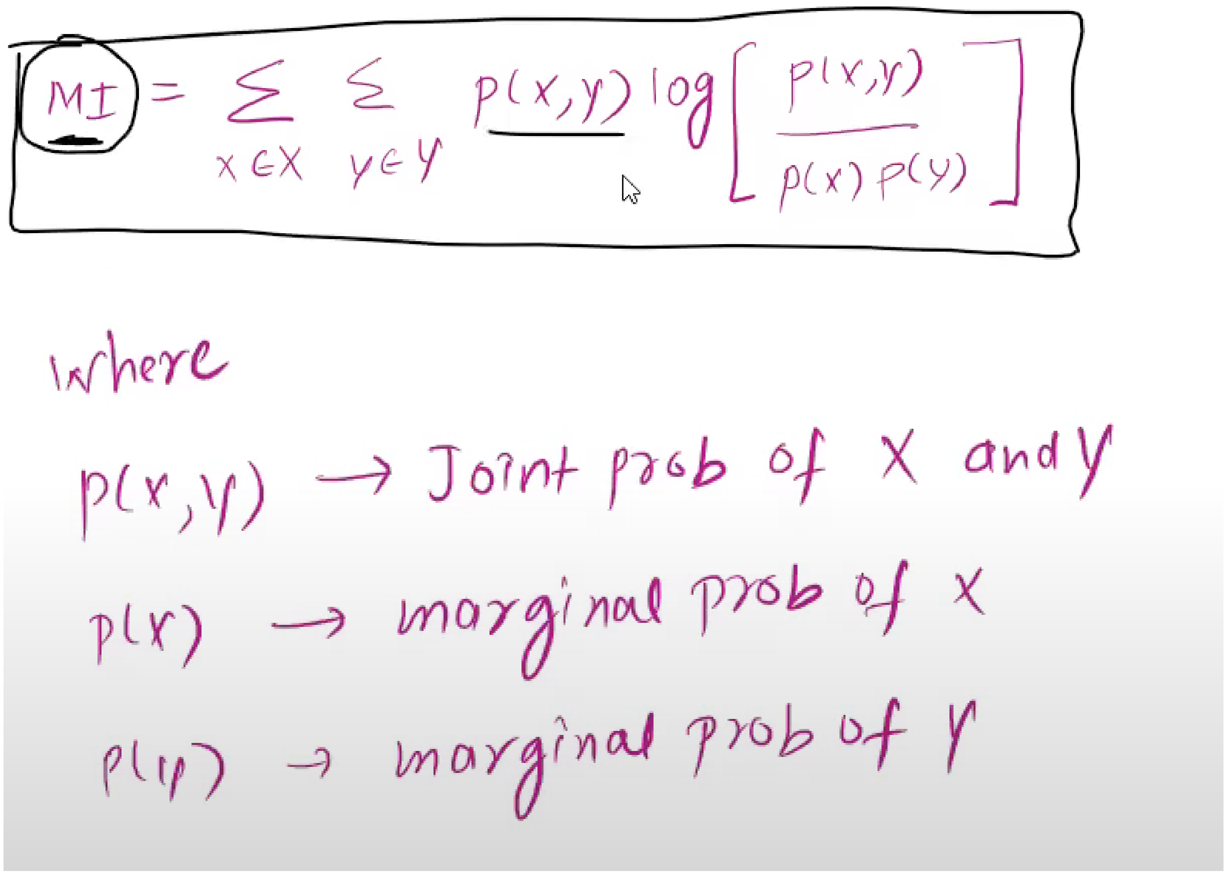
- MI captures **both linear and non-linear** relationships between features and the target.
- It does **not assume a specific data distribution**, unlike correlation.
- It helps rank features based on how much **useful information** they provide about the target.

Interpretation:

- **MI ≈ 0**: The feature and target are independent (no useful information).
- **MI > 0**: The feature helps predict the target.

- Measures the **dependency between two variables**.
    - How one column depends on other

- In feature selection, it helps determine **how much information a feature contributes** to predicting the target variable.
- If MI is high, the feature is strongly related to the target; if low, it is less useful.



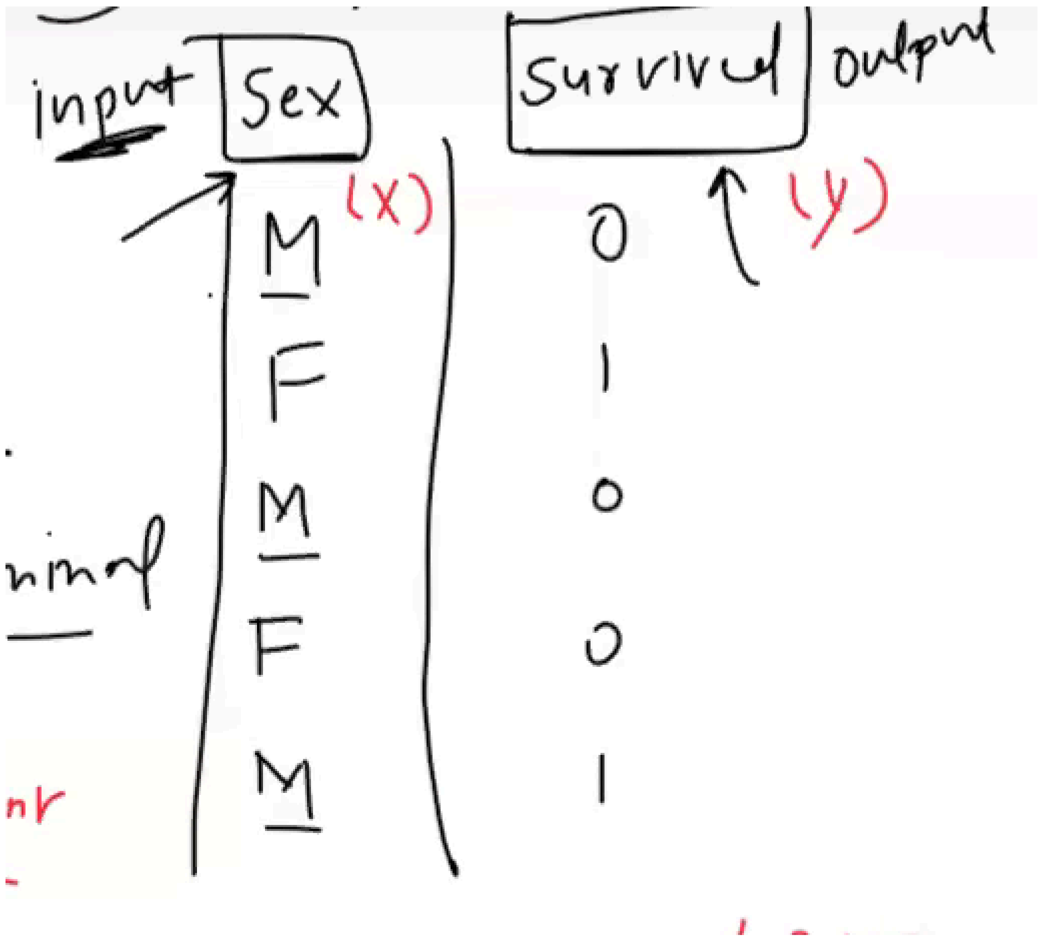
$$\boxed{MI = \sum_{x \in X} \sum_{y \in Y} \underline{p(x,y)} \log\left[\frac{p(x,y)}{p(x)\,p(y)}\right]}$$

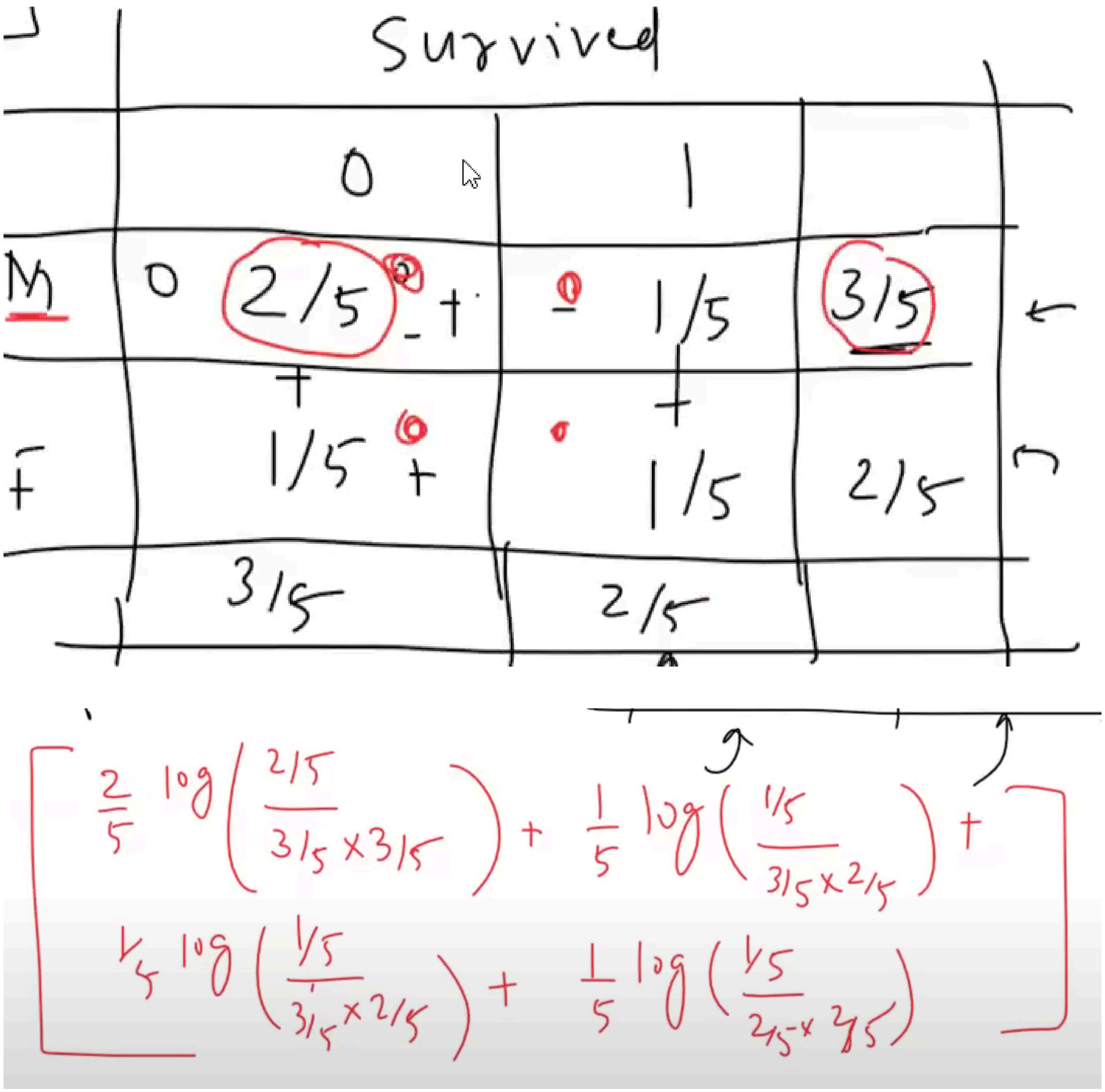
where

$p(x,y) \rightarrow$ Joint prob of X and Y

$p(x) \rightarrow$ marginal prob of X

$p(y) \rightarrow$ marginal prob of Y


input
Sex
(x)
Survived
output
(y)
M
F
M
F
M
0
1
0
0
1
nmal
nr



		Survived		
		0	1	
M	0	2/5	1/5	3/5
F		1/5	1/5	2/5
		3/5	2/5	

$$\left[\frac{2}{5} \log\left(\frac{2/5}{3/5 \times 3/5}\right) + \frac{1}{5} \log\left(\frac{1/5}{3/5 \times 2/5}\right) + \frac{1}{5} \log\left(\frac{1/5}{3/5 \times 2/5}\right) + \frac{1}{5} \log\left(\frac{1/5}{2/5 \times 3/5}\right) \right]$$

Key Points

1. Non-negative
2. Symmetric:

   $$MI(X,Y) = MI(Y,X)$$

3. It can capture any kind of statistical dependency

- Linear and non-linear
- Can be applied to numerical data → Internally histogram is created

Python code:

```
import pandas as pd

data = {
    'A': ['a1', 'a2', 'a1', 'a1', 'a2', 'a1', 'a2', 'a2'],
    'B': ['b1', 'b2', 'b2', 'b1', 'b1', 'b2', 'b2', 'b1']
}

df = pd.DataFrame(data)
```

```
from sklearn.feature_selection import mutual_info_classif
from sklearn.datasets import load_iris
import pandas as pd

# Load iris dataset
iris = load_iris()
X = iris['data']
y = iris['target']

# Compute mutual information
mi = mutual_info_classif(X, y)

# Print mutual information
for i, mi_value in enumerate(mi):
    print(f"Feature {i}: Mutual Information = {mi_value}")
```

Output:

```
Feature 0: Mutual Information = 0.5299968679612639
Feature 1: Mutual Information = 0.29450190713004587
Feature 2: Mutual Information = 0.9914331897550901
Feature 3: Mutual Information = 0.9972710833573024
```

`for i, mi_value in enumerate(mi):`

- `enumerate(mi)` :
    - `enumerate()` is a built-in Python function.
    - It is a function that loops through the list, and for each item in the list, it returns both:
        - `i` : The index of the feature (starting from 0).
        - `mi_value` : The **mutual information** value for the feature at index `i` .
    - In this case, `enumerate(mi)` will produce tuples like `(0, mi[0])` , `(1, mi[1])` , `(2, mi[2])` , and so on.

```
mi

Output:
array([0.52999687, 0.29450191, 0.99143319, 0.99727108])
```

You can use this with SelectKBest

```
from sklearn.feature_selection import SelectKBest, mutual_info_classif
from sklearn.datasets import load_iris

# Load iris dataset
iris = load_iris()
X = iris['data']
y = iris['target']

# Create SelectKBest feature selector
```

```
selector = SelectKBest(mutual_info_classif, k=2)

# Fit and transform
X_new = selector.fit_transform(X, y)

# Get columns to keep and create new dataframe with those only
cols = selector.get_support(indices=True)

print(iris.feature_names)
print(cols)
```

Output:

```
['sepal length (cm)', 'sepal width (cm)', 'petal length (cm)', 'petal width (cm)']
[2 3]
```

Disadvantages of Mutual Information (MI):

1. **Estimation Difficulty:** Sensitive to parameters/methods, especially with high dimensions or small samples.
2. **Needs Large Data:** Unreliable for small datasets.
3. **Computational Cost:** Slow for many features or continuous variables.
4. **Continuous Variables:** Hard to estimate due to density estimation challenges.
5. **No Relationship Insight:** Detects dependency but not type (linear/non-linear).
6. **Ignores Redundancy:** Selects relevant but potentially overlapping features.