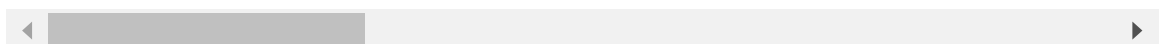


```
In [1]: import pandas as pd
dataset = pd.read_csv('Training.csv')
dataset
```

```
Out[1]:
```

	itching	skin_rash	nodal_skin_eruptions	continuous_sneezing	shivering	chills	jc
0	1	1	1	0	0	0	
1	0	1	1	0	0	0	
2	1	0	1	0	0	0	
3	1	1	0	0	0	0	
4	1	1	1	0	0	0	
...	...	...	...	...	...	...	...
4915	0	0	0	0	0	0	
4916	0	1	0	0	0	0	
4917	0	0	0	0	0	0	
4918	0	1	0	0	0	0	
4919	0	1	0	0	0	0	

4920 rows × 133 columns



```
In [2]: # vals = dataset.values.flatten()
dataset.shape
```

```
Out[2]: (4920, 133)
```

```
In [3]: #train test split
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import LabelEncoder
X = dataset.drop('prognosis', axis=1)
y = dataset['prognosis']

# encoding prognonsis
le = LabelEncoder()
le.fit(y)
Y = le.transform(y)

X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size=0.3, random_
```

```
In [4]: #Training top models
from sklearn.datasets import make_classification
from sklearn.model_selection import train_test_split
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import MultinomialNB
from sklearn.metrics import accuracy_score, confusion_matrix
import numpy as np

# Create a dictionary to store models
models = {
    'SVC': SVC(kernel='linear'),
    'RandomForest': RandomForestClassifier(n_estimators=100, random_state=42),
    'GradientBoosting': GradientBoostingClassifier(n_estimators=100, random_state=42),
    'KNeighbors': KNeighborsClassifier(n_neighbors=5),
    'MultinomialNB': MultinomialNB()
}

# Loop through the models, train, test, and print results
for model_name, model in models.items():
    # Train the model
    model.fit(X_train, y_train)

    # Test the model
    predictions = model.predict(X_test)

    # Calculate accuracy
    accuracy = accuracy_score(y_test, predictions)
    print(f"{model_name} Accuracy: {accuracy}")

    # Calculate confusion matrix
    cm = confusion_matrix(y_test, predictions)
    print(f"{model_name} Confusion Matrix:")
    print(np.array2string(cm, separator=', '))

    print("\n" + "="*40 + "\n")
```

```
SVC Accuracy: 1.0
SVC Confusion Matrix:
[[40,  0,  0, ...,  0,  0,  0],
 [ 0, 43,  0, ...,  0,  0,  0],
 [ 0,  0, 28, ...,  0,  0,  0],
 ...,
 [ 0,  0,  0, ..., 34,  0,  0],
 [ 0,  0,  0, ...,  0, 41,  0],
 [ 0,  0,  0, ...,  0,  0, 31]]

=====

RandomForest Accuracy: 1.0
RandomForest Confusion Matrix:
[[40,  0,  0, ...,  0,  0,  0],
 [ 0, 43,  0, ...,  0,  0,  0],
 [ 0,  0, 28, ...,  0,  0,  0],
 ...,
 [ 0,  0,  0, ..., 34,  0,  0],
 [ 0,  0,  0, ...,  0, 41,  0],
 [ 0,  0,  0, ...,  0,  0, 31]]

=====

GradientBoosting Accuracy: 1.0
GradientBoosting Confusion Matrix:
[[40,  0,  0, ...,  0,  0,  0],
 [ 0, 43,  0, ...,  0,  0,  0],
 [ 0,  0, 28, ...,  0,  0,  0],
 ...,
 [ 0,  0,  0, ..., 34,  0,  0],
 [ 0,  0,  0, ...,  0, 41,  0],
 [ 0,  0,  0, ...,  0,  0, 31]]

=====

KNeighbors Accuracy: 1.0
KNeighbors Confusion Matrix:
[[40,  0,  0, ...,  0,  0,  0],
 [ 0, 43,  0, ...,  0,  0,  0],
 [ 0,  0, 28, ...,  0,  0,  0],
 ...,
 [ 0,  0,  0, ..., 34,  0,  0],
 [ 0,  0,  0, ...,  0, 41,  0],
 [ 0,  0,  0, ...,  0,  0, 31]]

=====

MultinomialNB Accuracy: 1.0
MultinomialNB Confusion Matrix:
[[40,  0,  0, ...,  0,  0,  0],
 [ 0, 43,  0, ...,  0,  0,  0],
 [ 0,  0, 28, ...,  0,  0,  0],
 ...,
 [ 0,  0,  0, ..., 34,  0,  0],
 [ 0,  0,  0, ...,  0, 41,  0],
 [ 0,  0,  0, ...,  0,  0, 31]]

=====
```

```
In [5]: #single prediction
# selecting svc
svc = SVC(kernel='linear')
svc.fit(X_train,y_train)
ypred = svc.predict(X_test)
accuracy_score(y_test,ypred)
```

Out[5]: 1.0

```
In [6]: # save svc
import pickle
pickle.dump(svc,open('svc.pkl','wb'))
```

```
In [7]: # Load model
svc = pickle.load(open('svc.pkl','rb'))
# test 1:
print("predicted disease :",svc.predict(X_test.iloc[0].values.reshape(1,-1)))
print("Actual Disease :", y_test[0])
```

predicted disease : [40]  
Actual Disease : 40

C:\Users\gopik\AppData\Roaming\Python\Python313\site-packages\sklearn\utils\validation.py:2739: UserWarning: X does not have valid feature names, but SVC was fitted with feature names  
warnings.warn(

```
In [8]: # test 2:
print("predicted disease :",svc.predict(X_test.iloc[100].values.reshape(1,-1)))
print("Actual Disease :", y_test[100])
```

predicted disease : [39]  
Actual Disease : 39

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warnings.warn(

```
In [9]: #Recommendation System and Prediction
#Load database and use logic for recommendations
sym_des = pd.read_csv("symptoms_df.csv")
precautions = pd.read_csv("precautions_df.csv")
workout = pd.read_csv("workout_df.csv")
description = pd.read_csv("description.csv")
medications = pd.read_csv('medications.csv')
diets = pd.read_csv("diets.csv")
#=====
# custome and helping functions
#=====helper funtions=====
def helper(dis):
    desc = description[description['Disease'] == predicted_disease]['Description']
    desc = " ".join([w for w in desc])

    pre = precautions[precautions['Disease'] == dis][['Precaution_1', 'Precaution_2']]
    pre = [col for col in pre.values]

    med = medications[medications['Disease'] == dis]['Medication']
    med = [med for med in med.values]

    die = diets[diets['Disease'] == dis]['Diet']
```

```

die = [die for die in die.values]

wrkout = workout[workout['disease'] == dis] ['workout']

return desc,pre,med,die,wrkout

symptoms_dict = {'itching': 0, 'skin_rash': 1, 'nodal_skin_eruptions': 2, 'conti
diseases_list = {15: 'Fungal infection', 4: 'Allergy', 16: 'GERD', 9: 'Chronic c

# Model Prediction function
def get_predicted_value(patient_symptoms):
    input_vector = np.zeros(len(symptoms_dict))
    for item in patient_symptoms:
        input_vector[symptoms_dict[item]] = 1
    return diseases_list[svc.predict([input_vector])[0]]

# Test 1
# Split the user's input into a list of symptoms (assuming they are comma-separa
symptoms = input("Enter your symptoms.....")
user_symptoms = [s.strip() for s in symptoms.split(',')]
# Remove any extra characters, if any
user_symptoms = [symptom.strip("[]' ") for symptom in user_symptoms]
predicted_disease = get_predicted_value(user_symptoms)

desc, pre, med, die, wrkout = helper(predicted_disease)

print("=====predicted disease=====")
print(predicted_disease)
print("=====description=====")
print(desc)
print("=====precautions=====")
i = 1
for p_i in pre[0]:
    print(i, ": ", p_i)
    i += 1

print("=====medications=====")
for m_i in med:
    print(i, ": ", m_i)
    i += 1

print("=====workout=====")
for w_i in wrkout:
    print(i, ": ", w_i)
    i += 1

print("=====diets=====")
for d_i in die:
    print(i, ": ", d_i)
    i += 1

```

```

=====predicted disease=====
Urinary tract infection
=====description=====
Urinary tract infection is an infection in any part of the urinary system.
=====precautions=====
1 : drink plenty of water
2 : increase vitamin c intake
3 : drink cranberry juice
4 : take probiotics
=====medications=====
5 : ['Antibiotics', 'Urinary analgesics', 'Phenazopyridine', 'Antispasmodics',
'Probiotics']
=====workout=====
6 : Stay hydrated
7 : Consume cranberry products
8 : Include vitamin C-rich foods
9 : Limit caffeine and alcohol
10 : Consume probiotics
11 : Avoid spicy and acidic foods
12 : Consult a healthcare professional
13 : Follow medical recommendations
14 : Maintain good hygiene
15 : Limit sugary foods and beverages
=====diets=====
16 : ['UTI Diet', 'Hydration', 'Cranberry juice', 'Probiotics', 'Vitamin C-rich
foods']

```

```

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ation.py:2739: UserWarning: X does not have valid feature names, but SVC was fitt
ed with feature names
  warnings.warn(

```

```

In [10]: # Test 1
# Split the user's input into a list of symptoms (assuming they are comma-separa
symptoms = input("Enter your symptoms.....")
user_symptoms = [s.strip() for s in symptoms.split(',')]
# Remove any extra characters, if any
user_symptoms = [symptom.strip("[]' ") for symptom in user_symptoms]
predicted_disease = get_predicted_value(user_symptoms)

desc, pre, med, die, wrkout = helper(predicted_disease)

print("=====predicted disease=====")
print(predicted_disease)
print("=====description=====")
print(desc)
print("=====precautions=====")
i = 1
for p_i in pre[0]:
    print(i, ": ", p_i)
    i += 1

print("=====medications=====")
for m_i in med:
    print(i, ": ", m_i)
    i += 1

print("=====workout=====")
for w_i in wrkout:
    print(i, ": ", w_i)
    i += 1

```

```
print("=====diets=====")
for d_i in die:
    print(i, ": ", d_i)
    i += 1
```

```
=====predicted disease=====
Fungal infection
=====description=====
Fungal infection is a common skin condition caused by fungi.
=====precautions=====
1 : bath twice
2 : use detol or neem in bathing water
3 : keep infected area dry
4 : use clean cloths
=====medications=====
5 : ['Antifungal Cream', 'Fluconazole', 'Terbinafine', 'Clotrimazole', 'Ketocona
zole']
=====workout=====
6 : Avoid sugary foods
7 : Consume probiotics
8 : Increase intake of garlic
9 : Include yogurt in diet
10 : Limit processed foods
11 : Stay hydrated
12 : Consume green tea
13 : Eat foods rich in zinc
14 : Include turmeric in diet
15 : Eat fruits and vegetables
=====diets=====
16 : ['Antifungal Diet', 'Probiotics', 'Garlic', 'Coconut oil', 'Turmeric']
C:\Users\gopik\AppData\Roaming\Python\Python313\site-packages\sklearn\utils\valid
ation.py:2739: UserWarning: X does not have valid feature names, but SVC was fitt
ed with feature names
    warnings.warn(
```

In [ ]: