

```
In [74]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.tree import DecisionTreeClassifier
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import classification_report, confusion_matrix
from sklearn.metrics import accuracy_score
from sklearn.model_selection import train_test_split
from sklearn.neural_network import MLPClassifier
```

```
In [4]: import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))
```

```
In [5]: train_df=pd.read_csv("C:\\Users\\damma\\Downloads\\Test.csv")
df=train_df.copy()
```

```
In [6]: test_df=pd.read_csv("C:\\Users\\damma\\Downloads\\Training.csv")
df=test_df.copy()
```

Exploratory Data Analysis

```
In [7]: test_df.head()
```

Out[7]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...	scurrying	skin_
0	1	1	1	0	0	0	0	0	0	0	...	0	
1	0	1	1	0	0	0	0	0	0	0	...	0	
2	1	0	1	0	0	0	0	0	0	0	...	0	
3	1	1	0	0	0	0	0	0	0	0	...	0	
4	1	1	1	0	0	0	0	0	0	0	...	0	

5 rows × 134 columns



In [13]: `test_df.tail()`

Out[13]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...	scurrying	s
4915	0	0	0	0	0	0	0	0	0	0	...	0	
4916	0	1	0	0	0	0	0	0	0	0	...	1	
4917	0	0	0	0	0	0	0	0	0	0	...	0	
4918	0	1	0	0	0	0	1	0	0	0	...	0	
4919	0	1	0	0	0	0	0	0	0	0	...	0	

5 rows × 134 columns



```
In [8]: train_df.head()
```

```
Out[8]:
```

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...	blackheads	sc
0	1	1	1	0	0	0	0	0	0	0	...	0	
1	0	0	0	1	1	1	0	0	0	0	...	0	
2	0	0	0	0	0	0	0	1	1	1	...	0	
3	1	0	0	0	0	0	0	0	0	0	...	0	
4	1	1	0	0	0	0	0	1	0	0	...	0	

5 rows × 133 columns

```
In [14]: train_df.tail()
```

```
Out[14]:
```

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...	blackheads	s
37	0	1	0	0	0	0	0	0	0	0	...	1	
38	0	0	0	0	0	0	0	0	0	0	...	0	
39	0	1	0	0	0	0	1	0	0	0	...	0	
40	0	1	0	0	0	0	0	0	0	0	...	0	
41	1	1	0	0	0	0	0	0	0	0	...	0	

5 rows × 133 columns

```
In [9]: train_df.describe()
```

Out[9]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on_tongue	...
count	42.000000	42.000000	42.000000	42.000000	42.000000	42.000000	42.000000	42.000000	42.000000	42.000000	...
mean	0.166667	0.190476	0.023810	0.047619	0.023810	0.166667	0.142857	0.047619	0.047619	0.023810	...
std	0.377195	0.397437	0.154303	0.215540	0.154303	0.377195	0.354169	0.215540	0.215540	0.154303	...
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	...
25%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	...
50%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	...
75%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	...
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	...

8 rows × 132 columns



In [10]: `train_df.describe().T`

Out[10]:

	count	mean	std	min	25%	50%	75%	max
itching	42.0	0.166667	0.377195	0.0	0.0	0.0	0.0	1.0
skin_rash	42.0	0.190476	0.397437	0.0	0.0	0.0	0.0	1.0
nodal_skin_eruptions	42.0	0.023810	0.154303	0.0	0.0	0.0	0.0	1.0
continuous_sneezing	42.0	0.047619	0.215540	0.0	0.0	0.0	0.0	1.0
shivering	42.0	0.023810	0.154303	0.0	0.0	0.0	0.0	1.0
...
small_dents_in_nails	42.0	0.023810	0.154303	0.0	0.0	0.0	0.0	1.0
inflammatory_nails	42.0	0.023810	0.154303	0.0	0.0	0.0	0.0	1.0
blister	42.0	0.023810	0.154303	0.0	0.0	0.0	0.0	1.0
red_sore_around_nose	42.0	0.047619	0.215540	0.0	0.0	0.0	0.0	1.0
yellow_crust_ooze	42.0	0.023810	0.154303	0.0	0.0	0.0	0.0	1.0

132 rows × 8 columns

In [11]: test_df.describe()

Out[11]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_on
count	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000	4920.000000
mean	0.137805	0.159756	0.021951	0.045122	0.021951	0.162195	0.139024	0.045122	0.045122	0.045122
std	0.344730	0.366417	0.146539	0.207593	0.146539	0.368667	0.346007	0.207593	0.207593	0.207593
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
25%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
50%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
75%	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
max	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000

8 rows × 133 columns



In [12]: test_df.describe().T

Out[12]:

	count	mean	std	min	25%	50%	75%	max
itching	4920.0	0.137805	0.344730	0.0	0.0	0.0	0.0	1.0
skin_rash	4920.0	0.159756	0.366417	0.0	0.0	0.0	0.0	1.0
nodal_skin_eruptions	4920.0	0.021951	0.146539	0.0	0.0	0.0	0.0	1.0
continuous_sneezing	4920.0	0.045122	0.207593	0.0	0.0	0.0	0.0	1.0
shivering	4920.0	0.021951	0.146539	0.0	0.0	0.0	0.0	1.0
...
inflammatory_nails	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
blister	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
red_sore_around_nose	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
yellow_crust_ooze	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
Unnamed: 133	0.0	NaN	NaN	NaN	NaN	NaN	NaN	NaN

133 rows × 8 columns

In [15]: `train_df.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 42 entries, 0 to 41
Columns: 133 entries, itching to prognosis
dtypes: int64(132), object(1)
memory usage: 43.8+ KB
```

In [16]: `test_df.info()`

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 4920 entries, 0 to 4919
Columns: 134 entries, itching to Unnamed: 133
dtypes: float64(1), int64(132), object(1)
memory usage: 5.0+ MB
```

In [18]: `print(test_df.shape)`

```
(4920, 134)
```

```
In [17]: print(train_df.shape)
```

```
(42, 133)
```

```
In [17]: train_df.columns
```

```
Out[17]: Index(['itching', 'skin_rash', 'nodal_skin_eruptions', 'continuous_sneezing',  
              'shivering', 'chills', 'joint_pain', 'stomach_pain', 'acidity',  
              'ulcers_on_tongue',  
              ...  
              'blackheads', 'scurring', 'skin_peeling', 'silver_like_dusting',  
              'small_dents_in_nails', 'inflammatory_nails', 'blister',  
              'red_sore_around_nose', 'yellow_crust_ooze', 'prognosis'],  
             dtype='object', length=133)
```

```
In [19]: test_df.columns
```

```
Out[19]: Index(['itching', 'skin_rash', 'nodal_skin_eruptions', 'continuous_sneezing',  
              'shivering', 'chills', 'joint_pain', 'stomach_pain', 'acidity',  
              'ulcers_on_tongue',  
              ...  
              'scurring', 'skin_peeling', 'silver_like_dusting',  
              'small_dents_in_nails', 'inflammatory_nails', 'blister',  
              'red_sore_around_nose', 'yellow_crust_ooze', 'prognosis',  
              'Unnamed: 133'],  
             dtype='object', length=134)
```

```
In [55]: train_df.isna().sum()
```

```
Out[55]: itching                0  
skin_rash                    0  
nodal_skin_eruptions        0  
continuous_sneezing         0  
shivering                   0  
..  
inflammatory_nails          0  
blister                     0  
red_sore_around_nose        0  
yellow_crust_ooze           0  
prognosis                   0  
Length: 133, dtype: int64
```

```
In [22]: test_df.isna().sum()
```

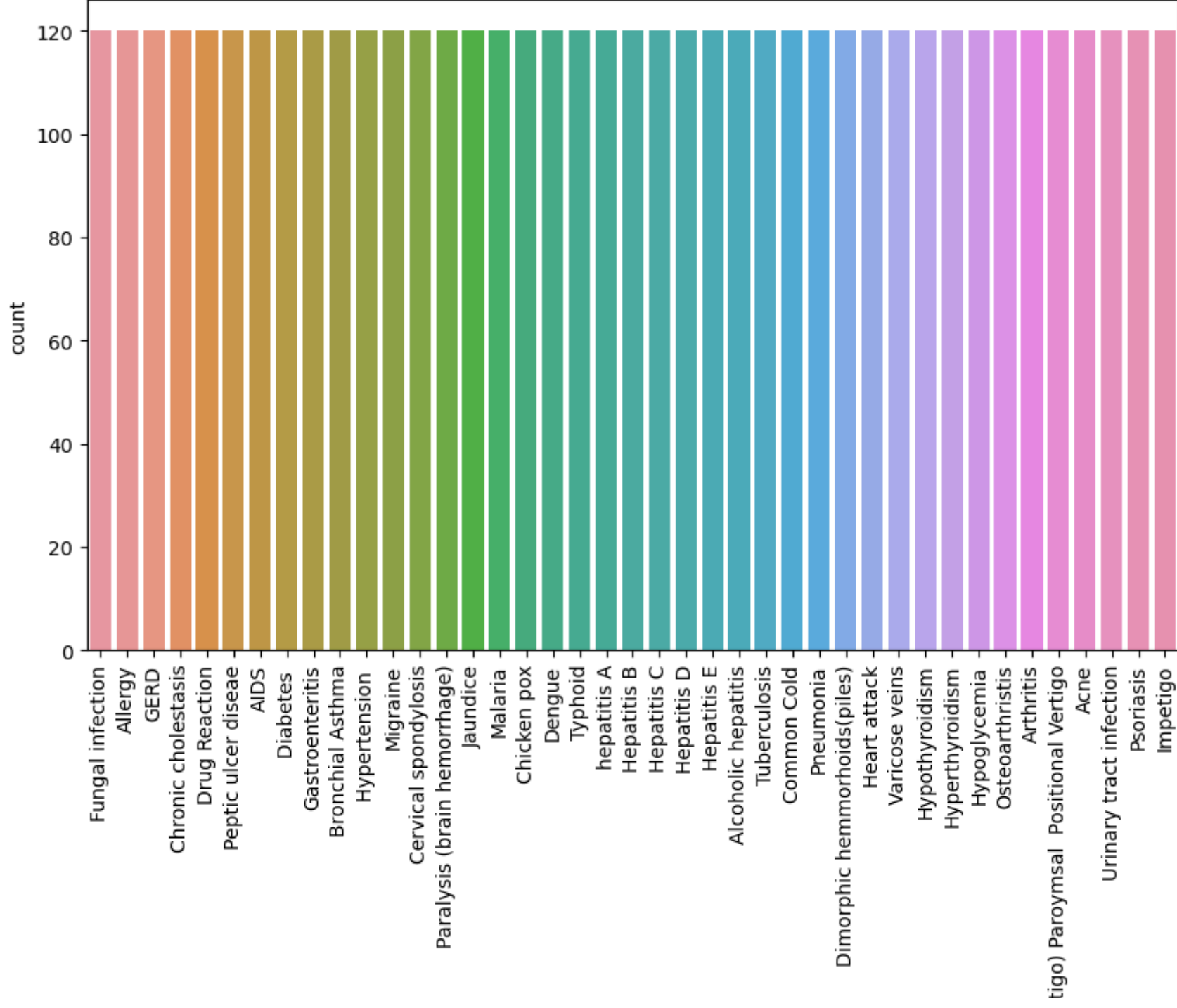


```
Out[22]: itching          0
          skin_rash       0
          nodal_skin_eruptions  0
          continuous_sneezing  0
          shivering       0
          ...
          blister         0
          red_sore_around_nose  0
          yellow_crust_ooze  0
          prognosis       0
          Unnamed: 133     4920
          Length: 134, dtype: int64
```

```
In [32]: df['prognosis'].value_counts()
```

```
Out[32]: Fungal infection      120
          Hepatitis C          120
          Hepatitis E          120
          Alcoholic hepatitis  120
          Tuberculosis         120
          Common Cold          120
          Pneumonia            120
          Dimorphic hemmorhoids(piles) 120
          Heart attack         120
          Varicose veins       120
          Hypothyroidism       120
          Hyperthyroidism      120
          Hypoglycemia         120
          Osteoarthritis       120
          Arthritis            120
          (vertigo) Paroymsal  Positional Vertigo 120
          Acne                 120
          Urinary tract infection 120
          Psoriasis            120
          Hepatitis D          120
          Hepatitis B          120
          Allergy              120
          hepatitis A          120
          GERD                 120
          Chronic cholestasis  120
          Drug Reaction        120
          Peptic ulcer disease 120
          AIDS                 120
          Diabetes             120
          Gastroenteritis     120
          Bronchial Asthma     120
          Hypertension         120
          Migraine             120
          Cervical spondylosis 120
          Paralysis (brain hemorrhage) 120
          Jaundice             120
          Malaria              120
          Chicken pox          120
          Dengue               120
          Typhoid              120
          Impetigo             120
          Name: prognosis, dtype: int64
```

```
In [31]: plt.figure(figsize= (10,6))
sns.countplot(data = df, x= 'prognosis')
plt.xticks(rotation=90)
plt.xlabel('Diseases');
```



Diseases

(ver

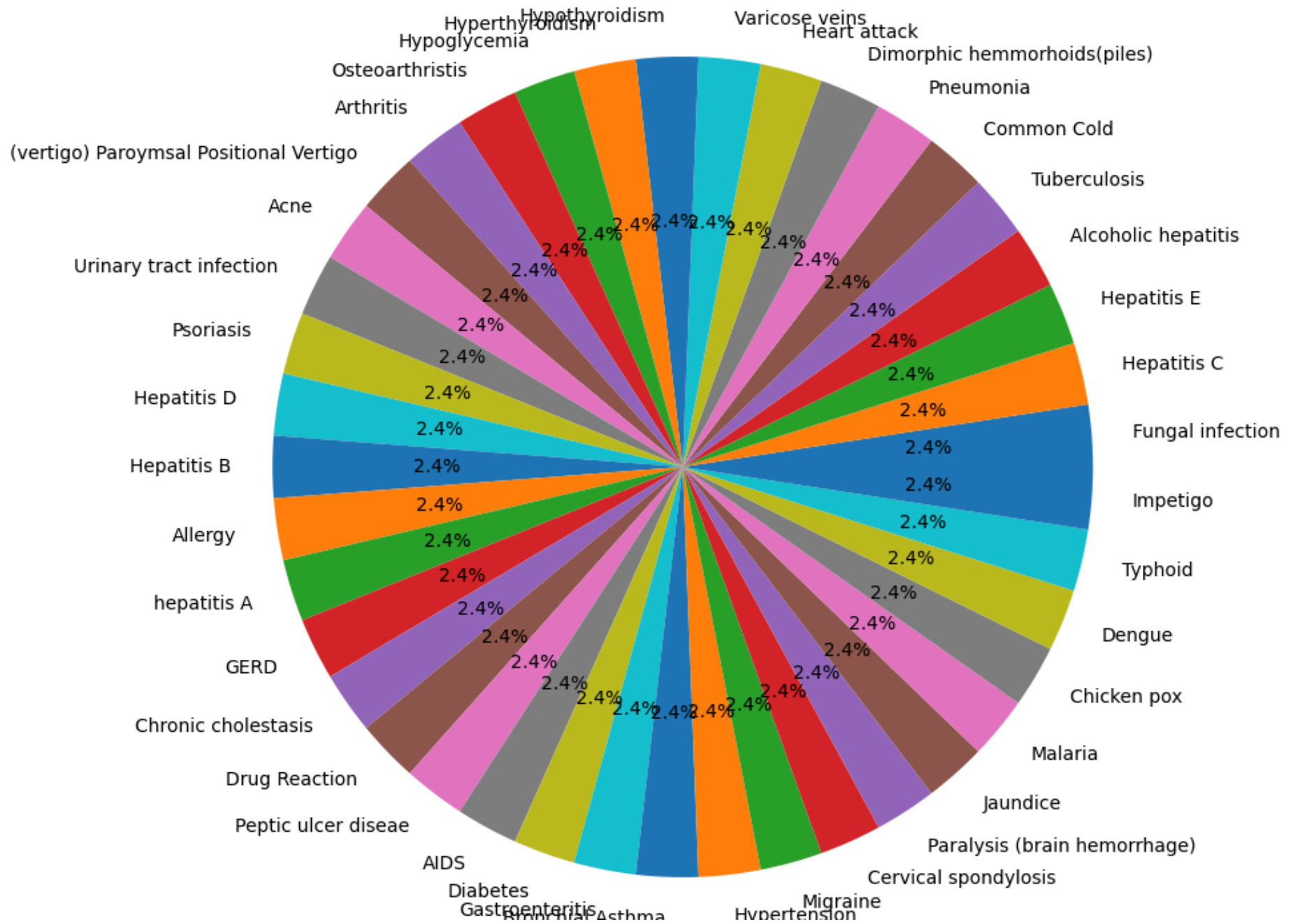
```
In [40]: mylabels = list(y.unique())  
mylabels
```

```
Out[40]: [120]
```

```
In [43]: y = df['prognosis'].value_counts()
```

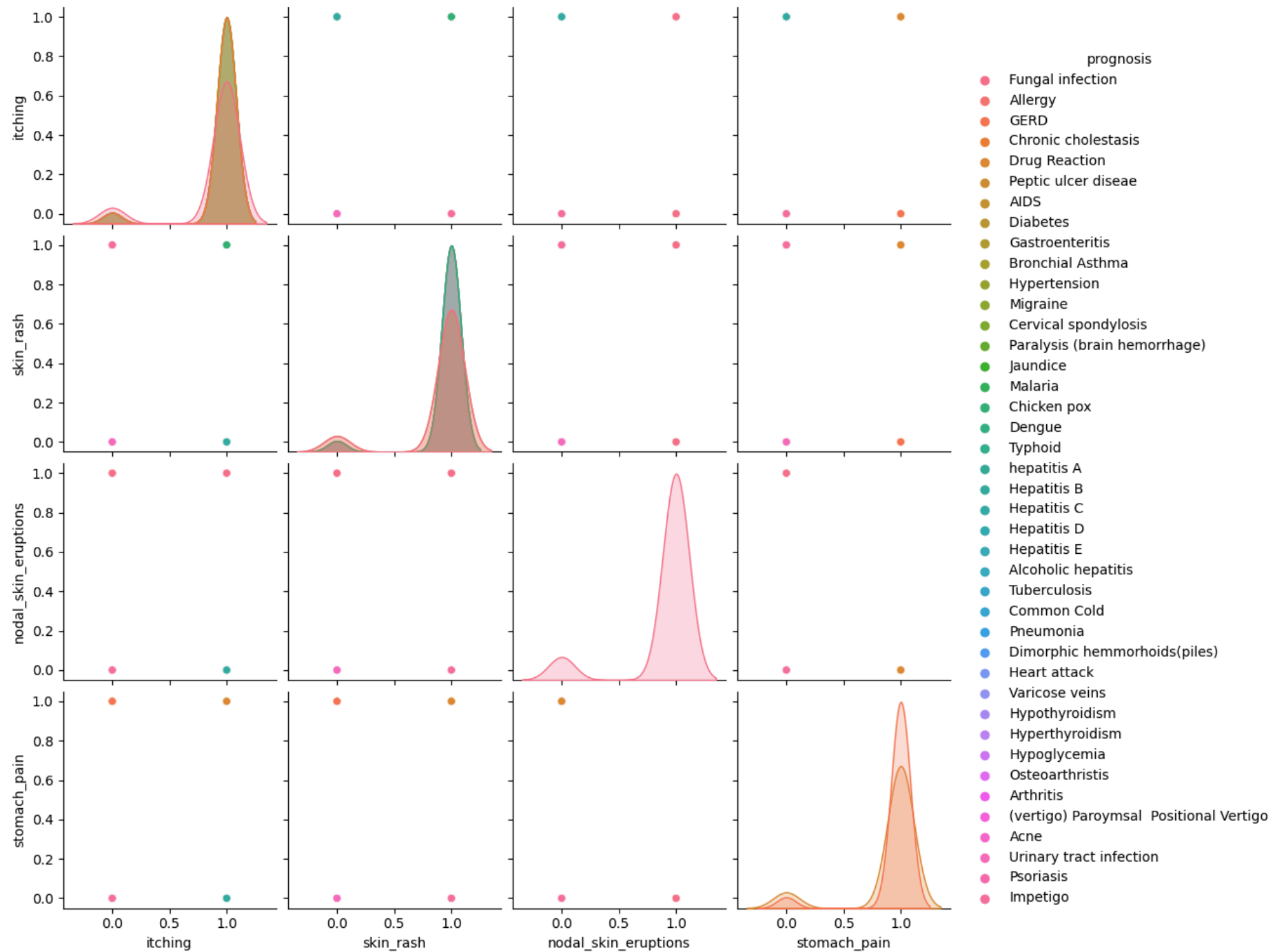
```
In [46]: diseases = ["Fungal infection", "Hepatitis C", "Hepatitis E", "Alcoholic hepatitis", "Tuberculosis", "Common Cold", "Pneumonia",  
  
cases = [120] * len(diseases)  
  
plt.figure(figsize=(10, 10))  
plt.pie(cases, labels=diseases, autopct='%1.1f%%')  
plt.title("Distribution of diseases")  
plt.show()
```

Distribution of diseases



```
In [58]: test_df=test_df.drop(["Unnamed: 133"],axis=1)
```

```
In [63]: selected_columns = ['itching', 'skin_rash', 'nodal_skin_eruptions', 'stomach_pain', 'prognosis']  
  
test_df_selected = test_df[selected_columns]  
  
sns.pairplot(test_df_selected, hue='prognosis')  
  
plt.show()
```



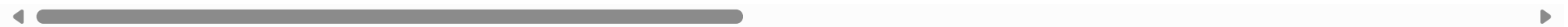

```
In [64]: num = ['itching', 'skin_rash', 'nodal_skin_eruptions', 'continuous_sneezing', 'shivering', 'chills', 'joint_pain',  
               'stomach_pain', 'acidity', 'ulcers_on_tongue', 'muscle_wasting', 'vomiting', 'burning_micturition',  
               'spotting_urination', 'fatigue', 'weight_gain', 'anxiety', 'cold_hands_and_feets', 'mood_swings',  
               'weight_loss', 'restlessness', 'lethargy', 'patches_in_throat', 'irregular_sugar_level', 'cough',  
               'high_fever', 'sunken_eyes', 'breathlessness', 'sweating', 'dehydration', 'indigestion', 'headache',  
               'yellowish_skin', 'dark_urine', 'nausea', 'loss_of_appetite', 'pain_behind_the_eyes', 'back_pain',  
               'constipation', 'abdominal_pain', 'diarrhoea', 'mild_fever', 'yellow_urine', 'yellowing_of_eyes',  
               'acute_liver_failure', 'fluid_overload', 'swelling_of_stomach', 'swelled_lymph_nodes', 'malaise', 'blurred_and_distorted_v  
               'runny_nose', 'congestion', 'chest_pain', 'weakness_in_limbs', 'fast_heart_rate',  
               'pain_during_bowel_movements', 'pain_in_anal_region', 'bloody_stool', 'irritation_in_anus', 'neck_pain',  
               'dizziness', 'cramps', 'bruising', 'obesity', 'swollen_legs', 'swollen_blood_vessels', 'puffy_face_and_eyes',  
               'enlarged_thyroid', 'brittle_nails', 'swollen_extremeties', 'excessive_hunger', 'extra_marital_contacts',  
               'drying_and_tingling_lips', 'slurred_speech', 'knee_pain', 'hip_joint_pain', 'muscle_weakness', 'stiff_neck',  
               'swelling_joints', 'movement_stiffness', 'spinning_movements', 'loss_of_balance', 'unsteadiness',  
               'weakness_of_one_body_side', 'loss_of_smell', 'bladder_discomfort', 'foul_smell_of_urine', 'continuous_feel_of_urine', 'pas  
               'irritability', 'muscle_pain', 'altered_sensorium', 'red_spots_over_body', 'belly_pain',  
               'abnormal_menstruation', 'dischromic_patches', 'watering_from_eyes', 'increased_appetite',  
               'polyuria', 'family_history', 'mucoid_sputum', 'rusty_sputum', 'lack_of_concentration',  
               'visual_disturbances', 'receiving_blood_transfusion', 'receiving_unsterile_injections', 'coma',  
               'stomach_bleeding', 'distention_of_abdomen', 'history_of_alcohol_consumption', 'fluid_overload.1',  
               'blood_in_sputum', 'prominent_veins_on_calf', 'palpitations', 'painful_walking', 'pus_filled_pimples',  
               'blackheads', 'scurring', 'skin_peeling', 'silver_like_dusting', 'small_dents_in_nails', 'inflammatory_nails', 'blister', '
```

```
In [65]: #correlation  
df[num].corr()
```

Out[65]:

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	joint_pain	stomach_pain	acidity	ulcers_o
itching	1.000000	0.318158	0.326439	-0.086906	-0.059893	-0.175905	-0.160650	0.202850	-0.086906	
skin_rash	0.318158	1.000000	0.298143	-0.094786	-0.065324	-0.029324	0.171134	0.161784	-0.094786	
nodal_skin_eruptions	0.326439	0.298143	1.000000	-0.032566	-0.022444	-0.065917	-0.060200	-0.032566	-0.032566	
continuous_sneezing	-0.086906	-0.094786	-0.032566	1.000000	0.608981	0.446238	-0.087351	-0.047254	-0.047254	
shivering	-0.059893	-0.065324	-0.022444	0.608981	1.000000	0.295332	-0.060200	-0.032566	-0.032566	
...
small_dents_in_nails	-0.061573	0.331087	-0.023073	-0.033480	-0.023073	-0.067765	0.359845	-0.033480	-0.033480	
inflammatory_nails	-0.061573	0.331087	-0.023073	-0.033480	-0.023073	-0.067765	0.359845	-0.033480	-0.033480	
blister	-0.061573	0.331087	-0.023073	-0.033480	-0.023073	-0.067765	-0.061889	-0.033480	-0.033480	
red_sore_around_nose	-0.061573	0.331087	-0.023073	-0.033480	-0.023073	-0.067765	-0.061889	-0.033480	-0.033480	
yellow_crust_ooze	-0.061573	0.331087	-0.023073	-0.033480	-0.023073	-0.067765	-0.061889	-0.033480	-0.033480	

132 rows × 132 columns

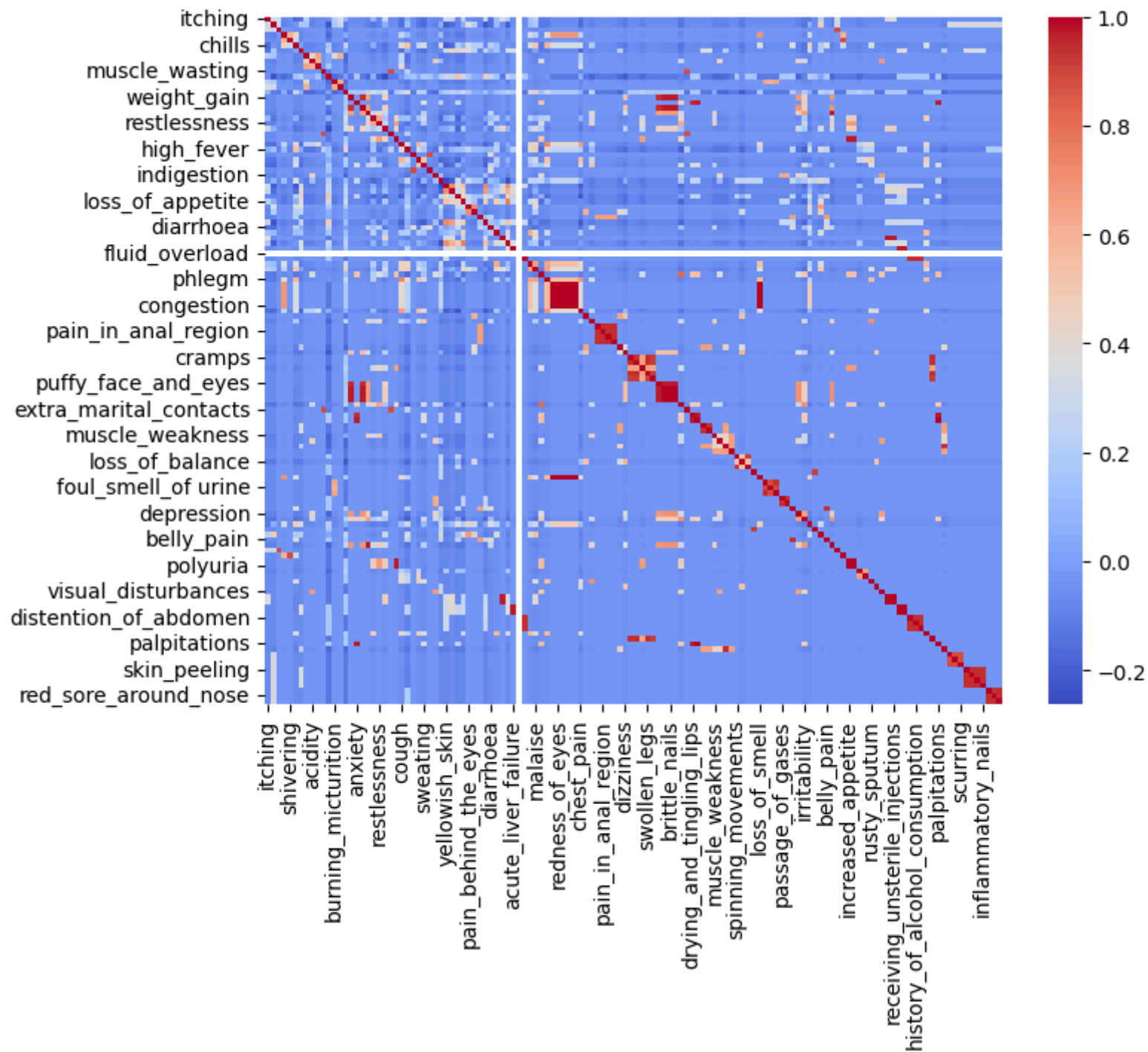


In [67]:

```
#heatmap
plt.figure(figsize=(8,6))
sns.heatmap(data=df[num].corr(),cmap='coolwarm')
```

Out[67]:

<Axes: >



```
In [72]: X_train = train_df.iloc[:, :-1].values
y_train = train_df.iloc[:, 132].values
X_test = test_df.iloc[:, :-1].values
y_test = test_df.iloc[:, 132].values
```

```
In [83]: classifierMLP = MLPClassifier()
classifierMLP.fit(X_train, y_train)
```

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\network_multilayer_perceptron.py:691: ConvergenceWarning: Stochastic Optimizer: Maximum iterations (200) reached and the optimization hasn't converged yet.

warnings.warn(

```
Out[83]: ▼ MLPClassifier
MLPClassifier()
```

```
In [81]: classifierDT = DecisionTreeClassifier(splitter='best', criterion='entropy', min_samples_leaf=2)
classifierDT.fit(X_train, y_train)
```

```
Out[81]: ▼ DecisionTreeClassifier
DecisionTreeClassifier(criterion='entropy', min_samples_leaf=2)
```

```
In [82]: classifierRF = RandomForestClassifier(criterion='entropy', min_samples_leaf=2)
classifierRF.fit(X_train, y_train)
```

```
Out[82]: ▼ RandomForestClassifier
RandomForestClassifier(criterion='entropy', min_samples_leaf=2)
```

```
In [84]: y_predMLP = classifierMLP.predict(X_test)
y_predDT = classifierDT.predict(X_test)
y_predRF = classifierRF.predict(X_test)
```

```
In [89]: print(confusion_matrix(y_test, y_predMLP))
print(classification_report(y_test, y_predMLP))

print("Train Accuracy: ", accuracy_score(y_train, classifierMLP.predict(X_train)))
print("Test Accuracy: ", accuracy_score(y_test, y_predMLP))
```

```

[[120  0  0 ...  0  0  0]
[  0 120  0 ...  0  0  0]
[  0  0 120 ...  0  0  0]
...
[  0  0  0 ... 120  0  0]
[  0  0  0 ...  0 120  0]
[  0  0  0 ...  0  0 120]]

```

	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	1.00	1.00	120
AIDS	1.00	1.00	1.00	120
Acne	1.00	1.00	1.00	120
Alcoholic hepatitis	1.00	1.00	1.00	120
Allergy	1.00	1.00	1.00	120
Arthritis	1.00	1.00	1.00	120
Bronchial Asthma	1.00	1.00	1.00	120
Cervical spondylosis	1.00	1.00	1.00	120
Chicken pox	1.00	1.00	1.00	120
Chronic cholestasis	1.00	1.00	1.00	120
Common Cold	1.00	1.00	1.00	120
Dengue	1.00	1.00	1.00	120
Diabetes	1.00	1.00	1.00	120
Dimorphic hemmorhoids(piles)	1.00	1.00	1.00	120
Drug Reaction	1.00	1.00	1.00	120
Fungal infection	1.00	1.00	1.00	120
GERD	1.00	1.00	1.00	120
Gastroenteritis	1.00	1.00	1.00	120
Heart attack	1.00	1.00	1.00	120
Hepatitis B	1.00	1.00	1.00	120
Hepatitis C	1.00	1.00	1.00	120
Hepatitis D	1.00	1.00	1.00	120
Hepatitis E	1.00	1.00	1.00	120
Hypertension	1.00	1.00	1.00	120
Hyperthyroidism	1.00	1.00	1.00	120
Hypoglycemia	1.00	1.00	1.00	120
Hypothyroidism	1.00	1.00	1.00	120
Impetigo	1.00	1.00	1.00	120
Jaundice	1.00	1.00	1.00	120
Malaria	1.00	1.00	1.00	120
Migraine	1.00	1.00	1.00	120
Osteoarthritis	1.00	1.00	1.00	120
Paralysis (brain hemorrhage)	1.00	1.00	1.00	120
Peptic ulcer disease	1.00	1.00	1.00	120
Pneumonia	1.00	1.00	1.00	120

Psoriasis	1.00	1.00	1.00	120
Tuberculosis	1.00	1.00	1.00	120
Typhoid	1.00	1.00	1.00	120
Urinary tract infection	1.00	1.00	1.00	120
Varicose veins	1.00	1.00	1.00	120
hepatitis A	1.00	1.00	1.00	120
accuracy			1.00	4920
macro avg	1.00	1.00	1.00	4920
weighted avg	1.00	1.00	1.00	4920

Train Accuracy: 1.0

Test Accuracy: 1.0

```
In [86]: print(confusion_matrix(y_test, y_predRF))
print(classification_report(y_test, y_predRF))

print("Train Accuracy: ", accuracy_score(y_train, classifierRF.predict(X_train)))
print("Test Accuracy: ", accuracy_score(y_test, y_predRF))
```

```

[[114  0  0 ...  0  0  0]
[  0 114  0 ...  0  0  0]
[  0  0  0 ...  0  0  0]
...
[  0  0  0 ...  0  0  0]
[  0  0  0 ...  0 120  0]
[  0  0  0 ...  0  0 120]]

```

	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	1.00	0.95	0.97	120
AIDS	0.95	0.95	0.95	120
Acne	0.00	0.00	0.00	120
Alcoholic hepatitis	1.00	0.95	0.97	120
Allergy	0.00	0.00	0.00	120
Arthritis	1.00	1.00	1.00	120
Bronchial Asthma	1.00	1.00	1.00	120
Cervical spondylosis	0.91	1.00	0.95	120
Chicken pox	1.00	1.00	1.00	120
Chronic cholestasis	1.00	1.00	1.00	120
Common Cold	1.00	1.00	1.00	120
Dengue	1.00	1.00	1.00	120
Diabetes	1.00	1.00	1.00	120
Dimorphic hemmorhoids(piles)	0.31	1.00	0.48	120
Drug Reaction	0.00	0.00	0.00	120
Fungal infection	0.20	1.00	0.34	120
GERD	1.00	1.00	1.00	120
Gastroenteritis	0.90	0.90	0.90	120
Heart attack	1.00	1.00	1.00	120
Hepatitis B	1.00	1.00	1.00	120
Hepatitis C	1.00	1.00	1.00	120
Hepatitis D	1.00	0.05	0.10	120
Hepatitis E	0.53	1.00	0.69	120
Hypertension	0.95	0.90	0.92	120
Hyperthyroidism	1.00	1.00	1.00	120
Hypoglycemia	1.00	1.00	1.00	120
Hypothyroidism	1.00	1.00	1.00	120
Impetigo	0.00	0.00	0.00	120
Jaundice	1.00	1.00	1.00	120
Malaria	1.00	1.00	1.00	120
Migraine	0.91	1.00	0.95	120
Osteoarthritis	1.00	1.00	1.00	120
Paralysis (brain hemorrhage)	1.00	0.80	0.89	120
Peptic ulcer diseae	0.95	1.00	0.98	120
Pneumonia	1.00	1.00	1.00	120

Psoriasis	0.00	0.00	0.00	120
Tuberculosis	1.00	1.00	1.00	120
Typhoid	1.00	1.00	1.00	120
Urinary tract infection	0.00	0.00	0.00	120
Varicose veins	1.00	1.00	1.00	120
hepatitis A	0.95	1.00	0.98	120
accuracy			0.82	4920
macro avg	0.79	0.82	0.78	4920
weighted avg	0.79	0.82	0.78	4920

Train Accuracy: 0.8333333333333334

Test Accuracy: 0.8170731707317073

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

```
_warn_prf(average, modifier, msg_start, len(result))
```

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

```
_warn_prf(average, modifier, msg_start, len(result))
```

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

```
_warn_prf(average, modifier, msg_start, len(result))
```

```
In [87]: print(confusion_matrix(y_test, y_predDT))
print(classification_report(y_test, y_predDT))

print("Train Accuracy: ", accuracy_score(y_train, classifierDT.predict(X_train)))
print("Test Accuracy: ", accuracy_score(y_test, y_predDT))
```



```

[[108  6  0 ...  0  0  0]
[  0 120  0 ...  0  0  0]
[  0  6 114 ...  0  0  0]
...
[  0 120  0 ...  0  0  0]
[  0  6  0 ...  0  0  0]
[  0  6  0 ...  0  0  0]]

```

	precision	recall	f1-score	support
(vertigo) Paroymsal Positional Vertigo	0.33	0.90	0.49	120
AIDS	0.15	1.00	0.26	120
Acne	0.32	0.95	0.47	120
Alcoholic hepatitis	0.46	0.90	0.61	120
Allergy	0.00	0.00	0.00	120
Arthritis	0.50	0.95	0.66	120
Bronchial Asthma	0.45	0.75	0.57	120
Cervical spondylosis	0.49	0.95	0.64	120
Chicken pox	0.32	0.90	0.47	120
Chronic cholestasis	0.47	0.85	0.61	120
Common Cold	0.48	0.80	0.60	120
Dengue	0.42	0.85	0.57	120
Diabetes	0.29	0.95	0.44	120
Dimorphic hemmorhoids(piles)	0.00	0.00	0.00	120
Drug Reaction	0.00	0.00	0.00	120
Fungal infection	0.47	0.80	0.59	120
GERD	0.29	0.90	0.43	120
Gastroenteritis	0.00	0.00	0.00	120
Heart attack	0.00	0.00	0.00	120
Hepatitis B	0.34	0.95	0.50	120
Hepatitis C	0.00	0.00	0.00	120
Hepatitis D	0.00	0.00	0.00	120
Hepatitis E	0.00	0.00	0.00	120
Hypertension	0.00	0.00	0.00	120
Hyperthyroidism	0.49	0.90	0.63	120
Hypoglycemia	0.00	0.00	0.00	120
Hypothyroidism	0.00	0.00	0.00	120
Impetigo	0.00	0.00	0.00	120
Jaundice	0.00	0.00	0.00	120
Malaria	0.00	0.00	0.00	120
Migraine	0.00	0.00	0.00	120
Osteoarthritis	0.00	0.00	0.00	120
Paralysis (brain hemorrhage)	0.00	0.00	0.00	120
Peptic ulcer diseae	0.00	0.00	0.00	120
Pneumonia	0.00	0.00	0.00	120

Psoriasis	0.00	0.00	0.00	120
Tuberculosis	0.00	0.00	0.00	120
Typhoid	0.00	0.00	0.00	120
Urinary tract infection	0.00	0.00	0.00	120
Varicose veins	0.00	0.00	0.00	120
hepatitis A	0.00	0.00	0.00	120
accuracy			0.35	4920
macro avg	0.15	0.35	0.21	4920
weighted avg	0.15	0.35	0.21	4920

Train Accuracy: 0.40476190476190477

Test Accuracy: 0.348780487804878

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

_warn_prf(average, modifier, msg_start, len(result))

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

_warn_prf(average, modifier, msg_start, len(result))

C:\Users\damma\anaconda4\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision and F-score are ill-defined and being set to 0.0 in labels with no predicted samples. Use `zero_division` parameter to control this behavior.

_warn_prf(average, modifier, msg_start, len(result))

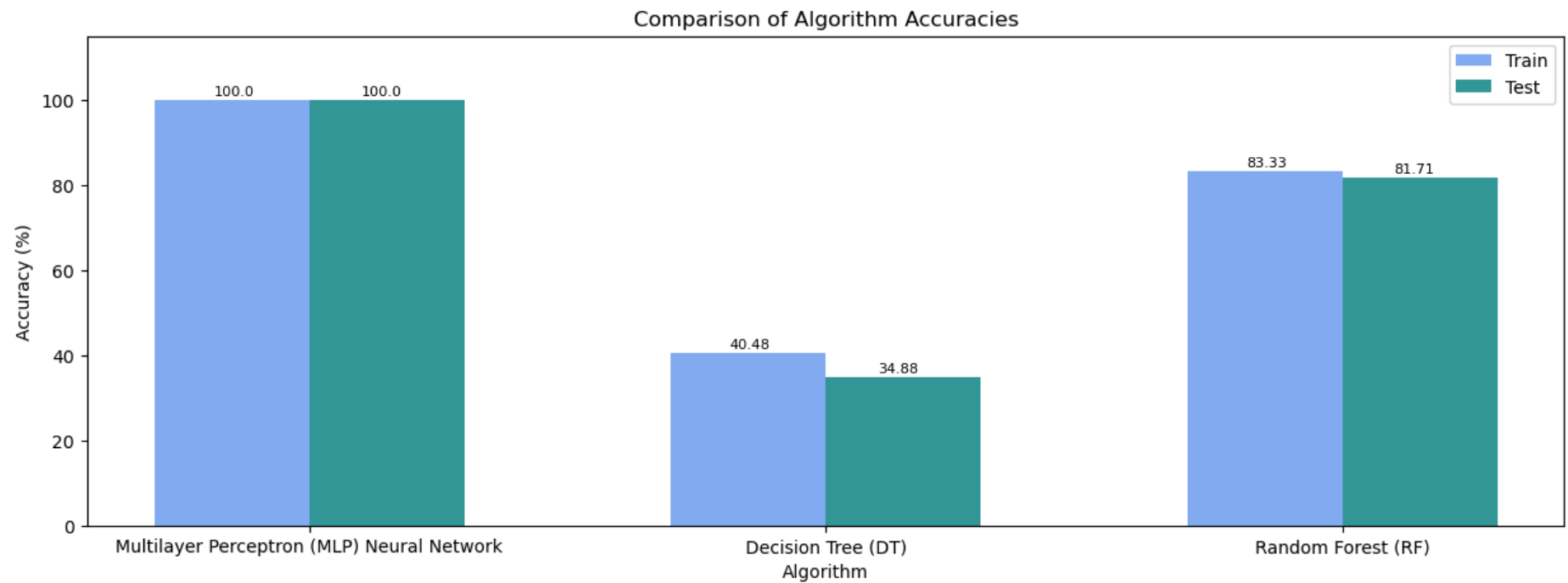
```
In [88]: # data to plot
n_groups = 3
algorithms = ('Multilayer Perceptron (MLP) Neural Network', 'Decision Tree (DT)', 'Random Forest (RF)')
train_accuracy = (accuracy_score(y_train, classifierMLP.predict(X_train))*100,
                  accuracy_score(y_train, classifierDT.predict(X_train))*100,
                  accuracy_score(y_train, classifierRF.predict(X_train))*100)
test_accuracy = (accuracy_score(y_test, y_predMLP)*100,
                 accuracy_score(y_test, y_predDT)*100,
                 accuracy_score(y_test, y_predRF)*100)

# create plot
fig, ax = plt.subplots(figsize=(15, 5))
index = np.arange(n_groups)
bar_width = 0.3
opacity = 0.8
rects1 = plt.bar(index, train_accuracy, bar_width, alpha = opacity, color='Cornflowerblue', label='Train')
rects2 = plt.bar(index + bar_width, test_accuracy, bar_width, alpha = opacity, color='Teal', label='Test')
```

```

plt.xlabel('Algorithm') # x axis label
plt.ylabel('Accuracy (%)') # y axis label
plt.ylim(0, 115)
plt.title('Comparison of Algorithm Accuracies') # plot title
plt.xticks(index + bar_width * 0.5, algorithms) # x axis data labels
plt.legend(loc = 'upper right') # show legend
for index, data in enumerate(train_accuracy):
    plt.text(x = index - 0.035, y = data + 1, s = round(data, 2), fontdict = dict(fontsize = 8))
for index, data in enumerate(test_accuracy):
    plt.text(x = index + 0.25, y = data + 1, s = round(data, 2), fontdict = dict(fontsize = 8))
plt.show()

```



In []: