

Devanshu Surana

PC-23, 1032210755

Panel C, Batch C1

ML Lab Assignment 4

FAQ's

1) What is a classifier?

→ A classifier is a type of algorithm used in machine learning to categorize input data into predefined classes or categories based on their features or attributes. Essentially a function that maps input data to a category or class label.

2) Compare SVM with decision tree classifiers.

→ Support Vector machines (SVM's) aim to find the optimal hyperplane that separates different classes in the data, maximizing the margin between classes. Decision trees split the data into subsets based on features, aiming to create simple decision rules for classification.

3) How would you tune SVM parameters?

→ To tune SVM parameters, focus on adjusting the regularization parameter C (tradeoff between misclassification and margin) and the choice of kernel (e.g. linear, polynomial, radial basis function). Use techniques like grid search or random search with cross validation to find the optimal values.

4) Describe various types of kernel functions.

- 1] Linear Kernel: Computes the dot product of input features.
- 2] Polynomial Kernel: Computes the dot product raised to a specific power.
- 3] Radial Basis Function (RBF) Kernel: Uses a Gaussian like function to map data into high dimensional space.
- 4] Sigmoid Kernel: Applies a hyperbolic tangent function to input features.

5) Give the applications of SVM classifier.

- Image Recognition: Identifying object/pattern in images.
- Text Classification: Categorizing documents into different topics or sentiments.
- Bioinformatics: Predicting protein function or classifying gene expression.

6) State the significance of kernel function.

- The kernel function allows SVM to map input data into high-dimensional space enabling the separation of complex patterns that may not be linearly separable in original feature space.

Paula
23/04/24

ml-lab-4

April 17, 2024

```
[51]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn import datasets
from sklearn.model_selection import cross_val_score, GridSearchCV
from sklearn.preprocessing import StandardScaler
from sklearn.svm import SVC
from sklearn.metrics import accuracy_score
from sklearn.decomposition import PCA
from mlxtend.plotting import plot_decision_regions
from sklearn.model_selection import train_test_split
```

```
cancer = datasets.load_breast_cancer()
X = cancer.data
y = cancer.target
target_names = cancer.target_names
```

```
df = pd.DataFrame(data=cancer.data)
print(df.head())
```

	0	1	2	3	4	5	6	7	8	\
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2419	
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1812	
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2069	
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2597	
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1809	

	9	...	20	21	22	23	24	25	26	27	\
0	0.07871	...	25.38	17.33	184.60	2019.0	0.1622	0.6656	0.7119	0.2654	
1	0.05667	...	24.99	23.41	158.80	1956.0	0.1238	0.1866	0.2416	0.1860	
2	0.05999	...	23.57	25.53	152.50	1709.0	0.1444	0.4245	0.4504	0.2430	
3	0.09744	...	14.91	26.50	98.87	567.7	0.2098	0.8663	0.6869	0.2575	
4	0.05883	...	22.54	16.67	152.20	1575.0	0.1374	0.2050	0.4000	0.1625	

	28	29
0	0.4601	0.11890
1	0.2750	0.08902
2	0.3613	0.08758


```
3 0.6638 0.17300
4 0.2364 0.07678
```

```
[5 rows x 30 columns]
```

```
[52]: scaler = StandardScaler()
      scaler.fit(X)
```

```
[52]: StandardScaler()
```

```
[53]: X_scaled = scaler.fit_transform(X)
      print(X_scaled)
```

```
[[ 1.09706398 -2.07333501  1.26993369 ...  2.29607613  2.75062224
   1.93701461]
 [ 1.82982061 -0.35363241  1.68595471 ...  1.0870843  -0.24388967
   0.28118999]
 [ 1.57988811  0.45618695  1.56650313 ...  1.95500035  1.152255
   0.20139121]
 ...
 [ 0.70228425  2.0455738   0.67267578 ...  0.41406869 -1.10454895
  -0.31840916]
 [ 1.83834103  2.33645719  1.98252415 ...  2.28998549  1.91908301
   2.21963528]
 [-1.80840125  1.22179204 -1.81438851 ... -1.74506282 -0.04813821
  -0.75120669]]
```

```
[54]: # Print the mean and standard deviation of each feature
      print("Mean of each feature:")
      print(scaler.mean_)
      print("\nStandard Deviation of each feature:")
      print(scaler.scale_)
```

```
Mean of each feature:
```

```
[1.41272917e+01 1.92896485e+01 9.19690334e+01 6.54889104e+02
 9.63602812e-02 1.04340984e-01 8.87993158e-02 4.89191459e-02
 1.81161863e-01 6.27976098e-02 4.05172056e-01 1.21685343e+00
 2.86605923e+00 4.03370791e+01 7.04097891e-03 2.54781388e-02
 3.18937163e-02 1.17961371e-02 2.05422988e-02 3.79490387e-03
 1.62691898e+01 2.56772232e+01 1.07261213e+02 8.80583128e+02
 1.32368594e-01 2.54265044e-01 2.72188483e-01 1.14606223e-01
 2.90075571e-01 8.39458172e-02]
```

```
Standard Deviation of each feature:
```

```
[3.52095076e+00 4.29725464e+00 2.42776193e+01 3.51604754e+02
 1.40517641e-02 5.27663291e-02 7.96497253e-02 3.87687325e-02
 2.73901809e-02 7.05415588e-03 2.77068942e-01 5.51163427e-01
 2.02007710e+00 4.54510134e+01 2.99987837e-03 1.78924359e-02]
```

```

3.01595231e-02 6.16486075e-03 8.25910439e-03 2.64374475e-03
4.82899258e+00 6.14085432e+00 3.35730016e+01 5.68856459e+02
2.28123569e-02 1.57198171e-01 2.08440875e-01 6.56745545e-02
6.18130785e-02 1.80453893e-02]

```

```
[55]: param_grid = {'C': [0.01, 0.1, 1, 10, 100], 'kernel': ['linear', 'rbf', 'poly']}
```

```
[56]: from sklearn.model_selection import KFold
      kfold = KFold(n_splits=10, shuffle=True, random_state=42)
```

```
[57]: pca = PCA(n_components=2)
      grid_search = GridSearchCV(estimator=SVC(), param_grid=param_grid,
      scoring='accuracy', cv=kfold)
      grid_search.fit(pca.fit_transform(X_scaled), y)
```

```
[57]: GridSearchCV(cv=KFold(n_splits=10, random_state=42, shuffle=True),
      estimator=SVC(),
      param_grid={'C': [0.01, 0.1, 1, 10, 100],
      'kernel': ['linear', 'rbf', 'poly']},
      scoring='accuracy')
```

```
[58]: best_model = grid_search.best_estimator_
      best_params = grid_search.best_params_
```

```
[59]: print("Best Params: ", best_params)
```

```
Best Params: {'C': 1, 'kernel': 'linear'}
```

```
[60]: y_pred = best_model.predict(pca.transform(X_scaled))
```

```
[61]: accuracy = accuracy_score(y, y_pred)
      print(f"Accuracy with best model: {accuracy:.4f}")
```

```
Accuracy with best model: 0.9543
```

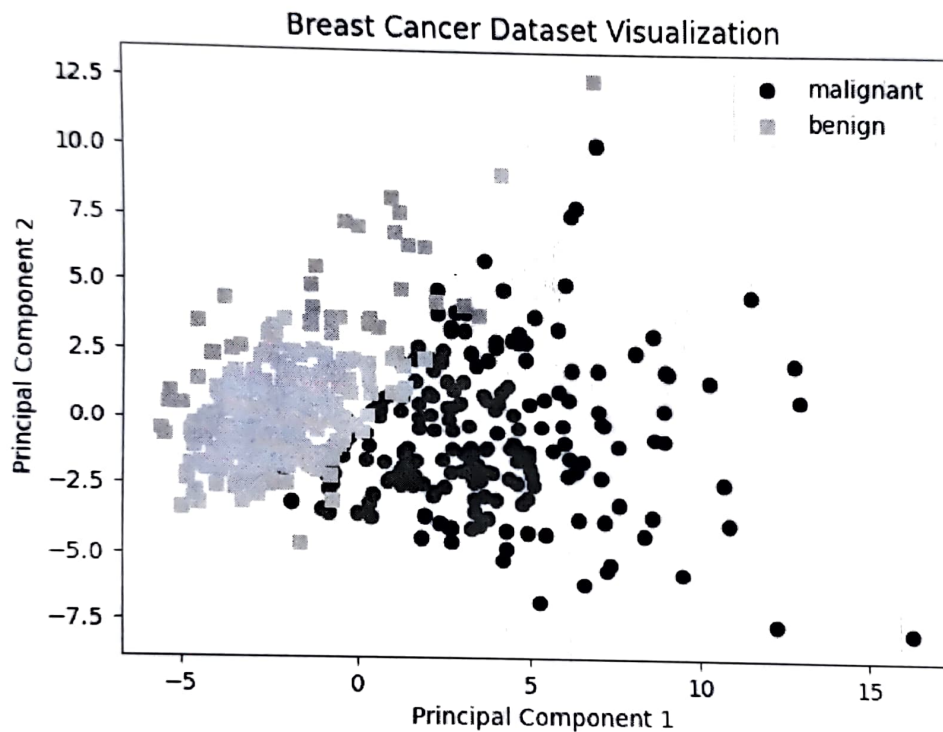
```
[62]: colors = ['red' if label == 0 else 'blue' for label in y]
      markers = ['o' if kernel == 'linear' else '^' if kernel == 'rbf' else 'x' for
      kernel in best_params['kernel']]
```

```
[63]: # Apply PCA
      pca = PCA(n_components=2)
      X_pca = pca.fit_transform(X_scaled)
```

```
[64]: # Plot the transformed data
      colors = ['navy', 'darkorange']
      markers = ['o', 's']
      for target, color, marker in zip(np.unique(y), colors, markers):
```

```
plt.scatter(X_pca[y == target, 0], X_pca[y == target, 1], color=color,
            marker=marker, label=target_names[target])

plt.xlabel('Principal Component 1')
plt.ylabel('Principal Component 2')
plt.title('Breast Cancer Dataset Visualization')
plt.legend(loc='upper right')
plt.show()
```



```
[65]: # Split the dataset into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
                                                    random_state=42)
y_pred = best_svm_classifier.predict(X_test_scaled)
```

NameError

Traceback (most recent call last)

Cell In[65], line 3

```
1 # Split the dataset into training and testing sets
2 X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2
random_state=42)
```

```
----> 3 y_pred = best_svm_classifier.predict(X_test_scaled)
```

```
NameError: name 'best_svm_classifier' is not defined
```

```
[ ]: print("\nClassification Report:")
print(classification_report(y_test, y_pred))
```

Classification Report:

	precision	recall	f1-score	support
0	1.00	0.95	0.98	43
1	0.97	1.00	0.99	71
accuracy			0.98	114
macro avg	0.99	0.98	0.98	114
weighted avg	0.98	0.98	0.98	114

```
[ ]: confusion_matrix(best_svm_classifier, X_test_scaled, y_test, cmap=plt.cm.Blues,
display_labels=data.target_names)
plt.title('Confusion Matrix')
plt.show()
```

Traceback (most recent call last)

TypeError

Cell In[35], line 1.

```
----> 1_
confusion_matrix(best_svm_classifier, X_test_scaled, y_test, cmap=plt.cm.Blues, display_la
2 plt.title('Confusion Matrix')
3 plt.show())
```

```
File ~/pyenv/versions/3.11.7/lib/python3.11/site-packages/sklearn/utils/
param_validation.py:191, in _validate_params<locals>decorator<locals>
188 func_sig = signature(func)
190 # Map *args/**kwargs to the function signature
--> 191 params = func_sig.bind(*args, **kwargs)
192 params.apply_defaults()
194 # ignore self/cls and positional/keyword markers
```

```
File ~/pyenv/versions/3.11.7/lib/python3.11/inspect.py:3212, in Signature
3207 def bind(self, /, *args, **kwargs):
3208     """Get a BoundArguments object, that maps the passed 'args'
3209     and 'kwargs' to the function's signature. Raises 'TypeError'
3210     if the passed arguments can not be bound.
```

```
3211     """
-> 3212     return self._bind(args, kwargs)
```

File ~/.pyenv/versions/3.11.7/lib/python3.11/inspect.py:3138, in Signature.
_bind(self, args, kwargs, partial)

```
3134 else:
3135     if param.kind in (_VAR_KEYWORD, _KEYWORD_ONLY):
3136         # Looks like we have no parameter for this positional
3137         # argument
-> 3138         raise TypeError(
3139             'too many positional arguments') from None
3141     if param.kind == _VAR_POSITIONAL:
3142         # We have an '*args'-like argument, let's fill it with
3143         # all positional arguments we have left and move on to
3144         # the next phase
3145         values = [arg_val]
```

TypeError: too many positional arguments

Pandey
25/4/24