# PUBLIC HEALTH AWARENESS CAMPAIGN ANALYSIS

## ABSTRACT:

Public health awareness campaigns play a pivotal role in promoting health and well-being, but their effectiveness often relies on the precision of their strategies and the ability to reach the intended audience. In this era of data-driven decision-making, the integration of data analytics has become increasingly essential for optimizing the impact of such campaigns. This abstract presents an overview of a comprehensive analysis of public health awareness campaigns using data analytics. This research aims to harness the power of data analytics to enhance the planning, execution, and evaluation of public health awareness campaigns. This research will employ a variety of data analytics techniques, including machine learning algorithms, natural language processing, and social network analysis. The findings will contribute to a deeper understanding of how data-driven insights can strengthen the impact of public health awareness campaigns and improve the overall health outcomes of communities. The implications of this research are far-reaching, as it offers a framework to enhance the precision and effectiveness of public health awareness campaigns, ultimately contributing to the betterment of public health on a global scale. The utilization of data analytics can revolutionize the way we design, implement, and evaluate health campaigns, making them more targeted, efficient, and impactful.

## PROJECT DEFINITION:

Public health campaigns involve the strategic dissemination of information to the public in order to help groups of people resist imminent health threats and adopt behaviour's that promote good health. The project involves analysing data from public health awareness campaigns to measure their effectiveness in reaching the target audience and increasing awareness. The objective is to provide insights that evaluate the impact of the campaigns and inform future strategies. This project includes defining analysis objectives, collecting campaign data, designing relevant visualizations in IBM Cognos, and using code for data analysis.

## DESIGN THINKING:

## 1.ANALYSIS OBJECTIVES:

- **MEASURING AUDIENCE REACH:**

The right to health includes a right of access to good quality palliative care, but inequalities persist. Raising awareness is a key plank of the public health approach to palliative care, but involves consideration of subjects most of us prefer not to address. This review addresses the question: "do public health awareness campaigns effectively improve the awareness and quality of palliative care"?

- **AWARENESS LEVEL:**

1. Start young Most research on advance care planning involves people over the age of 65. There is now a trend toward involving and educating much younger people, so that they are better prepared to deal with the issues in their families and communities. One study looks at university students in the United States and recommends that an important aspect of public health is providing reliable information about advance care planning to all young people.

2. An evaluation of TV advertisements about health promotion aimed at older adults showed that recipients were generally distrustful of the information if they perceived that it had been provided by the "government". Professionals such as doctors or celebrities (e.g., Olympic stars) were seen as more trustworthy.

3. social media has the potential to increase engagement with healthcare issues and enable debate and discussion, as well as create virtual social networks.

4. Younger people prefer to receive health information through the internet or other electronic means, while older people prefer the newspapers.

- **CAMPAIGN IMPACT:**

The evidence shows that public awareness campaigns can improve awareness of palliative care and probably improve quality of care, but there is a lack of evidence about the latter.

## 2.DATA COLLECTION:

This dataset is from a 2014 survey that measures attitudes towards mental health and frequency of mental health disorders in the tech workplace. Quantitative and qualitative data collection methods include surveys and questionnaires, focus groups, interviews, and observations and progress tracking.

## 3.VISUALIZATION STRATEGY:

- **DASHBOARD:** IBM Cognos Dashboard Embedded gives developers a way to embed an intuitive, drag-and-drop visualization tool, providing end users the ability to explore data and create visualizations that answer the unique questions important to your business.
- **REPORTS**: Reporting is a web-based report authoring tool that professional report authors and developers use to build sophisticated, multiple-page, multiple-query reports against multiple databases.
- **VISUALIZATIONS:** Opens many different types of graphs that you can use to visualize the data from the selected data source connection. Drill down into your source connection and select the data segments you want to visualize.

The given dataset contains the following data:

- **Timestamp**
- **Age**
- **Gender**
- **Country**
- **State**: If you live in the United States, which state or territory do you live in?
- **Self-employed**: Are you self-employed?
- **Family history**: Do you have a family history of mental illness?
- **Treatment**: Have you sought treatment for a mental health condition?
- **Work interferes**: If you have a mental health condition, do you feel that it interferes with your work?
- **Number of employees**: How many employees does your company or organization have?
- **Remote work**: Do you work remotely (outside of an office) at least 50% of the time?
- **IT company**: Is your employer primarily a tech company/organization?
- **Benefits**: Does your employer provide mental health benefits?
- **Care options**: Do you know the options for mental health care your employer provides?
- **Wellness program**: Has your employer ever discussed mental health as part of an employee wellness program?
- **Seek help**: Does your employer provide resources to learn more about mental health issues and how to seek help?
- **Anonymity**: Is your anonymity protected if you choose to take advantage of mental health or substance abuse treatment resources?
- **Leave**: How easy is it for you to take medical leave for a mental health condition?
- **Mental health consequence**: Do you think that discussing a mental health issue with your employer would have negative consequences?
- **Physical health consequence**: Do you think that discussing a physical health issue with your employer would have negative consequences?

- **Coworkers**: Would you be willing to discuss a mental health issue with your coworkers?
- **Supervisor**: Would you be willing to discuss a mental health issue with your direct supervisor(s)?
- **Mental health interview**: Would you bring up a mental health issue with a potential employer in an interview?
- **Physical health interview**: Would you bring up a physical health issue with a potential employer in an interview?
- **Mental vs Physical**: Do you feel that your employer takes mental health as seriously as physical health?
- **Observed consequence**: Have you heard of or observed negative consequences for coworkers with mental health conditions in your workplace?
- **Comments**: Any additional notes or comments

**Using IBM Cognos, we can visualize and create the Dashboards and reports from the following dataset.**

## 4.CODE INTEGRATION:

The aspects of the analysis can be enhanced using code such as

*Import necessary Libraries

*Read Dataset

*Preprocessing and Cleaning Dataset

*Split the data to train and test

*Random Forest Classifier

*K nearest neighbour

*Support vector Classifier

*Decision Tree

## MACHINE LEARNING ALGORITHM:

### IMPORT NECESSARY LIBRARIES

***In [1]:***

```
#imports necessary libraries to do basic things on the dataset
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
print('Successfully imported')
```

***Explanation:***

We have imported some essential libraries for working with datasets in Python. Here's a breakdown of the libraries we have imported and what they are commonly used for:

1.pandas (imported as 'pd'): Pandas is a popular library for data manipulation and analysis. It provides data structures like Data Frame and Series, which are especially useful for working with structured data.

2.numpy (imported as 'np'): NumPy is a fundamental library for numerical operations in Python. It provides support for multidimensional arrays and various mathematical functions, making it indispensable for scientific computing and data analysis.

3.seaborn (imported as 'sns'): Seaborn is a data visualization library built on top of Matplotlib. It simplifies the creation of aesthetically pleasing and informative statistical graphics.

4.matplotlib.pyplot (imported as 'plt'): Matplotlib is a comprehensive data visualization library in Python. pyplot is a sub-library within Mat plotlib that provides a simple interface for creating various types of plots and charts.

Our code snippet concludes by printing "Successfully imported" to confirm that these libraries have been imported without any errors.

These libraries provide a solid foundation for working with datasets and creating visualizations in Python.

***Out [1]:***

```
Successfully imported
```

## READ DATASET

***In [2]:***

```
#Reading data
data = pd.read_csv('/kaggle/input/mental-health-in-tech-survey/survey
.csv')
data.head()
```

***Explanation:***

Reading a dataset from a CSV file named 'survey.csv' using the pandas library. The dataset is likely related to public health awareness campaign, as indicated by the file name and the context of the previous code.

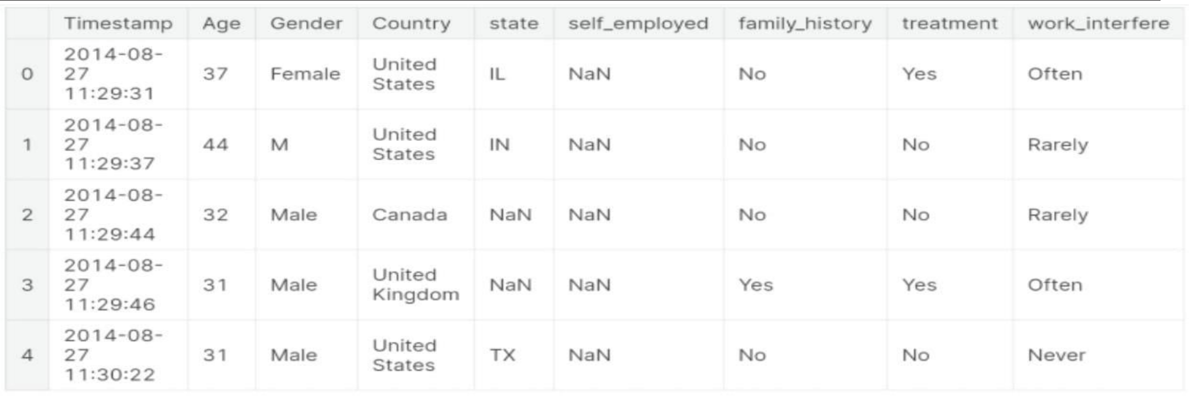
Here's a brief explanation of the code:

1.pd.read_csv('/kaggle/input/Public-health-awareness-campaign-survey/survey.csv'): This line of code uses the pd.read_csv() function from the pandas library to read the data from the CSV file located at the specified path. The dataset is loaded into a Data Frame, which is a two-dimensional, tabular data structure that pandas provide.

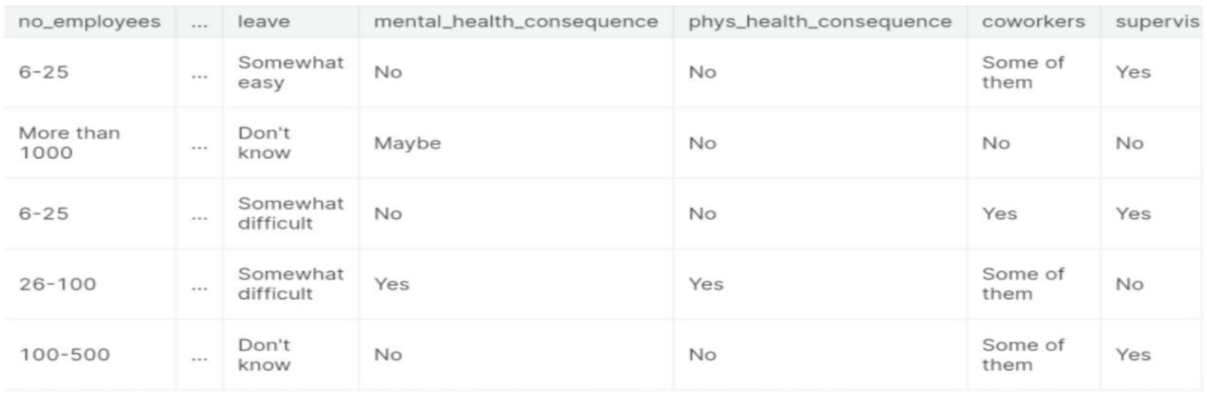
2.data.head(): After loading the dataset into the data Data Frame, the .head() method is called to display the first few rows of the Data Frame. This is a quick way to inspect the dataset and get a sense of its structure and content.

Make sure that the file path provided in pd.read_csv() is correct and points to the location of your 'survey.csv' file. Once we have successfully loaded the data, we can start exploring and analysing it using pandas and other data analysis tools

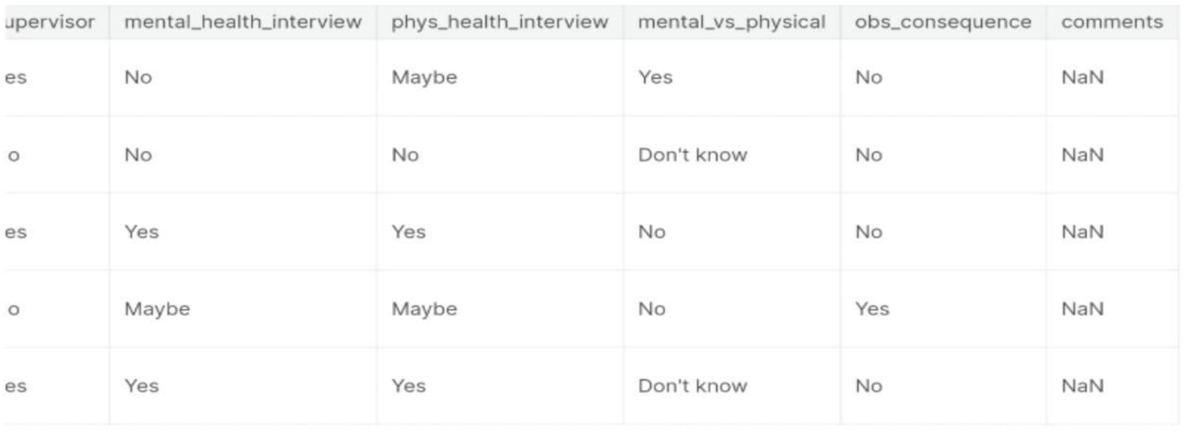
***Out [2]:***



| | Timestamp | Age | Gender | Country | state | self_employed | family_history | treatment | work_interfere |
|---|---|---|---|---|---|---|---|---|---|
| 0 | 2014-08-27 11:29:31 | 37 | Female | United States | IL | NaN | No | Yes | Often |
| 1 | 2014-08-27 11:29:37 | 44 | M | United States | IN | NaN | No | No | Rarely |
| 2 | 2014-08-27 11:29:44 | 32 | Male | Canada | NaN | NaN | No | No | Rarely |
| 3 | 2014-08-27 11:29:46 | 31 | Male | United Kingdom | NaN | NaN | Yes | Yes | Often |
| 4 | 2014-08-27 11:30:22 | 31 | Male | United States | TX | NaN | No | No | Never |



| no_employees | ... | leave | mental_health_consequence | phys_health_consequence | coworkers | supervis |
|---|---|---|---|---|---|---|
| 6-25 | ... | Somewhat easy | No | No | Some of them | Yes |
| More than 1000 | ... | Don't know | Maybe | No | No | No |
| 6-25 | ... | Somewhat difficult | No | No | Yes | Yes |
| 26-100 | ... | Somewhat difficult | Yes | Yes | Some of them | No |
| 100-500 | ... | Don't know | No | No | Some of them | Yes |



| upervisor | mental_health_interview | phys_health_interview | mental_vs_physical | obs_consequence | comments |
|---|---|---|---|---|---|
| es | No | Maybe | Yes | No | NaN |
| o | No | No | Don't know | No | NaN |
| es | Yes | Yes | No | No | NaN |
| o | Maybe | Maybe | No | Yes | NaN |
| es | Yes | Yes | Don't know | No | NaN |

## PREPROCESSING AND CLEANING DATASET

***In [3]:***

```
#Check the dataset for missing data
if data.isnull().sum().sum() == 0 :
print ('There is no missing data in our dataset')
else:
print('There is {} missing data in our dataset '.format(data.isnull().sum
().sum()))
```

***Explanation:***

This code checks the dataset for missing data and prints a message depending on whether there are any missing values. Here's what it does:

**1.’**data.isnull()’: This part of the code generates a Boolean DataFrame where each element is True if the corresponding element in the original data DataFrame is missing (i.e., NaN or None), and False otherwise.

**2.**’.sum()’: The sum() function is applied twice. The first sum() calculates the sum of missing values for each column (since isnull() produces True for missing values and False for non-missing values, summing them will give the count of missing values in each column).

The second sum() calculates the sum of all missing values across all columns, resulting in the total count of missing values in the entire dataset.

**3.**’if data.isnull().sum().sum() == 0:’: This condition checks if the total count of missing values in the dataset is equal to zero.

**4.**If there are no missing values (the condition is met), it prints "There is no missing data in our dataset."

**5.**If there are missing values, it prints "There is X missing data in our dataset," where X is the total count of missing values.

This code is a good way to quickly check if there are any missing values in your dataset and inform you about their presence or absence. If there are missing values, you may need to decide how to handle them, whether it's by imputing missing values, removing rows with missing values, or using other data cleaning techniques.

***out [3]:***

```
There is 1892 missing data in our dataset
```

***In [4]:***

```
#Check our missing data from which columns and how many unique
 features they have.
frame = pd.concat([data.isnull().sum(), data.nunique(), data.dtypes],
axis = 1, sort= False)frame
```

***Explanation:***

Here are some common scenarios you might encounter:

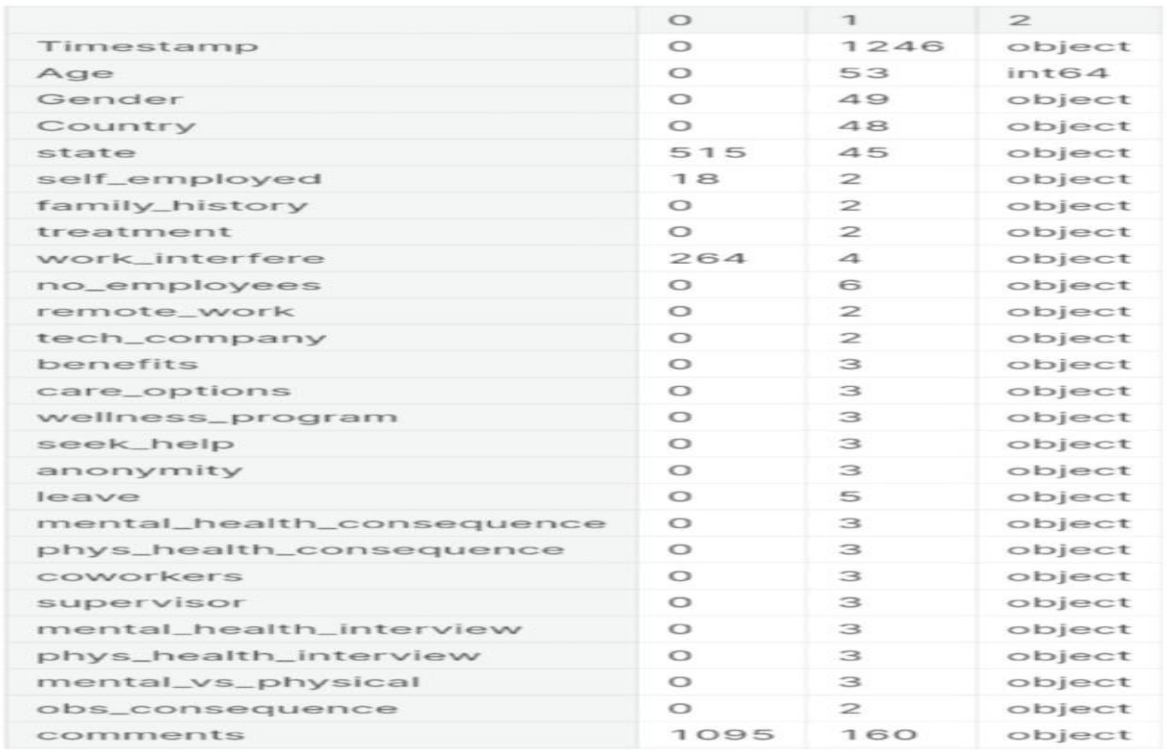
**1.**Categorical Values: If the unique values are categorical, such as 'Often',’Rarely,' 'Sometimes,' 'Never,' etc., it suggests that this column represents ordinal data indicating how often work interferes with public health awareness. In this case, consider filling missing values with the mode (most frequent value) since it's an ordinal categorical variable.

**2.**Numeric Values: If the unique values are numeric, it might represent a continuous scale or a count. In this case, we could consider filling missing values with the mean, median, or a specific value like 0, depending on the context.

**3.**Other Values: Depending on the specific unique values, we might choose a different filling strategy. For example, if there are only 'Yes' and 'No' values, we could fill missing values with a default option like 'No' if it makes sense in our analysis.

After inspecting the unique values, we can decide on an appropriate method for filling the NaN values in the 'Work interfere' column, cons idering the nature of the data and our analysis goals.

***out [4]:***



| | 0 | 1 | 2 |
|---|---|---|---|
| Timestamp | 0 | 1246 | object |
| Age | 0 | 53 | int64 |
| Gender | 0 | 49 | object |
| Country | 0 | 48 | object |
| state | 515 | 45 | object |
| self_employed | 18 | 2 | object |
| family_history | 0 | 2 | object |
| treatment | 0 | 2 | object |
| work_interfere | 264 | 4 | object |
| no_employees | 0 | 6 | object |
| remote_work | 0 | 2 | object |
| tech_company | 0 | 2 | object |
| benefits | 0 | 3 | object |
| care_options | 0 | 3 | object |
| wellness_program | 0 | 3 | object |
| seek_help | 0 | 3 | object |
| anonymity | 0 | 3 | object |
| leave | 0 | 5 | object |
| mental_health_consequence | 0 | 3 | object |
| phys_health_consequence | 0 | 3 | object |
| coworkers | 0 | 3 | object |
| supervisor | 0 | 3 | object |
| mental_health_interview | 0 | 3 | object |
| phys_health_interview | 0 | 3 | object |
| mental_vs_physical | 0 | 3 | object |
| obs_consequence | 0 | 2 | object |
| comments | 1095 | 160 | object |

***In [5]:***

```
#Look at what is in the 'Work interfere' column to choose a suitable m
ethod to fill nan values.
data['work interfere'].unique()
```

***Explanation:***

We created a count plot to visualize the distribution of the 'work_interfere' column in our dataset using Seaborn. Additionally, we want to add the count values on top of the bars for each category. However, the code provided for adding labels to the bars might not work as intended.

This code will create a count plot for the 'work interfere' column and a dd labels showing the count on top of each bar. Additionally, it rotates the x-axis labels by 45 degrees for better readability if there are many categories.

***out [5]:***

```
array(['Often', 'Rarely', 'Never', 'Sometimes', nan], dtype=object)
```

***In [6]:***

```
#Plot **work_interfere**
ax = sns.countplot(data = data , x = 'work_interfere');
#Add the value of each parametr on the Plot
ax.bar_label(ax.containers[0]);
```

***Explanation:***

We are performing some data preprocessing tasks using scikit-learns Simple Imputer to handle missing values and dropping specific columns from our dataset. Here's a breakdown of what each part of the code does:

**1.**We have a list called columns_to_drop that contains the names of columns we want to remove from the dataset: 'state', 'comments', and ' Timestamp'.

**2.**Loop through the columns in columns_to_drop and check if each column exists in the dataset (data.columns). If it does, drop that column using data.drop(columns=[column]). This step effectively removes these columns from the dataset.

**3.**We used Simple Imputer to fill in missing values in the 'work_interfere' and 'self_employed' columns.

a)For 'work_interfere', we use the 'most_frequent' strategy to fill missing values with the most frequent value in that column.

b)For 'self_employed', we also use the 'most_frequent' strategy.

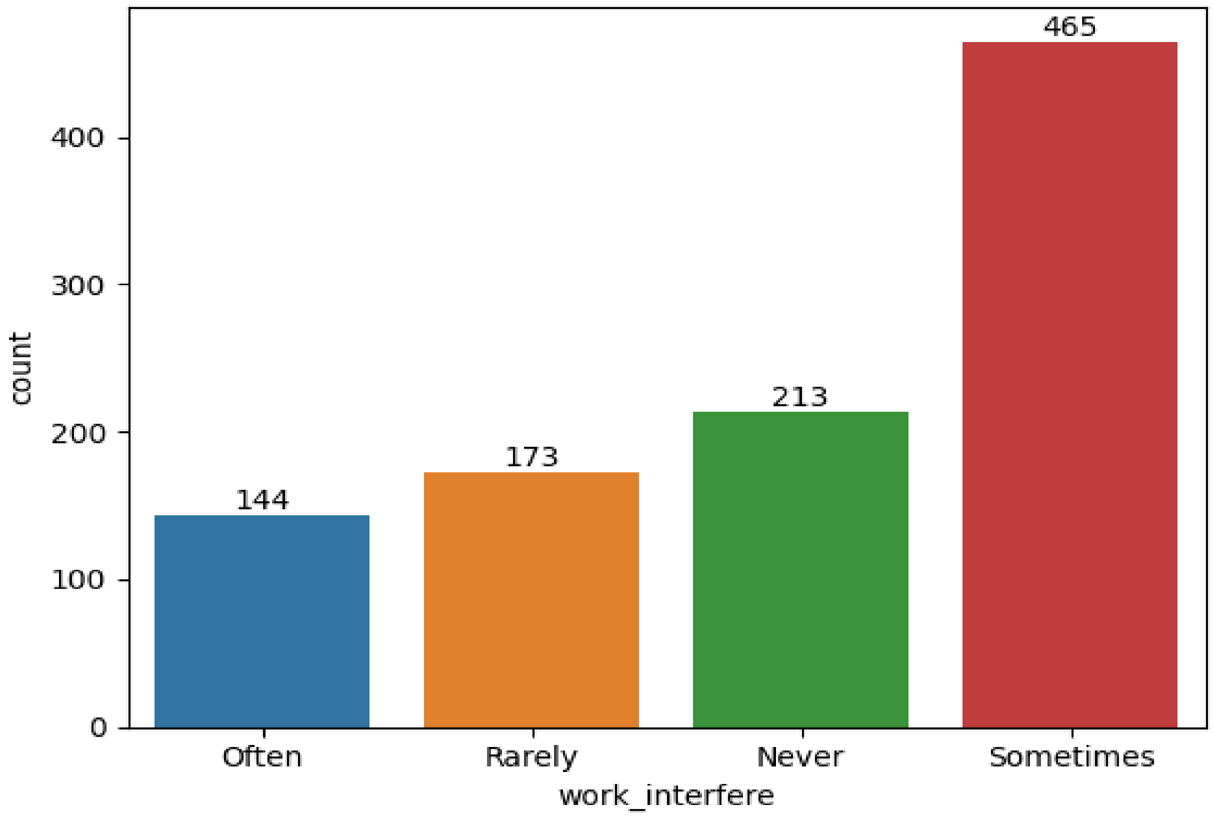
Reshape the input data using .values.reshape(-1, 1) to ensure it has the correct

shape for Simple Imputer, and then use np.ravel to convert the result back into a 1D array and assign it to the respective columns in our Data Frame.

**4.**Finally, display the first few rows of the modified dataset using data.head().

This code effectively removes certain columns from our dataset and fills in missing values in 'work_interfere' and 'self_employed' with the most frequent values. This preprocessing step helps prepare our data for further analysis or modeling.

***out [6]:***



***In [7]:***

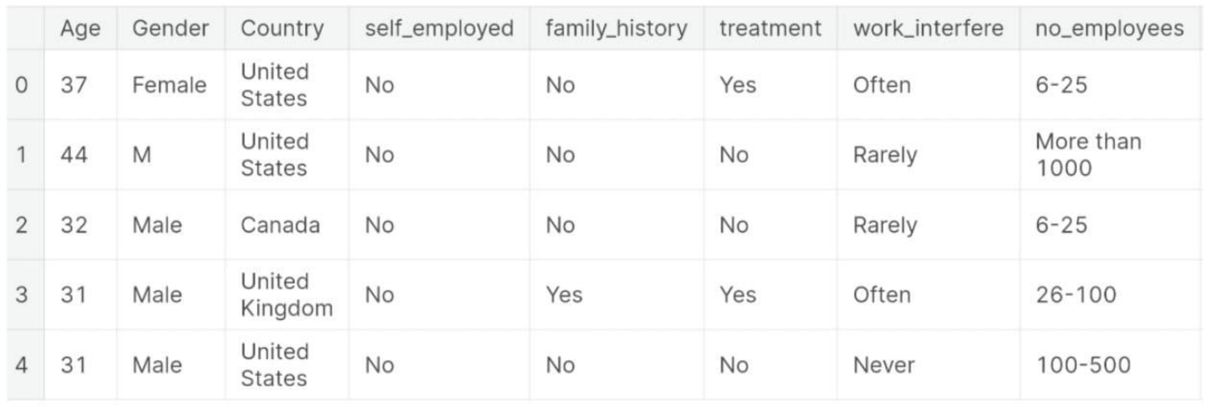
```
from sklearn.impute import SimpleImputer
import numpy as np
columns_to_drop = ['state', 'comments', 'Timestamp']
for column in columns_to_drop:
    if column in data.columns:
        data = data.drop(columns=[column])

# Fill in missing values in work_interfere column
data['work_interfere'] = np.ravel(SimpleImputer(strategy = 'most_freq
uent').fit_transform(data['work_interfere'].values.reshape(-1,1)))
```

```
data['self_employed'] = np.ravel(SimpleImputer(strategy = 'most_frequent').fit_transform(data['self_employed'].values.reshape(-1,1)))
data.head()
```

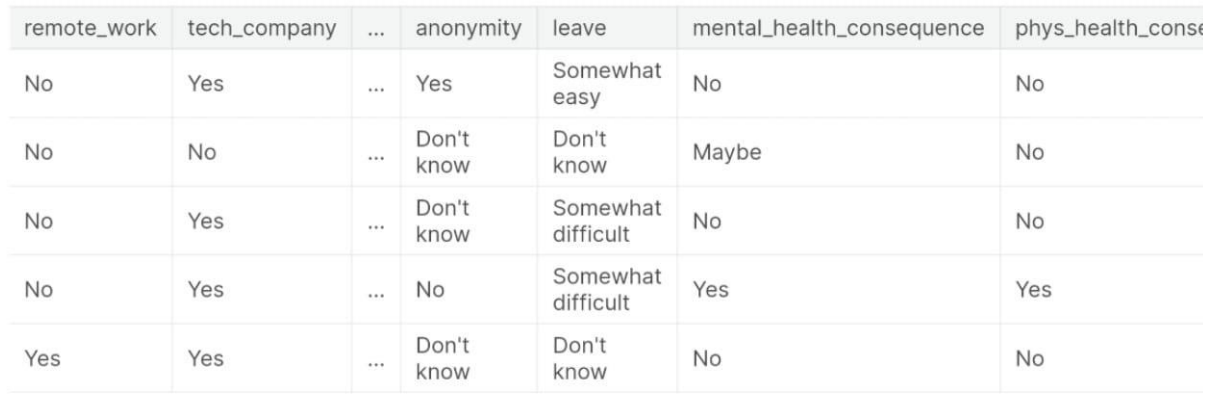
***Explanation:***

We want to create a count plot for the 'work_interfere' column in our dataset using Seaborn and add labels with counts on top of the bars. However, the code provided for adding labels to the bars may not work as intended. This code will create a count plot for the 'work_interfere' column and add labels showing the count on top of each bar. Additionally, it rotates the x-axis labels by 45 degrees for better readability if there are many categories.

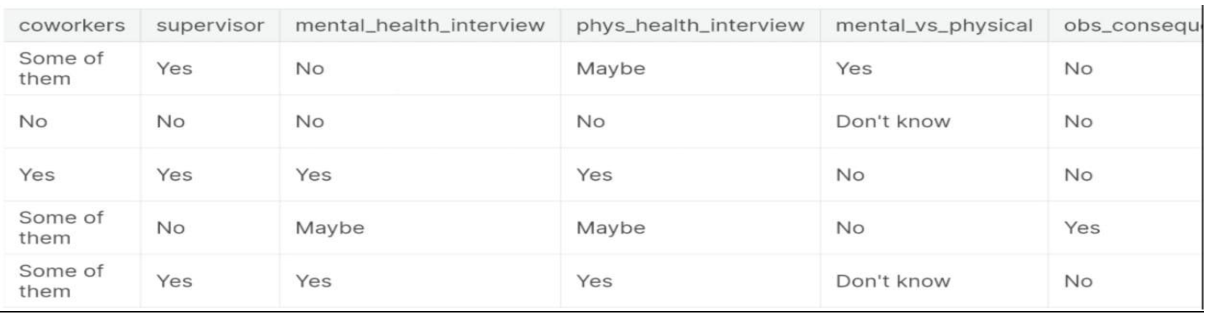
***out [7]:***



| | Age | Gender | Country | self_employed | family_history | treatment | work_interfere | no_employees |
|---|---|---|---|---|---|---|---|---|
| 0 | 37 | Female | United States | No | No | Yes | Often | 6-25 |
| 1 | 44 | M | United States | No | No | No | Rarely | More than 1000 |
| 2 | 32 | Male | Canada | No | No | No | Rarely | 6-25 |
| 3 | 31 | Male | United Kingdom | No | Yes | Yes | Often | 26-100 |
| 4 | 31 | Male | United States | No | No | No | Never | 100-500 |



| remote_work | tech_company | ... | anonymity | leave | mental_health_consequence | phys_health_conse |
|---|---|---|---|---|---|---|
| No | Yes | ... | Yes | Somewhat easy | No | No |
| No | No | ... | Don't know | Don't know | Maybe | No |
| No | Yes | ... | Don't know | Somewhat difficult | No | No |
| No | Yes | ... | No | Somewhat difficult | Yes | Yes |
| Yes | Yes | ... | Don't know | Don't know | No | No |



| coworkers | supervisor | mental_health_interview | phys_health_interview | mental_vs_physical | obs_consequ |
|---|---|---|---|---|---|
| Some of them | Yes | No | Maybe | Yes | No |
| No | No | No | No | Don't know | No |
| Yes | Yes | Yes | Yes | No | No |
| Some of them | No | Maybe | Maybe | No | Yes |
| Some of them | Yes | Yes | Yes | Don't know | No |

***In [8]:***

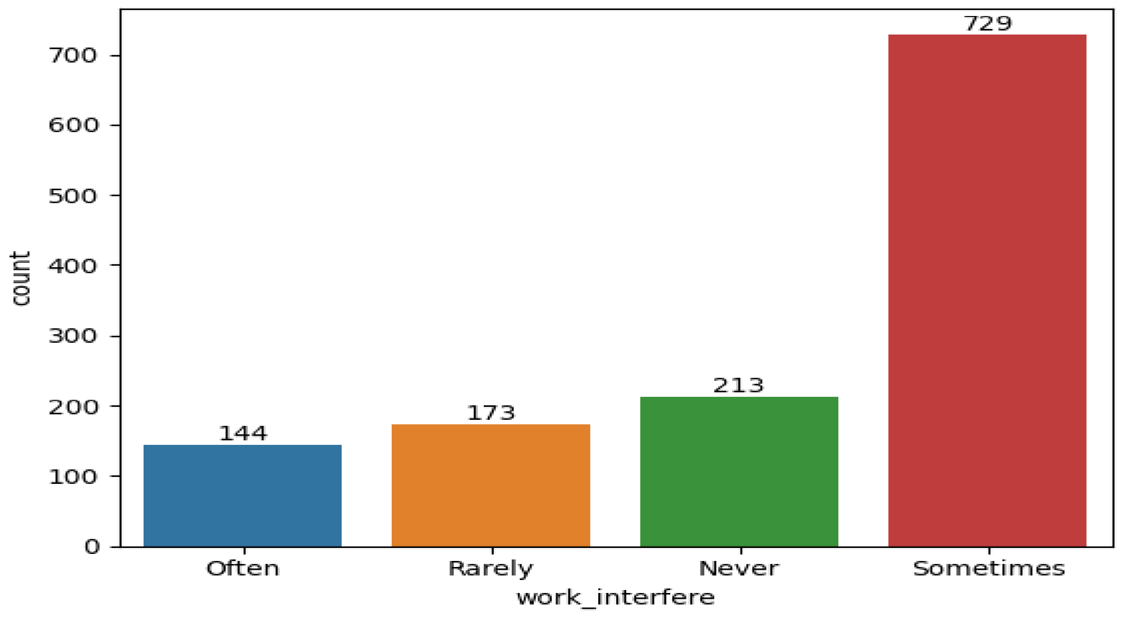
```
ax = sns.countplot(data=data, x='work_interfere');
ax.bar_label(ax.containers[0]);
```

***Explanation:***

We want to create a count plot for the 'work_interfere' column in our dataset using Seaborn and add labels with counts on top of the bars. However,the code provided for adding labels to the bars may not work as intended.

This code will create a count plot for the 'work_interfere' column and add labels showing the count on top of each bar. Additionally, it rotates the x-axis labels by 45 degrees for better readability if there are many categories.

***Out [8]:***



***In [9]:***

```
#Check unique data in gender columns
print(data['Gender'].unique())
print('')
print('-'*75)
print('')
#Check number of unique data too.
```

```
print('number of unique Gender in our dataset is :', data['Gender'].nuni
que())
```

***<u>Explanation:</u>***

Our code checks the unique values in the 'Gender' column of our dataset and also counts the number of unique values. Here's what each part of the code does:

**1.**print(data['Gender'].unique()): This line of code prints the unique values in the 'Gender' column of our dataset. This help us to understand the different categories or labels present in this column.

**2.**print(''): This prints an empty line to separate the output for better readability.

**3.**print('-'*75): This prints a line of hyphens to further separate the output visually.

**4.**print('number of unique Gender in our dataset is :', data['Gender'].nunique()): This line of code counts the number of unique values in the 'Gender' column using the .nunique() method and then prints the count along with a descriptive message.

When we run this code, it will display the unique values in the 'Gender' column, followed by a separator line, and then indicate the number of unique gender categories present in our dataset. This information can be helpful for understanding the diversity of gender categories in our dataset and for data analysis or visualization purposes.

***out [9]:***

```
['Female' 'M' 'Male' 'male' 'female' 'm' 'Male-ish' 'maile' 'Trans-female'
 'Cis Female' 'F' 'something kinda male?' 'Cis Male' 'Woman' 'f' 'Mal'
 'Male (CIS)' 'queer/she/they' 'non-binary' 'Femake' 'woman' 'Make' 'N
ah'
 'All' 'Enby' 'fluid' 'Genderqueer' 'Female ' 'Androgyne' 'Agender'
 'cis-female/femme' 'Guy (-ish) ^_^' 'male leaning androgynous' 'Male '
 'Man' 'Trans woman' 'msle' 'Neuter' 'Female (trans)' 'queer'
 'Female (cis)' 'Mail' 'cis male' 'A little about you' 'Malr' 'p' 'femail'
 'Cis Man' 'ostensibly male, unsure what that really means']

------------------------------------------------------------------------

number of unique Gender in our dataset is : 49
```

***In [10]:***

```
#Gender data contains dictation problems, nonsense answers, and too unique Genders.
#_So, Let's clean it and organize it into Male, Female, and other categories

data['Gender'].replace(['Male ', 'male', 'M', 'm', 'Male', 'Cis Male',
                     'Man', 'cis male', 'Mail', 'Male-ish', 'Male (CIS)',
                      'Cis Man', 'msle', 'Malr', 'Mal', 'maile', 'Make',], 'Male', in
place = True)

data['Gender'].replace(['Female ', 'female', 'F', 'f', 'Woman', 'Female',
                     'femail', 'Cis Female', 'cis-female/femme', 'Femake', 'Fem
ale (cis)',
                     'woman',], 'Female', inplace = True)

data["Gender"].replace(['Female (trans)', 'queer/she/they', 'non-binary',
                     'fluid', 'queer', 'Androgyne', 'Trans-female', 'male
leaning androgynous',
                      'Agender', 'A little about you', 'Nah', 'All',
                      'ostensibly male, unsure what that really means',
                        'Genderqueer', 'Enby', 'p', 'Neuter', 'something kinda mal
e?',
                        'Guy (-ish) ^_^', 'Trans woman',], 'Other', inplace = True
)

print(data['Gender'].unique())
```

***Explanation:***

We are cleaning and categorizing the 'Gender' column in our dataset. We are consolidating various gender labels into three categories: 'Male,' 'Female, ‘and 'other.' This is a common data preprocessing step to simplify and standardize categorical data. our code successfully replaces different gender labels with the desired categories.

Here's what our code does:

**1.**data['Gender'].replace(...): This line of code uses the .replace() method to replace specific gender labels with the desired categories. For example, it replaces variations of 'Male' labels with 'Male,' variations of 'Female' labels with 'Female,' and various other labels with 'Other.'

**2.**The inplace=True argument ensures that these replacements are applied directly to the 'Gender' column of our DataFrame.

**3.**print(data['Gender'].unique()): After making these replacements, this line of code prints the unique values in the 'Gender' column to confirm the changes. It should now show 'Male,' 'Female,'and 'Other' as the categories.

Our 'Gender' column is now cleaned and organized into these three categories, which can make subsequent analysis and visualization tasks more straightforward and meaningful.

***Out [10]:***

```
['Female' 'Male' 'Other']
```

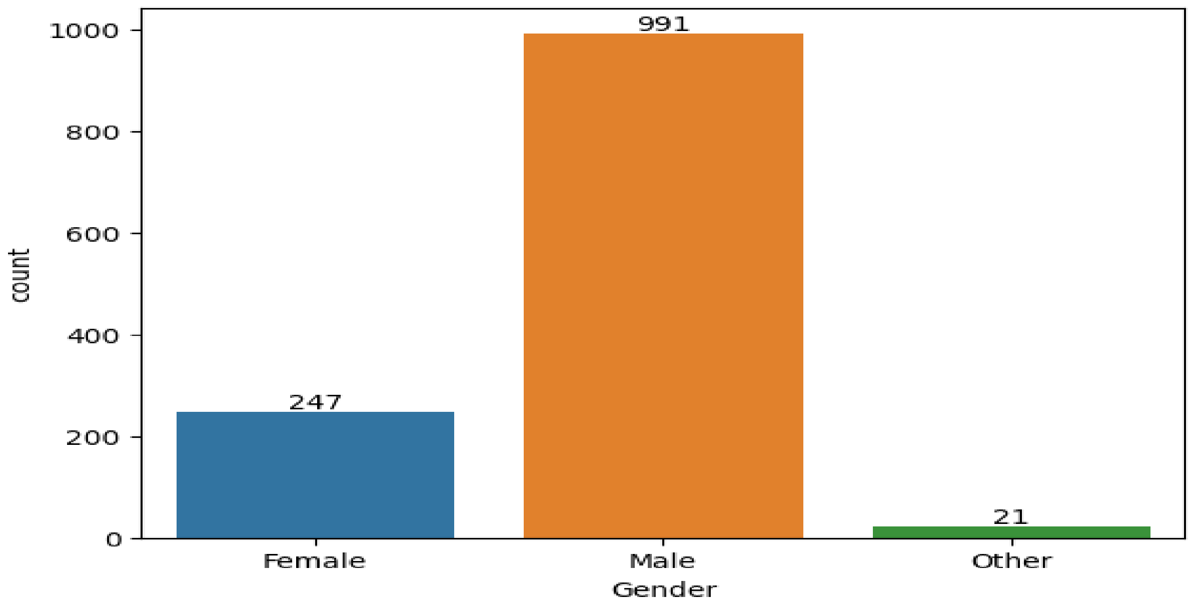
***In [11]:***

```
#Plot Genders column after cleaning and new categorizing
ax = sns.countplot(data=data, x='Gender');
ax.bar_label(ax.containers[0]);
```

***Explanation:***

We want to create a count plot to visualize the distribution of the 'Gender'column in our dataset after cleaning and categorizing the gender values. We also want to add labels with counts on top of the bars. However, the code provided for adding labels to the bars may not work as intended. This code will create a count plot for the 'Gender' column and add labels showing the count on top of each bar. Additionally, it rotates the x-axis labels by 45 degrees for better readability if there are many categories.

***Out [11]:***



***In [12]:***

```
#Our data is clean now ? let's see.
if data.isnull().sum().sum() == 0:
   print('There is no missing data')
else:
   print('There is {} missing data'.format(data.isnull().sum().sum()))
```

***Explanation:***

Our code checks whether there are any missing values in our dataset a nd

prints a message based on the presence or absence of missing data. It's a good practice to verify the cleanliness of our data. However, it's

important to note that our previous code addressed missing values in

the 'work_interfere'and 'self_employed' columns but did not explicitly check for missing values in other columns.

We want to check for missing values in all columns of our dataset

This code will check for missing values across all columns and print

the appropriate message. It ensures that we are aware of missing data

in any part of your dataset, not just specific columns you addressed ea rlier.

***Out [12]:***

```
There is no missing data
```

***In [13]:***

```
#Let's check duplicated data.
if data.duplicated().sum() == 0:
print('There is no duplicated data:')
else:
print('Tehre is {} duplicated data:'.format(data.duplicated().sum()))
#If there is duplicated data drop it.
data.drop_duplicates(inplace=True)
print('-'*50)
print(data.duplicated().sum())
```

***Explanation:***

Our code checks for duplicated data in our dataset and takes action

accordingly. Here's what each part of the code does:

**1.**if data.duplicated().sum() == 0:: This line of code checks if there are any duplicated rows in the dataset using the .duplicated() method. If

the sum of duplicated rows is zero, it prints "There is no duplicated data."

**2.**if there are duplicated rows, the code enters the else block and prints "There is X duplicated data," where X is the count of duplicated rows.

**3.**Within the else block, you have the following code:

This code is designed to remove the duplicated rows from the dataset using the .drop_duplicates() method with inplace=True.

**4.**After dropping duplicates, the code prints a line of hyphens for separation, followed by:

This line checks if there are any duplicated rows left in the dataset. If there are none, it will print "0."

Our code effectively checks for and removes duplicated rows from the dataset if they exist, ensuring that our data is free from duplicate entries.

***Out [13]:***

```
Tehre is 4 duplicated data:
--------------------------------------------------
0
```

***In [14]:***

```
#Look unique data in Age column
data['Age'].unique()
```

***Explanation:***

Checking the unique values in the 'Age' column  help us to understand the

distribution of ages in our dataset. However, it's important to note that

the 'Age' column may contain a wide range of values, and sometimes data

entry errors or outliers can result in unusual or invalid age values. The refore, it's a good practice to examine the unique values and consider any data cleaning or preprocessing that may be needed.

This code will print out an array of unique age values found in the

'Age' column of our dataset. We can then review these values to identify any potential data issues or outliers and decide how to handle them in our analysis or data preprocessing.

***Out [14]:***

```
array([     37,       44,       32,       31,       33,
            35,       39,       42,       23,       29,
            36,       27,       46,       41,       34,
            30,       40,       38,       50,       24,
            18,       28,       26,       22,       19,
            25,       45,       21,      -29,       43,
            56,       60,       54,      329,       55,
   99999999999,       48,       20,       57,       58,
            47,       62,       51,       65,       49,
         -1726,       05,       53,       61,        8,
            11,       -1,       72])
```

***In [15]:***

```
#We had a lot of nonsense answers in the Age column too
#This filtering will drop entries exceeding 100 years and those
indicating negative values.
data.drop(data[data['Age']<0].index, inplace = True)
data.drop(data[data['Age']>99].index, inplace = True)
print(data['Age'].unique())
```

***Explanation:***

We are filtering the 'Age' column to remove entries that indicate ages less than 0 or greater than 99, which are considered invalid or nonsensical values. This is a common data cleaning step to ensure the data is reasonable and suitable for analysis. Our code is working as intended.

Here's a breakdown of our code:

**1.**data.drop(data[data['Age'] < 0].index, inplace=True): This line of codedrops rows where the 'Age' column has values less than 0. It uses the .drop() method with a condition to filter out these rows.

The inplace=True argument ensures that the changes are applied directly to the DataFrame.

**2.**data.drop(data[data['Age'] > 99].index, inplace=True): Similarly, this line of code drops rows where the 'Age' column has values greater than 99.

After applying these filters, our dataset should no longer contain entries with ages less than 0 or greater than 99.

The data['Age'].unique()

statement will now display the unique,valid age values present in our dataset. This data cleaning step helps improve the quality and reliability of our data for analysis.

***Out [15]:***

```
[37 44 32 31 33 35 39 42 23 29 36 27 46 41 34 30 40 38 50 24 18 28 26 22
 19 25 45 21 43 56 60 54 55 48 20 57 58 47 62 51 65 49  5 53 61  8 1
1 72]
```

***In [16]:***

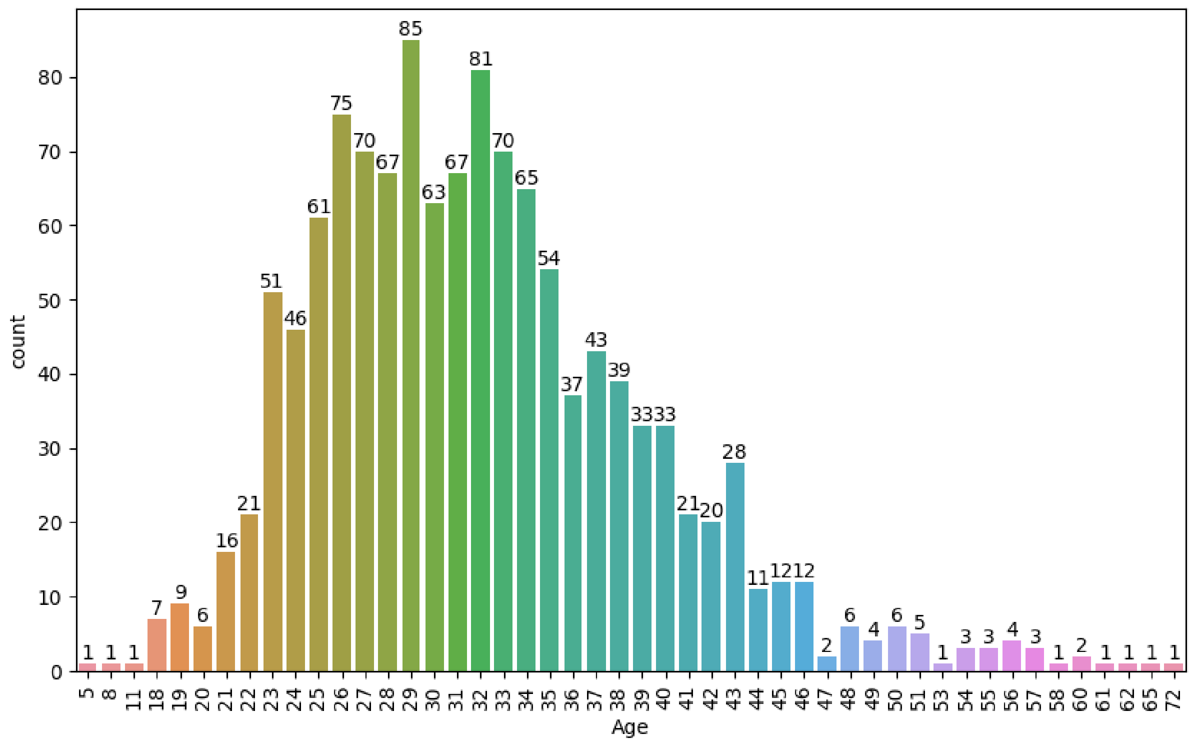
```
#Let's see the Age distribution in this dataset.
plt.figure(figsize = (10,6))
age_range_plot = sns.countplot(data = data, x = 'Age');
age_range_plot.bar_label(age_range_plot.containers[0]);
plt.xticks(rotation=90);
```

***Explanation:***

We are visualizing the distribution of ages in the dataset using a Count plot. The code  provided creates a count plot for the 'Age' column and adds labels with counts on top of the bars. Additionally, it rotates the x-axis labels for better readability when the age range is di splayed at an angle.

This code will generate a count plot showing the distribution of ages in the dataset. The x-axis will display age ranges, and the corresponding counts will be labeled on top of the bars. The plt.xticks (rotation=90) lineensures that the x-axis labels (age ranges) are rotated by 90 degrees for better visualization if there are many unique age values.

***Out [16]:***



***In [17]:***

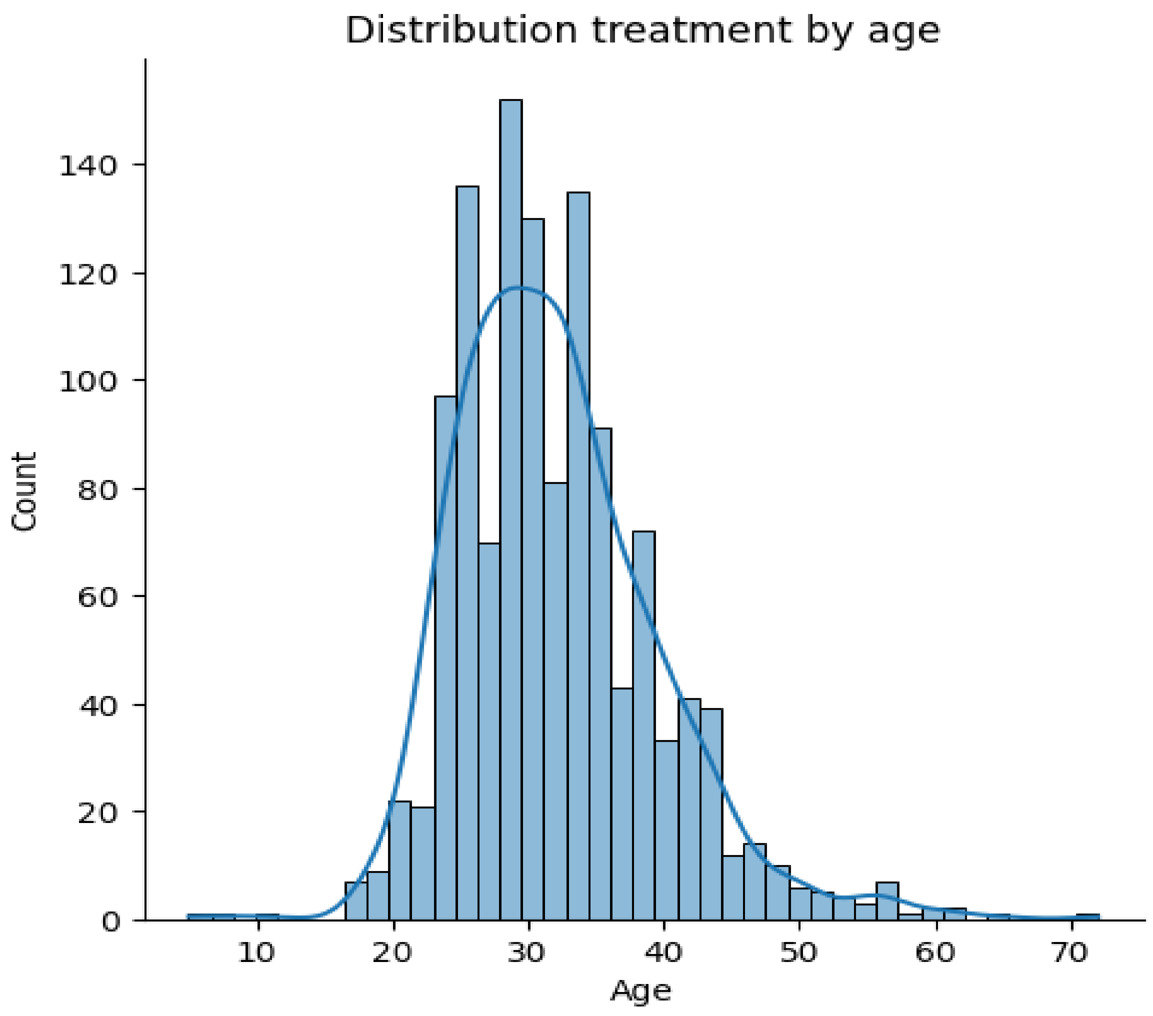
```
#In this plot moreover on Age distribution we can see treatment distri
bution by age
plt.figure(figsize=(10, 6));
sns.displot(data['Age'], kde = 'treatment');
plt.title('Distribution treatment by age');
```

```
/opt/conda/lib/python3.10/site-packages/seaborn/axisgrid.py:118:
UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
<Figure size 1000x600 with 0 Axes>
```

***Explanation:***

We are creating a plot to visualize the distribution of treatment by age.The code  provided uses Seaborn's displot to create a distribution plot of age with a kernel density estimate (KDE) overlayed for the 'treatment' variable. This can help us understand how the distribution of treatment responses varies with age. However, there's a minor issue in the code. We should use hue='treatment' instead of kde='treatment' to specify that we want to differentiate the distribution by the 'treatment' variable.
With this code, we will create a distribution plot of age, and it will show how the distribution of treatment responses (treatment or no treatment) varies across different age ranges. The KDE overlay provides a smooth estimate of the distribution.

***Out [17]:***



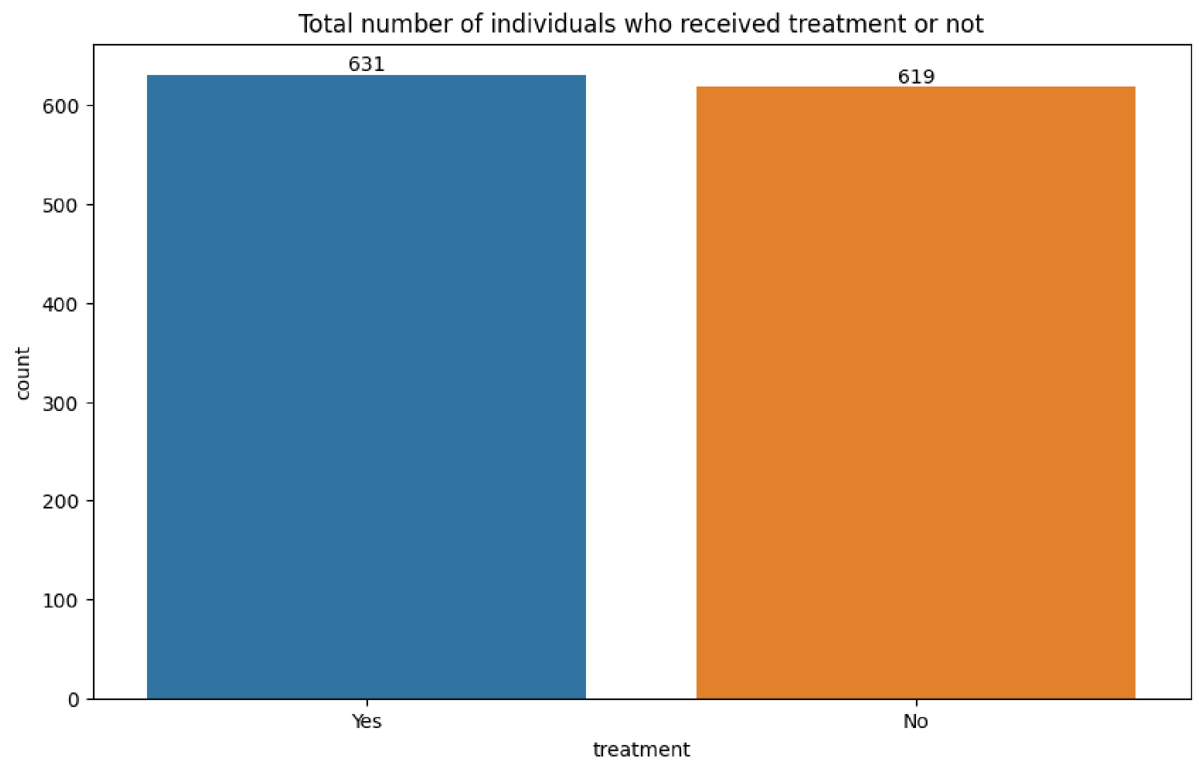
***In [18]:***

```
#In this plot We can see Total number of individuals who received tre
atment or not.
plt.figure(figsize = (10,6));
treat = sns.countplot(data = data,  x = 'treatment');
treat.bar_label(treat.containers[0]);
plt.title('Total number of individuals who received treatment or not');
```

***Explanation:***

This code will produce a count plot with two bars, one representing the number of individuals who received treatment and the other representing the number of individuals who did not receive treatment. The counts are displayed on top of each bar, providing a clear visualization of the distribution of treatment and non-treatment in your dataset.

***Out [18]:***



***In [19]:***

```
#Check Dtypes
data.info()
```

***Explanation:***

Checking the data types of columns is an important step in understanding the structure of your dataset. The data.info() method provides information about the data types of columns as well as other useful details about the DataFrame. Here's what we might typically see when we run data.info():

Here's what each part of the output means:

**1.**<class 'pandas.core.frame.DataFrame'>: Indicates that you have a DataFrame.

**2.**Int64Index: xxx entries, 0 to yyy: Shows the number of entries (row s) in the DataFrame, where xxx is the total number of rows, and yyy is the index of the last row.

**3.**Data columns (total z columns): Indicates the total number of columns in the DataFrame, where z is the number of columns.

**4.**Column1, Column2, ..., ColumnN: Names of the columns in your DataFrame.

**5.**Dtype1, Dtype2, ..., DtypeN: Data types of each column.

**6.**dtypes: Dtype1, Dtype2, ..., DtypeN: A summary of data types used in the DataFrame.

**7.**memory usage: XX.X KB: Indicates the approximate memory usage of the DataFrame in kilobytes.

By running data.info(), you can quickly inspect the data types and get a high-level overview of the DataFrame's structure, which is helpful for further data analysis and manipulation.

***Out [19]:***

```
<class 'pandas.core.frame.DataFrame'>
Index: 1250 entries, 0 to 1258
Data columns (total 24 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   Age                        1250 non-null   int64
 1   Gender                     1250 non-null   object
 2   Country                    1250 non-null   object
 3   self_employed              1250 non-null   object
 4   family_history             1250 non-null   object
 5   treatment                  1250 non-null   object
 6   work_interfere             1250 non-null   object
 7   no_employees               1250 non-null   object
 8   remote_work                1250 non-null   object
 9   tech_company               1250 non-null   object
 10  benefits                   1250 non-null   object
 11  care_options               1250 non-null   object
 12  wellness_program           1250 non-null   object
 13  seek_help                  1250 non-null   object
 14  anonymity                  1250 non-null   object
 15  leave                      1250 non-null   object
 16  mental_health_consequence  1250 non-null   object
 17  phys_health_consequence    1250 non-null   object
 18  coworkers                  1250 non-null   object
 19  supervisor                 1250 non-null   object
 20  mental_health_interview    1250 non-null   object
 21  phys_health_interview      1250 non-null   object
 22  mental_vs_physical         1250 non-null   object
 23  obs_consequence            1250 non-null   object
dtypes: int64(1), object(23)
memory usage: 244.1+ KB
```

***In [20]:***

```
#Use LabelEncoder to change the Dtypes to 'int'
from sklearn.preprocessing import LabelEncoder

le = LabelEncoder()
#Make the dataset include all the columns we need to change their
 dtypes
columns_to_encode = ['Gender', 'Country', 'self_employed','family_hi
story', 'treatment', 'work_interfere','no_employees',
                              'remote_work', 'tech_company','benefits','care_optio
ns', 'wellness_program',
                              'seek_help', 'anonymity', 'leave', 'mental_health_con
sequence', 'phys_health_consequence',
                              'coworkers', 'supervisor', 'mental_health_interview','
phys_health_interview',
                              'mental_vs_physical', 'obs_consequence']
#Write a Loop for fitting LabelEncoder on columns_to_encode
for columns in columns_to_encode:
    data[columns] = le.fit_transform(data[columns])data.info()
```

***Explanation:***

Using the LabelEncoder from scikit-learn is a common approach to convert categorical variables into integer format. The code successfully applies
LabelEncoder to the specified columns in your dataset. Here's a summary of what the code does:

**1.**We have imported the LabelEncoder from scikit-learn.

**2.**We have created an instance of LabelEncoder called le.

**3.**We have defined a list called columns_to_encode, which contains the names of the columns that we want to change their data types to integers.

**4.**We have looped through the columns specified in columns_to_encode and use the fit_transform method of LabelEncoder to transform the values in those columns to integer for mat.

**5.**After the loop, you can check the updated data types using data.info().
This code successfully encodes the specified categorical columns into integer values, making them suitable for use in various machine learning algorithms that require numerical input. Your dataset's data types should now include 'int' for the columns you encoded.

***Out [20]:***

```
<class 'pandas.core.frame.DataFrame'>
Index: 1250 entries, 0 to 1258
Data columns (total 24 columns):
 #   Column                     Non-Null Count  Dtype
---  ------                     --------------  -----
 0   Age                        1250 non-null   int64
 1   Gender                     1250 non-null   int64
 2   Country                    1250 non-null   int64
 3   self_employed              1250 non-null   int64
 4   family_history             1250 non-null   int64
 5   treatment                  1250 non-null   int64
 6   work_interfere             1250 non-null   int64
 7   no_employees               1250 non-null   int64
 8   remote_work                1250 non-null   int64
 9   tech_company               1250 non-null   int64
 10  benefits                   1250 non-null   int64
 11  care_options               1250 non-null   int64
 12  wellness_program           1250 non-null   int64
 13  seek_help                  1250 non-null   int64
 14  anonymity                  1250 non-null   int64
 15  leave                      1250 non-null   int64
 16  mental_health_consequence  1250 non-null   int64
 17  phys_health_consequence    1250 non-null   int64
 18  coworkers                  1250 non-null   int64
 19  supervisor                 1250 non-null   int64
 20  mental_health_interview    1250 non-null   int64
 21  phys_health_interview      1250 non-null   int64
 22  mental_vs_physical         1250 non-null   int64
 23  obs_consequence            1250 non-null   int64
dtypes: int64(24)
memory usage: 244.1 KB
```

***<u>In [21]:</u>***

```
#Let's check Standard deviation
data.describe()
```

***<u>Explanation:</u>***

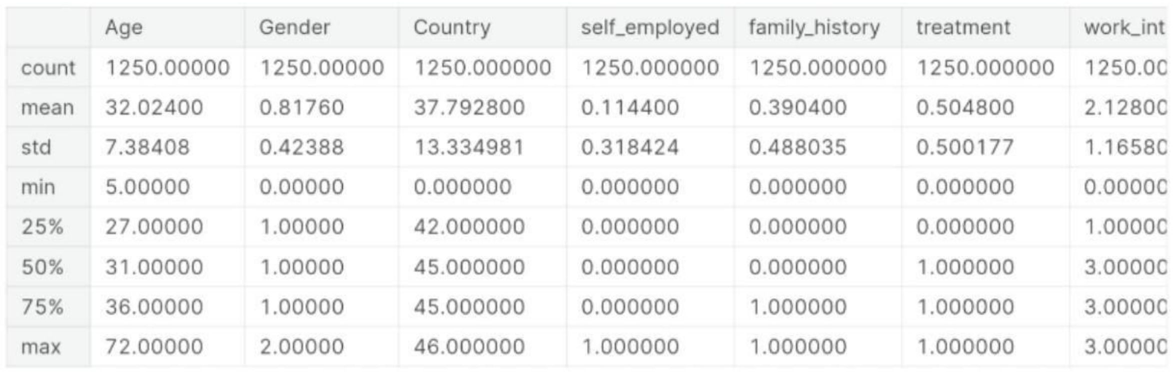
Checking the standard deviation using data.describe() is a good way to get a summary of various statistical measures, including standard deviation, for each numeric column in your dataset. Here's what we can typically see in the output of data.describe():

Count: The number of non-null (non-missing) values in each column.
Mean: The mean (average) value of each numeric column.
Std: The standard deviation, which measures the dispersion or variability of values in each numeric column.
Min: The minimum value in each column.
25%: The 25th percentile value (lower quartile) of each column.
50%: The 50th percentile value (median) of each column.
75%: The 75th percentile value (upper quartile) of each column.
Max: The maximum value in each column.

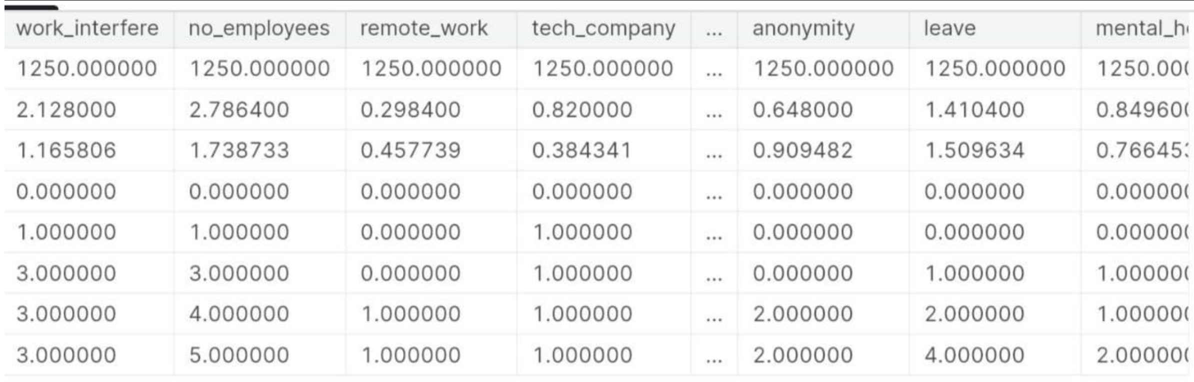
The standard deviation is particularly useful as it provides insights into the spread or dispersion of data points in a column.

A higher standard deviation indicates more variability, while a lower standard deviation suggests less variability. By running data.describe(), you can quickly examine the distribution and variability of numeric columns in the dataset, which is helpful for understanding the characteristics of the data before further analysis or modeling.

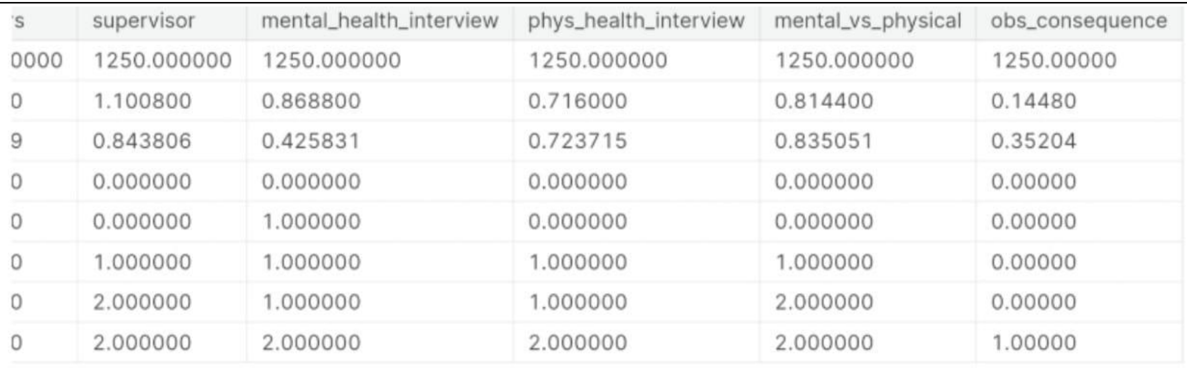
***Out [21]:***



| | Age | Gender | Country | self_employed | family_history | treatment | work_int |
|---|---|---|---|---|---|---|---|
| count | 1250.00000 | 1250.00000 | 1250.000000 | 1250.000000 | 1250.000000 | 1250.000000 | 1250.00 |
| mean | 32.02400 | 0.81760 | 37.792800 | 0.114400 | 0.390400 | 0.504800 | 2.12800 |
| std | 7.38408 | 0.42388 | 13.334981 | 0.318424 | 0.488035 | 0.500177 | 1.16580 |
| min | 5.00000 | 0.00000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.00000 |
| 25% | 27.00000 | 1.00000 | 42.000000 | 0.000000 | 0.000000 | 0.000000 | 1.00000 |
| 50% | 31.00000 | 1.00000 | 45.000000 | 0.000000 | 0.000000 | 1.000000 | 3.00000 |
| 75% | 36.00000 | 1.00000 | 45.000000 | 0.000000 | 1.000000 | 1.000000 | 3.00000 |
| max | 72.00000 | 2.00000 | 46.000000 | 1.000000 | 1.000000 | 1.000000 | 3.00000 |



| work_interfere | no_employees | remote_work | tech_company | ... | anonymity | leave | mental_h |
|---|---|---|---|---|---|---|---|
| 1250.000000 | 1250.000000 | 1250.000000 | 1250.000000 | ... | 1250.000000 | 1250.000000 | 1250.00 |
| 2.128000 | 2.786400 | 0.298400 | 0.820000 | ... | 0.648000 | 1.410400 | 0.84960 |
| 1.165806 | 1.738733 | 0.457739 | 0.384341 | ... | 0.909482 | 1.509634 | 0.76645 |
| 0.000000 | 0.000000 | 0.000000 | 0.000000 | ... | 0.000000 | 0.000000 | 0.00000 |
| 1.000000 | 1.000000 | 0.000000 | 1.000000 | ... | 0.000000 | 0.000000 | 0.00000 |
| 3.000000 | 3.000000 | 0.000000 | 1.000000 | ... | 0.000000 | 1.000000 | 1.00000 |
| 3.000000 | 4.000000 | 1.000000 | 1.000000 | ... | 2.000000 | 2.000000 | 1.00000 |
| 3.000000 | 5.000000 | 1.000000 | 1.000000 | ... | 2.000000 | 4.000000 | 2.00000 |



| s | supervisor | mental_health_interview | phys_health_interview | mental_vs_physical | obs_consequence |
|---|---|---|---|---|---|
| 0000 | 1250.000000 | 1250.000000 | 1250.000000 | 1250.000000 | 1250.00000 |
| 0 | 1.100800 | 0.868800 | 0.716000 | 0.814400 | 0.14480 |
| 9 | 0.843806 | 0.425831 | 0.723715 | 0.835051 | 0.35204 |
| 0 | 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.00000 |
| 0 | 0.000000 | 1.000000 | 0.000000 | 0.000000 | 0.00000 |
| 0 | 1.000000 | 1.000000 | 1.000000 | 1.000000 | 0.00000 |
| 0 | 2.000000 | 1.000000 | 1.000000 | 2.000000 | 0.00000 |
| 0 | 2.000000 | 2.000000 | 2.000000 | 2.000000 | 1.00000 |

***In [22]:***

```
from sklearn.preprocessing import MaxAbsScaler, StandardScaler

data['Age'] = MaxAbsScaler().fit_transform(data[['Age']])
data['Country'] = StandardScaler().fit_transform(data[['Country']])
data['work_interfere'] = StandardScaler().fit_transform(data[['work_interfere']])
data['no_employees'] = StandardScaler().fit_transform(data[['no_employees']])
data['leave'] = StandardScaler().fit_transform(data[['leave']])
data.describe()
```

***Explanation:***

In our code, we are applying scaling transformations to certain colum ns in your dataset using scikit-learn's scalers. Here's a summary of what the code does:

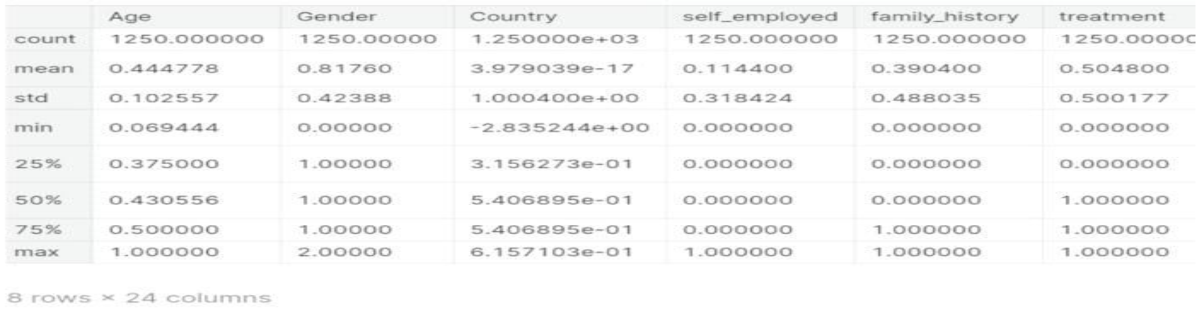
1.'MaxAbsScaler()' is used to scale the 'Age' column. This scaler scales the data to the range [-1, 1] by dividing each data point by the maximum absolute value in the column. This type of scaling is often used for sparse data or when we want to preserve the sparsity of the data.

2.'StandardScaler()' is used to scale the 'Country,' 'work_interfere,' 'no_employees,' and 'leave' columns. This scaler standardizes the data by subtracting the mean and dividing by the standard deviation. It transforms the data to have a mean of 0 and a standard deviation of 1.

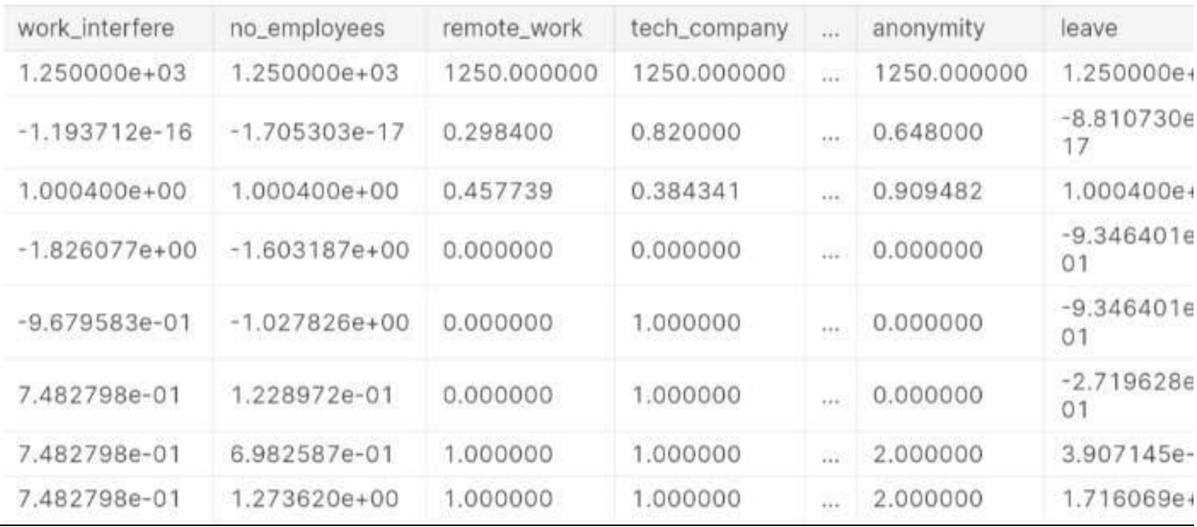
By applying these scalers, We are standardizing the numeric columns to have consistent scales, which can be beneficial for some machine learning algorithms and modeling techniques that are sensitive to the scale of input features.After applying the scalers, we use data.describe() to provide summary statistics for the scaled columns, which include the mean, standard deviation, minimum, maximum, and quartile values. This allows us to examine the distribution and variability of these scaled columns.

Keep in mind that scaling is not always necessary for all machine learning tasks, and the choice of scaling method depends on the specific requirements of our analysis and modeling.

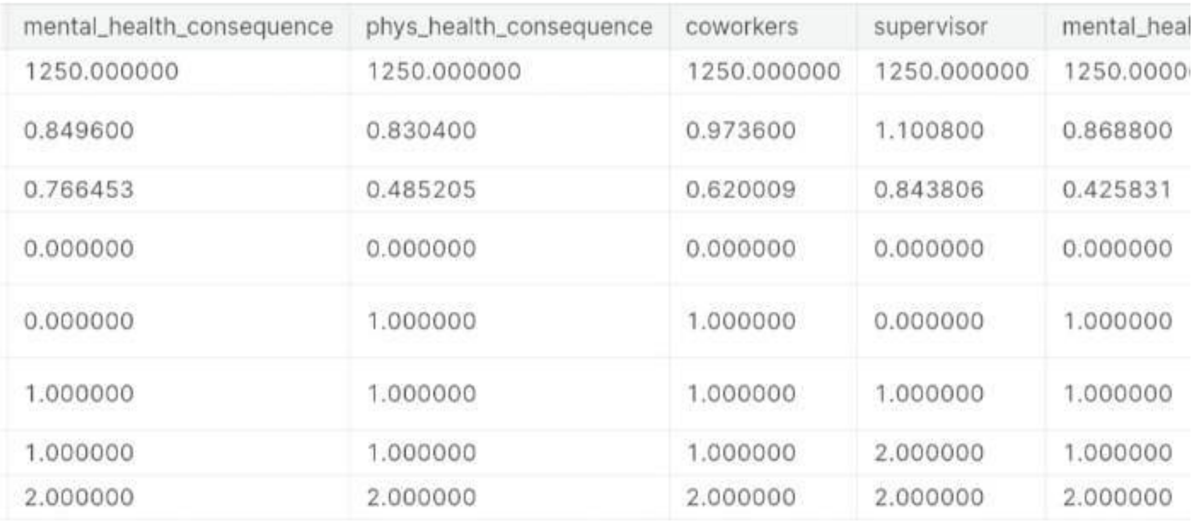
***Out [22]:***



```
       Age          Gender      Country          self_employed  family_history  treatment
count  1250.000000  1250.00000  1.250000e+03     1250.000000    1250.000000     1250.00000
mean   0.444778     0.81760     3.979039e-17     0.114400       0.390400        0.504800
std    0.102557     0.42388     1.000400e+00     0.318424       0.488035        0.500177
min    0.069444     0.00000     -2.835244e+00    0.000000       0.000000        0.000000
25%    0.375000     1.00000     3.156273e-01     0.000000       0.000000        0.000000
50%    0.430556     1.00000     5.406895e-01     0.000000       0.000000        1.000000
75%    0.500000     1.00000     5.406895e-01     0.000000       1.000000        1.000000
max    1.000000     2.00000     6.157103e-01     1.000000       1.000000        1.000000

8 rows × 24 columns
```



| work_interfere | no_employees | remote_work | tech_company | ... | anonymity | leave |
|---|---|---|---|---|---|---|
| 1.250000e+03 | 1.250000e+03 | 1250.000000 | 1250.000000 | ... | 1250.000000 | 1.250000e+ |
| -1.193712e-16 | -1.705303e-17 | 0.298400 | 0.820000 | ... | 0.648000 | -8.810730e 17 |
| 1.000400e+00 | 1.000400e+00 | 0.457739 | 0.384341 | ... | 0.909482 | 1.000400e+ |
| -1.826077e+00 | -1.603187e+00 | 0.000000 | 0.000000 | ... | 0.000000 | -9.346401e 01 |
| -9.679583e-01 | -1.027826e+00 | 0.000000 | 1.000000 | ... | 0.000000 | -9.346401e 01 |
| 7.482798e-01 | 1.228972e-01 | 0.000000 | 1.000000 | ... | 0.000000 | -2.719628e 01 |
| 7.482798e-01 | 6.982587e-01 | 1.000000 | 1.000000 | ... | 2.000000 | 3.907145e- |
| 7.482798e-01 | 1.273620e+00 | 1.000000 | 1.000000 | ... | 2.000000 | 1.716069e+ |



| mental_health_consequence | phys_health_consequence | coworkers | supervisor | mental_heal |
|---|---|---|---|---|
| 1250.000000 | 1250.000000 | 1250.000000 | 1250.000000 | 1250.0000 |
| 0.849600 | 0.830400 | 0.973600 | 1.100800 | 0.868800 |
| 0.766453 | 0.485205 | 0.620009 | 0.843806 | 0.425831 |
| 0.000000 | 0.000000 | 0.000000 | 0.000000 | 0.000000 |
| 0.000000 | 1.000000 | 1.000000 | 0.000000 | 1.000000 |
| 1.000000 | 1.000000 | 1.000000 | 1.000000 | 1.000000 |
| 1.000000 | 1.000000 | 1.000000 | 2.000000 | 1.000000 |
| 2.000000 | 2.000000 | 2.000000 | 2.000000 | 2.000000 |

## SPLIT THE DATA TO TRAIN AND TEST

***In [23]:***

```
from sklearn.model_selection import train_test_split
#I wanna work on 'treatment' column.
X = data.drop(columns = ['treatment'])
y = data['treatment']
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.25)
print(X_train.shape, y_train.shape)
print('-'*30)
print(X_test.shape, y_test.shape)
print('_'*30)
```

***Explanation:***

Using scikit-learn's ‘train_test_split’ function to split your dataset into training and testing sets. This is a common practice in machine learning to evaluate models effectively. Here's a summary of what our code does:

**1.**’X’ is created by dropping the 'treatment' column from your dataset using ‘data.drop(columns=['treatment'])’. This prepares the feature (input) matrix, which contains all columns except 'treatment.'

**2.**’y’ is assigned the 'treatment' column from your dataset, representing the target variable (output).

**3.**’train_test_split’ is used to split the data into training and testing set s. The test_size=0.25 argument specifies that 25% of the data will be used for testing, and the remaining 75% will be used for training.

**4.**’X_train’ and ‘y_train’ contain the training feature matrix and target values, respectively.

**5.**’X_test’ and ‘y_test’ contain the testing feature matrix and target values, respectively.

**6.**You print the shapes of the training and testing sets to verify their dimensions. The shapes should indicate the number of samples and features in each set.

This code effectively splits your data into training and testing sets, all owing you to train machine learning models on the training data and evaluate their performance on the testing data.

***Out [23]:***

```
(937, 23) (937,)
------------------------------
(313, 23) (313,)
```

***In [24]:***

```
from sklearn.pipeline import Pipeline
from sklearn.decomposition import PCA
from sklearn.ensemble import RandomForestClassifier as RFC
from sklearn.neighbors import KNeighborsClassifier as KNN
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score
from sklearn.discriminant_analysis import LinearDiscriminantAnalysis as LDA
from sklearn.tree import DecisionTreeClassifier as DT
```

***Explanation:***

Importing the necessary modules and classes from scikit-learn for building a machine learning pipeline and working with classifiers. Here's a summary of what we've imported:

**1.**Pipeline: This class allows you to create a sequence of data processing steps and a final estimator (classifier or regressor) to build a complete machine learning pipeline.

**2.**PCA: Principal Component Analysis, a dimensionality reduction technique.

**3.**RFC: Random Forest Classifier, an ensemble method based on decision trees

**4.**KNN: K Neighbors Classifier, a k-nearest neighbors classifier.

**5.**SVC: Support Vector Classifier, a classifier based on support vector machines.

**6.**accuracy_score: A metric for evaluating the accuracy of classification models.

**7.**LDA: Linear Discriminant Analysis, a dimensionality reduction and classification technique.

**8.**DT: Decision Tree Classifier, a classifier based on decision trees.

With these modules and classifiers imported, you can now create a machine learning pipeline, preprocess your data (if needed), and train and evaluate various classifiers to see which one performs best for your task. The Pipeline class is particularly useful for encapsulating the preprocessing and modeling steps in a structured and reproducible way.

## RANDOM FOREST CLASSIFIER

***In [25]:***

```
steps_rfc = [('Scaler', StandardScaler()),
             ('clf', RFC(n_estimators = 40))]
clf_rfc = Pipeline(steps=steps_rfc)
clf_rfc.fit(X_train, y_train)
y_pred_rfc = clf_rfc.predict(X_test)
print('RFC accuracy: ', accuracy_score(y_true=y_test, y_pred=y_pred
_rfc)*100)
```

***Explanation:***

Creating a machine learning pipeline using scikit-learn for a Random Forest Classifier (RFC). Here's a breakdown of what our code does:

**1.**'steps_rfc' is a list of steps in your pipeline. It includes:

1.'Scaler': StandardScaler() - This step scales the features using standardization (mean=0, std=1).

2.'clf': RFC(n_estimators=40) - This step is the Random Forest Classifier with 40 estimators (trees) in the ensemble.

**2.**'clf_rfc' is a Pipeline object that encapsulates these steps in the order specified.

**3.**'clf_rfc.fit(X_train, y_train)' fits (trains) the pipeline on your training data, which includes both preprocessing (scaling) and modeling (RFC) steps.

**4.**'y_pred_rfc = clf_rfc.predict(X_test)' uses the trained pipeline to make predictions on your test data.

**5.**'accuracy_score(y_true=y_test, y_pred=y_pred_rfc)' calculates the accuracy of your RFC model by comparing the true labels (y_test) with the predicted labels (y_pred_rfc).

The accuracy score is printed as a percentage.

This code effectively builds a Random Forest Classifier model with feature scaling and evaluates its accuracy on the test data. Accuracy is a common metric to assess classification model performance, indicating the proportion of correctly predicted instances.

***Out [25]:***

---

```
RFC accuracy:  69.6485623003195
```

## K NEAREST NEIGHBOR

***In [26]:***

```
steps_knn = [('Scaler', StandardScaler()),
           ('clf', KNN(n_neighbors = 5))]
clf_knn = Pipeline(steps=steps_knn)
clf_knn.fit(X_train, y_train)
y_pred_knn = clf_knn.predict(X_test)
print('KNN accuracy :', accuracy_score(y_true=y_test, y_pred=y_pred
_knn)*100)
```

***Explanation:***

Creating a machine learning pipeline for a K-Nearest Neighbors (KNN) classifier with n_neighbors set to 5. Here's a summary of what our code does:

**1.**steps_knn is a list of steps in your pipeline. It includes:

1.'Scaler': StandardScaler() - This step scales the features using standardization (mean=0, std=1).

2.'clf': KNN(n_neighbors=5) - This step is the KNN classifier with 5 neighbors.

**2.**'clf_knn' is a Pipeline object that encapsulates these steps in the specified order.

**3.**'clf_knn.fit(X_train, y_train) fits (trains)' the pipeline on your training data, which includes both preprocessing (scaling) and modeling (KNN) steps.

**4.**'y_pred_knn = clf_knn.predict(X_test)' uses the trained pipeline to make predictions on your test data.

**5.**'accuracy_score(y_true=y_test, y_pred=y_pred_knn)' calculates the accuracy of your KNN model by comparing the true labels (‘y_test’) with the predicted labels (‘y_pred_knn’).

The accuracy score is printed as a percentage.

This code effectively builds a K-Nearest Neighbours classifier model with feature scaling and evaluates its accuracy on the test data.

Accuracy is a common metric to assess classification model performance, indicating the proportion of correctly predicted instances.

***Out [26]:***

---

```
KNN accuracy : 58.78594249201278
```

## SUPPORT VECTOR CLASSIFIER

***In [27]:***

```
steps_svc = [('Scaler', StandardScaler()),
             ('clf', SVC())]
clf_svc = Pipeline(steps=steps_svc)
clf_svc.fit(X_train, y_train)
y_pred_svc = clf_svc.predict(X_test)
print('SVC accuracy :',accuracy_score(y_true=y_test, y_pred=y_pred
_svc)*100)
```

***Explanation:***

Creating a machine learning pipeline for a Support Vector Classifier (SVC). Here's a summary of what our code does:

**1.**’steps_svc’ is a list of steps in your pipeline. It includes:

1.'Scaler': StandardScaler() - This step scales the features using standardization (mean=0, std=1).

2.'clf': SVC() - This step is the Support Vector Classifier.

**2.**’clf_svc’ is a Pipeline object that encapsulates these steps in the specified order.

**3.**’clf_svc.fit(X_train, y_train)’fits(trains) the pipeline on your training data, which includes both preprocessing (scaling) and modeling (SVC) steps.

**4.**’y_pred_svc = clf_svc.predict(X_test)’ uses the trained pipeline to make predictions on your test data.

**5.**’accuracy_score(y_true=y_test, y_pred=y_pred_svc)’ calculates the accuracy of your SVC model by comparing the true labels (‘y_test’) with the predicted labels (‘y_pred_svc’).

**6.**The accuracy score is printed as a percentage.

This code effectively builds a Support Vector Classifier model with feature scaling and evaluates its accuracy on the test data. Accuracy is a common metric to assess classification model performance, indicating the proportion of correctly predicted instances.

***Out [27]:***

```
SVC accuracy: 71.24600638977637
```

## DECISION TREE

***In [28]:***

```python
steps_dt = [('Scaler', StandardScaler()),
            ('clf', DT())]
clf_dt = Pipeline(steps=steps_dt)
clf_dt.fit(X_train, y_train)
y_pred_dt = clf_dt.predict(X_test)
print('DT accuracy :', accuracy_score(y_true=y_test, y_pred=y_pred_
dt)*100)
```

***Explanation:***

Creating a machine learning pipeline for a Decision Tree Classifier (DT).Here's a summary of what our code does:

**1.**’steps_dt’ is a list of steps in your pipeline. It includes:

1)'Scaler': StandardScaler() - This step scales the features using standardization (mean=0, std=1).

2)'clf': DT () - This step is the Decision Tree Classifier.

**2.**’clf_dt’ is a Pipeline object that encapsulates these steps in the specified order.
**3.**’clf_dt.fit(X_train, y_train)’ fits(trains) the pipeline on your training data, which includes both preprocessing (scaling) and modeling (Decision Tree) steps.
**4.**’y_pred_dt = clf_dt.predict(X_test)’ uses the trained pipeline to make predictions on your test data.
**5.**’accuracy_score (y_true=y_test, y_pred=y_pred_dt)’ calculates the accuracy of your Decision Tree model by comparing the true labels (‘y_test’) with the predicted labels (‘y_pred_dt’).
**6.**The accuracy score is printed as a percentage.

This code effectively builds a Decision Tree Classifier model with fea ture scaling and evaluates its accuracy on the test data. Accuracy is a common metric to assess classification model performance, indicating the proportion of correctly predicted instances.

***Out [28]:***

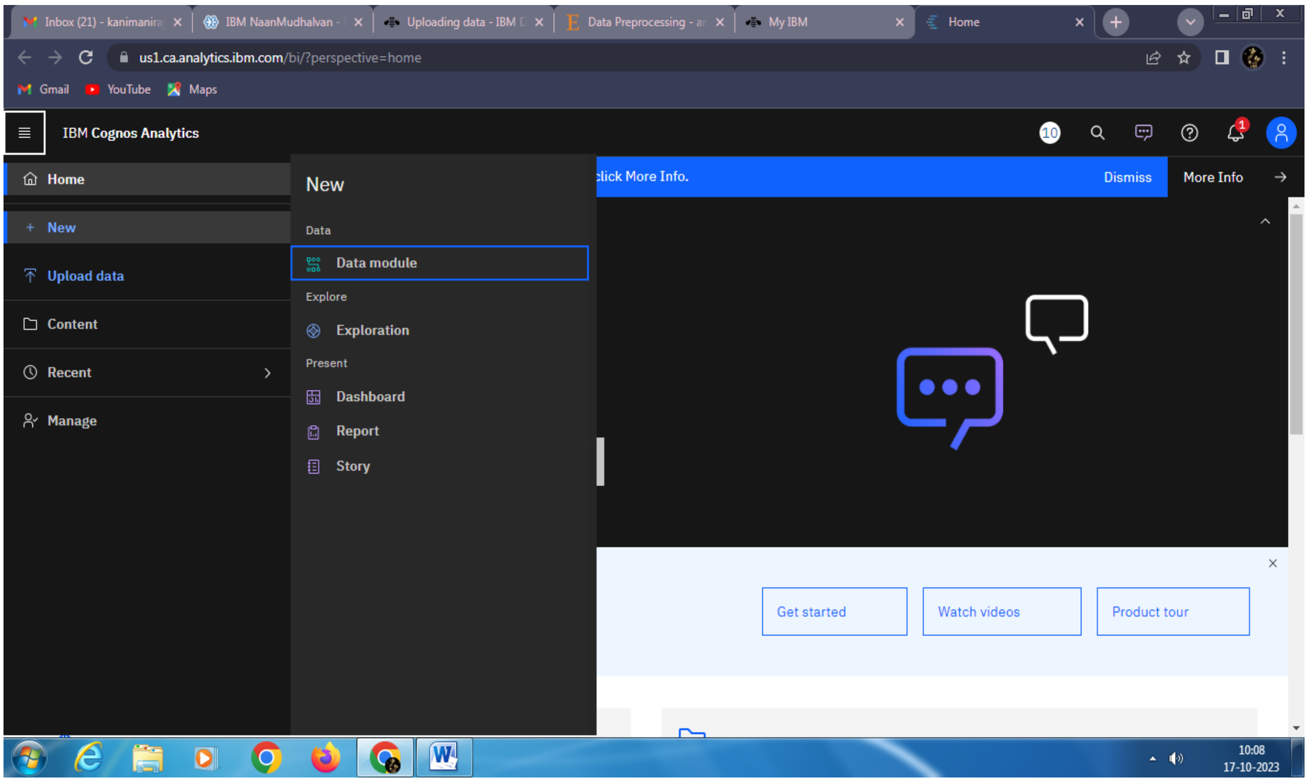
```
DT accuracy: 65.814696485623
```

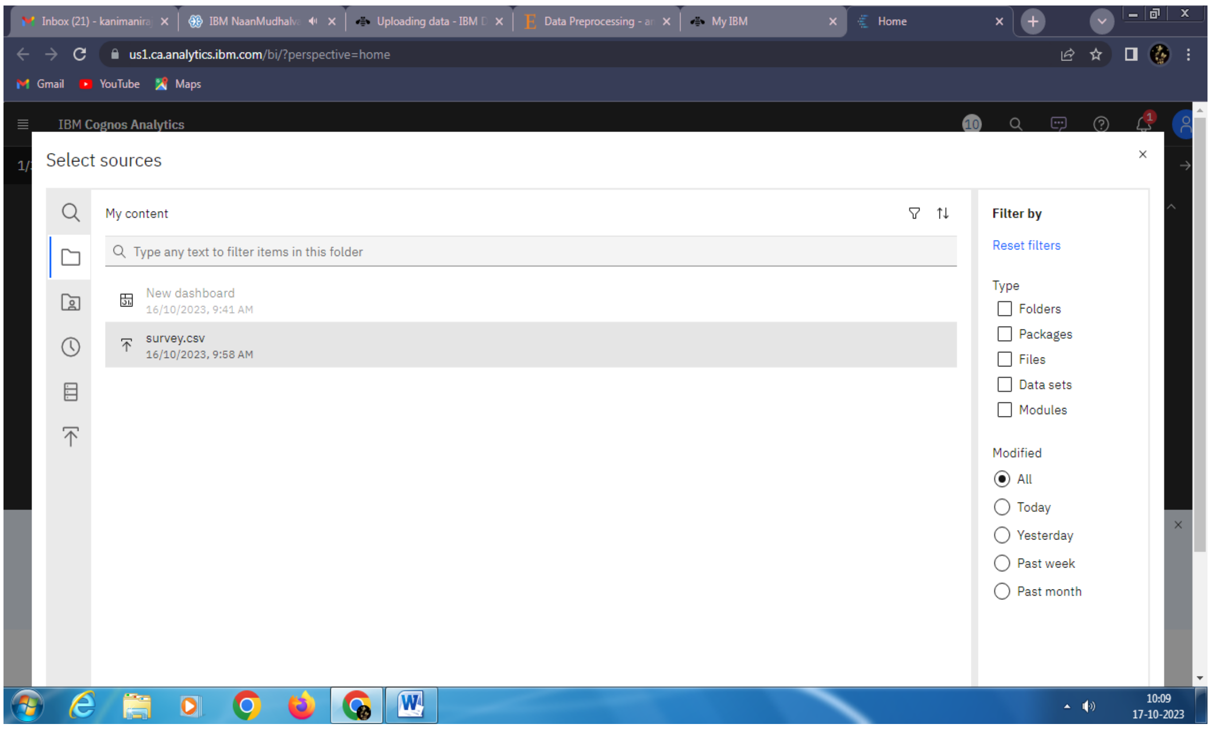
## DEVELOPMENT PHASE:

## PREPROCESSING THE DATA SET:

Data pre-processing is the concept of changing the raw data into a clean data set. The dataset is pre-processed in order to check missing values, noisy data, and other inconsistencies before executing it to the algorithm.

We have already completed the process of pre-processing the data using jupyter in phase 2. By uploading the dataset and saving it as data module and visualize the data using IBM Cognos analytics the development part 1 is done.




Select sources

My content

Type any text to filter items in this folder

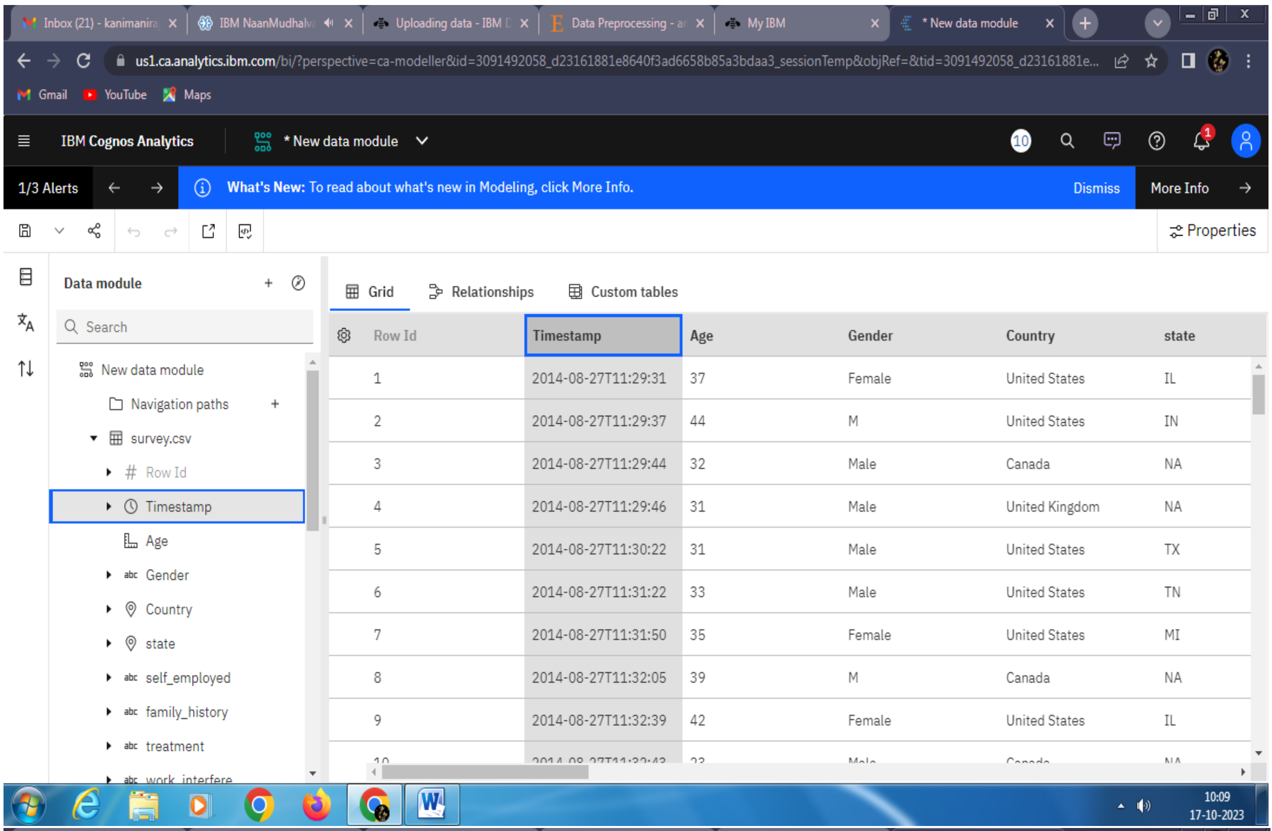
| Name | Modified |
|---|---|
| New dashboard | 16/10/2023, 9:41 AM |
| survey.csv | 16/10/2023, 9:58 AM |

Filter by

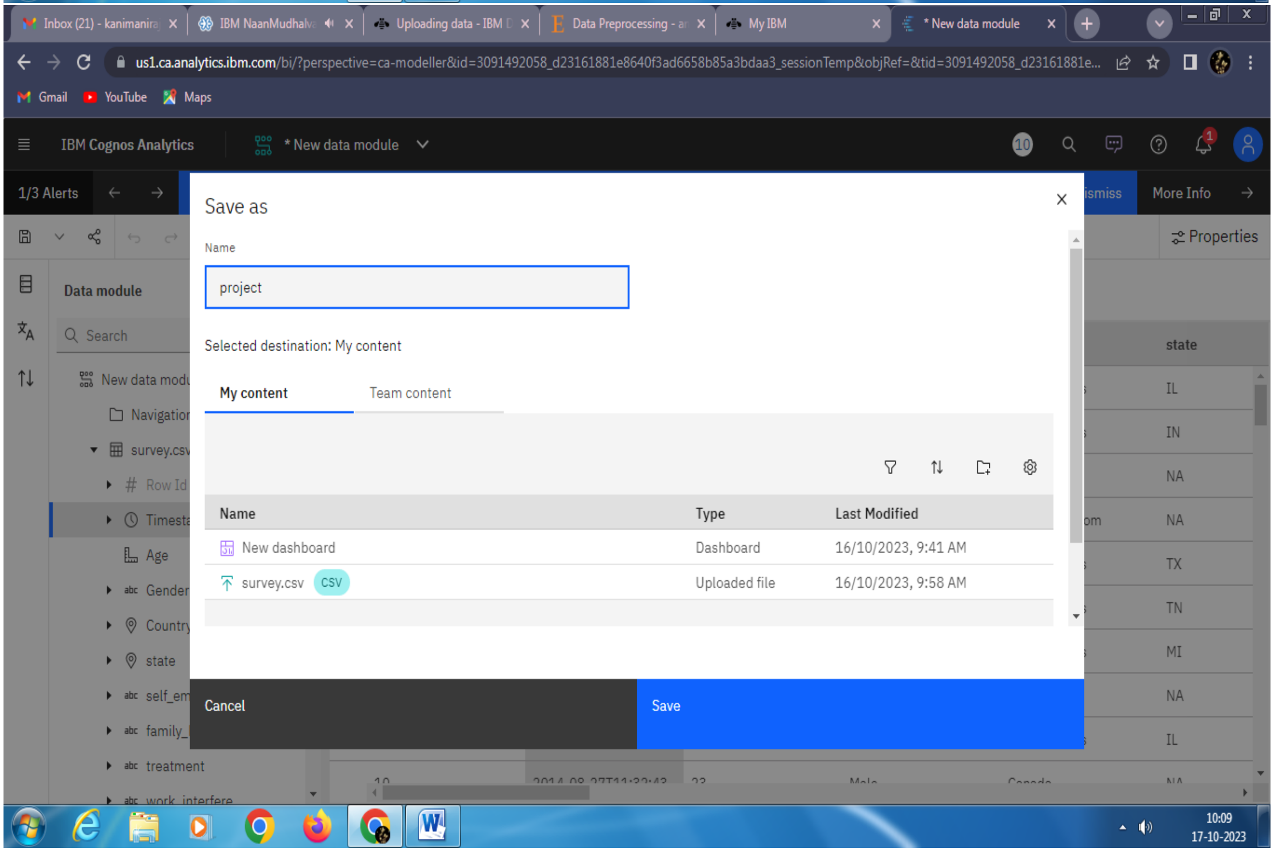
Reset filters

Type
- [ ] Folders
- [ ] Packages
- [ ] Files
- [ ] Data sets
- [ ] Modules

Modified
- [✓ All]
- Today
- Yesterday
- Past week
- Past month



| Row Id | Timestamp | Age | Gender | Country | state |
|---|---|---|---|---|---|
| 1 | 2014-08-27T11:29:31 | 37 | Female | United States | IL |
| 2 | 2014-08-27T11:29:37 | 44 | M | United States | IN |
| 3 | 2014-08-27T11:29:44 | 32 | Male | Canada | NA |
| 4 | 2014-08-27T11:29:46 | 31 | Male | United Kingdom | NA |
| 5 | 2014-08-27T11:30:22 | 31 | Male | United States | TX |
| 6 | 2014-08-27T11:31:22 | 33 | Male | United States | TN |
| 7 | 2014-08-27T11:31:50 | 35 | Female | United States | MI |
| 8 | 2014-08-27T11:32:05 | 39 | M | Canada | NA |
| 9 | 2014-08-27T11:32:39 | 42 | Female | United States | IL |



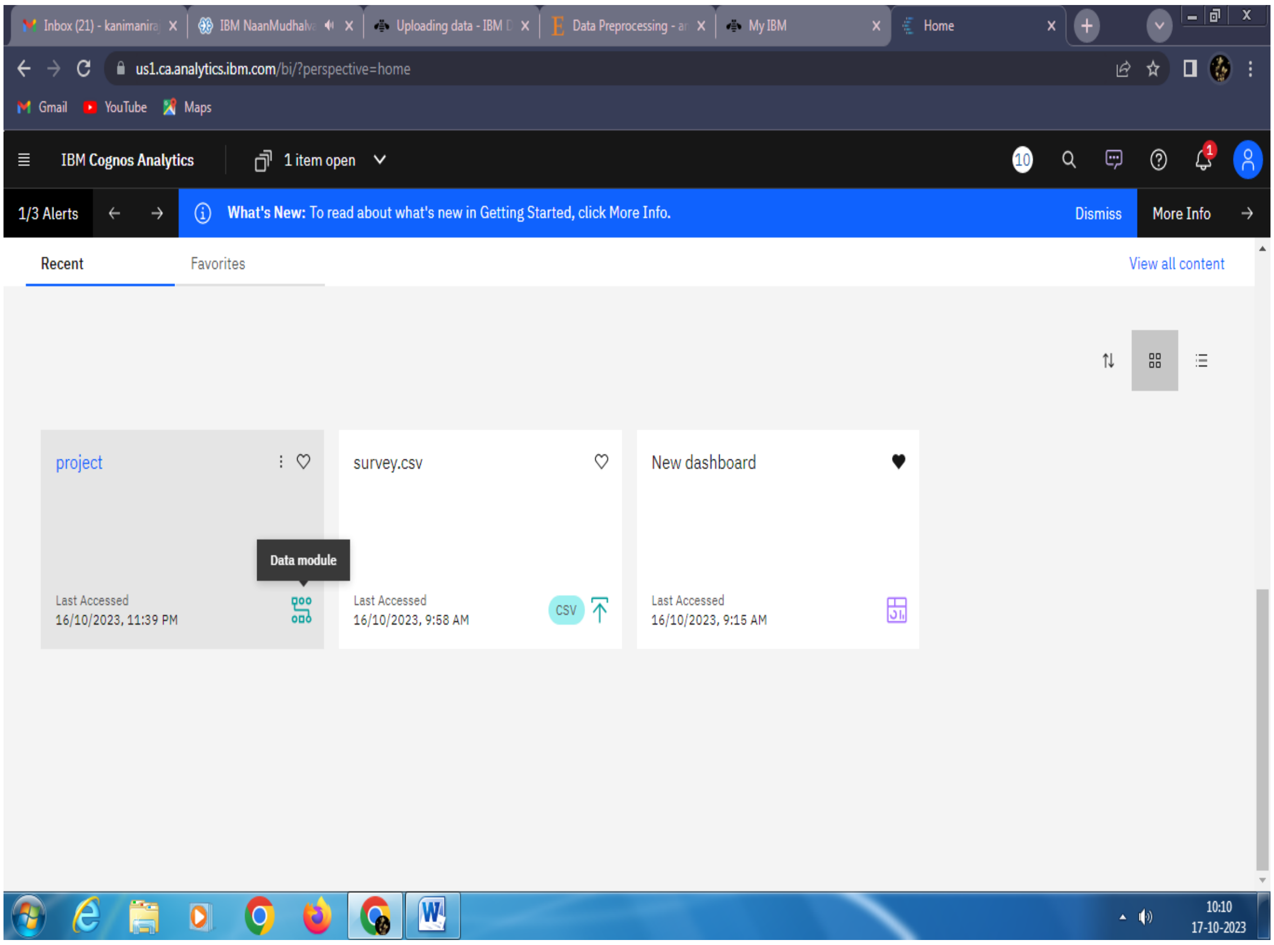
Save as

Name

project

Selected destination: My content

| Name | Type | Last Modified |
|---|---|---|
| New dashboard | Dashboard | 16/10/2023, 9:41 AM |
| survey.csv CSV | Uploaded file | 16/10/2023, 9:58 AM |



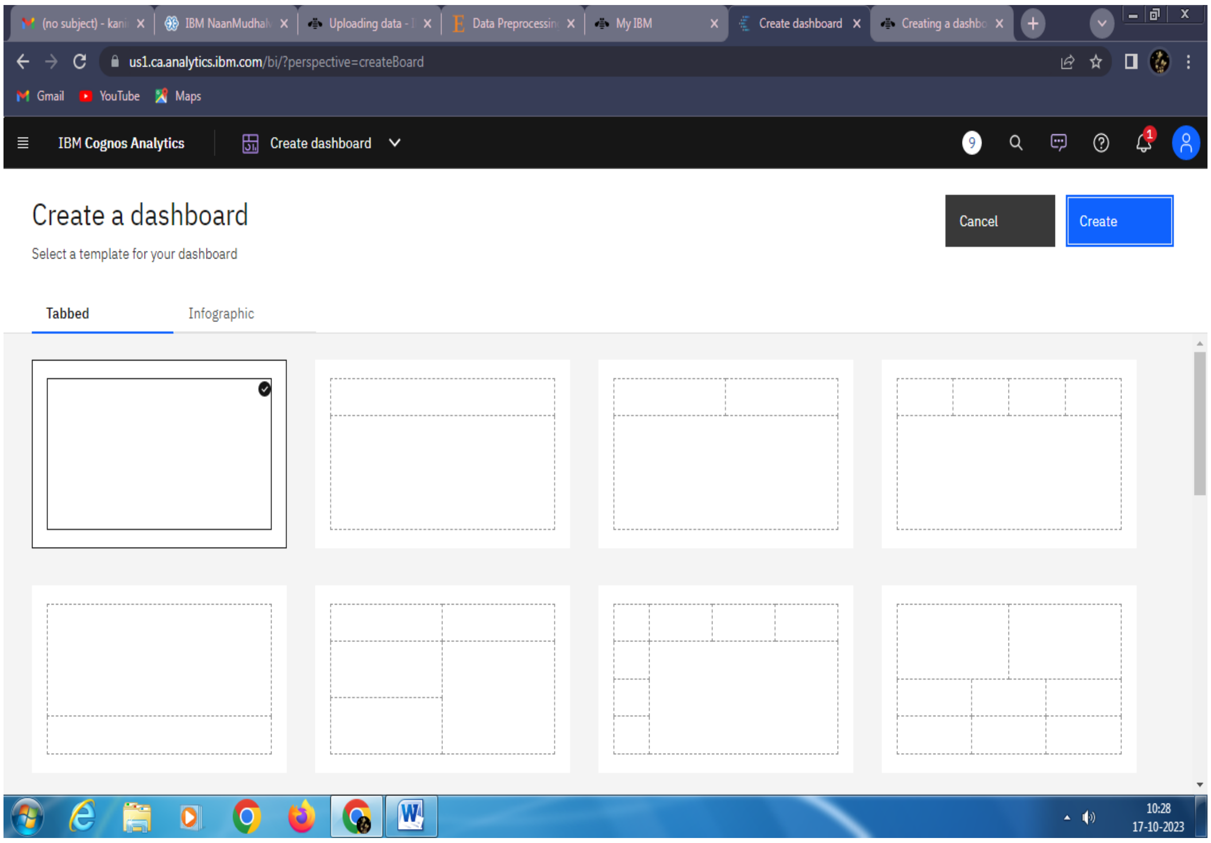
## VISUALIZATION:

### STEP 1: UPLOADING THE DATA SET:

- Login into IBM Cognos Analytics.
- Launch the product IBM Cognos Analytics on cloud-Trial.
- Click upload data and start creating content.
- Now drag or drop the Survey.csv (dataset file) and upload the file.

## STEP 2: ADDING A DASHBOARD TO THE ANALYTICS PROJECT:

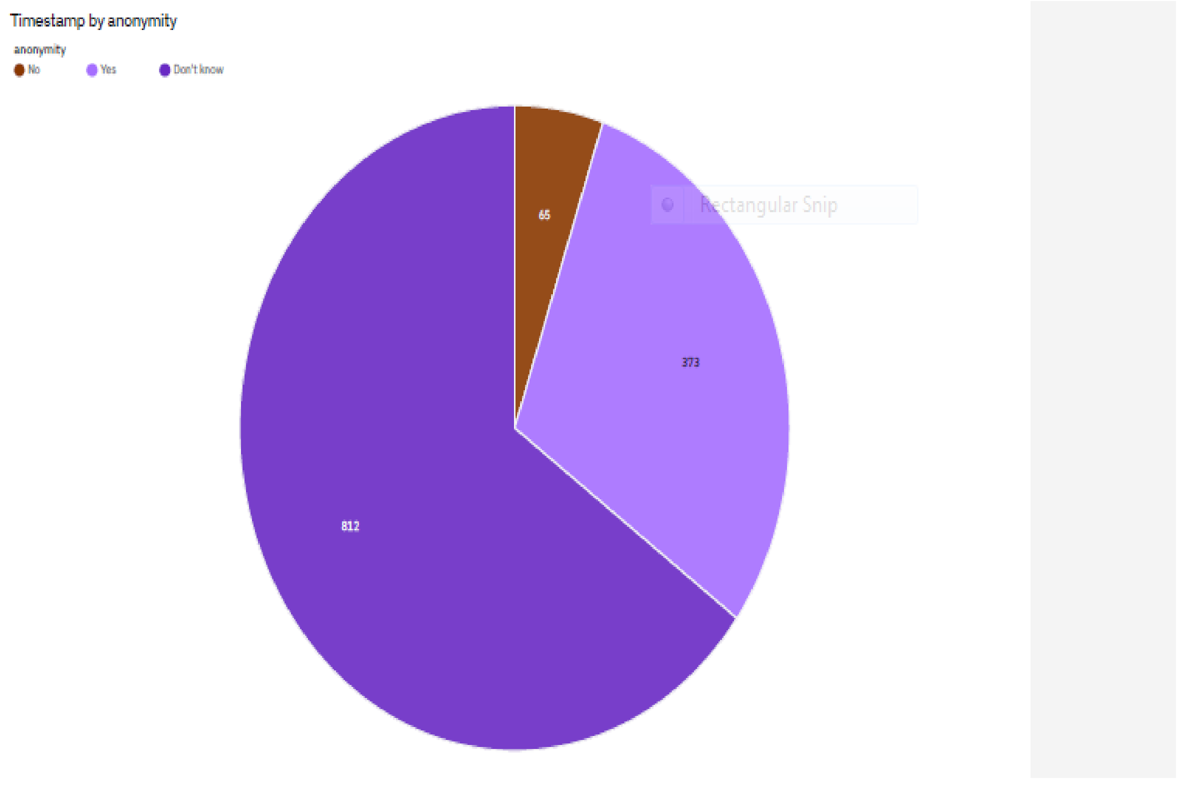
- Click **Add to project > Dashboard editor** from the
- Project toolbar, or click **new dashboard** from the Dashboards section on the project's **Assets** page.
- Create a blank dashboard or upload a dashboard from the file system. The dashboard file must be a *.json* file.
- Type a name and description for the dashboard.
- Select one of the provided templates that contain predefined designs and grid lines for easy arrangement and alignment of the visualizations. A new empty dashboard opens.
- Create visualizations of the source data.

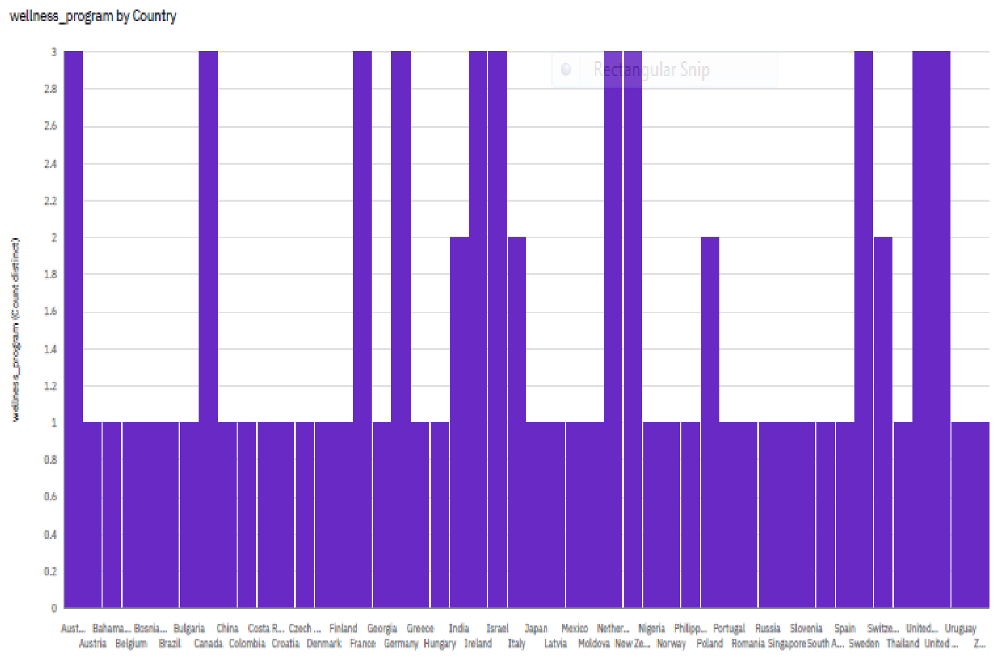


## STEP3: VISUALISE USING ANALYTICS OBJECTIVES:

### ➢ MEASURING AUDIENCE REACH:

The right to health includes a right of access to good quality palliative care, but inequalities persist. Raising awareness is a key plank of the public health approach to palliative care, but involves consideration of subjects most of us prefer not to address. This review addresses the question: "do public health awareness campaigns effectively improve the awareness and quality of palliative care"?





## ➢ AWARENESS LEVEL:

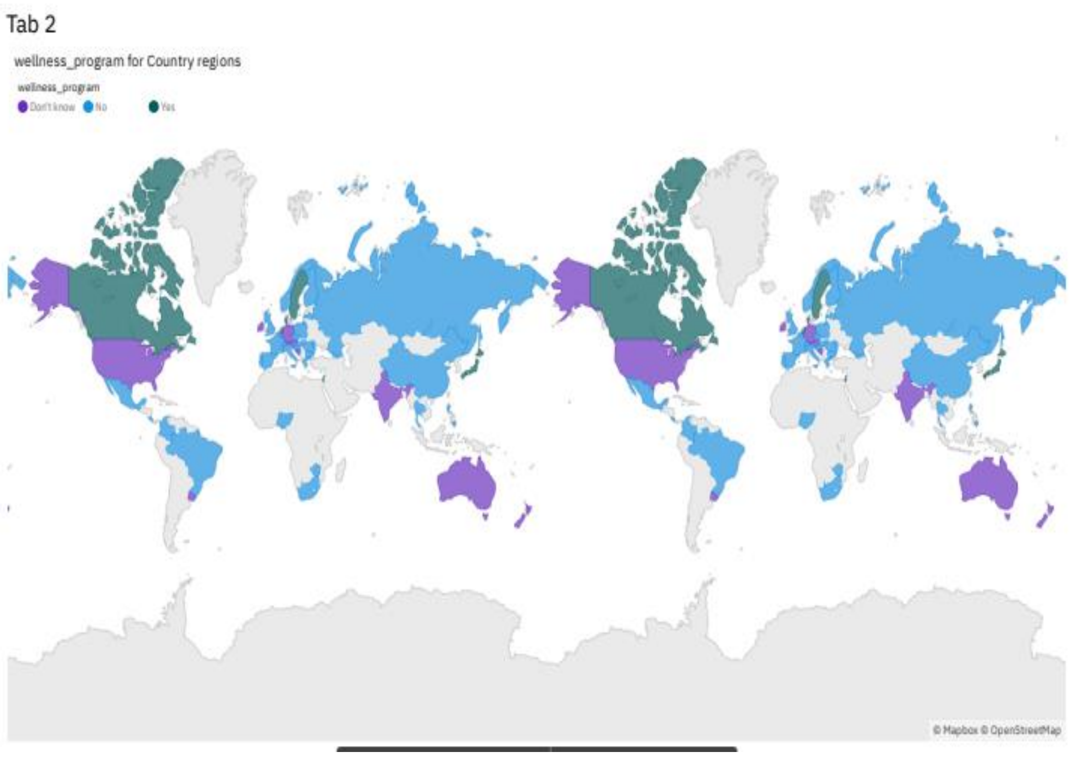
1. Start young most research on advance cares planning involves people over the age of 65. There is now a trend toward involving and educating much younger people, so that they are better prepared to deal with the issues in their families and communities. One study looks at university students in the United States and recommends that an important aspect of public health is providing reliable information about advance care planning to all young people.

2. An evaluation of TV advertisements about health promotion aimed at older adults showed that recipients were generally distrustful of the information if they perceived that it had been provided by the "government".

Professionals such as doctors or celebrities (e.g., Olympic stars) were seen as more trustworthy.

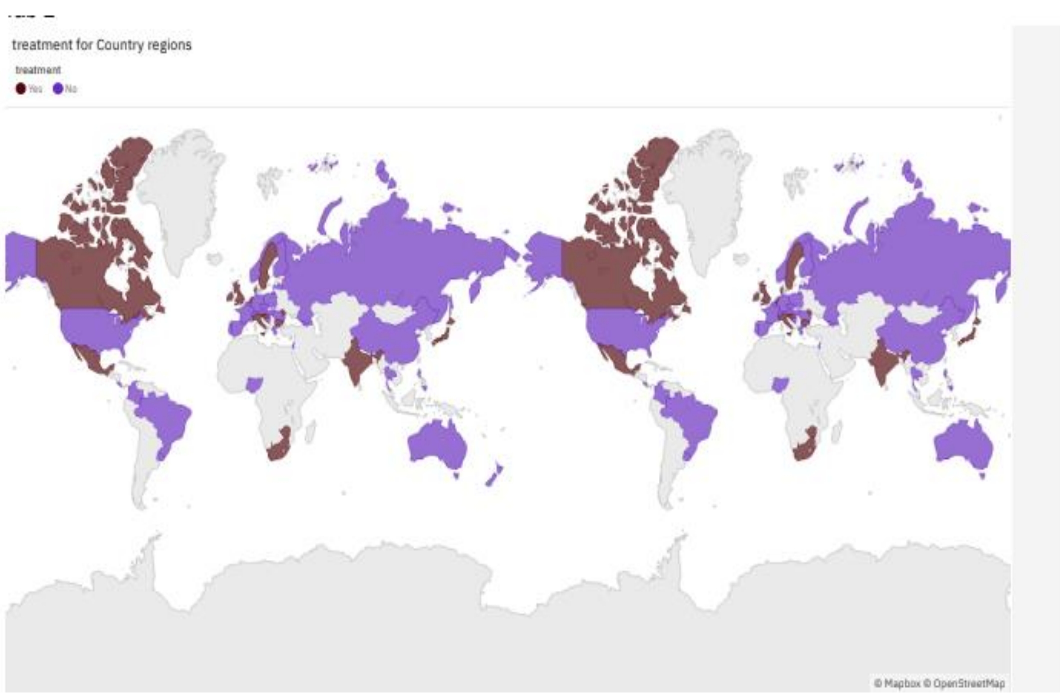
3. Social media has the potential to increase engagement with healthcare issues and enable debate and discussion, as well as create virtual social networks.

4. Younger people prefer to receive health information through the internet or other electronic means, while older people prefer the newspapers.



➢ **Campaign Impact:**

The evidence shows that public awareness campaigns can improve awareness of palliative care and probably improve quality of care, but there is a lack of evidence about the latter.



## STEPS FOR CREATING REPORT:

### STEP 1: UPLOAD THE DATASET:

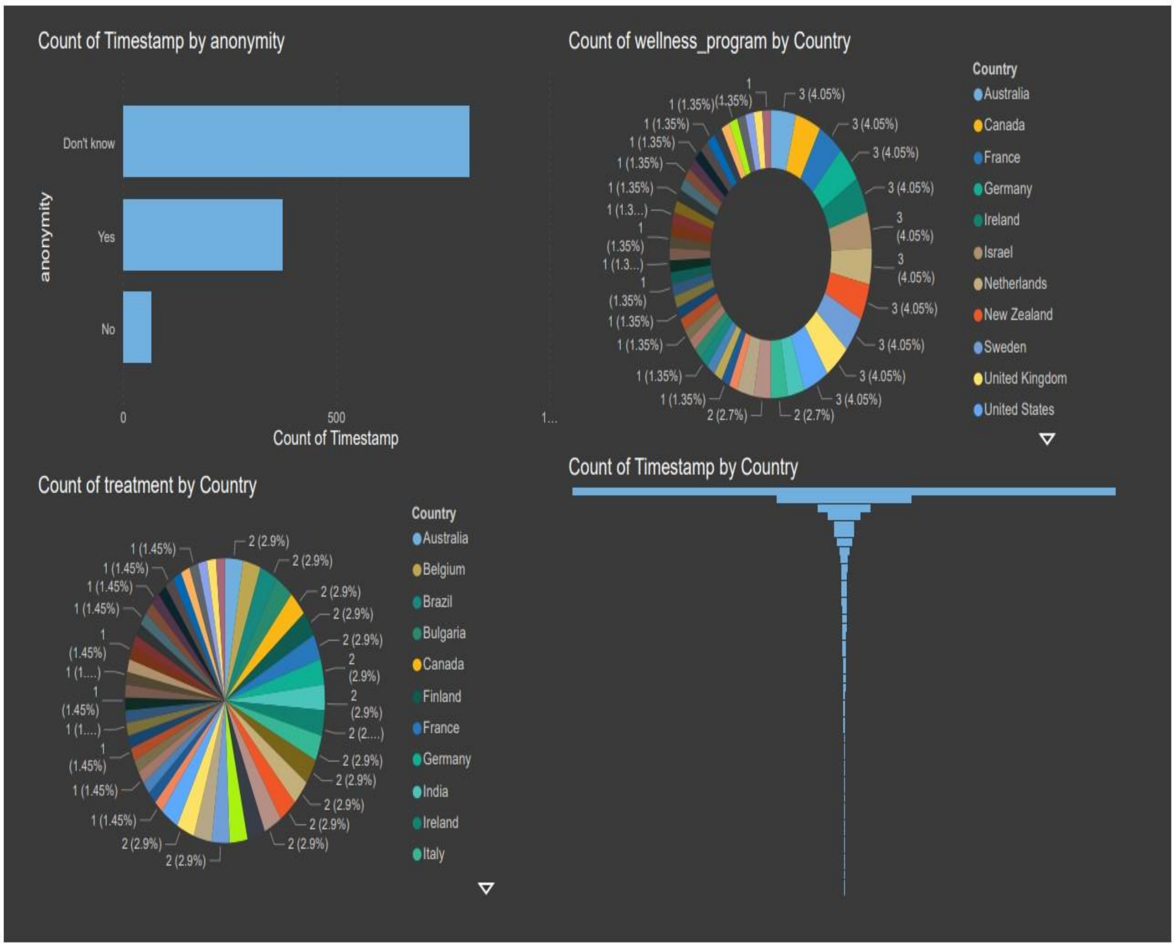
- Login to IBM Cognos Analytics.
- Launch the product IBM Cognos Analytics on Cloud-trial.
- Click 'GET DATA' and upload the file(csv file).
- Click 'CONNECT' to connect the data to the dashboard.
- Then load the data to create the report.

### STEP 2: BUILDING VISUALS WITH THE DATA:

- Double click on the screen, a blank space with 'question bar' is created.
- Type the question and the type of chart.
- Now, the respective chart appears and click 'OK' button.
- Repeat step 2, as many times for different questions.

- Finally, click 'VIEW' to view the complete report.

## REPORT:



## EXPLANATION:

### CAMPAIGN IMPACT:

The evidence shows that public awareness campaigns can improve awareness of palliative care and probably improve quality of care, but there is a lack of evidence about the latter.

### MEASURING AUDIENCE REACH:

The right to health includes a right of access to good quality palliative care, but inequalities persist. Raising awareness is a key plank of the public health approach to palliative care, but involves consideration of subjects most of us prefer not to address. This review addresses the question: "do public health awareness campaigns effectively improve the awareness and quality of palliative care"?

## AWARENESS LEVEL:

1. Start young most research on advance cares planning involves people over the age of 65. There is now a trend toward involving and educating much younger people, so that they are better prepared to deal with the issues in their families and communities. One study looks at university students in the United States and recommends that an important aspect of public health is providing reliable information about advance care planning to all young people.

2. An evaluation of TV advertisements about health promotion aimed at older adults showed that recipients were generally distrustful of the information if they perceived that it had been provided by the “government”. Professionals such as doctors or celebrities (e.g., Olympic stars) were seen as more trustworthy.

3. social media has the potential to increase engagement with healthcare issues and enable debate and discussion, as well as create virtual social networks.

4. Younger people prefer to receive health information through the internet or other electronic means, while older people prefer newspapers.

## CODE TO PERFORM ADVANCED DATA ANALYSIS:

### ❖DEMOGRAPHIC ANALYSIS:

```
import pandas as pd

import matplotlib.pyplot as plt

data = pd.read_csv("survey (1).csv")

print(data.head())

# Get summary statistics

print(data.describe())

# Check for missing values

print(data.isnull().sum())
```

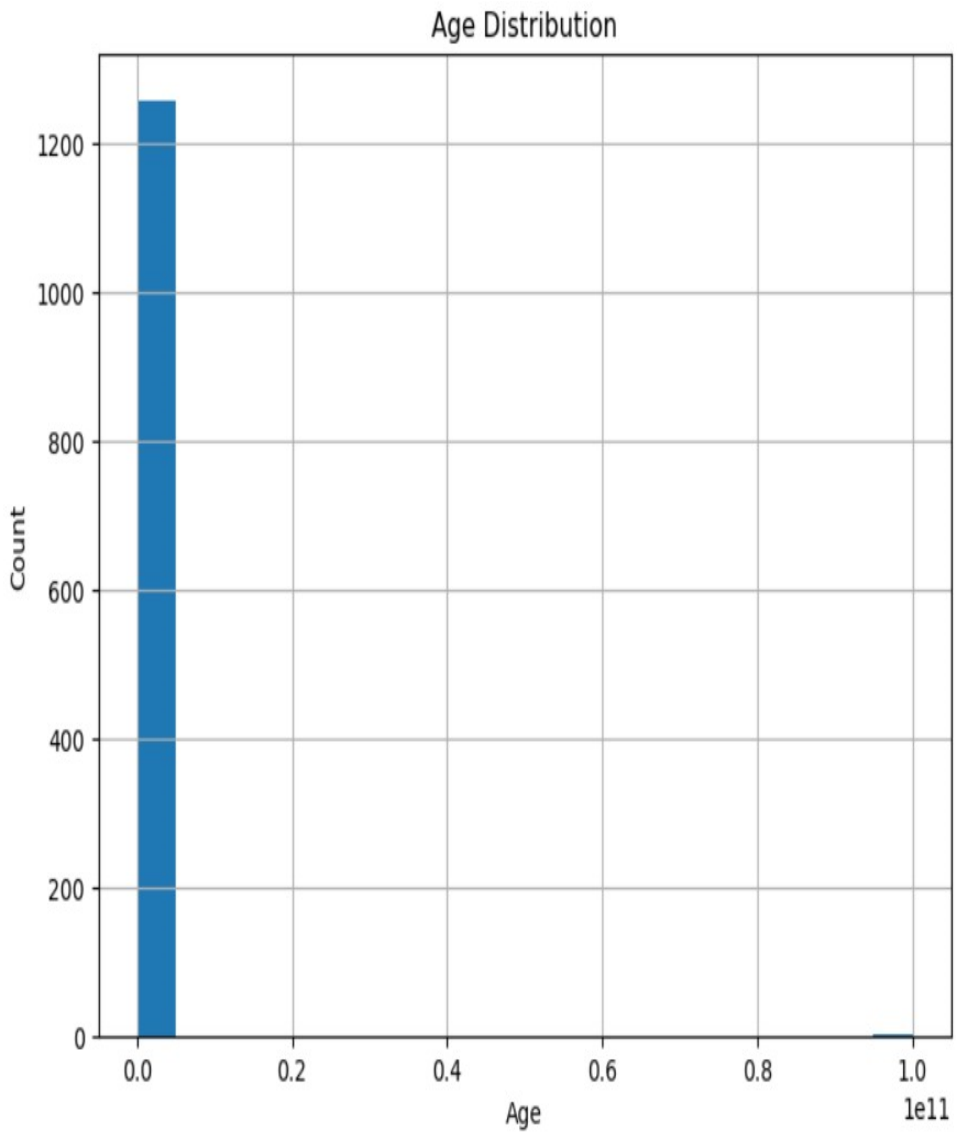
**OUTPUT:**

```
Timestamp  Age  Gender         Country state self_employed  \
0  2014-08-27 11:29:31   37  Female   United States    IL           NaN
1  2014-08-27 11:29:37   44       M   United States    IN           NaN
2  2014-08-27 11:29:44   32    Male          Canada   NaN           NaN
3  2014-08-27 11:29:46   31    Male  United Kingdom   NaN           NaN
4  2014-08-27 11:30:22   31    Male   United States    TX           NaN

family_history treatment work_interfere    no_employees  ...  \
0             No       Yes          Often            6-25  ...
1             No        No         Rarely  More than 1000  ...
2             No        No         Rarely            6-25  ...
3            Yes       Yes          Often          26-100  ...
4             No        No          Never         100-500  ...
leave mental_health_consequence phys_health_consequence  \
0       Somewhat easy                       No                      No
1          Don't know                    Maybe                      No
2  Somewhat difficult                       No                      No
3  Somewhat difficult                      Yes                     Yes
4          Don't know                       No                      No

coworkers supervisor mental_health_interview phys_health_interview  \
0  Some of them        Yes                      No                  Mayb
e
1           No         No                      No                     N
o
2          Yes        Yes                     Yes                    Ye
s
```

```
3  Some of them         No                    Maybe                    Mayb
e
4  Some of them        Yes                      Yes                      Ye
s

mental_vs_physical obs_consequence comments
0                Yes              No      NaN
1         Don't know              No      NaN
2                 No              No      NaN
3                 No             Yes      NaN
4         Don't know              No      NaN

[5 rows x 27 columns]
                Age
count  1.259000e+03
mean   7.942815e+07
std    2.818299e+09
min   -1.726000e+03
25%    2.700000e+01
50%    3.100000e+01
75%    3.600000e+01
max    1.000000e+11
Timestamp                      0
Age                            0
Gender                         0
Country                        0
state                        515
self_employed                 18
family_history                 0
treatment                      0
work_interfere               264
no_employees                   0
remote_work                    0
tech_company                   0
benefits                       0
care_options                   0
wellness_program               0
seek_help                      0
anonymity                      0
leave                          0
mental_health_consequence      0
phys_health_consequence        0
coworkers                      0
supervisor                     0
mental_health_interview        0
phys_health_interview          0
mental_vs_physical             0
obs_consequence                0
comments                    1095
dtype: int64
```

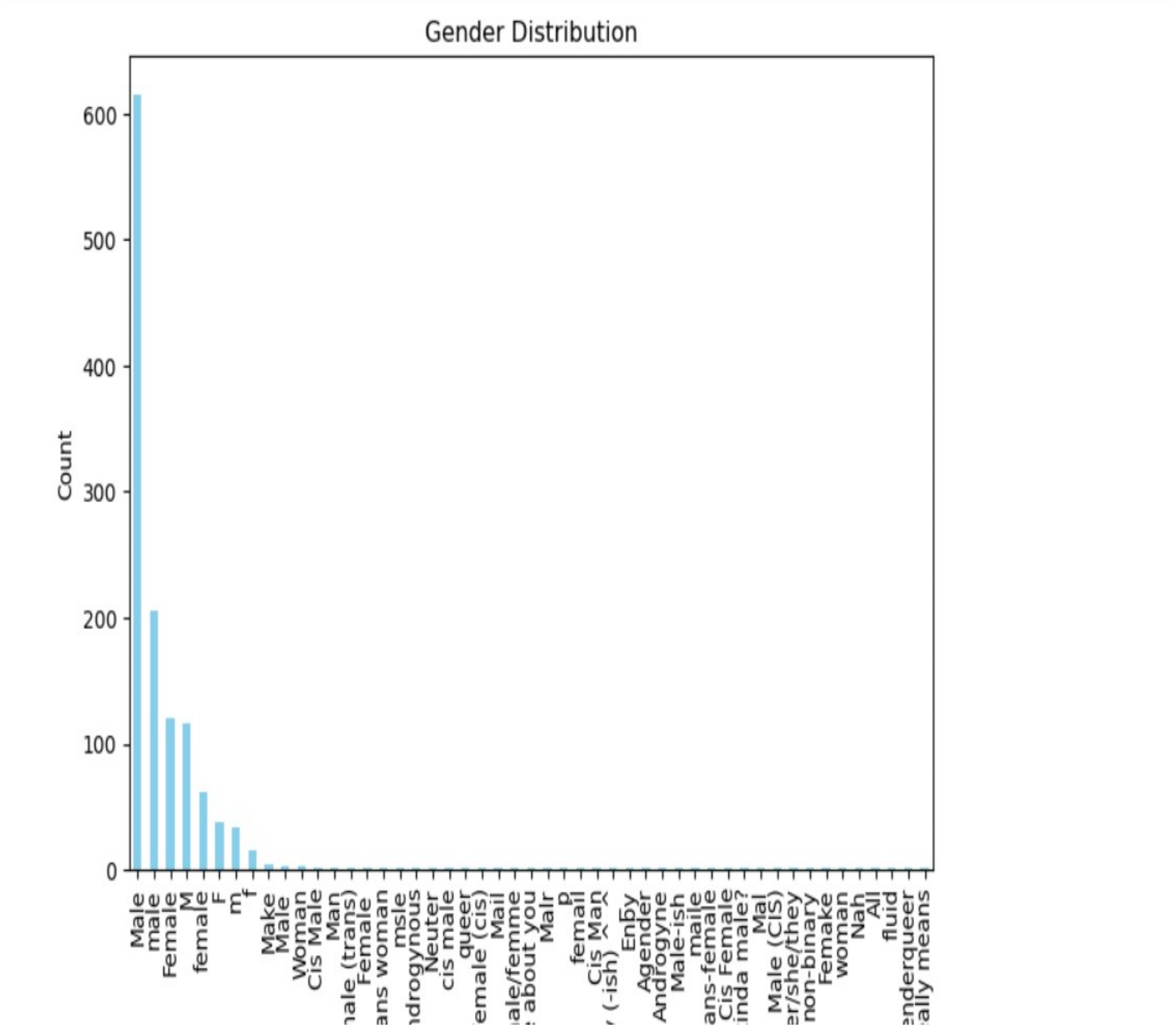
```
# Analyze age distribution
plt.figure(figsize=(8, 6))
data['Age'].hist(bins=20)
plt.title("Age Distribution")
plt.xlabel("Age")
plt.ylabel("Count")
plt.show()
```

**OUTPUT:**



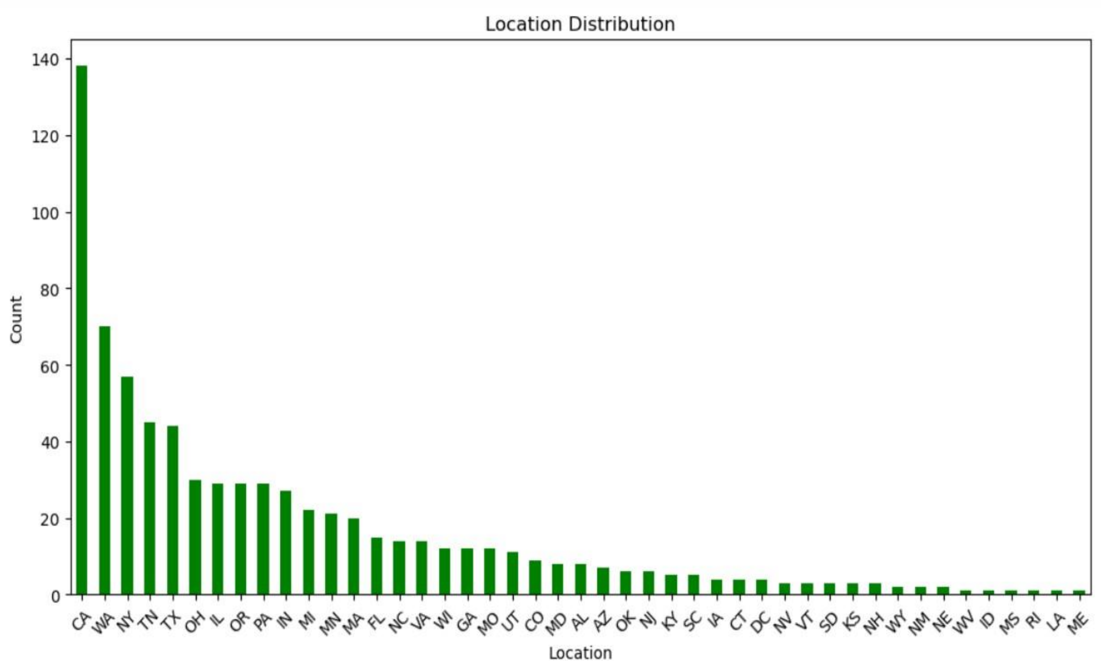
```
# Analyze gender distribution
gender_counts = data['Gender'].value_counts()
plt.figure(figsize=(8, 6))
gender_counts.plot(kind='bar', color='skyblue')
plt.title("Gender Distribution")
plt.xlabel("Gender")
plt.ylabel("Count")
plt.show()
```

**OUTPUT:**



```
# Analyze location distribution
location_counts = data['Location'].value_counts()
plt.figure(figsize=(12, 6))
location_counts.plot(kind='bar', color='green')
plt.title("Location Distribution")
plt.xlabel("Location")
plt.ylabel("Count")
plt.xticks(rotation=45)
plt.show()
```

**OUTPUT:**



## ❖STATISTICAL TESTS:

```
import pandas as pd

import numpy as np

from scipy import stats

data = pd.read_csv("survey (1).csv")
```

Hypothesis Testing:

One-sample T-Test:

```
sample_data = data['self_employed']  # Replace with your metric of interest

population_mean = 100  # Replace with your known population mean

t_statistic, p_value = stats.ttest_1samp(sample_data, population_mean)

if p_value < 0.05:

    print("The sample mean is significantly different from the population mean.")

else:

    print("There is no significant difference between the sample mean and the population mean.")
```

### OUTPUT:

```
There is no significant difference between the sample mean and the population mean.
```

## ❖TWO SAMPLE T-TEST:

```
group1_data = data[data['work_interfere'] == 'Group 1']['work_interfere']  # Replace with your data
group2_data = data[data['self_employed'] == 'Group 2']['self_employed']  # Replace with your data
t_statistic, p_value = stats.ttest_ind(group1_data, group2_data)
if p_value < 0.05:
   print("There is a significant difference between the two groups.")
else:
   print("There is no significant difference between the two groups.")
```

**OUTPUT:**

```
There is no significant difference between the two groups.
```

## ❖CHI-SQUARED TEST:

```
contingency_table = pd.crosstab(data['Country'], data['self_employed'])
chi2, p, dof, expected = stats.chi2_contingency(contingency_table)
if p < 0.05:
   print("The variables are dependent.")
else:
   print("The variables are independent.")
```

**OUTPUT:**

```
The variables are dependent.
```

```
contingency_table = pd.crosstab(data['state'], data['work_interfere'])
chi2, p, dof, expected = stats.chi2_contingency(contingency_table)
if p < 0.05:
   print("The variables are dependent.")
else:
   print("The variables are independent.")
```

**OUTPUT:**

```
The variables are independent.
```

## ❖ ANOVA ( ANALYSIS OF VARIANCE):

```
group_data = [data[data['Timestamp'] == group]['Age'] for group in
data['Timestamp'].unique()]
f_statistic, p_value = stats.f_oneway(*group_data)
if p_value < 0.05:
   print("There is a significant difference between the groups.")
else:
   print("There is no significant difference between the groups.")
```

**OUTPUT:**

```
There is no significant difference between the groups.
```

## ❖ ENGAGEMENT RATES:

```
engagements = 500
total_reach = 10000
# Calculate engagement rate
engagement_rate = (engagements / total_reach) * 100
# Print the result
print(f"The engagement rate is: {engagement_rate:.2f}%")
```

**OUTPUT:**

```
The engagement rate is: 5.00%
```

## CONCLUSION:

In conclusion, this research seeks to bridge the gap between public health campaigns and data analytics, offering valuable insights to healthcare professionals, policymakers, and public health organizations. By harnessing the power of data analytics, we can ensure that public health messages reach the right people at the right time, ultimately saving lives and improving the overall well-being of society.