# **Exploratory Data Analysis (EDA)**

```
In [3]: |#Importing the Required Libraries
         import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plot
         import seaborn as sns
         from sklearn.utils import resample
         from imblearn.over_sampling import SMOTENC,RandomOverSampler,KMeansSMOTE
         from sklearn.impute import KNNImputer
         from sklearn.preprocessing import LabelEncoder
         sns.set()
In [4]: | df = pd.read_csv("InputFile.csv")
In [5]:
Out[5]:
                        on_thyroxine
                                    query_on_thyroxine on_antithyroid_medication sick
               age
                    sex
             0
                41
             1
                23
                                  f
                                                     f
                                                                            f
                                                                                 f
             2
                46
                     М
             3
                70
                70
            ...
          3767
                30
                      F
                                  f
                                                     f
                                                                                 f
          3768
          3769
                74
          3770
                72
          3771
                64
         3772 rows × 30 columns
```

Problem Statement: To build a classification methodology to predict the type of Thyroid a person has ,based on the below features.

age - Age of the person

sex - Male or Female

on\_thyroxine - true or false

on\_antithyroid\_medication - true or false

sick - true or false

pregnant - true or false

thyroid surgery - true or false

1131 treatment - true or false

query hypothyroid - true or false

query hyperthyroid -true or false

lithium - true or false

goitre - true or false

tumor - true or false

hypopituitary- true or false

psych - true or false

TSH\_measured - true or false

TSH - thyroid stimulating hormone floating value

T3 measured - true or false

T3 - triiodothyronine value

TT4\_measured- true or false

TT4 - Thyroxine value

T4U measured- true or false

T4U - numerical value

FTI\_measured- true or false

FTI -Free Thyroxine Index

TBG measured- true or false

TBG -Thyroid-Binding Globulin value

referral\_source - different sources of referals

Class - different types of thyroid

In [6]: df.describe()

Out[6]:		age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_medication	sick	pre
	count	3772	3772	3772	3772	3772	3772	
	unique	94	3	2	2	2	2	
	top	59	F	f	f	f	f	
	freq	95	2480	3308	3722	3729	3625	

4 rows × 30 columns

```
In [8]:
         for column in df.columns:
              count = df[column][df[column]=="?"].count()
              if count != 0:
                  print(column, count)
          age 1
          sex 150
          TSH 369
          T3 769
          TT4 231
          T4U 387
          FTI 385
          TBG 3772
 In [9]: | df = df.drop(["TBG"], axis = 1)
In [10]: df[["T4U_measured", "T4U"]]
Out[10]:
                T4U_measured T4U
             0
                           t 1.14
                               ?
             1
             2
                           t 0.91
                               ?
             3
                           t 0.87
          3767
                               ?
          3768
                           t 1.08
          3769
                           t 1.07
          3770
                           t 0.94
          3771
                           t 1.07
          3772 rows × 2 columns
In [11]: | df = df.drop(['TSH_measured','T3_measured','TT4_measured','T4U_measured','F
In [12]: for column in df.columns:
              count = df[column][df[column] == "?"].count()
                  df[column] = df[column].replace("?", np.nan)
```

```
In [13]: df.isnull().sum()
Out[13]: age
                                            1
                                         150
          sex
                                            0
          on_thyroxine
                                            0
          query_on_thyroxine
          on_antithyroid_medication
                                            0
                                            0
          sick
          pregnant
                                            0
          thyroid_surgery
                                            0
          I131_treatment
                                            0
          query_hypothyroid
                                            0
          query_hyperthyroid
                                            0
          lithium
                                            0
                                            0
          goitre
                                            0
          tumor
                                            0
          hypopituitary
                                            0
          psych
          TSH
                                         369
          T3
                                         769
          TT4
                                         231
          T4U
                                         387
          FTI
                                         385
          referral_source
                                           0
          Class
                                            0
          dtype: int64
In [15]: df['sex'] = df['sex'].map(\{"F" : 0, "M" : 1\})
In [16]: for column in df.columns:
              if len(df[column].unique()) == 2:
                   df[column] = df[column].map({"f":0, "t":1})
In [17]: df.head()
Out[17]:
             age sex on_thyroxine query_on_thyroxine on_antithyroid_medication sick pregnant tl
           0
              41
                  0.0
                                0
                                                                          0
                                                                               0
                                                                                       0
           1
              23
                  0.0
                                0
                                                  0
                                                                          0
                                                                               0
                                                                                       0
           2
              46
                  1.0
                                0
                                                  0
                                                                          0
                                                                               0
                                                                                       0
           3
              70
                  0.0
                                1
                                                  0
                                                                          0
                                                                               0
                                                                                       0
                                                                          0
                                                                                       0
              70
                  0.0
                                0
                                                  0
                                                                               0
          5 rows × 23 columns
In [18]: df = df.drop(columns=["referral_source"], axis = True)
In [19]: |df["Class"].unique()
Out[19]: array(['negative', 'compensated_hypothyroid', 'primary_hypothyroid',
                  'secondary_hypothyroid'], dtype=object)
```

```
In [20]:
           lbn = LabelEncoder()
           df["Class"] = lbn.fit_transform(df["Class"])
In [21]: df.head()
Out[21]:
                                     query_on_thyroxine on_antithyroid_medication
                                                                                  sick pregnant tl
               age
                   sex
                        on_thyroxine
            0
                41
                    0.0
                                   0
                                                                                     0
                                                                                               0
                                   0
            1
                23
                    0.0
                                                       0
                                                                                0
                                                                                     0
                                                                                               0
                                   0
            2
                46
                    1.0
                                                       0
                                                                                0
                                                                                     0
                                                                                               0
            3
                70
                    0.0
                                                                                0
                                                                                     0
                                   1
                                                       0
                                                                                               0
                70
                    0.0
                                                                                0
                                                                                     0
                                                                                               0
           5 rows × 22 columns
          df.describe(include='all')
In [22]:
Out[22]:
                                 sex on_thyroxine query_on_thyroxine on_antithyroid_medication
                    age
                         3622.000000
                                                                                    3772.000000
             count 3771
                                       3772.000000
                                                          3772.000000
                                                                                           NaN
            unique
                      93
                                 NaN
                                              NaN
                                                                 NaN
                      59
                                 NaN
                                              NaN
                                                                 NaN
                                                                                           NaN
               top
                                                                                           NaN
                      95
                                 NaN
                                              NaN
                                                                 NaN
              freq
                                                             0.013256
                                                                                       0.011400
                    NaN
                            0.315295
                                          0.123012
             mean
                    NaN
                            0.464698
                                          0.328494
                                                             0.114382
                                                                                       0.106174
               std
                    NaN
                            0.000000
                                          0.000000
                                                             0.000000
                                                                                       0.000000
               min
              25%
                    NaN
                            0.000000
                                          0.000000
                                                             0.000000
                                                                                       0.000000
              50%
                    NaN
                            0.000000
                                          0.000000
                                                             0.000000
                                                                                       0.000000
              75%
                    NaN
                             1.000000
                                          0.000000
                                                             0.000000
                                                                                       0.000000
              max
                    NaN
                             1.000000
                                          1.000000
                                                              1.000000
                                                                                       1.000000
           11 rows × 22 columns
           imputer = KNNImputer(n_neighbors=3, weights='uniform', missing_values=np.na
In [23]:
           new arr = imputer.fit transform(df)
In [25]: new_df = pd.DataFrame(new_arr)
```

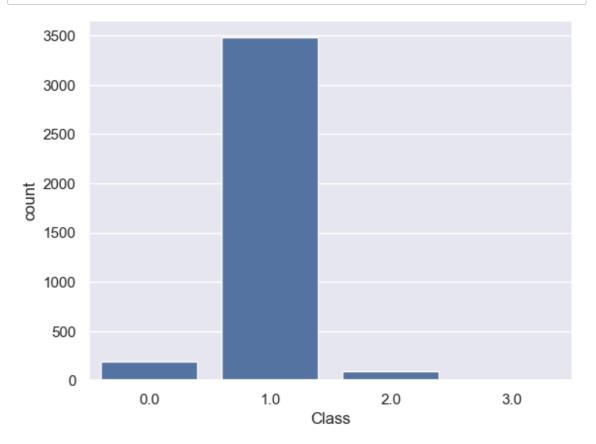
```
In [26]:
          new_df
Out[26]:
                        1
                            2
                                                 7
                   0
                                3
                                     4
                                         5
                                             6
                                                     8
                                                          9 ...
                                                                12
                                                                    13
                                                                         14
                                                                             15
                                                                                      16
                      0.0
                          0.0 0.0
                                   0.0
                                       0.0
                                           0.0
                                               0.0
                                                    0.0 0.0 ...
                                                                0.0
                                                                    0.0
                                                                        0.0
                                                                            0.0
                                                                                1.300000
                          0.0
                              0.0
                                  0.0
                                       0.0
                                           0.0
                                               0.0
                                                    0.0
                                                       0.0 ...
                                                               0.0
                                                                   0.0
                                                                        0.0
                                                                            0.0
                                                                                4.100000
                          0.0
                               0.0
                                  0.0
                                       0.0
                                           0.0
                                               0.0
                                                    0.0
                                                        0.0
                                                               0.0
                                                                   0.0
                                                                        0.0
                                                                                0.980000
                               0.0
                                           0.0
                                               0.0
                                                    0.0
                                                        0.0
                                                                0.0
                                                                    0.0
                                                                        0.0
                                                                                0.160000
                          0.0
                               0.0
                                       0.0
                                           0.0
                                               0.0
                                                    0.0
                                                        0.0 ...
                                                               0.0
                                                                    0.0
                                                                        0.0
                                                                                0.720000
                                                                                         1.2000
           3767
                 30.0
                      0.0
                          0.0
                               0.0
                                  0.0
                                       0.0
                                           0.0
                                               0.0
                                                    0.0
                                                        0.0 ...
                                                                0.0
                                                                        0.0
                                                                            0.0
                                                                                1.566667 2.5333
                                                                   1.0
           3768 68.0
                      0.0
                          0.0
                              0.0
                                  0.0
                                       0.0 0.0 0.0
                                                    0.0
                                                       0.0 ... 0.0
                                                                   0.0
                                                                        0.0
                                                                            0.0
                                                                                1.000000
                                                                                         2.1000
           3769 74.0 0.0
                          0.0
                              0.0 0.0
                                      0.0 0.0
                                               0.0
                                                    0.0 \quad 0.0 \quad \dots \quad 0.0 \quad 0.0
                                                                       0.0 0.0
                                                                                5.100000
                                                                                         1.8000
           3770 72.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0
                                                    0.0 0.0 ... 0.0 0.0 0.0
                                                                            0.0
                                                                                0.700000 2.0000
           3772 rows × 22 columns
          new_df.isnull().sum()
In [27]:
Out[27]:
                 0
          1
                 0
          2
                 0
          3
                 0
          4
                 0
          5
                 0
          6
                 0
          7
                 0
          8
                 0
          9
                 0
          10
                 0
          11
                 0
                 0
          12
          13
                 0
          14
                 0
          15
                 0
          16
                 0
          17
                 0
          18
                 0
          19
                 0
                 0
          20
          21
                 0
          dtype: int64
```

		0	1	2	3	4		5	
coun	3772	2.000000	3772.000000	3772.000000	3772.000000	3772.000000	3772.0	000000	3772.
mear	51	.737275	0.308855	0.123012	0.013256	0.011400	0.0	038971	0.
sto	1 20	0.082478	0.458819	0.328494	0.114382	0.106174	0.1	193552	0.
mir	1	.000000	0.000000	0.000000	0.000000	0.000000	0.0	000000	0.
25%	36	0.000000	0.000000	0.000000	0.000000	0.000000	0.0	000000	0.
50%	54	.000000	0.000000	0.000000	0.000000	0.000000	0.0	000000	0.
75%	67	7.000000	1.000000	0.000000	0.000000	0.000000	0.0	000000	0.
max	455	5.000000	1.000000	1.000000	1.000000	1.000000	1.0	000000	1.
8 row	s × 22	columns	3						
4									•
colum	ns =	df.col	umns						
new_d	f = p	d.Data	Frame(new_a	rr, columns	=columns)				
new_d		d.Datal	Frame(new_a	rr, columns	=columns)				
				rr, columns		hyroid_medica	ation s	sick p	regnan
	f					hyroid_medica	ation s	sick p	regnan
new_d	f age	sex on	_thyroxine q		xine on_antit	hyroid_medica			
new_d	f age 41.0	sex on	thyroxine q		xine on_antit	hyroid_medica	0.0	0.0	0.0
new_d	f age 41.0 23.0 46.0	sex on 0.0 0.0	0.0 0.0		xine on_antit	hyroid_medica	0.0	0.0	0.0
new_d	f age 41.0 23.0 46.0 70.0	sex on 0.0 0.0 1.0	0.0 0.0 0.0		xine on_antit  0.0  0.0  0.0  0.0	hyroid_medica	0.0 0.0 0.0	0.0 0.0 0.0	0.0
new_d 0 1 2 3	f age 41.0 23.0 46.0 70.0	sex on 0.0 0.0 1.0 0.0	0.0 0.0 0.0 0.0		xine on_antit  0.0  0.0  0.0  0.0  0.0	hyroid_medica	0.0 0.0 0.0 0.0	0.0 0.0 0.0 0.0	0.0
new_d 0 1 2 3	f age 41.0 23.0 46.0 70.0	sex on 0.0 0.0 1.0 0.0 0.0	0.0 0.0 0.0 0.0 1.0 0.0		xine on_antit 0.0 0.0 0.0 0.0 0.0	hyroid_medica	0.0 0.0 0.0 0.0 0.0	0.0 0.0 0.0 0.0 0.0	0.0
new_d  1 2 3 4	f  age 41.0 23.0 46.0 70.0 70.0	sex on 0.0 0.0 1.0 0.0 0.0	0.0 0.0 0.0 0.0 1.0 0.0		xine on_antit  0.0  0.0  0.0  0.0  0.0	hyroid_medica	0.0 0.0 0.0 0.0 0.0	0.0 0.0 0.0 0.0 0.0	0.0 0.0 0.0 0.0
0 1 2 3 4 	f  age 41.0 23.0 46.0 70.0 70.0 30.0	sex on 0.0 0.0 1.0 0.0 0.0 0.0	0.0 0.0 0.0 0.0 1.0 0.0 		on_antit  0.0  0.0  0.0  0.0  0.0   0.0	hyroid_medica	0.0 0.0 0.0 0.0 0.0 	0.0 0.0 0.0 0.0 0.0 	0.0 0.0 0.0 0.0 0.0
new_d  0  1  2  3  4   3767  3768	f  age 41.0 23.0 46.0 70.0 70.0 30.0 68.0	sex on 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	0.0 0.0 0.0 1.0 0.0  0.0		on_antit  0.0  0.0  0.0  0.0  0.0  0.0  0.0	hyroid_medica	0.0 0.0 0.0 0.0 0.0  0.0	0.0 0.0 0.0 0.0 0.0  0.0	0.0 0.0 0.0 0.0 0.0
new_d  0  1  2  3  4   3767  3768  3769  3770	f  age 41.0 23.0 46.0 70.0 70.0 30.0 68.0 74.0	sex on 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.	0.0 0.0 0.0 1.0 0.0  0.0 0.0		on_antit  0.0  0.0  0.0  0.0  0.0  0.0  0.0	hyroid_medica	0.0 0.0 0.0 0.0 0.0  0.0 0.0	0.0 0.0 0.0 0.0 0.0  0.0 0.0	0.0 0.0 0.0 0.0 0.0 0.0
new_d  0 1 2 3 4 3767 3768 3769 3770 3771	f  age 41.0 23.0 46.0 70.0 70.0 30.0 68.0 74.0 72.0 64.0	sex on 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.0 1.0	0.0 0.0 0.0 1.0 0.0  0.0 0.0 0.0 0.0		xine on_antit  0.0  0.0  0.0  0.0  0.0  0.0  0.0	hyroid_medica	0.0 0.0 0.0 0.0 0.0  0.0 0.0	0.0 0.0 0.0 0.0 0.0  0.0 0.0	0.0 0.0 0.0 0.0 0.0 0.0 0.0

```
columns = ['age','TSH','T3','TT4','T4U','FTI']
In [39]:
         plot.figure(figsize=(10,15),facecolor='white')
         plotnumber = 1
         for column in columns:
             ax = plot.subplot(3,2,plotnumber)
             sns.distplot(new_df[column])
             plot.xlabel(column,fontsize=10)
             plotnumber+=1
         plot.show()
         enimital lievinitital of hierbior (all avee-level laucaton for hierori
         ams).
         For a guide to updating your code to use the new functions, please see
         https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751 (http
         s://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751)
           sns.distplot(new_df[column])
         C:\Users\Dinesh\AppData\Local\Temp\ipykernel_39476\1990233037.py:8: Us
         erWarning:
         `distplot` is a deprecated function and will be removed in seaborn v0.
         14.0.
         Please adapt your code to use either `displot` (a figure-level functio
         similar flexibility) or `histplot` (an axes-level function for histogr
         ams).
         For a guide to updating your code to use the new functions, please see
```

```
plot.figure(figsize=(10,15),facecolor='white')
In [40]:
         plotnumber = 1
         for column in columns:
             new df[column]+=1
             ax = plot.subplot(3,2,plotnumber)
             sns.distplot(np.log(new df[column]))
             plot.xlabel(column, fontsize=10)
             plotnumber+=1
         plot.show()
         C:\Users\Dinesh\AppData\Local\Temp\ipykernel_39476\3553379851.py:7: Us
         erWarning:
         `distplot` is a deprecated function and will be removed in seaborn v0.
         14.0.
         Please adapt your code to use either `displot` (a figure-level functio
         similar flexibility) or `histplot` (an axes-level function for histogr
         ams).
         For a guide to updating your code to use the new functions, please see
         https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751 (http
         s://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751)
           sns.distplot(np.log(new_df[column]))
         C:\Users\Dinesh\AppData\Local\Temp\ipykernel_39476\3553379851.py:7: Us
         erWarning:
         . . . . . . .
                                                J 211 L
In [41]: new_df = new_df.drop(columns="TSH")
In [43]: new df.shape
Out[43]: (3772, 21)
```

```
In [52]: sns.countplot(data = new_df, x = "Class")
plot.show()
```



```
In [54]: x = new_df.drop(["Class"], axis = 1)
y = new_df["Class"]
rdsmple = RandomOverSampler()
x_sampled, y_sampled = rdsmple.fit_resample(x, y)

In [55]: x_sampled.shape

Out[55]: (13924, 20)

In [56]: y_sampled.shape

Out[56]: (13924,)

In [62]: df_y = pd.DataFrame(y_sampled, columns=["Class"])
```

```
In [63]: df_y
```

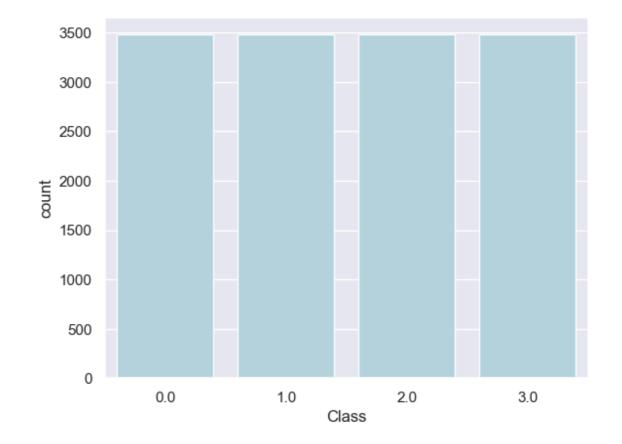
Out	[63]	:

	Class
0	1.0
1	1.0
2	1.0
3	1.0
4	1.0
13919	3.0
13920	3.0
13921	3.0
13922	3.0
13923	3.0

13924 rows × 1 columns

```
In [67]: sns.countplot(data = df_y, x = "Class", color="lightblue")
```

Out[67]: <AxesSubplot: xlabel='Class', ylabel='count'>



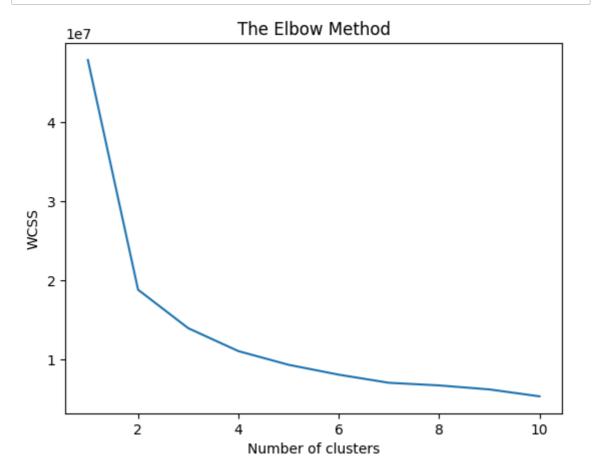
In [69]: df\_x Out[69]: nant thyroid\_surgery I131\_treatment query\_hypothyroid query\_hyperthyroid lithium goitre 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 ... ... ... ... 0.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 In [71]: merged\_df = pd.merge(df\_x, df\_y, left\_index=True, right\_index=True) In [72]: merged\_df Out[72]: age sex on\_thyroxine query\_on\_thyroxine on\_antithyroid\_medication sick pregna 0 42.0 0.0 0.0 0 0.0 0.0 0.0 24.0 0.0 0.0 0.0 0.0 0.0 0 **2** 47.0 1.0 0.0 0.0 0.0 0.0 0 **3** 71.0 0.0 1.0 0.0 0.0 0.0 0 71.0 0.0 0.0 0.0 0.0 0.0 0 0 **13919** 42.0 1.0 0.0 0.0 0.0 0.0 **13920** 47.0 0.0 0.0 0.0 0.0 0 0.0 **13921** 42.0 0.0 0 1.0 0.0 0.0 0.0 **13922** 47.0 0.0 0.0 0.0 0.0 0 0.0 **13923** 47.0 0.0 0.0 0.0 0.0 0.0 0 13924 rows × 21 columns In [81]: merged\_df.to\_csv("Data/preprocessed\_data.csv", index=False)

In [76]:	<pre># for saving the label encoder for model output printing to front end from joblib import dump dump(lbn, "Encoder/label_encoder_class.joblib")</pre>
Out[76]:	['Encoder/label_encoder_class.joblib']
In [ ]:	
In [ ]:	

### Clustering

```
In [1]:
        import matplotlib.pyplot as plt
         from sklearn.cluster import KMeans
         from kneed import KneeLocator
         import pandas as pda
         C:\Users\Dinesh\AppData\Roaming\Python\Python39\site-packages\scipy\__ini
         t__.py:177: UserWarning: A NumPy version >=1.18.5 and <1.26.0 is required
         for this version of SciPy (detected version 1.26.4
           warnings.warn(f"A NumPy version >={np_minversion} and <{np_maxversion}"</pre>
In [2]: | df = pd.read_csv('Data/preprocessed_data.csv')
In [3]: df
Out[3]:
                 age sex on_thyroxine query_on_thyroxine on_antithyroid_medication sick pregna
              0 42.0
                      0.0
                                                                                 0.0
                                  0.0
                                                    0.0
                                                                            0.0
                                                                                          0
              1 24.0
                      0.0
                                                                                 0.0
                                  0.0
                                                    0.0
                                                                            0.0
                                                                                          0
              2 47.0
                      1.0
                                  0.0
                                                    0.0
                                                                                 0.0
                                                                                          0
                                                                            0.0
              3 71.0 0.0
                                                                                 0.0
                                  1.0
                                                    0.0
                                                                            0.0
                                                                                          0
              4 71.0 0.0
                                  0.0
                                                    0.0
                                                                                 0.0
                                                                                          0
                                                                            0.0
          13919 42.0
                     1.0
                                  0.0
                                                    0.0
                                                                            0.0
                                                                                 0.0
                                                                                          0
          13920 47.0 0.0
                                  0.0
                                                    0.0
                                                                            0.0
                                                                                 0.0
                                                                                          0
          13921 42.0
                      1.0
                                  0.0
                                                    0.0
                                                                                 0.0
                                                                                          0
                                                                            0.0
          13922 47.0 0.0
                                  0.0
                                                    0.0
                                                                            0.0
                                                                                 0.0
                                                                                          0
          13923 47.0 0.0
                                  0.0
                                                    0.0
                                                                            0.0
                                                                                 0.0
                                                                                          0
         13924 rows × 21 columns
In [4]: | X = df.drop(["Class"], axis = 1)
         y = df["Class"]
        wcss = [] #within cluster sum of square
In [5]:
         for i in range(1, 11):
             kmeans = KMeans(n clusters=i, init='k-means++', random state=42)
             kmeans.fit(X)
             wcss.append(kmeans.inertia )
```

```
In [9]: plt.plot(range(1,11),wcss) # creating the graph between WCSS and the number
plt.title('The Elbow Method')
plt.xlabel('Number of clusters')
plt.ylabel('WCSS')
plt.show()
```



```
In [11]: kn = KneeLocator(range(1, 11), wcss, curve='convex', direction='decreasing
num_cluster = kn.knee

In [14]: #creating the number of cluster using KMeans++ as the number of cluster is
kmeans = KMeans(n_clusters=3, init='k-means++', random_state=42)

In [15]: y_kmeans = kmeans.fit_predict(X)

In [16]: # created the cluster and stored the number of cluster
y_kmeans

Out[16]: array([2, 0, 2, ..., 1, 1, 1])
In [17]: X['Cluster'] = y_kmeans
```

In [18]:	X.I	nead(	)					
Out[18]:		age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_medication	sick	pregnant
	0	42.0	0.0	0.0	0.0	0.0	0.0	0.0
	1	24.0	0.0	0.0	0.0	0.0	0.0	0.0
	2	47.0	1.0	0.0	0.0	0.0	0.0	0.0
		71.0	0.0	1.0	0.0	0.0	0.0	0.0
	4	71.0	0.0	0.0	0.0	0.0	0.0	0.0
	5 r	ows ×	21 c	olumns				
	4							•
n [19]:	X['	"Labe	1"] :	= y				
n [20]:	x.I	nead(	)					
ut[20]:		age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_medication	sick	pregnant
	0	42.0	0.0	0.0	0.0	0.0	0.0	0.0
	1	24.0	0.0	0.0	0.0	0.0	0.0	0.0
	2	47.0	1.0	0.0	0.0	0.0	0.0	0.0
		71.0	0.0	1.0	0.0	0.0	0.0	0.0
	4	71.0	0.0	0.0	0.0	0.0	0.0	0.0
	5 r	ows ×	22 c	olumns				
	4							•
n [21]:	<b>X.</b> 1	to_cs	v("Da	ata/Cluster_	_data.csv", index	= False)		
n [22]:	im	oort	pick:	le				
n [24]:	wi			Cluster_mode dump(kmeans,	el/clustering.pkl f)	", 'wb') as f:		
In [ ]:								

# Model\_Selection\_Training\_Cluster\_1

```
In [2]: import pandas as pd
         import numpy as np
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.model_selection import GridSearchCV
         from sklearn.metrics import roc auc score,accuracy score
         from sklearn.neighbors import KNeighborsClassifier
         from sklearn.svm import SVC
         from sklearn.tree import DecisionTreeClassifier
         from sklearn.model_selection import train_test_split
         import pickle
         C:\Users\Dinesh\AppData\Roaming\Python\Python39\site-packages\scipy\__ini
         t__.py:177: UserWarning: A NumPy version >=1.18.5 and <1.26.0 is required
         for this version of SciPy (detected version 1.26.4
           warnings.warn(f"A NumPy version >={np_minversion} and <{np_maxversion}"</pre>
In [3]: df = pd.read_csv("Data/Cluster_data.csv")
In [4]: | df.head()
Out[4]:
            age sex on_thyroxine query_on_thyroxine on_antithyroid_medication sick pregnant t
         0 42.0
                 0.0
                             0.0
                                               0.0
                                                                      0.0
                                                                          0.0
                                                                                   0.0
         1 24.0
                 0.0
                             0.0
                                               0.0
                                                                      0.0
                                                                          0.0
                                                                                   0.0
         2 47.0
                 1.0
                             0.0
                                               0.0
                                                                      0.0
                                                                          0.0
                                                                                   0.0
         3 71.0 0.0
                             1.0
                                               0.0
                                                                      0.0
                                                                          0.0
                                                                                   0.0
         4 71.0 0.0
                             0.0
                                               0.0
                                                                      0.0
                                                                          0.0
                                                                                   0.0
         5 rows × 22 columns
In [5]: |list_of_clusters = df["Cluster"].unique()
In [6]: list of clusters
Out[6]: array([2, 0, 1], dtype=int64)
In [7]: | cluster_data_2 = df[df["Cluster"] == list_of_clusters[2]]
```

```
cluster_data_2.head()
 In [8]:
 Out[8]:
                     sex on_thyroxine query_on_thyroxine on_antithyroid_medication sick pregnant
                45.0
            40
                      1.0
                                   0.0
                                                      0.0
                                                                              0.0
                                                                                   0.0
                                                                                             0.0
                40.0
                     0.0
                                   0.0
                                                      0.0
                                                                              0.0
                                                                                   0.0
            88
                                                                                             0.0
            89
                50.0
                     0.0
                                   0.0
                                                      0.0
                                                                              0.0
                                                                                   0.0
                                                                                             0.0
            91 81.0
                     1.0
                                   0.0
                                                      0.0
                                                                              0.0
                                                                                   0.0
                                                                                             0.0
           116 51.0 1.0
                                   0.0
                                                      0.0
                                                                              0.0
                                                                                   0.0
                                                                                             0.0
           5 rows × 22 columns
          cluster_feature_2 = cluster_data_2.drop(["Cluster", "Label"], axis = 1)
           cluster_label_2 = cluster_data_2["Label"]
In [10]: x_train, x_test, y_train, y_test = train_test_split(cluster_feature_2, cluster_
```

#### **Random Forest**

In [11]: | clf = RandomForestClassifier()

```
grid = GridSearchCV(estimator=clf, param_grid=param_clf, cv=10, n_jobs=-1,
In [16]:
In [16]: grid.fit(x_train, y_train)
Out[16]: GridSearchCV(cv=10, error_score='raise', estimator=RandomForestClassifier
          (),
                       n_jobs=-1,
                       param_grid={'criterion': ['gini', 'entropy'],
                                    'max_depth': range(2, 8),
                                    'max_features': ['sqrt', 'log2'],
                                    'n_estimators': [10, 50, 100, 130, 160, 200, 25
          0]})
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [17]: grid.best_params_
Out[17]: {'criterion': 'entropy',
           'max_depth': 7,
           'max_features': 'sqrt',
           'n_estimators': 10}
In [17]: | clf = RandomForestClassifier(criterion='entropy', max_depth=7, max_features
In [18]: clf.fit(x_train, y_train)
```

Out[18]: RandomForestClassifier(criterion='entropy', max\_depth=7, n\_estimators=10)
In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [19]: clf.score(x_test, y_test)
Out[19]: 0.9961070559610705
In [20]: clf.score(x_train, y_train)
Out[20]: 0.9979136240350511
In [22]: prediction_clf = clf.predict_proba(x_test)
```

```
In [25]: if len(y_test.unique()) == 1:
    clf_score = accuracy_score(y_test, prediction_clf)
else:
    clf_score = roc_auc_score(y_test, prediction_clf, multi_class="ovr")
```

```
In [26]: clf_score
```

Out[26]: 0.9932519073016862

#### **KNN**

```
In [27]: knn = KNeighborsClassifier()
```

```
In [28]: knn.fit(x_train, y_train)
```

Out[28]: KNeighborsClassifier()

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [29]: knn.score(x_test, y_test)

Out[29]: 0.9951338199513382

In [30]: param_knn = {
        'n_neighbors' : [i for i in range(5, 25)],
        'algorithm' : ['auto', 'ball_tree', 'kd_tree', 'brute'],
        'leaf_size' : [10, 15, 20, 25, 30, 35, 40, 50],
        'p' : [1,2],
        'weights' : ['uniform', 'distance']
}
```

```
In [44]: grid_knn = GridSearchCV(estimator=knn, param_grid=param_knn, cv = 10, error
```

```
In [45]: grid_knn.fit(x_train, y_train)
Out[45]: GridSearchCV(cv=10, error_score='raise', estimator=KNeighborsClassifier
          (),
                       n_jobs=-1,
                       param_grid={'algorithm': ['auto', 'ball_tree', 'kd_tree', 'b
          rute'],
                                    'leaf size': [10, 15, 20, 25, 30, 35, 40, 50],
                                     'n_neighbors': [5, 6, 7, 8, 9, 10, 11, 12, 13, 1
          4, 15,
                                                     16, 17, 18, 19, 20, 21, 22, 23,
          24],
                                    'p': [1, 2], 'weights': ['uniform', 'distanc
          e']})
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [46]: |grid_knn.best_params_
Out[46]: {'algorithm': 'auto',
           'leaf_size': 10,
           'n_neighbors': 5,
           'p': 1,
           'weights': 'distance'}
In [31]: knn = KNeighborsClassifier(algorithm='auto', leaf size=10, n neighbors = 5,
In [32]: knn.fit(x_test, y_test)
Out[32]: KNeighborsClassifier(leaf_size=10, p=1, weights='distance')
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [33]: knn.score(x_train, y_train)
Out[33]: 0.9912372209472147
In [34]: knn.score(x_test, y_test)
Out[34]: 1.0
In [35]: prediction score = knn.predict proba(x test)
```

#### **SVM**

```
In [39]: svm = SVC()
In [40]: svm.fit(x_train, y_train)
Out[40]: SVC()
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

```
In [65]: grid_svc.best_params_
Out[65]: {'kernel': 'linear'}
```

```
In [44]: svm = SVC(kernel = 'linear')
In [45]: svm.fit(x_train, y_train)
Out[45]: SVC(kernel='linear')
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

```
In [46]: svm.score(x_test, y_test)
Out[46]: 0.9664233576642336
In [47]: svm.score(x_train, y_train)
Out[47]: 0.9609847694554559
In [58]: prediction_svm = svm.score(x_test, y_test)
In [59]: prediction_svm
Out[59]: 0.9664233576642336
In []:
```

### **Decision Tree**

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [62]: dt.score(x_test, y_test)
Out[62]: 0.9965936739659368
In [63]: dt.score(x_train, y_train)
Out[63]: 1.0
```

```
param_dt = {"criterion" : ['gini', 'entropy'],
In [64]:
                       "splitter" : ['best', 'random'],
                       "max_depth" : range(2, 40, 1),
                       "min_samples_split" : range(2, 10, 1),
                       "min_samples_leaf" : range(1, 10, 1)
         }
In [65]: grid_dt = GridSearchCV(estimator=dt, param_grid=param_dt, n_jobs=3, cv = 10
In [66]: grid_dt.fit(x_train, y_train)
Out[66]: GridSearchCV(cv=10, error_score='raise', estimator=DecisionTreeClassifier
         (),
                       n_jobs=3,
                       param_grid={'criterion': ['gini', 'entropy'],
                                   'max_depth': range(2, 40),
                                   'min_samples_leaf': range(1, 10),
                                   'min_samples_split': range(2, 10),
                                   'splitter': ['best', 'random']})
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [72]: dt.score(x_test, y_test)
Out[72]: 0.9975669099756691
```

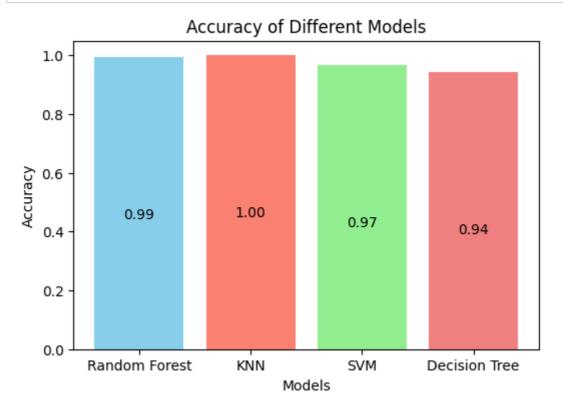
```
In [73]: dt.score(x_train, y_train)
Out[73]: 1.0
In [74]: prediction_dt = dt.predict_proba(x_test)
In [76]: dt_score = roc_auc_score(y_test, prediction_dt, multi_class='ovr')
In [77]: dt_score
Out[77]: 0.9426115627073657
```

# **Model Accuracy**

```
In [79]: import matplotlib.pyplot as plt
```

```
In [102]:
    models = ['Random Forest', 'KNN', 'SVM', 'Decision Tree']
    accuracies = [clf_score, knn_score, prediction_svm, dt_score]
    colors = ['skyblue', 'salmon', 'lightgreen', 'lightcoral']

    plt.figure(figsize=(6, 4))
    bars = plt.bar(models, accuracies, color=colors)
    plt.xlabel('Models')
    plt.ylabel('Accuracy')
    plt.title('Accuracy of Different Models')
    for bar, acc in zip(bars, accuracies):
        plt.text(bar.get_x() + bar.get_width() / 2, bar.get_height() - 0.55, f
    plt.show()
```



# Here the KNN is performing well on the cluster data 2 so we are using knn to predict the data

```
In [101]: with open("Models/KNN2/knn.pkl", 'wb') as f:
    pickle.dump(knn, f)
In []:
```

# Model\_Selection\_Training\_Cluster\_2\_0

```
In [1]: import pandas as pd
         import numpy as np
         from sklearn.ensemble import RandomForestClassifier
         from sklearn.model_selection import GridSearchCV
         from sklearn.metrics import roc auc score,accuracy score
         from sklearn.neighbors import KNeighborsClassifier
         from sklearn.svm import SVC
         from sklearn.tree import DecisionTreeClassifier
         from sklearn.linear_model import LogisticRegression
         from sklearn.model_selection import train_test_split
         import pickle
         C:\Users\Dinesh\AppData\Roaming\Python\Python39\site-packages\scipy\__ini
         t__.py:177: UserWarning: A NumPy version >=1.18.5 and <1.26.0 is required
         for this version of SciPy (detected version 1.26.4
           warnings.warn(f"A NumPy version >={np_minversion} and <{np_maxversion}"</pre>
In [2]: df = pd.read csv("Data/Cluster data.csv")
In [3]: |df.head()
Out[3]:
            age sex on_thyroxine query_on_thyroxine on_antithyroid_medication
                                                                         sick pregnant t
         0 42.0
                 0.0
                             0.0
                                              0.0
                                                                     0.0
                                                                          0.0
                                                                                  0.0
         1 24.0 0.0
                             0.0
                                              0.0
                                                                         0.0
                                                                     0.0
                                                                                  0.0
         2 47.0
                1.0
                             0.0
                                              0.0
                                                                         0.0
                                                                                  0.0
                                                                     0.0
         3 71.0 0.0
                             1.0
                                              0.0
                                                                     0.0
                                                                         0.0
                                                                                  0.0
         4 71.0 0.0
                             0.0
                                              0.0
                                                                     0.0
                                                                         0.0
                                                                                  0.0
         5 rows × 22 columns
In [4]: list_of_clusters = df["Cluster"].unique()
In [5]: list of clusters
Out[5]: array([2, 0, 1], dtype=int64)
         Cluster 2
In [6]: | cluster_data_2 = df[df["Cluster"] == list_of_clusters[0]]
```

```
cluster_data_2.head()
In [7]:
Out[7]:
                       on thyroxine query on thyroxine on antithyroid medication
                                                                                 sick pregnant
          0 42.0
                   0.0
                                                    0.0
                                                                                  0.0
                                 0.0
                                                                             0.0
                                                                                            0.0
          2 47.0
                                0.0
                                                    0.0
                                                                                  0.0
                   1.0
                                                                             0.0
                                                                                            0.0
          3 71.0
                   0.0
                                 1.0
                                                    0.0
                                                                             0.0
                                                                                  0.0
                                                                                            0.0
            19.0
                   0.0
                                 1.0
                                                    0.0
                                                                             0.0
                                                                                  0.0
                                                                                            0.0
          8 67.0 0.0
                                0.0
                                                    0.0
                                                                             0.0
                                                                                  0.0
                                                                                            0.0
          5 rows × 22 columns
         cluster_feature_2 = cluster_data_2.drop(["Cluster", "Label"], axis = 1)
          cluster_label_2 = cluster_data_2["Label"]
In [9]: x_train, x_test, y_train, y_test = train_test_split(cluster_feature_2, cluster_feature_2)
```

#### **Random Forest**

In [10]: | clf = RandomForestClassifier()

```
grid = GridSearchCV(estimator=clf, param_grid=param_clf, cv=10, n_jobs=-1,
In [17]:
In [23]: grid.fit(x_train, y_train)
Out[23]: GridSearchCV(cv=10, error_score='raise', estimator=RandomForestClassifier
          (),
                       n_jobs=-1,
                       param_grid={'criterion': ['gini', 'entropy'],
                                    'max_depth': range(2, 8),
                                    'max_features': ['sqrt', 'log2'],
                                    'n_estimators': [10, 50, 100, 130, 160, 200, 25
          0]})
In [24]: |grid.best_params_
Out[24]: {'criterion': 'entropy',
           'max_depth': 7,
           'max_features': 'sqrt',
           'n_estimators': 100}
In [15]: | clf = RandomForestClassifier(criterion='entropy', max_depth=7, max_features
In [16]: clf.fit(x train, y train)
Out[16]: RandomForestClassifier(criterion='entropy', max_depth=7)
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [17]: | clf.score(x test, y test)
Out[17]: 0.886039886039886
In [18]: clf.score(x train, y train)
Out[18]: 0.9016493585827734
In [19]: | prediction_clf = clf.predict_proba(x_test)
          if len(y_test.unique()) == 1:
              clf_score_2 = accuracy_score(y_test, prediction_clf)
              clf_score_2 = roc_auc_score(y_test, prediction_clf, multi_class="ovr")
          clf_score_2
Out[19]: 0.9848749197961503
```

### **KNN**

In [20]: knn = KNeighborsClassifier()

```
In [21]: knn.fit(x_train, y_train)
Out[21]: KNeighborsClassifier()
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [22]: knn.score(x_test, y_test)
Out[22]: 0.9301994301994302
In [23]: knn.score(x_train, y_train)
Out[23]: 0.9578497251069029
In [48]: | param_knn = {
              'n_neighbors' : [i for i in range(5, 25)],
              'algorithm' : ['auto', 'ball_tree', 'kd_tree', 'brute'],
              'leaf_size' : [8,9,11,12,21,24,23,45,67,78,],
              'p' : [1,2],
              'weights' : ['uniform','distance']
          }
In [49]: grid = GridSearchCV(estimator=knn, param_grid=param_knn, cv=10, n_jobs=-1,
In [50]: grid.fit(x_train, y_train)
Out[50]: GridSearchCV(cv=10, error_score='raise',
                       estimator=KNeighborsClassifier(leaf_size=10, weights='distan
          ce'),
                       n jobs=-1,
                       param_grid={'algorithm': ['auto', 'ball_tree', 'kd_tree', 'b
          rute'],
                                    'leaf size': [8, 9, 11, 12, 21, 24, 23, 45, 67,
          78],
                                    'n_neighbors': [5, 6, 7, 8, 9, 10, 11, 12, 13, 1
          4, 15,
                                                    16, 17, 18, 19, 20, 21, 22, 23,
          24],
                                    'p': [1, 2], 'weights': ['uniform', 'distanc
          e']})
In [51]: grid.best_params_
Out[51]: {'algorithm': 'auto',
           'leaf size': 8,
           'n neighbors': 5,
           'p': 2,
           'weights': 'distance'}
```

```
In [24]: knn = KNeighborsClassifier(algorithm='auto', leaf_size=8, n_neighbors=5,p=2)
In [25]: knn.fit(x_train, y_train)
```

Out[25]: KNeighborsClassifier(leaf\_size=8, weights='distance')

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

On GitHub, the HTML representation is unable to render, please try loading this page with nbviewer.org.

```
In [26]: knn.score(x_test, y_test)
Out[26]: 0.9387464387464387

In [27]: knn.score(x_train,y_train)
Out[27]: 1.0

In [28]: prediction_score = knn.predict_proba(x_test)
    if len(y_test.unique()) == 1:
        knn_score_2 = accuracy_score(y_test, prediction_score)
    else:
        knn_score_2 = roc_auc_score(y_test, prediction_score, multi_class="ovr")
```

#### **SVM**

```
In [29]: svm = SVC()
In [30]: svm.fit(x_train, y_train)
Out[30]: SVC()
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [31]: svm.score(x_test, y_test)
Out[31]: 0.6723646723646723
In [32]: svm.score(x_train,y_train)
Out[32]: 0.6945632254123396
```

```
In [70]: | param_svm = {
              'kernel' :['linear', 'poly', 'rbf', 'sigmoid']
          }
In [71]: grid = GridSearchCV(estimator=svm, param_grid=param_svm, cv=10, n_jobs=3,
In [72]: |grid.fit(x_train, y_train)
Out[72]: GridSearchCV(cv=10, error_score='raise', estimator=SVC(), n_jobs=3,
                       param_grid={'kernel': ['linear', 'poly', 'rbf', 'sigmoid']})
In [73]: |grid.best_params_
Out[73]: {'kernel': 'linear'}
In [33]: | svm = SVC(kernel='linear')
In [34]: | svm.fit(x_train, y_train)
Out[34]: SVC(kernel='linear')
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [35]: svm.score(x_test, y_test)
Out[35]: 0.7165242165242165
```

```
In [35]: svm.score(x_test, y_test)
Out[35]: 0.7165242165242165
In [36]: svm.score(x_train, y_train)
Out[36]: 0.7532070861331704
In [37]: prediction_svm_2 = svm.score(x_test,y_test)
```

# **Decision Tree**

```
In [38]: dt = DecisionTreeClassifier()
In [39]: dt.fit(x_train, y_train)
Out[39]: DecisionTreeClassifier()
```

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [40]: dt.score(x_test, y_test)
Out[40]: 0.9672364672364673
In [41]: dt.score(x_train, y_train)
Out[41]: 1.0
"max_depth" : range(2, 40, 1),
                      "min_samples_split" : range(2, 10, 1),
                      "min_samples_leaf" : range(1, 10, 1)}
In [94]: grid = GridSearchCV(estimator=dt, param_grid=parm_dt, cv=10, n_jobs=3, error
In [95]: grid.fit(x_train, y_train)
Out[95]: GridSearchCV(cv=10, error_score='raise', estimator=DecisionTreeClassifier
         (),
                      n jobs=3,
                      param_grid={'criterion': ['gini', 'entropy'],
                                  'max_depth': range(2, 40),
                                  'min_samples_leaf': range(1, 10),
                                  'min_samples_split': range(2, 10),
                                  'splitter': ['best', 'random']})
In [96]: grid.best params
Out[96]: {'criterion': 'gini',
          'max_depth': 35,
          'min_samples_leaf': 1,
          'min_samples_split': 2,
          'splitter': 'random'}
In [42]: dt = DecisionTreeClassifier(criterion='gini', max depth= 35, min samples le
In [43]: |dt.fit(x_train, y_train)
Out[43]: DecisionTreeClassifier(max_depth=35, splitter='random')
         In a Jupyter environment, please rerun this cell to show the HTML representation or
         trust the notebook.
         On GitHub, the HTML representation is unable to render, please try loading this page
         with nbviewer.org.
In [44]: | dt.score(x test, y test)
Out[44]: 0.9786324786324786
```

```
In [45]: dt.score(x_train, y_train)
Out[45]: 1.0
In [46]: prediction_dt = dt.predict_proba(x_test)
dt_score_2 = roc_auc_score(y_test, prediction_dt, multi_class='ovr')
```

#### Cluster 0

<pre>In [47]: cluster_data_0 = df[df["Cluster"] == list_of_clusters[1]]</pre>											
In [48]:	cluster_data_0.head()										
Out[48]:	age	sex	on_thyroxine	query_on_thyroxine	on_antithyroid_medication	sick	pregnant t				
	<b>1</b> 24.0	0.0	0.0	0.0	0.0	0.0	0.0				
	<b>4</b> 71.0	0.0	0.0	0.0	0.0	0.0	0.0				
	<b>6</b> 60.0	0.0	0.0	0.0	0.0	0.0	0.0				
	<b>7</b> 81.0	0.0	0.0	0.0	0.0	0.0	0.0				
	<b>9</b> 69.0	1.0	0.0	0.0	0.0	0.0	0.0				
	5 rows ×	22 cc	lumns								
	4						•				
In [49]:	<pre>In [49]: cluster_features_0 = cluster_data_0.drop(columns = ['Cluster','Label'],axis</pre>										
In [50]:	n [50]: cluster_label_0 = cluster_data_0['Label']										
In [51]:	x_train	, x_t	est, y_trai	n,y_test = train	_test_split(cluster_f	eatur	es_0, clus				

### **Random Forest**

```
In [54]: clf_0.score(x_test, y_test)
 Out[54]: 0.9922644163150492
 In [55]: clf_0.score(x_train, y_train)
 Out[55]: 1.0
 In [56]: param_clf_0 = {"n_estimators" : [10, 20, 67, 240, 110, 100, 250],
                          "criterion" : ['gini', 'entropy'],
                          "max_depth" : range(2,8,1),
                          "max_features" : ['sqrt', 'log2']
           }
In [120]: grid = GridSearchCV(estimator =clf_0, param_grid = param_clf_0,cv= 10, n_jc
In [121]: |grid.fit(x_train, y_train)
Out[121]: GridSearchCV(cv=10, error_score='raise', estimator=RandomForestClassifier
           (),
                        n jobs=-1,
                        param_grid={'criterion': ['gini', 'entropy'],
                                     'max_depth': range(2, 8),
                                     'max_features': ['sqrt', 'log2'],
                                     'n_estimators': [10, 20, 67, 240, 110, 100, 25
           0]})
In [122]: grid.best params
Out[122]: {'criterion': 'gini',
            'max_depth': 7,
            'max features': 'log2',
            'n estimators': 250}
 In [57]: clf_0 = RandomForestClassifier(criterion= 'gini', max_depth= 7,max_features
 In [58]: | clf_0.fit(x_train, y_train)
 Out[58]: RandomForestClassifier(max_depth=7, max_features='log2', n_estimators=25
           0)
           In a Jupyter environment, please rerun this cell to show the HTML representation or
           trust the notebook.
           On GitHub, the HTML representation is unable to render, please try loading this page
           with nbviewer.org.
 In [59]: | clf_0.score(x_test, y_test)
 Out[59]: 0.8291139240506329
```

```
In [60]: clf_0.score(x_train, y_train)
Out[60]: 0.8395173453996984

In [61]: prediction_clf = clf_0.predict_proba(x_test)
    if len(y_test.unique()) == 1:
        clf_score_0 = accuracy_score(y_test, prediction_clf)
    else:
        clf_score_0 = roc_auc_score(y_test, prediction_clf, multi_class="ovr")
    clf_score_0

Out[61]: 0.934690768293213
```

#### KNN

```
In [62]: knn_0 = KNeighborsClassifier()
In [63]: knn_0.fit(x_train, y_train)
```

Out[63]: KNeighborsClassifier()

In a Jupyter environment, please rerun this cell to show the HTML representation or trust the notebook.

```
In [137]: grid.fit(x_train, y_train)
Out[137]: GridSearchCV(cv=10, error_score='raise', estimator=KNeighborsClassifier
          (),
                        n_jobs=-1,
                        param_grid={'algorithm': ['auto', 'ball_tree', 'kd_tree', 'b
          rute'],
                                     'leaf_size': [8, 9, 11, 12, 21, 50, 20, 60, 70,
          100],
                                     'n neighbors': [5, 6, 7, 8, 9, 10, 11, 12, 13, 1
          4, 15,
                                                     16, 17, 18, 19, 20, 21, 22, 23,
          24],
                                     'p': [1, 2], 'weights': ['uniform', 'distanc
          e']})
In [138]: grid.best_params_
Out[138]: {'algorithm': 'auto',
            'leaf_size': 8,
            'n neighbors': 5,
            'p': 1,
            'weights': 'distance'}
In [66]: knn_0 = KNeighborsClassifier(algorithm= 'auto', leaf_size= 8, n_neighbors=
In [67]: knn_0.fit(x_train, y_train)
Out[67]: KNeighborsClassifier(leaf_size=8, p=1, weights='distance')
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
 In [68]: knn 0.score(x test, y test)
Out[68]: 0.9240506329113924
In [69]: knn_0.score(x_train, y_train)
Out[69]: 1.0
 In [70]: prediction score = knn 0.predict proba(x test)
          if len(y test.unique()) == 1:
               knn_score_0 = accuracy_score(y_test, prediction_score)
          else:
               knn_score_0 = roc_auc_score(y_test, prediction_score, multi_class="ovr"
```

### **SVM**

```
In [71]: svm_0 = SVC()
 In [72]: svm_0.fit(x_train, y_train)
Out[72]: SVC()
           In a Jupyter environment, please rerun this cell to show the HTML representation or
           trust the notebook.
           On GitHub, the HTML representation is unable to render, please try loading this page
           with nbviewer.org.
 In [73]: svm_0.score(x_test, y_test)
Out[73]: 0.6315049226441631
In [74]: | svm_0.score(x_train, y_train)
Out[74]: 0.6132730015082957
In [148]: | param_svm_0 = {
               'kernel' :['linear', 'poly', 'rbf', 'sigmoid']
In [149]: grid = GridSearchCV(estimator = svm_0, param_grid = param_svm_0, cv= 10, n
In [150]: |grid.fit(x_train, y_train)
Out[150]: GridSearchCV(cv=10, error_score='raise', estimator=SVC(), n_jobs=-1,
                        param_grid={'kernel': ['linear', 'poly', 'rbf', 'sigmoid']})
In [151]: |grid.best_params_
Out[151]: {'kernel': 'linear'}
In [75]: svm 0 = SVC(kernel= 'linear')
 In [76]: |svm_0.fit(x_train, y_train)
 Out[76]: SVC(kernel='linear')
           In a Jupyter environment, please rerun this cell to show the HTML representation or
           trust the notebook.
           On GitHub, the HTML representation is unable to render, please try loading this page
           with nbviewer.org.
 In [77]: | svm_0.score(x_test, y_test)
 Out[77]: 0.6870604781997187
```

```
In [78]: svm_0.score(x_train, y_train)
Out[78]: 0.6911010558069381
In [79]: prediction_svm_0 = svm_0.score(x_test,y_test)
```

### **Decision Tree**

In [80]: dt 0 = DecisionTreeClassifier()

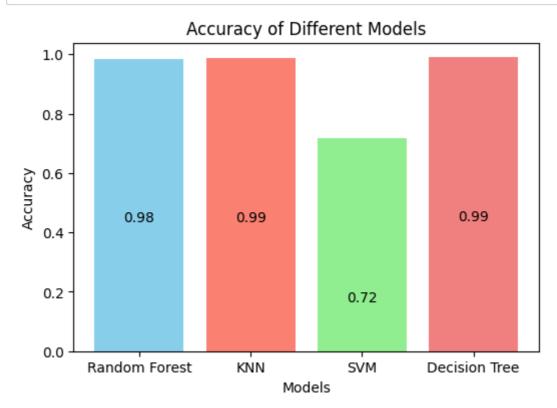
```
In [81]: dt_0.fit(x_train, y_train)
Out[81]: DecisionTreeClassifier()
          In a Jupyter environment, please rerun this cell to show the HTML representation or
          trust the notebook.
          On GitHub, the HTML representation is unable to render, please try loading this page
          with nbviewer.org.
In [82]: dt_0.score(x_test, y_test)
Out[82]: 0.9683544303797469
 In [83]: dt_0.score(x_train, y_train)
Out[83]: 1.0
In [163]: param_dt_0 = { "criterion" : ['gini', 'entropy'],
                        "splitter" : ['best', 'random'],
                        "max depth" : range(2, 40, 1),
                        "min_samples_split" : range(2, 10, 1),
                        "min_samples_leaf" : range(1, 10, 1)
          }
In [164]: | grid = GridSearchCV(estimator = dt_0, param_grid = param_dt_0, cv= 10, n_j
In [165]: grid.fit(x train, y train)
Out[165]: GridSearchCV(cv=10, error_score='raise', estimator=DecisionTreeClassifier
           (),
                        n jobs=-1,
                        param_grid={'criterion': ['gini', 'entropy'],
                                     'max_depth': range(2, 40),
                                     'min_samples_leaf': range(1, 10),
                                     'min_samples_split': range(2, 10),
                                     'splitter': ['best', 'random']})
```

```
In [166]: grid.best_params_
Out[166]: {'criterion': 'gini',
            'max_depth': 39,
            'min_samples_leaf': 1,
            'min_samples_split': 2,
            'splitter': 'random'}
 In [84]: dt_0 = DecisionTreeClassifier(criterion= 'gini', max_depth= 39, min_samples
 In [85]: |dt_0.fit(x_train, y_train)
Out[85]: DecisionTreeClassifier(max_depth=39, splitter='random')
           In a Jupyter environment, please rerun this cell to show the HTML representation or
           trust the notebook.
           On GitHub, the HTML representation is unable to render, please try loading this page
           with nbviewer.org.
 In [86]: dt_0.score(x_test, y_test)
Out[86]: 0.9669479606188467
 In [87]: dt_0.score(x_train,y_train)
Out[87]: 1.0
 In [88]: | prediction_dt = dt_0.predict_proba(x_test)
           dt_score_0 = roc_auc_score(y_test, prediction_dt, multi_class='ovr')
```

## **Model Accuracy**

#### Cluster number 2

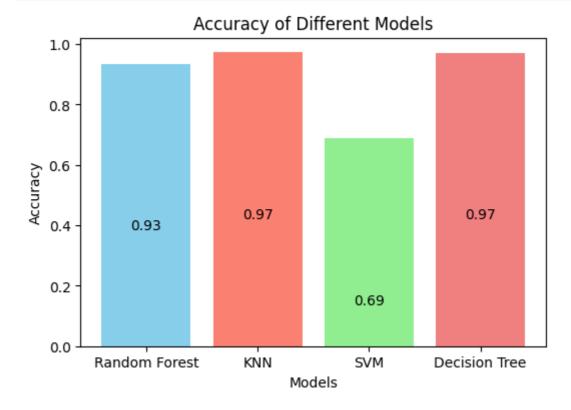
```
In [89]: import matplotlib.pyplot as plt
```



## As Decision Tree has the highest accuracy score we will consider DT as our Model for cluster number 2

```
In [91]: with open("dt.pkl", 'wb') as f:
    pickle.dump(dt,f)
```

#### Cluster number 0



# As we have chosen KNN and DT for other two clusters so we will be considering Random Forest for cluster number 0

```
In [94]: with open("clf.pkl", 'wb') as f:
    pickle.dump(clf_0,f)
```

#### Flask API for Backend

```
from flask import Flask, request, render_template
import pickle
import os
import joblib
app = Flask(__name__)
kmeans = pickle.load(open("../Cluster_model/clustering.pkl", "rb"))
encoder = joblib.load(open("../Encoder/label_encoder_class.joblib", "rb"))
def find_model(cluster):
    if(cluster == 0):
        with open('../Models/CLF0/clf.pkl', 'rb') as f:
            model = pickle.load(f)
    elif(cluster == 1):
        with open('../Models/KNN1/knn.pkl', 'rb') as f:
            model = pickle.load(f)
    else:
        with open('../Models/DT2/dt.pkl', 'rb') as f:
            model = pickle.load(f)
    return model
@app.route("/", methods=['GET'])
def index():
    return render_template("main.html")
@app.route("/predict", methods=['POST'])
def predict():
    if request.method == 'POST':
        age = int(request.form["age"])
        T3 = float(request.form["T3"])
        TT4 = float(request.form["TT4"])
        T4U = float(request.form["T4U"])
        FTI = float(request.form["FTI"])
        sex = request.form['sex']
        if (sex_ == "Male"):
            sex = 1
        else:
            sex = 0
        thyroxine = request.form["on thyroxine"]
        if (thyroxine == "true"):
            on thyroxine = 1
        else:
            on_thyroxine = 0
        query_thyroxine = request.form["query_thyroxine"]
        if (query_thyroxine == "true"):
            query on thyroxine = 1
```

```
query on thyroxine = 0
antithyroid_medication = request.form["antithyroid_medication"]
if( antithyroid_medication == "true"):
    on_antithyroid_medication = 1
else:
    on antithyroid medication = 0
I131_treatment_ = request.form["I131_treatment"]
if(I131_treatment_ == "true"):
    I131_treatment = 1
else:
    I131_treatment = 0
query_hypothyroid_ = request.form["query_hypothyroid"]
if(query_hypothyroid_ == "true"):
    query_hypothyroid = 1
else:
    query_hypothyroid = 0
hypopituitary_ = request.form["hypopituitary"]
if(hypopituitary_ == "true"):
    hypopituitary = 1
else:
    hypopituitary = 0
psych_ = request.form["psych"]
if(psych_ == "true"):
    psych = 1
else:
    psych = 0
sick_ = request.form['sick']
if (sick_ == 'true'):
    sick = 1
else:
    sick = 0
lithium_ = request.form["lithium"]
if(lithium_ == "true"):
   lithium = 1
else:
   lithium = 0
pregnant_ = request.form['pregnant']
if (pregnant_ == 'true'):
   pregnant = 1
else:
    pregnant = 0
thyroid_surgery_ = request.form['thyroid_surgery']
if (thyroid_surgery_ == 'true'):
    thyroid surgery = 1
```

```
thyroid surgery = 0
        goitre_ = request.form['goitre']
        if(goitre_ == 'true'):
            goitre = 1
        else:
            goitre = 0
        tumor_ = request.form['tumor']
        if (tumor == 'true'):
            tumor = 1
        else:
            tumor = 0
        cluster_output = kmeans.predict([[age,
                                    sex, on_thyroxine, query_on_thyroxine,
on_antithyroid_medication, sick, pregnant, thyroid_surgery, I131_treatment,
                                     query_hypothyroid, query_hypothyroid,
lithium, goitre, tumor, hypopituitary, psych, T3,
                                     TT4,
                                     T4U,
                                     FTI]])
        cluster_num = cluster_output
        model = find_model(cluster_num)
        prediction_output = model.predict([[age,
                                    sex, on_thyroxine, query_on_thyroxine,
on_antithyroid_medication, sick, pregnant, thyroid_surgery, I131_treatment,
                                     query_hypothyroid, query_hypothyroid,
lithium, goitre, tumor, hypopituitary, psych, T3,
                                     TT4,
                                     T4U,
                                     FTI
                                    ]])
        prediction = int(prediction_output[0])
        encoded_prediction = encoder.inverse_transform([prediction])
        return f"<div style='display: flex; justify-content: center; align-items: center;
height: 100vh;'><h1>You have {encoded_prediction[0]}</h1></div>"
if __name__ == '__main__':
    app.run(debug=True)
```

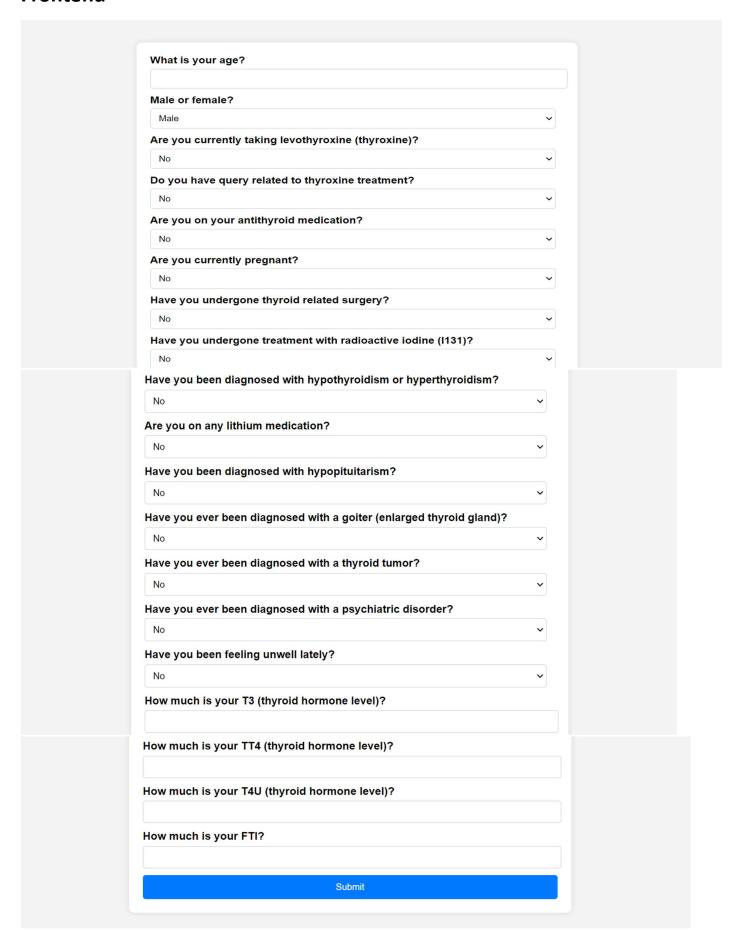
#### **HTML & CSS For Frontend**

```
<!DOCTYPE html>
<html lang="en">
   <meta charset="UTF-8">
   <meta name="viewport" content="width=device-width, initial-scale=1.0">
   <title>Thyroid Form</title>
   <style>
       body {
            font-family: Arial, sans-serif;
            background-color: #f4f4f4;
           margin: 0;
           padding: 0;
        .container {
           max-width: 600px;
           margin: 50px auto;
            background-color: #fff;
            padding: 20px;
           border-radius: 8px;
           box-shadow: 0 0 10px rgba(0,0,0,0.1);
        form label {
           display: block;
           margin-bottom: 5px;
            font-weight: bold;
        form input[type="text"], form select, form input[type="checkbox"] {
            width: calc(100% - 12px);
            padding: 8px;
           margin-bottom: 10px;
            border: 1px solid #ccc;
           border-radius: 4px;
        form input[type="submit"] {
           width: 100%;
            padding: 10px;
            background-color: #007bff;
            color: #fff;
            border: none;
            border-radius: 4px;
            cursor: pointer;
        form input[type="submit"]:hover {
            background-color: #0056b3;
   </style>
   <div class="container">
    <form action="/predict" method="post">
        <label for="age">What is your age?</label>
```

```
<input type="text" name="age"><br>
        <label for="sex">Male or female?</label>
        <select name="sex">
            <option value="Male">Male</option>
            <option value="Female">Female</option>
        </select><br>
        <label for="on_thyroxine">Are you currently taking levothyroxine
(thyroxine)?</label>
        <select name="on thyroxine">
            <option value="true">Yes</option>
            <option value="false" selected>No</option>
        </select><br>
        <label for="query thyroxine">Do you have query related to thyroxine
treatment?</label>
        <select name="query thyroxine">
            <option value="true">Yes</option>
            <option value="false" selected>No</option>
       </select><br>
        <label for="antithyroid medication">Are you on your antithyroid
medication?</label>
        <select name="antithyroid medication">
            <option value="true">Yes</option>
            <option value="false" selected>No</option>
        </select><br>
        <label for="pregnant">Are you currently pregnant?</label>
        <select name="pregnant">
            <option value="true">Yes</option>
            <option value="false" selected>No</option>
        </select><br>
        <label for="thyroid_surgery">Have you undergone thyroid related surgery?</label>
        <select name="thyroid surgery">
            <option value="true">Yes</option>
            <option value="false" selected>No</option>
        </select><br>
        <label for="I131_treatment">Have you undergone treatment with radioactive iodine
(I131)?</label>
        <select name="I131 treatment">
           <option value="true">Yes</option>
```

```
<option value="false" selected>No</option>
       </select><br>
       <label for="query_hypothyroid">Have you been diagnosed with hypothyroidism or
hyperthyroidism?</label>
       <select name="query hypothyroid">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
       <label for="lithium">Are you on any lithium medication?</label>
       <select name="lithium">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
       <label for="hypopituitary">Have you been diagnosed with hypopituitarism?
       <select name="hypopituitary">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
       <label for="goitre">Have you ever been diagnosed with a goiter (enlarged thyroid
gland)?</label>
       <select name="goitre">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
       <label for="tumor">Have you ever been diagnosed with a thyroid tumor?</label>
       <select name="tumor">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
       <label for="psych">Have you ever been diagnosed with a psychiatric
disorder?</label>
       <select name="psych">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
       <label for="sick">Have you been feeling unwell lately?</label>
       <select name="sick">
           <option value="true">Yes</option>
           <option value="false" selected>No</option>
       </select><br>
```

#### **Frontend**



You have compensated\_hypothyroid

You have negative

You have primary\_hypothyroid

You have secondary\_hypothyroid