

21BCE7371
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ML LAB

SVM for Multiclass Classification

DATA

1. Allhyper.csv

1	41	F	f	f	f	f	f	f	f	f	f	f	f	f	t	1.3	t	2.5	t	125	t	1.14	t	109	f	?	SVHC	negative.]3733	
2	23	F	f	f	f	f	f	f	f	f	f	f	f	f	t	4.1	t	2	t	102	f	?	f	?	f	?	other	negative.]1442	
3	46	M	f	f	f	f	f	f	f	f	f	f	f	f	t	0.98	f	?	t	109	t	0.91	t	120	f	?	other	negative.]2965	
4	70	F	t	f	f	f	f	f	f	f	f	f	f	f	t	0.16	t	1.9	t	175	f	?	f	?	f	?	other	negative.]806	
5	70	F	f	f	f	f	f	f	f	f	f	f	f	f	t	0.72	t	1.2	t	61	t	0.87	t	70	f	?	SVI	negative.]2807	
6	18	F	t	f	f	f	f	f	f	f	f	f	f	f	t	0.03	f	?	t	183	t	1.3	t	141	f	?	other	negative.]3434	
7	59	F	f	f	f	f	f	f	f	f	f	f	f	f	f	?	f	?	t	72	t	0.92	t	78	f	?	other	negative.]1595	
8	80	F	f	f	f	f	f	f	f	f	f	f	f	f	t	2.2	t	0.6	t	80	t	0.7	t	115	f	?	SVI	negative.]1367	
9	66	F	f	f	f	f	f	f	f	f	f	f	t	f	t	0.6	t	2.2	t	123	t	0.93	t	132	f	?	SVI	negative.]1787	
10	68	M	f	f	f	f	f	f	f	f	f	f	f	f	t	2.4	t	1.6	t	83	t	0.89	t	93	f	?	SVI	negative.]2534	
11	84	F	f	f	f	f	f	f	f	f	f	f	t	f	t	1.1	t	2.2	t	115	t	0.95	t	121	f	?	SVI	negative.]1485	
12	67	F	t	f	f	f	f	f	f	f	f	f	f	f	t	0.03	f	?	t	152	t	0.99	t	153	f	?	other	negative.]3448	
13	71	F	f	f	f	t	f	f	f	f	t	f	f	f	f	t	0.03	t	3.8	t	171	t	1.13	t	151	f	?	other	negative.]1027
14	59	F	f	f	f	f	f	f	f	f	f	f	f	f	t	2.8	t	1.7	t	97	t	0.91	t	107	f	?	SVI	negative.]3331	
15	28	M	f	f	f	f	f	f	f	f	f	f	f	f	t	3.3	t	1.8	t	109	t	0.91	t	119	f	?	SVHC	negative.]2043	
16	65	F	f	f	f	f	f	f	f	f	f	f	f	f	t	1.2	f	?	t	90	t	1.14	t	87	f	?	other	negative.]2169	

2. Allhypo.csv

1	41	F	f	f	f	f	f	f	f	f	f	f	f	f	t	1.3	t	2.5	t	125	t	1.14	t	109	f	?	SVHC	negative.[3733	
2	23	F	f	f	f	f	f	f	f	f	f	f	f	f	t	4.1	t	2	t	102	f	?	f	?	f	?	other	negative.[1442	
3	46	M	f	f	f	f	f	f	f	f	f	f	f	f	t	0.98	f	?	t	109	t	0.91	t	120	f	?	other	negative.[2965	
4	70	F	t	f	f	f	f	f	f	f	f	f	f	f	t	0.16	t	1.9	t	175	f	?	f	?	f	?	other	negative.[806	
5	70	F	f	f	f	f	f	f	f	f	f	f	f	f	t	0.72	t	1.2	t	61	t	0.87	t	70	f	?	SVI	negative.[2807	
6	18	F	t	f	f	f	f	f	f	f	f	f	f	f	t	0.03	f	?	t	183	t	1.3	t	141	f	?	other	negative.[3434	
7	59	F	f	f	f	f	f	f	f	f	f	f	f	f	f	?	f	?	t	72	t	0.92	t	78	f	?	other	negative.[1595	
8	80	F	f	f	f	f	f	f	f	f	f	f	f	f	t	2.2	t	0.6	t	80	t	0.7	t	115	f	?	SVI	negative.[1367	
9	66	F	f	f	f	f	f	f	f	f	f	f	f	t	f	0.6	t	2.2	t	123	t	0.93	t	132	f	?	SVI	negative.[1787	
0	68	M	f	f	f	f	f	f	f	f	f	f	f	f	t	2.4	t	1.6	t	83	t	0.89	t	93	f	?	SVI	negative.[2534	
1	84	F	f	f	f	f	f	f	f	f	f	f	f	t	f	1.1	t	2.2	t	115	t	0.95	t	121	f	?	SVI	negative.[1485	
2	67	F	t	f	f	f	f	f	f	f	f	f	f	f	t	0.03	f	?	t	152	t	0.99	t	153	f	?	other	negative.[3448	
3	71	F	f	f	f	t	f	f	f	f	t	f	f	f	f	t	0.03	t	3.8	t	171	t	1.13	t	151	f	?	other	negative.[1027
4	59	F	f	f	f	f	f	f	f	f	f	f	f	f	t	2.8	t	1.7	t	97	t	0.91	t	107	f	?	SVI	negative.[3331	
5	28	M	f	f	f	f	f	f	f	f	f	f	f	f	t	3.3	t	1.8	t	109	t	0.91	t	119	f	?	SVHC	negative.[2043	
6	65	F	f	f	f	f	f	f	f	t	f	f	f	f	f	t	12	f	?	t	99	t	1.14	t	87	f	?	other	compensated hypothyroid.[3169
7	42	?	f	f	f	f	f	f	f	f	f	f	f	f	t	1.2	t	1.8	t	70	t	0.86	t	81	f	?	other	negative.[2755	
8	63	F	f	f	f	f	f	f	f	f	f	f	f	f	t	1.5	t	1.2	t	117	t	0.96	t	121	f	?	SVI	negative.[1010	
9	80	F	f	f	f	f	f	f	f	f	f	f	f	f	t	6	t	1.6	t	99	t	0.95	t	104	f	?	SVI	negative.[803	

3. Sick.csv

1	41	F	f	f	f	f	f	f	f	f	f	f	f	f	f	t	1.3	t	2.5	t	125	t	1.14	t	109	f	?	SVHC	negative.13733		
2	23	F	f	f	f	f	f	f	f	f	f	f	f	f	f	t	4.1	t	2	t	102	f	?	f	?	f	?	other	negative.11442		
3	46	M	f	f	f	f	f	f	f	f	f	f	f	f	f	t	0.98	f	?	t	109	t	0.91	t	120	f	?	other	negative.12965		
4	70	F	t	f	f	f	f	f	f	f	f	f	f	f	f	t	0.16	t	1.9	t	175	f	?	f	?	f	?	other	negative.1806		
5	70	F	f	f	f	f	f	f	f	f	f	f	f	f	f	t	0.72	t	1.2	t	61	t	0.87	t	70	f	?	SVI	negative.12807		
6	18	F	t	f	f	f	f	f	f	f	f	f	f	f	f	t	0.03	f	?	t	183	t	1.3	t	141	f	?	other	negative.13434		
7	59	F	f	f	f	f	f	f	f	f	f	f	f	f	f	f	?	f	?	t	72	t	0.92	t	78	f	?	other	negative.11595		
8	80	F	f	f	f	f	f	f	f	f	f	f	f	f	f	t	2.2	t	0.6	t	80	t	0.7	t	115	f	?	SVI	sick.11367		
9	66	F	f	f	f	f	f	f	f	f	f	f	f	f	t	f	f	t	0.6	t	2.2	t	123	t	0.93	t	132	f	?	SVI	negative.11787
10	68	M	f	f	f	f	f	f	f	f	f	f	f	f	f	t	2.4	t	1.6	t	83	t	0.89	t	93	f	?	SVI	negative.12534		
11	84	F	f	f	f	f	f	f	f	f	f	f	f	f	t	f	f	t	1.1	t	2.2	t	115	t	0.95	t	121	f	?	SVI	negative.11485
12	67	F	t	f	f	f	f	f	f	f	f	f	f	f	f	t	0.03	f	?	t	152	t	0.99	t	153	f	?	other	negative.13448		
13	71	F	f	f	f	t	f	f	f	f	t	f	f	f	f	t	0.03	t	3.8	t	171	t	1.13	t	151	f	?	other	negative.11027		
14	59	F	f	f	f	f	f	f	f	f	f	f	f	f	f	t	2.8	t	1.7	t	97	t	0.91	t	107	f	?	SVI	negative.13331		
15	28	M	f	f	f	f	f	f	f	f	f	f	f	f	f	t	3.3	t	1.8	t	109	t	0.91	t	119	f	?	SVHC	negative.12043		
16	65	F	f	f	f	f	f	f	f	t	f	f	f	f	f	t	12	f	?	t	99	t	1.14	t	87	f	?	other	negative.13169		
17	42	?	f	f	f	f	f	f	f	f	f	f	f	f	f	t	1.2	t	1.8	t	70	t	0.86	t	81	f	?	other	negative.12755		
18	63	F	f	f	f	f	f	f	f	f	f	f	f	f	f	t	1.5	t	1.2	t	117	t	0.96	t	121	f	?	SVI	negative.11010		
19	80	F	f	f	f	f	f	f	f	f	f	f	f	f	t	t	6	t	1.6	t	99	t	0.95	t	104	f	?	SVI	negative.1803		

CODE

```
import warnings
warnings.filterwarnings("ignore")

import pandas as pd
import numpy as np

from sklearn.svm import SVC
from sklearn.preprocessing import label_binarize
from sklearn.impute import SimpleImputer
from sklearn.preprocessing import MinMaxScaler
from sklearn.utils.class_weight import compute_class_weight
from sklearn.model_selection import GridSearchCV,
train_test_split, cross_val_score
from sklearn.metrics import classification_report,
accuracy_score, confusion_matrix
from sklearn.preprocessing import LabelEncoder
from sklearn.decomposition import PCA

import matplotlib.pyplot as plt
%matplotlib inline
```

```

def parse_row(row):
    row = row.split(".")[0]
    return row

def to_hyperthyroid(row):
    if row != "negative":
        row = "hyperthyroid"
    return row

def to_hypothyroid(row):
    if row != "negative":
        row = "hypothyroid"
    return row

def convert_category(dataframe, column):

    if column == 'Sex':
        conditionF = dataframe[column] == 'F' # For sex column
        conditionT = dataframe[column] == 'M' # For sex column
    else:
        conditionF = dataframe[column] == 'f'
        conditionT = dataframe[column] == 't'

    dataframe.loc[conditionF, column] = 0
    dataframe.loc[conditionT, column] = 1

```

Data Retrieval

```

columns = ["Age", "Sex", "On Thyroxine", "Query on Thyroxine",
           "On Antithyroid Medication", "Sick", "Pregnant",
           "Thyroid Surgery", "I131 Treatment", "Query
Hypothyroid",
           "Query Hyperthyroid", "Lithium", "Goitre", "Tumor",
           "Hypopituitary", "Psych", "TSH Measured", "TSH", "T3
Measured",
           "T3", "TT4 Measured", "TT4", "T4U Measured", "T4U",

```

```
"FTI Measured", "FTI", "TBG Measured", "TBG",
"Referral Source", "Category"]
```

```
hyper_data = pd.read_csv("../Datasets/allhyper.csv",
names=columns)
hypo_data = pd.read_csv("../Datasets/allhypo.csv", names=columns)
sick_data = pd.read_csv("../Datasets/sick.csv", names=columns)
```

```
hyper_data['Category'] = hyper_data['Category'] \
    .apply(parse_row) \
    .apply(to_hypothyroid)
```

```
hypo_data['Category'] = hypo_data['Category'] \
    .apply(parse_row) \
    .apply(to_hypothyroid)
```

```
sick_data['Category'] = sick_data['Category'] \
    .apply(parse_row)
```

```
# Combined Thyroid Data
```

```
thyroid_frames = [hyper_data, hypo_data, sick_data]
thyroid_data = pd.concat(thyroid_frames) \
    .drop_duplicates() \
    .drop(['Referral Source', 'TBG', 'TBG
Measured'], axis=1)
```

```
classes = thyroid_data['Category'].unique()
```

```
print("Number of samples:", len(thyroid_data))
```

```
thyroid_data.head()
```

	Age	Sex	On Thyroxine	Query on Thyroxine	On Antithyroid Medication	Sick	Pregnant	Thyroid Surgery	I131 Treatment	Query Hypothyroid	...	TSH	T3 Measured	T3	TT4 Measured	TT4	T4U Measured	T4U
0	41	F	f	f	f	f	f	f	f	f	...	1.3	t	2.5	t	125	t	1.14
1	23	F	f	f	f	f	f	f	f	f	...	4.1	t	2	t	102	f	?
2	46	M	f	f	f	f	f	f	f	f	...	0.98	f	?	t	109	t	0.91
3	70	F	t	f	f	f	f	f	f	f	...	0.16	t	1.9	t	175	f	?
4	70	F	f	f	f	f	f	f	f	f	...	0.72	t	1.2	t	61	t	0.87

5 rows x 27 columns

Data Cleaning

```
# A quick fix needed
thyroid_data.loc[thyroid_data['Age'] == '455', 'Age'] = '45'
```

```
# Binarize Category Columns
binary_cols = ['On Thyroxine', 'Query on Thyroxine', 'Sex',
               'On Antithyroid Medication', 'Sick', 'Pregnant',
               'Thyroid Surgery', 'I131 Treatment', 'Query
Hypothyroid',
               'Query Hyperthyroid', 'Lithium', 'Goitre',
               'Tumor',
               'Hypopituitary', 'Psych', 'TSH Measured', 'T3
Measured',
               'TT4 Measured', 'T4U Measured', 'FTI Measured']

for col in binary_cols: convert_category(thyroid_data, col)
```

```
# Convert '?' to np.nan and convert numeric data to numeric dtype
for col in thyroid_data.columns:
    if col != 'Category':
        thyroid_data.loc[thyroid_data[col] == '?', col] = np.nan
        thyroid_data[col] = pd.to_numeric(thyroid_data[col])
```

```
curr_columns = thyroid_data.columns.difference(['Category'])

imputer = SimpleImputer(missing_values=np.nan, strategy='median')
imputed_data =
imputer.fit_transform(thyroid_data.drop('Category', axis=1))
imputed_data = pd.DataFrame(imputed_data, columns=curr_columns)

thyroid_data = pd.concat([
    imputed_data.reset_index(),
    thyroid_data['Category'].reset_index()],
    axis=1).drop('index', axis=1)
```

```
thyroid_data.head()
```

	Age	FTI	FTI Measured	Goitre	Hypopituitary	I131 Treatment	Lithium	On Antithyroid Medication	On Thyroxine	Pregnant	...	T3 Measured	T4U	T4U Measured	TSH	TSH Measured	TT4	Mei
0	41.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	1.30	1.0	2.5	1.0	125.0	1.0	
1	23.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	4.10	1.0	2.0	1.0	102.0	0.0	
2	46.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.98	0.0	1.9	1.0	109.0	1.0	
3	70.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.16	1.0	1.9	1.0	175.0	0.0	
4	70.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	...	0.72	1.0	1.2	1.0	61.0	1.0	

5 rows × 27 columns

Split Data

```
X = thyroid_data.drop('Category', axis=1)
y = thyroid_data['Category']

col_names = X.columns

X_train, X_test, y_train, y_test = train_test_split(X, y,
                                                    test_size=0.25, stratify=y)

scaler = MinMaxScaler()
X_train = pd.DataFrame(scaler.fit_transform(X_train))
X_test = pd.DataFrame(scaler.transform(X_test))
```

Visualize Data with PCA

```
def plot_pca_data(X, y):

    LE = LabelEncoder()
    y_encoded = LE.fit_transform(y)

    pca = PCA(n_components=2)
    pca.fit(X)
    pca_X = pca.transform(X)

    x_axis = pca_X[:,0]
```

```
y_axis = pca_X[:,1]

fig = plt.figure(figsize=(10,10))
ax = fig.add_subplot(111)

for label in np.unique(y):
    ax.scatter(pca_X[y==label, 0],
               pca_X[y==label, 1],
               label=label,
               s=100,
               edgecolor='k')

ax.legend()
plt.xticks([])
plt.yticks([])

plot_pca_data(X, y)
```



```

cv=cv,n_jobs=-1)

grid_clf.fit(X_data, y_data)

print("The best parameters are: ", grid_clf.best_params_)

return grid_clf.best_params_

```

```

svm_clf = SVC(class_weight='balanced')

svm_params_list = {'C':[1,2,4,8],
                   'kernel':['poly', 'rbf', 'sigmoid'],
                   'degree':[3,4,5],
                   'gamma':['auto', 'scale']}

svm_parameters = search_for_parameters(estimator=svm_clf,
                                       X_data=X_train,
                                       y_data=y_train, cv=5,
                                       grid_parameters=svm_params_list)

svm_clf.set_params(**svm_parameters)

svm_clf.fit(X_train, y_train)

```

The best parameters are: {'C': 8, 'degree': 5, 'gamma': 'scale', 'kernel': 'poly'}

▼ SVC
 SVC(C=8, class_weight='balanced', degree=5, kernel='poly')

Evaluate Parameters

```

def cross_validate(estimator, X_data, y_data, scoring='accuracy',
cv=3, Z=2):

    classes = y_data.unique()

    # Execute Cross Validation

```

```

scores = cross_val_score(estimator=estimator, X=X_data,
y=y_data, cv=cv, scoring=scoring)

print("Model Scoring Evaluation Results")
print("The mean score and the confidence interval of the
score estimate are:")
print("Accuracy: %0.2f (+/- %0.2f)" % (scores.mean(),
scores.std() * 2))

cross_validate(estimator=svm_clf, X_data=X_train, y_data=y_train,
cv=5)

```

```

Model Scoring Evaluation Results
The mean score and the confidence interval of the score estimate are:
Accuracy: 0.73 (+/- 0.07)

```

Predict on Test Set

```

y_true, y_pred = y_test, svm_clf.predict(X_test)

print("Accuracy:", accuracy_score(y_test, y_pred))
print("*"*50)
print()
print("\t\t\tClassification Report")
print()
print(classification_report(y_true, y_pred))

```

Accuracy: 0.6985111662531017

Classification Report

	precision	recall	f1-score	support
hyperthyroid	0.19	0.42	0.26	19
hypothyroid	0.27	0.51	0.35	55
negative	0.92	0.73	0.81	689
sick	0.23	0.63	0.33	43
accuracy			0.70	806
macro avg	0.40	0.57	0.44	806
weighted avg	0.83	0.70	0.74	806

```
# Confusion Matrix
```

```
cm = confusion_matrix(y_true, y_pred, labels=classes)
```

```
print(cm)
```

```
[[500  31  75  83]
 [  8   8   0   3]
 [ 21   0  28   6]
 [ 12   3   1  27]]
```