

# CA4

April 18, 2024

Imports

```
[119]: import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split, RandomizedSearchCV
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.svm import SVC
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import f1_score
from mlxtend.feature_selection import SequentialFeatureSelector as SFS
from scipy.stats import expon, loguniform
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay
from sklearn.model_selection import StratifiedKFold
from sklearn.metrics import roc_curve
import numpy as np
from sklearn.pipeline import make_pipeline
from sklearn.model_selection import cross_val_predict, cross_val_score
from sklearn.model_selection import GridSearchCV
```

## 0.1 Reading data

```
[120]: # Load data
df = pd.read_csv("train.csv", index_col=0)
df = df.drop(['index'], axis=1)
df
```

```
[120]:
```

	AFP (ng/mL)	ALP (U/L)	ALT (U/L)	AST (U/L)	Age	Albumin (g/dL)	\
0	13.571425	1653.138489	40.405592	45.598427	4	4.477126	
1	13.649342	1940.518305	21.336986	34.064095	55	3.190724	
2	10.898943	1557.369920	29.665496	16.044488	30	4.506351	
3	13.872275	1273.840525	142.418649	64.204257	0	3.665655	
4	10.102457	1461.622515	22.437303	23.940205	59	4.005109	
..	...	...	...	...	...	...	
698	13.086307	1663.149063	94.844911	81.525503	82	3.893254	
699	12.425079	1580.772607	19.152473	29.765881	8	4.434494	

700	12.887508	1164.383286	116.825787	71.610295	14	4.002324
701	8.947665	1178.449705	7.818343	46.739457	2	3.866326
702	11.885037	1493.989598	74.664804	31.270461	5	4.516665

	Alcohol_Use (yes/no)	Bilirubin (mg/dL)	CRP (mg/L)	Diabetes (yes/no)	\
0	yes	0.541997	1.002121	no	
1	yes	1.199063	0.582746	no	
2	no	0.740952	1.670375	no	
3	yes	1.939879	1.220646	no	
4	no	0.769535	0.139863	no	
..	...	...	...	...	
698	yes	1.514709	4.102990	no	
699	yes	2.497997	3.827726	no	
700	no	1.760204	2.456043	no	
701	no	0.552524	4.907847	no	
702	no	1.969524	1.298070	no	

	...	Serum_Creatinine (mg/dL)	Serum_Iron (g/dL)	Serum_Lactate (mmol/L)	\
0	...	2.569954	97.242495	2.923385	
1	...	3.024642	128.597676	2.719966	
2	...	2.219844	98.026938	3.267757	
3	...	1.704282	63.105133	1.937625	
4	...	2.656926	89.966713	1.979801	
..	...	...	...	...	
698	...	2.510571	71.561815	3.255364	
699	...	3.267194	139.135093	3.741368	
700	...	3.056218	141.278410	2.945887	
701	...	2.322946	112.506385	2.180009	
702	...	2.586336	125.523874	2.225373	

	Serum_Urea (mg/dL)	Serum_Zinc (g/dL)	TIBC (g/dL)	\
0	26.696110	96.124260	315.439318	
1	23.021218	50.554650	268.492437	
2	20.123808	82.900681	312.107620	
3	36.436855	72.360010	182.506010	
4	20.036074	63.216136	212.261519	
..	...	...	...	
698	13.806666	74.751383	331.761651	
699	24.133150	51.577230	266.947184	
700	13.363649	95.869655	260.085180	
701	15.892570	72.641767	344.926350	
702	23.713673	71.472957	330.848442	

	Transferrin_Saturation (%)	WBC (10 <sup>9</sup> /L)	pH	\
0	30.827639	4.180007	6.163600	
1	47.896200	4.590995	5.244266	
2	31.408057	4.524580	5.769592	

3	34.577016	4.234483	5.982228
4	42.384844	4.306892	4.837404
..	...	...	...
698	21.570249	4.239866	6.525677
699	52.120832	4.374619	6.071335
700	54.320054	4.369082	5.059313
701	32.617510	4.249171	6.546267
702	37.939993	4.249528	6.838394

	Diagnosis
0	Healthy
1	Cirrhosis
2	Healthy
3	Drug-induced Liver Injury
4	Healthy
..	...
698	Hepatitis
699	Cirrhosis
700	Hepatitis
701	Healthy
702	Hepatitis

[703 rows x 31 columns]

### 0.1.1 Data exploration and visualisation

```
[121]: # for comparing different features to each other from the dataset, with hue as ↵
↵ Edible
#I just made comments out of this so you dont have to read all the output

# sns.pairplot(df, hue='Diagnosis')
# plt.legend
# plt.show()
```

```
[122]: # For looking at the distribution of the data of each feature in the dataset
# I just made comments out of this so you dont have to read all the output

# for column in df.columns:
#     plt.figure(figsize=(10, 4))
#     sns.histplot(df[column], kde=True) # kde (Kernel Density Estimate) adds ↵
↵ a density curve
#     plt.title(f'Distribution of {column}')
#     plt.xlabel(column)
#     plt.ylabel('Frequency')
#     plt.show()
```

```
[123]: df.describe()
```

[123]:

	AFP (ng/mL)	ALP (U/L)	ALT (U/L)	AST (U/L)	Age \
count	703.000000	703.000000	703.000000	703.000000	703.000000
mean	23.804227	1624.337402	58.262199	46.855946	27.206259
std	54.938736	517.367426	36.372428	30.838523	23.632185
min	-22.836893	546.609117	-14.313734	-16.215535	0.000000
25%	8.029213	1229.735749	29.939330	24.163363	5.000000
50%	10.195074	1553.771408	48.857238	38.720602	23.000000
75%	12.656547	1931.433883	84.583900	70.023374	45.000000
max	449.925304	3769.332343	178.226798	154.173314	86.000000

	Albumin (g/dL)	Bilirubin (mg/dL)	CRP (mg/L)	Fibroscan (kPa) \
count	703.000000	703.000000	703.000000	703.000000
mean	4.155568	1.056841	2.021190	8.899789
std	0.432317	0.617223	2.638333	3.822241
min	2.625845	0.130291	0.075035	2.323530
25%	3.880943	0.634089	0.651623	6.273365
50%	4.166995	0.801903	1.238123	7.966800
75%	4.437957	1.396853	2.449216	10.588808
max	5.447072	3.712815	32.356076	26.691648

	GGT (U/L) ...	Serum_Copper (g/dL)	Serum_Creatinine (mg/dL) \
count	703.000000 ...	703.000000	703.000000
mean	347.457426 ...	105.754889	2.901900
std	371.157528 ...	26.159403	0.647559
min	17.056568 ...	30.099096	1.525736
25%	131.695741 ...	88.632128	2.441051
50%	244.400101 ...	102.842960	2.844621
75%	419.660403 ...	118.722674	3.275906
max	3426.981860 ...	227.617474	5.729147

	Serum_Iron (g/dL)	Serum_Lactate (mmol/L)	Serum_Urea (mg/dL) \
count	703.000000	703.000000	703.000000
mean	105.901892	2.867523	21.440875
std	33.699054	0.936050	6.946169
min	8.328732	0.711997	7.641927
25%	84.737590	2.211484	16.422281
50%	104.670558	2.700933	20.668951
75%	125.937089	3.393898	25.096926
max	223.915730	8.010270	51.875943

	Serum_Zinc (g/dL)	TIBC (g/dL)	Transferrin_Saturation (%) \
count	703.000000	703.000000	703.000000
mean	78.021500	288.708468	38.220427
std	15.826557	54.223207	15.438507
min	34.170231	102.896996	2.496813
25%	66.617374	248.832647	28.598082
50%	78.024893	290.278094	35.617342

75%	88.452369	326.508987	46.630605
max	120.279580	484.581225	156.858874

	WBC (10 <sup>9</sup> /L)	pH
count	703.000000	703.000000
mean	5.000254	6.072044
std	2.025527	0.642783
min	4.129884	4.416868
25%	4.243197	5.724293
50%	4.331605	6.085019
75%	4.762898	6.485114
max	21.195702	8.368522

[8 rows x 26 columns]

```
[124]: nan_per_column = df.isna().sum()
total_nan = df.isna().sum().sum()

# To display the number of NaNs per column
print(nan_per_column)

# To display the total number of NaNs in the DataFrame
print(f"Total number of NaN values in the DataFrame: {total_nan}")
```

AFP (ng/mL)	0
ALP (U/L)	0
ALT (U/L)	0
AST (U/L)	0
Age	0
Albumin (g/dL)	0
Alcohol_Use (yes/no)	0
Bilirubin (mg/dL)	0
CRP (mg/L)	0
Diabetes (yes/no)	0
Fibroscan (kPa)	0
GGT (U/L)	0
Gender	0
Hemoglobin (g/dL)	0
IL-6 (pg/mL)	0
Obesity (yes/no)	0
PT/INR	0
Platelets (10 <sup>9</sup> /L)	0
RBC (10 <sup>12</sup> /L)	0
Serum_Ammonia (mol/L)	0
Serum_Copper (g/dL)	0
Serum_Creatinine (mg/dL)	0
Serum_Iron (g/dL)	0
Serum_Lactate (mmol/L)	0

```

Serum_Urea (mg/dL)          0
Serum_Zinc (g/dL)          0
TIBC (g/dL)                0
Transferrin_Saturation (%)  0
WBC (109/L)                0
pH                          0
Diagnosis                   0
dtype: int64
Total number of NaN values in the DataFrame: 0

```

## 0.2 Comments on the visualisation

I found no missing values. There was features that had some outliers, but maybe some of them have their purpose, so i haven't removed them. There was some negative values in the dataset that didn't make sense, so i'm removing them

### 0.2.1 Data cleaning

```

[125]: # Replace negative values with zero for specified columns
for column in ['AFP (ng/mL)', 'ALT (U/L)', 'AST (U/L)']:
    df[column] = df[column].apply(lambda x: max(x, 0))

```

## 0.3 Preprocessing

```

[126]: # Separate features and target
X = df.drop('Diagnosis', axis=1)
y = df['Diagnosis']

# Identify column types
numerical_cols = X.select_dtypes(include=['int64', 'float64']).columns
categorical_cols = X.select_dtypes(include=['object']).columns

# Preprocessing steps, i make it ignore unkown categories in the OneHotEncoder
preprocessor = ColumnTransformer([
    ('num', StandardScaler(), numerical_cols), # Apply standard scaling to
    ↪numerical columns
    ('cat', OneHotEncoder(handle_unknown='ignore'), categorical_cols) # Apply
    ↪one-hot encoding to categorical columns
])

# Split data into train and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
    ↪random_state=42)

```

## 0.4 Modelling

```
[128]: # SVM Pipeline, focusing on getting the highest f1-macro score
svm_pipeline = Pipeline([
    ('preprocessor', preprocessor), #adding the preprocessor
    ('feature_selector', SFS(SVC(kernel='rbf', random_state=42), #using
    ↪rbf-kernel
                                k_features=(5, 20), #the different combos of
    ↪features i want to try
                                forward=True, #forward SFS
                                floating=True, #allowing both inclusion and
    ↪exclusion of features during the process
                                scoring='f1_macro', # getting the highest f1-macro
    ↪score
                                cv=5)), #5-fold cross validation
    ('classifier', RandomizedSearchCV(SVC(kernel='rbf', random_state=42),
                                     {'C': expon(scale=1), #Finding the best
    ↪value for C
                                     'gamma': ['scale', 'auto'] +
    ↪list(expon(scale=0.1).rvs(size=20))}, #finding the best value for gamma
                                     n_iter=200, #how many iterations
                                     cv=10, #10-Fold Cross-Validation, because
    ↪i felt like it
                                     scoring='f1_macro', # Focusing on getting
    ↪the best f1_macro score
                                     random_state=42,
                                     n_jobs=-1)) #using all processors
    ↪available when running
                                     ])

# Fit the pipeline
svm_pipeline.fit(X_train, y_train) #fitting the training, so i can evaluate

# Evaluate the model
y_pred_svm = svm_pipeline.predict(X_test)
f1_svm = f1_score(y_test, y_pred_svm, average='macro')
print("F1-Score (Macro):", f1_svm) # getting the F1 score from the evaluation

# getting the best paramters from the evaluation
best_params_svm = svm_pipeline.named_steps['classifier'].best_params_
print("Best Parameters:", best_params_svm)
```

```
c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\model_selection\_validation.py:73: FutureWarning: `fit_params`
is deprecated and will be removed in version 1.6. Pass parameters via `params`
instead.
warnings.warn(
```





```

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```

F1-Score (Macro): 0.6942705187338093

Best Parameters: {'C': 3.8581438253895746, 'gamma': 0.01538872159151384}

After using RandomSearch, i tried grid sarch on a smaller range around the best paramters i've found earlier.

```

[129]: param_grid = {
    'C': np.linspace(best_params_svm['C'] * 0.5, best_params_svm['C'] * 2, 10),
    ↪ # Creating 10 points between half and twice the best 'C'
    'gamma': np.linspace(best_params_svm['gamma'] * 0.5,
    ↪ best_params_svm['gamma'] * 2, 10) # Creating 10 points between half and
    ↪ twice the best 'gamma'

```



```

}

# Since we are doing a grid search, we do not need the RandomizedSearchCV part
# anymore.
# We directly plug in the GridSearchCV in place of the RandomizedSearchCV in
# the pipeline
svm_pipeline.named_steps['classifier'] = GridSearchCV(
    SVC(kernel='rbf', random_state=42),
    param_grid,
    cv=10, # 10-Fold Cross-Validation
    scoring='f1_macro',
    n_jobs=-1
)

# Fit the pipeline with the new GridSearchCV
svm_pipeline.fit(X_train, y_train)

# Evaluate the model with the updated classifier
y_pred_svm = svm_pipeline.predict(X_test)
f1_svm = f1_score(y_test, y_pred_svm, average='macro')
print("F1-Score (Macro) with Grid Search:", f1_svm)

# Get the best parameters from the grid search
best_params_svm_grid = svm_pipeline.named_steps['classifier'].best_params_
print("Best Parameters from Grid Search:", best_params_svm_grid)

```

```

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c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-

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File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\base.py:1351, in
↳ _fit_context.<locals>.decorator.<locals>.wrapper(estimator, *args, **kwargs)
    1344     estimator._validate_params()
    1346 with config_context(
    1347     skip_parameter_validation=(
    1348         prefer_skip_nested_validation or global_skip_validation
    1349     )
    1350 ):
-> 1351     return fit_method(estimator, *args, **kwargs)

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\pipeline.py:471, in
↳ Pipeline.fit(self, X, y, **params)
    428 """Fit the model.
    429
    430 Fit all the transformers one after the other and sequentially transform
↳ the
    (...)
    468     Pipeline with fitted steps.
    469 """
    470 routed_params = self._check_method_params(method="fit", props=params)
-> 471 Xt = self._fit(X, y, routed_params)
    472 with _print_elapsed_time("Pipeline", self._log_message(len(self.steps)
↳ 1)):
    473     if self._final_estimator != "passthrough":

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\pipeline.py:408, in
↳ Pipeline._fit(self, X, y, routed_params)
    406     cloned_transformer = clone(transformer)
    407 # Fit or load from cache the current transformer
-> 408 X, fitted_transformer = fit_transform_one_cached(
    409     cloned_transformer,
    410     X,
    411     y,
    412     None,
    413     message_clsname="Pipeline",
    414     message=self._log_message(step_idx),
    415     params=routed_params[name],
    416 )
    417 # Replace the transformer of the step with the fitted
    418 # transformer. This is necessary when loading the transformer
    419 # from the cache.
    420 self.steps[step_idx] = (name, fitted_transformer)

```

```

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\joblib\memory.py:353, in
↳ NotMemorizedFunc.__call__(self, *args, **kwargs)
    352 def __call__(self, *args, **kwargs):
--> 353     return self.func(*args, **kwargs)

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\pipeline.py:1303, in
↳ _fit_transform_one(transformer, X, y, weight, message_clsname, message, param)
    1301 with _print_elapsed_time(message_clsname, message):
    1302     if hasattr(transformer, "fit_transform"):
-> 1303         res = transformer.fit_transform(X, y, **params.
↳ get("fit_transform", {}))
    1304     else:
    1305         res = transformer.fit(X, y, **params.get("fit", {})).transform(
    1306             X, **params.get("transform", {}))
    1307         )

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\mlxtend\feature_selection\sequential_fea
↳ py:854, in SequentialFeatureSelector.fit_transform(self, X, y, groups,
↳ **fit_params)
    828 """Fit to training data then reduce X to its most important features.
    829
    830 Parameters
    (...)
    851
    852 """
    853 self.fit(X, y, groups=groups, **fit_params)
--> 854 return self.transform(X)

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\mlxtend\feature_selection\sequential_fea
↳ py:823, in SequentialFeatureSelector.transform(self, X)
    807 def transform(self, X):
    808     """Reduce X to its most important features.
    809
    810     Parameters
    (...)
    821
    822     """
--> 823     self._check_fitted()
    824     X_, _ = _preprocess(X)
    825     return X_[ :, self.k_feature_idx_]

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\mlxtend\feature_selection\sequential_fea
↳ py:898, in SequentialFeatureSelector._check_fitted(self)
    896 def _check_fitted(self):

```

```

897     if not self.fitted:
--> 898         raise AttributeError(
899             "SequentialFeatureSelector has not been " " fitted, yet."
900         )

```

**AttributeError:** SequentialFeatureSelector has not been fitted, yet.

```

[ ]: # Logistic Regression Pipeline, same procedure, just a different classifier
logreg_pipeline = Pipeline([
    ('preprocessor', preprocessor),
    ('feature_selector', SFS(LogisticRegression(random_state=42),
                             k_features=(5, 20),
                             forward=True,
                             floating=False,
                             scoring='f1_macro',
                             cv=5)),
    ('classifier', RandomizedSearchCV(LogisticRegression(random_state=42),
                                      {'C': loguniform(1e-4, 1e2), #getting the
↳best value for C
                                      'penalty': ['l1', 'l2']}, #finding out
↳which regularization works best
                                      n_iter=50,
                                      cv=5,
                                      scoring='f1_macro',
                                      random_state=42,
                                      n_jobs=-1))
])

logreg_pipeline.fit(X_train, y_train)

y_pred_lr = logreg_pipeline.predict(X_test)
f1_lr = f1_score(y_test, y_pred_lr, average='macro')
print("F1-Score (Macro):", f1_lr)

best_params_lr = logreg_pipeline.named_steps['classifier'].best_params_
print("Best Parameters:", best_params_lr)

#I made comments on the earlier pipeline

```

c:\Users\Kristian Røhne\anaconda3\envs\dat200\_env\lib\site-packages\sklearn\model\_selection\\_validation.py:73: FutureWarning: `fit\_params` is deprecated and will be removed in version 1.6. Pass parameters via `params` instead.

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c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-

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```

STOPPING EARLY DUE TO KEYBOARD INTERRUPT...

```

-----
AttributeError                                Traceback (most recent call last)
Cell In[93], line 20
      1 # Logistic Regression Pipeline, same procedure, just a different_
      ↪ classifier
      2 logreg_pipeline = Pipeline([
      3     ('preprocessor', preprocessor),
      4     ('feature_selector', SFS(LogisticRegression(random_state=42),
      (...))
      17                                     n_jobs=-1))
      18 ])
----> 20 logreg_pipeline.fit(X_train, y_train)
      22 y_pred_lr = logreg_pipeline.predict(X_test)
      23 f1_lr = f1_score(y_test, y_pred_lr, average='macro')

```

```

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\base.py:1351, in
↳ _fit_context.<locals>.decorator.<locals>.wrapper(estimator, *args, **kwargs)
    1344     estimator._validate_params()
    1346 with config_context(
    1347     skip_parameter_validation=(
    1348         prefer_skip_nested_validation or global_skip_validation
    1349     )
    1350 ):
-> 1351     return fit_method(estimator, *args, **kwargs)

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\pipeline.py:471, in
↳ Pipeline.fit(self, X, y, **params)
    428 """Fit the model.
    429
    430 Fit all the transformers one after the other and sequentially transform
↳ the
    (...)
    468     Pipeline with fitted steps.
    469 """
    470 routed_params = self._check_method_params(method="fit", props=params)
-> 471 Xt = self._fit(X, y, routed_params)
    472 with _print_elapsed_time("Pipeline", self._log_message(len(self.steps)
↳ 1)):
    473     if self._final_estimator != "passthrough":

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\pipeline.py:408, in
↳ Pipeline._fit(self, X, y, routed_params)
    406     cloned_transformer = clone(transformer)
    407 # Fit or load from cache the current transformer
-> 408 X, fitted_transformer = fit_transform_one_cached(
    409     cloned_transformer,
    410     X,
    411     y,
    412     None,
    413     message_clsname="Pipeline",
    414     message=self._log_message(step_idx),
    415     params=routed_params[name],
    416 )
    417 # Replace the transformer of the step with the fitted
    418 # transformer. This is necessary when loading the transformer
    419 # from the cache.
    420 self.steps[step_idx] = (name, fitted_transformer)

```

```

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\joblib\memory.py:353, in
↳ NotMemorizedFunc.__call__(self, *args, **kwargs)
    352 def __call__(self, *args, **kwargs):
--> 353     return self.func(*args, **kwargs)

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\sklearn\pipeline.py:1303, in
↳ _fit_transform_one(transformer, X, y, weight, message_clsname, message, param)
    1301 with _print_elapsed_time(message_clsname, message):
    1302     if hasattr(transformer, "fit_transform"):
-> 1303         res = transformer.fit_transform(X, y, **params.
↳ get("fit_transform", {}))
    1304     else:
    1305         res = transformer.fit(X, y, **params.get("fit", {})).transform(
    1306             X, **params.get("transform", {})
    1307         )

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\mlxtend\feature_selection\sequential_fea
↳ py:854, in SequentialFeatureSelector.fit_transform(self, X, y, groups,
↳ **fit_params)
    828 """Fit to training data then reduce X to its most important features.
    829
    830 Parameters
    (...)
    851
    852 """
    853 self.fit(X, y, groups=groups, **fit_params)
--> 854 return self.transform(X)

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\mlxtend\feature_selection\sequential_fea
↳ py:823, in SequentialFeatureSelector.transform(self, X)
    807 def transform(self, X):
    808     """Reduce X to its most important features.
    809
    810     Parameters
    (...)
    821
    822     """
--> 823     self._check_fitted()
    824     X_, _ = _preprocess(X)
    825     return X_[ :, self.k_feature_idx_]

File c:\Users\Kristian
↳ Røhne\anaconda3\envs\dat200_env\lib\site-packages\mlxtend\feature_selection\sequential_fea
↳ py:898, in SequentialFeatureSelector._check_fitted(self)
    896 def _check_fitted(self):

```

```

897         if not self.fitted:
--> 898             raise AttributeError(
899                 "SequentialFeatureSelector has not been " " fitted, yet."
900             )

```

**AttributeError:** SequentialFeatureSelector has not been fitted, yet.

## 0.5 Confusion matrix for the best pipeline

SVM-pipeline performed best! Now i'm making a confusion matrix for the best pipeline.

```

[ ]: #Splitting the dataset
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.4,
    ↪random_state=42)

# Fit the pipeline
svm_pipeline.fit(X_train, y_train)

# Predict on the test set
y_pred_full = svm_pipeline.predict(X_test)

# Calculate confusion matrix
cm = confusion_matrix(y_test, y_pred_full)

# Plot the confusion matrix
disp = ConfusionMatrixDisplay(confusion_matrix=cm)
disp.plot(cmap=plt.cm.Blues)
plt.title('Confusion Matrix')
plt.show()

```

```

c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\model_selection\_validation.py:73: FutureWarning: `fit_params`
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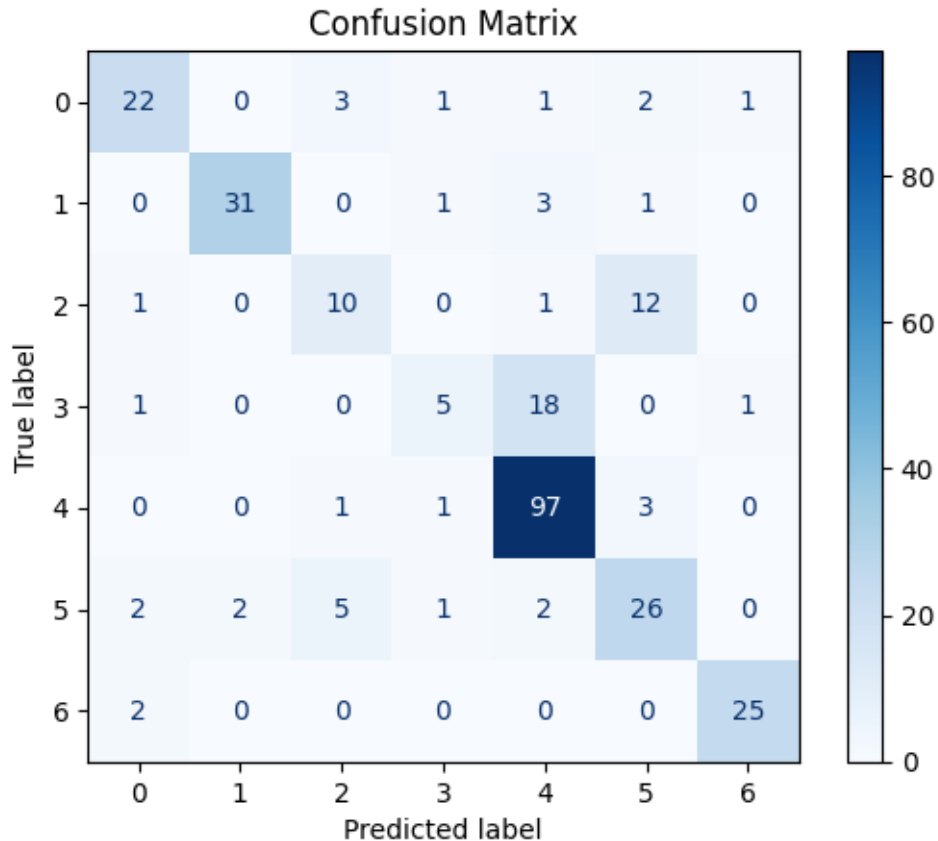
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```



```
[ ]: # Fit the svm-model with the whole dataset
svm_pipeline.fit(X, y)
```

```
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```
[ ]: Pipeline(steps=[('preprocessor',
                        ColumnTransformer(transformers=[('num', StandardScaler(),
                                                         Index(['AFP (ng/mL)', 'ALP
(U/L)', 'ALT (U/L)', 'AST (U/L)', 'Age',
'Albumin (g/dL)', 'Bilirubin (mg/dL)', 'CRP (mg/L)', 'Fibroscan (kPa)',
'GGT (U/L)', 'Hemoglobin (g/dL)', 'IL-6 (pg/mL)', 'PT/INR',
'Platelets (10^9/L)', 'RBC (10^12/L)', 'Serum_Ammonia (mol/L)',
'Serum_Copper (g/dL)', 'Seru...
0.09425809734513582,
0.14899223965207048,
0.44552817161009256,
0.020419819065547195,
0.09734896956908318,
0.005383367283785567,
0.172046627692541,
0.13345988175740695,
0.0015515010020265224,
0.14106608367836024,
0.027487288507156073,
0.013030507671881963,
0.04405125880001592,
0.25501221647094435,
0.1998244597487973,
0.027608676665662392]]),

                                random_state=42, scoring='f1_macro'))])
```

```
[ ]: #fit the logreg model with the whole dataset
logreg_pipeline.fit(X, y)
```

```
c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\model_selection\_validation.py:73: FutureWarning: `fit_params`
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c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\model_selection\_validation.py:542: FitFailedWarning:
90 fits failed out of a total of 250.
The score on these train-test partitions for these parameters will be set to
nan.
If these failures are not expected, you can try to debug them by setting
error_score='raise'.
```

Below are more details about the failures:

```
-----
90 fits failed with the following error:
Traceback (most recent call last):
  File "c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\model_selection\_validation.py", line 890, in _fit_and_score
    estimator.fit(X_train, y_train, **fit_params)
  File "c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\base.py", line 1351, in wrapper
    return fit_method(estimator, *args, **kwargs)
  File "c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\linear_model\_logistic.py", line 1172, in fit
    solver = _check_solver(self.solver, self.penalty, self.dual)
  File "c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\linear_model\_logistic.py", line 67, in _check_solver
    raise ValueError(
ValueError: Solver lbfgs supports only 'l2' or None penalties, got l1 penalty.
```

```
warnings.warn(some_fits_failed_message, FitFailedWarning)
c:\Users\Kristian Røhne\anaconda3\envs\dat200_env\lib\site-
packages\sklearn\model_selection\_search.py:1051: UserWarning: One or more of
the test scores are non-finite: [      nan 0.13594482      nan      nan
0.07495178 0.59305403
0.75261915 0.07495178 0.73918839 0.07495178 0.13594482      nan
      nan      nan 0.07495178      nan      nan 0.75827056
0.72754179      nan      nan 0.69765971 0.73502868 0.7429208
      nan 0.31935677      nan 0.75845532 0.07495178 0.66138413
0.75925009 0.68382221 0.73699938 0.07495178 0.74533009 0.66277111
0.74741578 0.57560511      nan      nan 0.6623792 0.73361218
0.62185705      nan      nan      nan 0.73502868 0.66277111
      nan 0.18758749]
warnings.warn(
```

```
[ ]: Pipeline(steps=[('preprocessor',
                      ColumnTransformer(transformers=[('num', StandardScaler(),
                                                    Index(['AFP (ng/mL)', 'ALP
(U/L)', 'ALT (U/L)', 'AST (U/L)', 'Age',
'Albumin (g/dL)', 'Bilirubin (mg/dL)', 'CRP (mg/L)', 'Fibroscan (kPa)',
'GGT (U/L)', 'Hemoglobin (g/dL)', 'IL-6 (pg/mL)', 'PT/INR',
```

```

        'Platelets (10^9/L)', 'RBC (10^12/L)', 'Serum_Ammonia (mol/L)',
        'Serum_Copper (g/dL)', 'Seru...
SequentialFeatureSelector(estimator=LogisticRegression(random_state=42),
                           k_features=(5, 20),
                           scoring='f1_macro')),

        ('classifier',
         RandomizedSearchCV(cv=5,
estimator=LogisticRegression(random_state=42),
                             n_iter=50, n_jobs=-1,
                             param_distributions={'C':
<scipy.stats._distn_infrastructure.rv_continuous_frozen object at
0x00000252B2533FA0>,

                                                'penalty': ['l1',
                                                         'l2']},
                             random_state=42, scoring='f1_macro'))))

```

## 0.6 Kaggle submission

```

[ ]: # Evaluate and save results
X_test = pd.read_csv("test.csv").drop(['index'], axis=1)
svm_predictions = svm_pipeline.predict(X_test)
# logreg_predictions = logreg_pipeline.predict(X_test)

# Save predictions to CSV files
pd.DataFrame({'index': X_test.index, 'Diagnosis': svm_predictions}).
    to_csv('svm_predictions.csv', index=False)
# pd.DataFrame({'index': X_test.index, 'Diagnosis': logreg_predictions}).
    to_csv('logreg_predictions.csv', index=False)

```

## 0.7 Seperate part of task

```

[ ]: # Load data again, so the dataset is right every time i run this box
df = pd.read_csv("train.csv", index_col=0)
df = df.drop(['index'], axis=1)

# Replace negative values with zero for specified columns
for column in ['AFP (ng/mL)', 'ALT (U/L)', 'AST (U/L)']:
    df[column] = df[column].apply(lambda x: max(x, 0))

#Creating Condition binary
df['ConditionBinary'] = df['Diagnosis'].apply(lambda x: 0 if x == 'Healthy'
    else 1) #Will be 0 if healthy and 1 if sick
df = df.drop(['Diagnosis'], axis=1)

# Separate features and target
X = df.drop('ConditionBinary', axis=1)
y = df['ConditionBinary']

```

```

# Initializes Stratified K-Fold cross-validator with 5 folds
skf = StratifiedKFold(n_splits=5, shuffle=True, random_state=42)

# Set up pipeline
pipe_lr = make_pipeline(preprocessor,
                        LogisticRegression(penalty='l2', random_state=42))

# Obtain predicted probabilities using cross-validation
y_probas = cross_val_predict(pipe_lr, X, y, cv=skf, method='predict_proba')

# Compute ROC AUC scores directly during cross-validation
auc_scores = cross_val_score(pipe_lr, X, y, cv=skf, scoring='roc_auc')

# Compute mean and standard deviation of the AUC scores
mean_auc = np.mean(auc_scores)
std_auc = np.std(auc_scores)

# Calculate ROC curve
fpr, tpr, thresholds = roc_curve(y, y_probas[:, 1])

# Plot ROC Curve
plt.figure(figsize=(8, 6))
plt.plot(fpr, tpr, color='blue', label=f'Mean ROC (AUC = {mean_auc:.2f} ± {std_auc:.2f})')
plt.plot([0, 1], [0, 1], linestyle='--', lw=2, color='red', label='Chance', alpha=.8)
plt.xlim([-0.05, 1.05])
plt.ylim([-0.05, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic')
plt.legend(loc="lower right")
plt.show()

```

