

Heart Failure Prediction

June 12, 2024

```
[3]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

```
[4]: %matplotlib inline
```

```
[5]: from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
```

```
[86]: from sklearn.model_selection import train_test_split, cross_val_score
from sklearn.model_selection import RandomizedSearchCV, GridSearchCV
from sklearn.metrics import confusion_matrix, classification_report
from sklearn.metrics import precision_score, recall_score, f1_score
from sklearn.metrics import RocCurveDisplay
```

```
[11]: df = pd.read_csv("heart_failure_clinical_records_dataset.csv")
df.shape
```

```
[11]: (299, 13)
```

```
[12]: df.head()
```

```
[12]:
```

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	\
0	75.0	0	582	0	20	
1	55.0	0	7861	0	38	
2	65.0	0	146	0	20	
3	50.0	1	111	0	20	
4	65.0	1	160	1	20	

	high_blood_pressure	platelets	serum_creatinine	serum_sodium	sex	\
0	1	265000.00	1.9	130	1	
1	0	263358.03	1.1	136	1	
2	0	162000.00	1.3	129	1	
3	0	210000.00	1.9	137	1	
4	0	327000.00	2.7	116	0	

	smoking	time	DEATH_EVENT
--	---------	------	-------------

0	0	4	1
1	0	6	1
2	1	7	1
3	0	7	1
4	0	8	1

```
[13]: df.tail()
```

```
[13]:
```

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	\
294	62.0	0	61	1	38	
295	55.0	0	1820	0	38	
296	45.0	0	2060	1	60	
297	45.0	0	2413	0	38	
298	50.0	0	196	0	45	

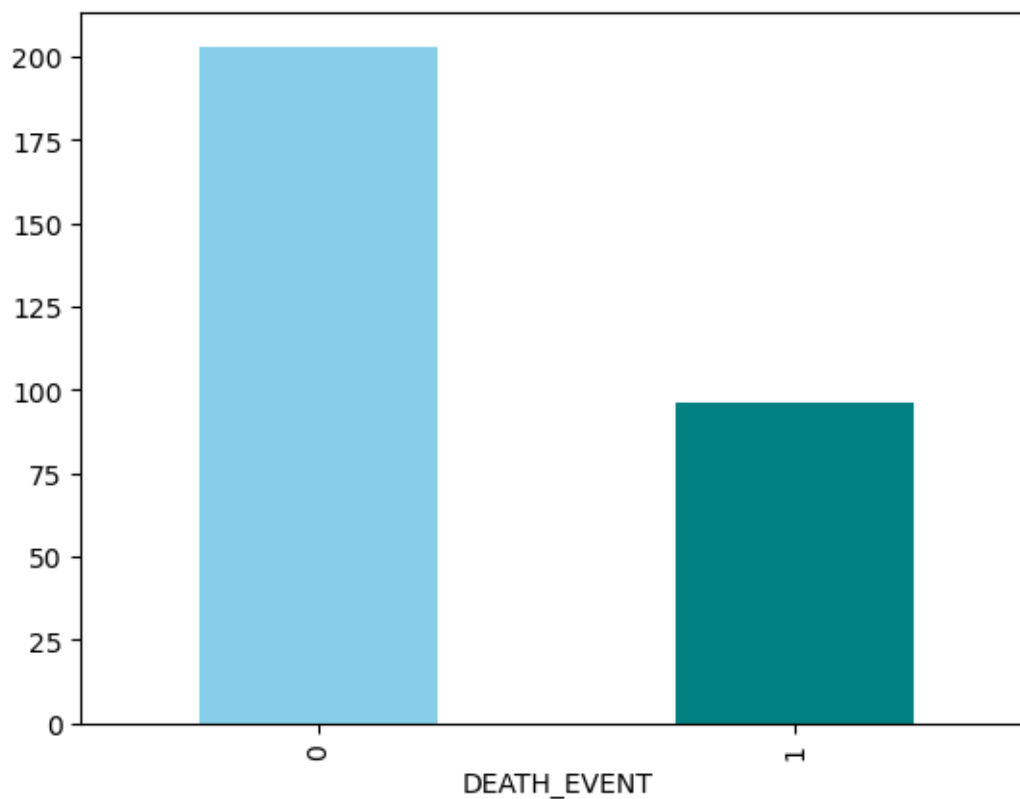
	high_blood_pressure	platelets	serum_creatinine	serum_sodium	sex	\
294	1	155000.0	1.1	143	1	
295	0	270000.0	1.2	139	0	
296	0	742000.0	0.8	138	0	
297	0	140000.0	1.4	140	1	
298	0	395000.0	1.6	136	1	

	smoking	time	DEATH_EVENT
294	1	270	0
295	0	271	0
296	0	278	0
297	1	280	0
298	1	285	0

```
[14]: df['DEATH_EVENT'].value_counts()
```

```
[14]: DEATH_EVENT
0    203
1     96
Name: count, dtype: int64
```

```
[19]: df["DEATH_EVENT"].value_counts().plot(kind="bar", color=["skyblue", "teal"]);
```



```
[20]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 299 entries, 0 to 298
Data columns (total 13 columns):
#   Column                                Non-Null Count  Dtype
---  -
0   age                                   299 non-null    float64
1   anaemia                              299 non-null    int64
2   creatinine_phosphokinase             299 non-null    int64
3   diabetes                             299 non-null    int64
4   ejection_fraction                    299 non-null    int64
5   high_blood_pressure                  299 non-null    int64
6   platelets                            299 non-null    float64
7   serum_creatinine                     299 non-null    float64
8   serum_sodium                         299 non-null    int64
9   sex                                  299 non-null    int64
10  smoking                              299 non-null    int64
11  time                                 299 non-null    int64
12  DEATH_EVENT                          299 non-null    int64
dtypes: float64(3), int64(10)
memory usage: 30.5 KB
```

```
[21]: df.isna().sum()
```

```
[21]: age                0
      anaemia           0
      creatinine_phosphokinase  0
      diabetes          0
      ejection_fraction  0
      high_blood_pressure  0
      platelets          0
      serum_creatinine    0
      serum_sodium        0
      sex                 0
      smoking             0
      time                0
      DEATH_EVENT         0
      dtype: int64
```

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

```
[22]:
```

	age	anaemia	creatinine_phosphokinase	diabetes	\
count	299.000000	299.000000	299.000000	299.000000	
mean	60.833893	0.431438	581.839465	0.418060	
std	11.894809	0.496107	970.287881	0.494067	
min	40.000000	0.000000	23.000000	0.000000	
25%	51.000000	0.000000	116.500000	0.000000	
50%	60.000000	0.000000	250.000000	0.000000	
75%	70.000000	1.000000	582.000000	1.000000	
max	95.000000	1.000000	7861.000000	1.000000	

	ejection_fraction	high_blood_pressure	platelets	\
count	299.000000	299.000000	299.000000	
mean	38.083612	0.351171	263358.029264	
std	11.834841	0.478136	97804.236869	
min	14.000000	0.000000	25100.000000	
25%	30.000000	0.000000	212500.000000	
50%	38.000000	0.000000	262000.000000	
75%	45.000000	1.000000	303500.000000	
max	80.000000	1.000000	850000.000000	

	serum_creatinine	serum_sodium	sex	smoking	time	\
count	299.00000	299.000000	299.000000	299.00000	299.000000	
mean	1.39388	136.625418	0.648829	0.32107	130.260870	
std	1.03451	4.412477	0.478136	0.46767	77.614208	
min	0.50000	113.000000	0.000000	0.00000	4.000000	
25%	0.90000	134.000000	0.000000	0.00000	73.000000	
50%	1.10000	137.000000	1.000000	0.00000	115.000000	
75%	1.40000	140.000000	1.000000	1.00000	203.000000	

```
max          9.40000    148.000000    1.000000    1.00000    285.000000
```

```
      DEATH_EVENT
count    299.00000
mean      0.32107
std       0.46767
min       0.00000
25%       0.00000
50%       0.00000
75%       1.00000
max       1.00000
```

```
[23]: df.diabetes.value_counts()
```

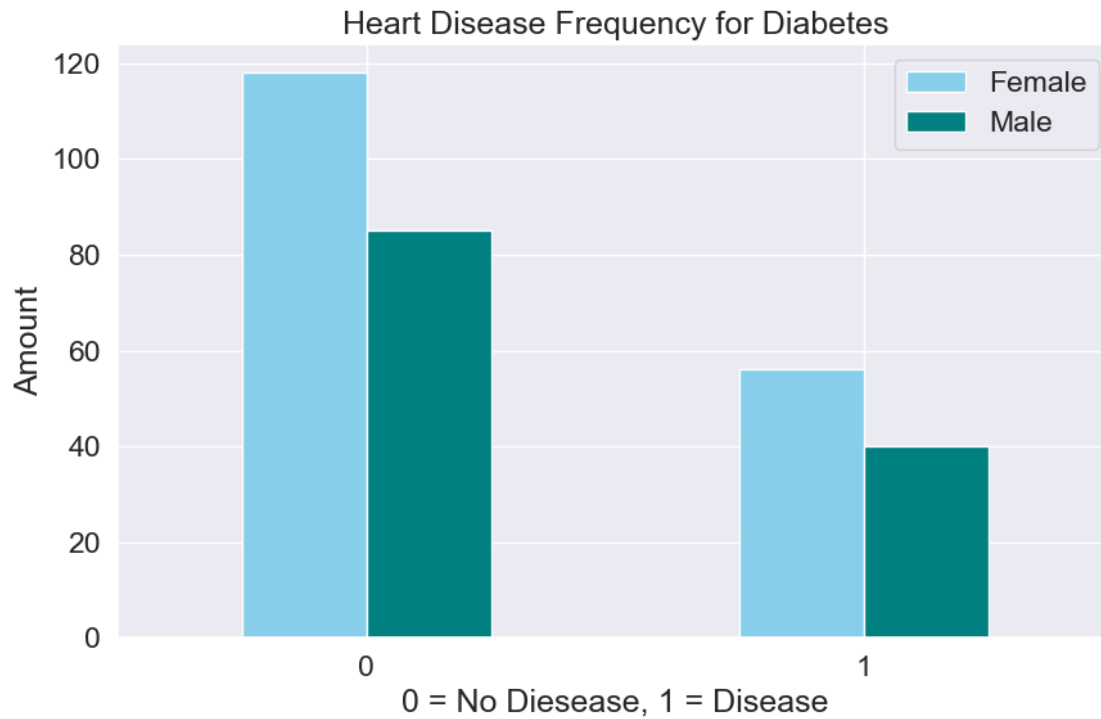
```
[23]: diabetes
0     174
1     125
Name: count, dtype: int64
```

```
[24]: pd.crosstab(df.DEATH_EVENT, df.diabetes)
```

```
[24]: diabetes      0      1
DEATH_EVENT
0         118    85
1         56    40
```

```
[109]: pd.crosstab(df.DEATH_EVENT, df.diabetes).plot(kind="bar",
                                                    figsize=(10, 6),
                                                    color=["skyblue", "teal"])

plt.title("Heart Disease Frequency for Diabetes")
plt.xlabel("0 = No Disease, 1 = Disease")
plt.ylabel("Amount")
plt.legend(["Female", "Male"]);
plt.xticks(rotation=0);
```

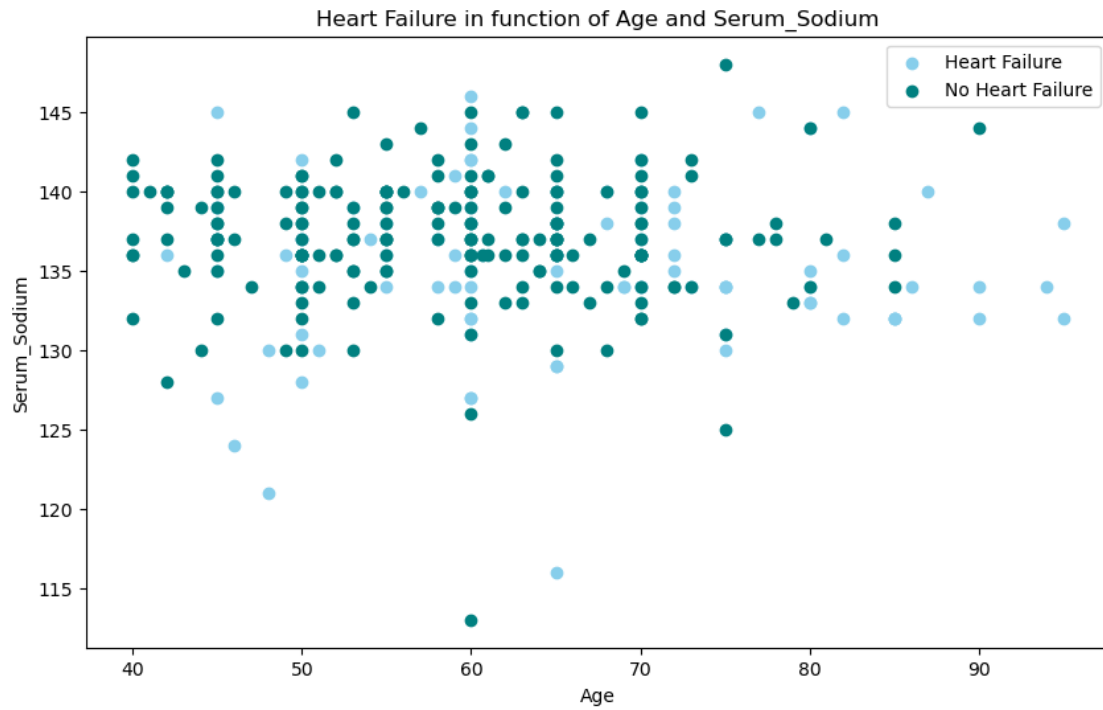


```
[30]: plt.figure(figsize=(10, 6))

plt.scatter(df.age[df.DEATH_EVENT==1],
            df.serum_sodium[df.DEATH_EVENT==1],
            c="skyblue")

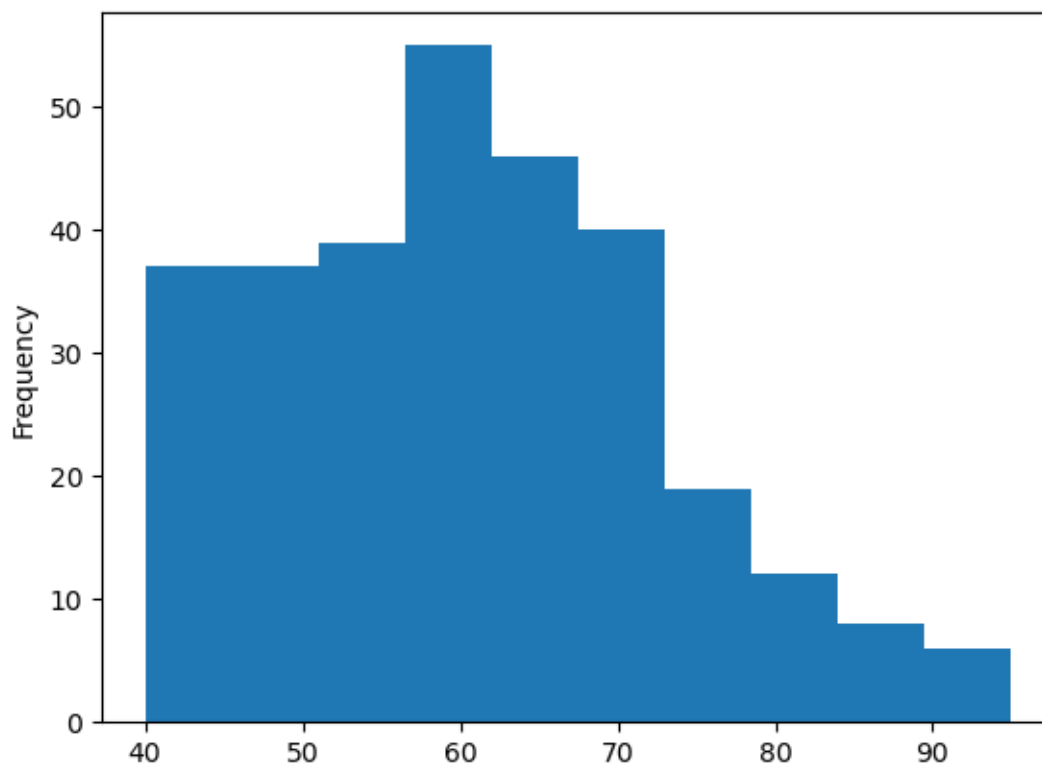
plt.scatter(df.age[df.DEATH_EVENT==0],
            df.serum_sodium[df.DEATH_EVENT==0],
            c="teal")

plt.title("Heart Failure in function of Age and Serum_Sodium")
plt.xlabel("Age")
plt.ylabel("Serum_Sodium")
plt.legend(["Heart Failure", "No Heart Failure"]);
```



```
[36]: df.age.plot.hist()
```

```
[36]: <Axes: ylabel='Frequency'>
```



```
[42]: df.corr()
```

```
[42]:
```

	age	anaemia	creatinine_phosphokinase \
age	1.000000	0.088006	-0.081584
anaemia	0.088006	1.000000	-0.190741
creatinine_phosphokinase	-0.081584	-0.190741	1.000000
diabetes	-0.101012	-0.012729	-0.009639
ejection_fraction	0.060098	0.031557	-0.044080
high_blood_pressure	0.093289	0.038182	-0.070590
platelets	-0.052354	-0.043786	0.024463
serum_creatinine	0.159187	0.052174	-0.016408
serum_sodium	-0.045966	0.041882	0.059550
sex	0.065430	-0.094769	0.079791
smoking	0.018668	-0.107290	0.002421
time	-0.224068	-0.141414	-0.009346
DEATH_EVENT	0.253729	0.066270	0.062728

	diabetes	ejection_fraction	high_blood_pressure \
age	-0.101012	0.060098	0.093289
anaemia	-0.012729	0.031557	0.038182
creatinine_phosphokinase	-0.009639	-0.044080	-0.070590
diabetes	1.000000	-0.004850	-0.012732

ejection_fraction	-0.004850	1.000000	0.024445
high_blood_pressure	-0.012732	0.024445	1.000000
platelets	0.092193	0.072177	0.049963
serum_creatinine	-0.046975	-0.011302	-0.004935
serum_sodium	-0.089551	0.175902	0.037109
sex	-0.157730	-0.148386	-0.104615
smoking	-0.147173	-0.067315	-0.055711
time	0.033726	0.041729	-0.196439
DEATH_EVENT	-0.001943	-0.268603	0.079351

	platelets	serum_creatinine	serum_sodium	sex \
age	-0.052354	0.159187	-0.045966	0.065430
anaemia	-0.043786	0.052174	0.041882	-0.094769
creatinine_phosphokinase	0.024463	-0.016408	0.059550	0.079791
diabetes	0.092193	-0.046975	-0.089551	-0.157730
ejection_fraction	0.072177	-0.011302	0.175902	-0.148386
high_blood_pressure	0.049963	-0.004935	0.037109	-0.104615
platelets	1.000000	-0.041198	0.062125	-0.125120
serum_creatinine	-0.041198	1.000000	-0.189095	0.006970
serum_sodium	0.062125	-0.189095	1.000000	-0.027566
sex	-0.125120	0.006970	-0.027566	1.000000
smoking	0.028234	-0.027414	0.004813	0.445892
time	0.010514	-0.149315	0.087640	-0.015608
DEATH_EVENT	-0.049139	0.294278	-0.195204	-0.004316

	smoking	time	DEATH_EVENT
age	0.018668	-0.224068	0.253729
anaemia	-0.107290	-0.141414	0.066270
creatinine_phosphokinase	0.002421	-0.009346	0.062728
diabetes	-0.147173	0.033726	-0.001943
ejection_fraction	-0.067315	0.041729	-0.268603
high_blood_pressure	-0.055711	-0.196439	0.079351
platelets	0.028234	0.010514	-0.049139
serum_creatinine	-0.027414	-0.149315	0.294278
serum_sodium	0.004813	0.087640	-0.195204
sex	0.445892	-0.015608	-0.004316
smoking	1.000000	-0.022839	-0.012623
time	-0.022839	1.000000	-0.526964
DEATH_EVENT	-0.012623	-0.526964	1.000000

```
[44]: corr_matrix = df.corr()
fig, ax = plt.subplots(figsize=(15, 10))
ax = sns.heatmap(corr_matrix,
                  annot=True,
                  linewidths=0.5,
                  fmt=".2f",
                  cmap="YlGnBu");
```

```
bottom, top = ax.get_ylim()
ax.set_ylim(bottom + 0.5, top)
```

[44]: (13.5, 0.0)



```
[56]: X = df.drop("DEATH_EVENT", axis=1)
      y = df["DEATH_EVENT"]
```

[57]: X

```
[57]:
```

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	\
0	75.0	0	582	0	20	
1	55.0	0	7861	0	38	
2	65.0	0	146	0	20	
3	50.0	1	111	0	20	
4	65.0	1	160	1	20	
..	
294	62.0	0	61	1	38	
295	55.0	0	1820	0	38	

296	45.0	0	2060	1	60
297	45.0	0	2413	0	38
298	50.0	0	196	0	45

	high_blood_pressure	platelets	serum_creatinine	serum_sodium	sex	\
0	1	265000.00	1.9	130	1	
1	0	263358.03	1.1	136	1	
2	0	162000.00	1.3	129	1	
3	0	210000.00	1.9	137	1	
4	0	327000.00	2.7	116	0	
...	
294	1	155000.00	1.1	143	1	
295	0	270000.00	1.2	139	0	
296	0	742000.00	0.8	138	0	
297	0	140000.00	1.4	140	1	
298	0	395000.00	1.6	136	1	

	smoking	time
0	0	4
1	0	6
2	1	7
3	0	7
4	0	8
...
294	1	270
295	0	271
296	0	278
297	1	280
298	1	285

[299 rows x 12 columns]

[48]: y

[48]:

0	1
1	1
2	1
3	1
4	1
...	
294	0
295	0
296	0
297	0
298	0

Name: DEATH_EVENT, Length: 299, dtype: int64

```
[54]: np.random.seed(42)
```

```
X_train, X_test, y_train, y_test = train_test_split(X,  
                                                    y,  
                                                    test_size=0.2)
```

```
[55]: X_train
```

```
[55]:
```

	age	anaemia	creatinine_phosphokinase	diabetes	ejection_fraction	\
6	75.000	1	246	0		15
183	75.000	0	99	0		38
185	60.667	1	104	1		30
146	52.000	0	132	0		30
30	94.000	0	582	1		38
..
188	60.667	1	151	1		40
71	58.000	0	582	1		35
106	55.000	0	748	0		45
270	44.000	0	582	1		30
102	80.000	0	898	0		25

	high_blood_pressure	platelets	serum_creatinine	serum_sodium	sex	\
6	0	127000.00	1.20	137	1	
183	1	224000.00	2.50	134	1	
185	0	389000.00	1.50	136	1	
146	0	218000.00	0.70	136	1	
30	1	263358.03	1.83	134	1	
..
188	1	201000.00	1.00	136	0	
71	0	122000.00	0.90	139	1	
106	0	263000.00	1.30	137	1	
270	1	263358.03	1.60	130	1	
102	0	149000.00	1.10	144	1	

	smoking	time
6	0	10
183	0	162
185	0	171
146	1	112
30	0	27
..
188	0	172
71	1	71
106	0	88
270	1	244
102	1	87

[239 rows x 12 columns]

```
[58]: y_train
```

```
[58]: 6      1
      183   1
      185   1
      146   0
      30    1
      ..
      188   0
      71    0
      106   0
      270   0
      102   0
      Name: DEATH_EVENT, Length: 239, dtype: int64
```

```
[65]: models = {"Logistic Regression": LogisticRegression(),
               "Random Forest": RandomForestClassifier()}

def fit_and_score(models, X_train, X_test, y_train, y_test):

    np.random.seed(42)

    model_scores = {}

    for name, model in models.items():
        model.fit(X_train, y_train)
        model_scores[name] = model.score(X_test, y_test)

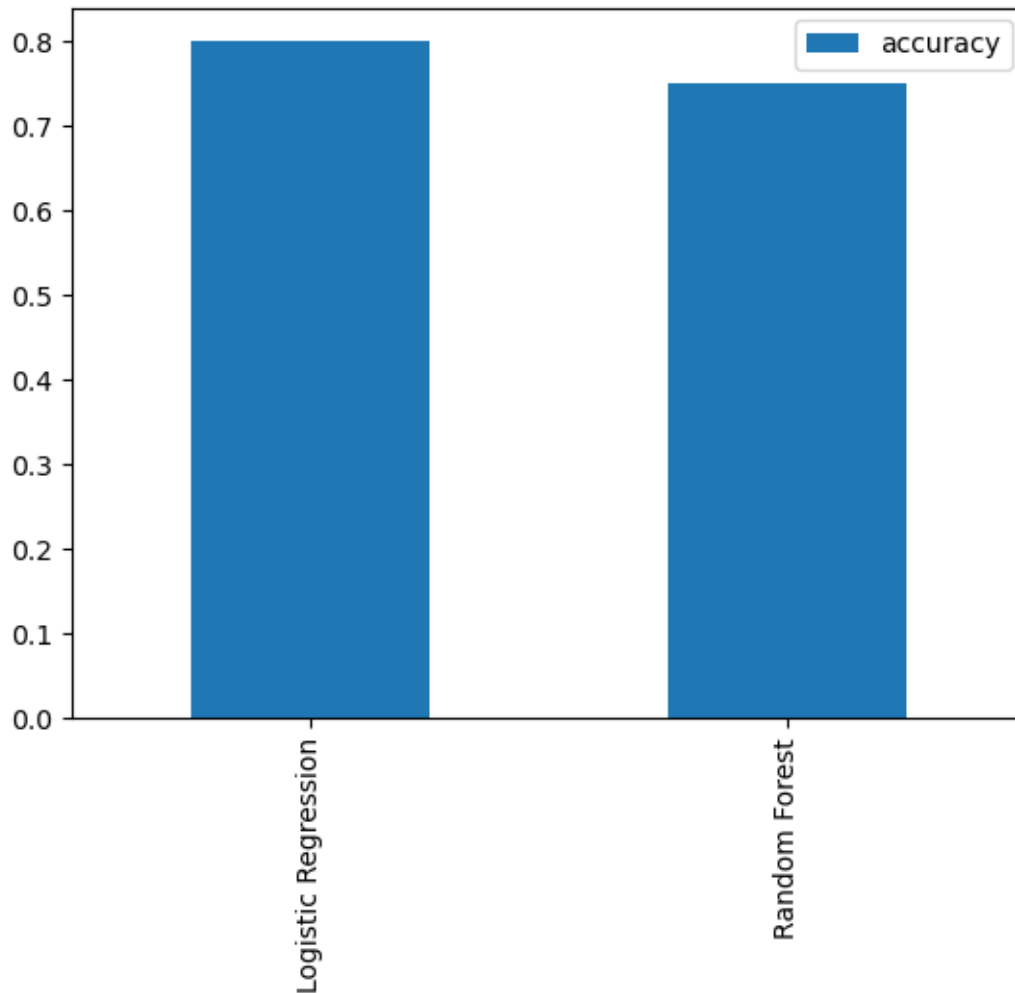
    return model_scores
```

```
[66]: model_scores = fit_and_score(models=models,
                                   X_train=X_train,
                                   X_test=X_test,
                                   y_train=y_train,
                                   y_test=y_test)

model_scores
```

```
[66]: {'Logistic Regression': 0.8, 'Random Forest': 0.75}
```

```
[67]: model_compare = pd.DataFrame(model_scores, index=["accuracy"])
      model_compare.T.plot.bar();
```



```
[68]: log_reg_grid = {"C": np.logspace(-4, 4, 20),  
                    "solver": ["liblinear"]}  
  
rf_grid = {"n_estimators": np.arange(10, 1000, 50),  
          "max_depth": [None, 3, 5, 10],  
          "min_samples_split": np.arange(2, 20, 2),  
          "min_samples_leaf": np.arange(1, 20, 2)}  
  
[69]: np.random.seed(42)  
  
rs_log_reg = RandomizedSearchCV(LogisticRegression(),  
                                param_distributions=log_reg_grid,  
                                cv=5,  
                                n_iter=20,  
                                verbose=True)
```

```
rs_log_reg.fit(X_train, y_train)
```

Fitting 5 folds for each of 20 candidates, totalling 100 fits

```
[69]: RandomizedSearchCV(cv=5, estimator=LogisticRegression(), n_iter=20,
      param_distributions={'C': array([1.00000000e-04,
      2.63665090e-04, 6.95192796e-04, 1.83298071e-03,
      4.83293024e-03, 1.27427499e-02, 3.35981829e-02, 8.85866790e-02,
      2.33572147e-01, 6.15848211e-01, 1.62377674e+00, 4.28133240e+00,
      1.12883789e+01, 2.97635144e+01, 7.84759970e+01, 2.06913808e+02,
      5.45559478e+02, 1.43844989e+03, 3.79269019e+03, 1.00000000e+04])},
      'solver': ['liblinear']},
      verbose=True)
```

```
[70]: rs_log_reg.best_params_
```

```
[70]: {'solver': 'liblinear', 'C': 0.08858667904100823}
```

```
[71]: rs_log_reg.score(X_test, y_test)
```

```
[71]: 0.75
```

```
[72]: np.random.seed(42)
```

```
rs_rf = RandomizedSearchCV(RandomForestClassifier(),
      param_distributions=rf_grid,
      cv=5,
      n_iter=20,
      verbose=True)

rs_rf.fit(X_train, y_train)
```

Fitting 5 folds for each of 20 candidates, totalling 100 fits

```
[72]: RandomizedSearchCV(cv=5, estimator=RandomForestClassifier(), n_iter=20,
      param_distributions={'max_depth': [None, 3, 5, 10],
      'min_samples_leaf': array([ 1,  3,  5,
      7,  9, 11, 13, 15, 17, 19])},
      'min_samples_split': array([ 2,  4,  6,
      8, 10, 12, 14, 16, 18])},
      'n_estimators': array([ 10,  60, 110,
      160, 210, 260, 310, 360, 410, 460, 510, 560, 610,
      660, 710, 760, 810, 860, 910, 960])},
      verbose=True)
```

```
[74]: rs_rf.best_params_
```

```
[74]: {'n_estimators': 260,  
      'min_samples_split': 16,  
      'min_samples_leaf': 9,  
      'max_depth': 10}
```

```
[75]: rs_rf.score(X_test, y_test)
```

```
[75]: 0.75
```

```
[77]: log_reg_grid = {"C": np.logspace(-4, 4, 30),  
                    "solver": ["liblinear"]}  
  
gs_log_reg = GridSearchCV(LogisticRegression(),  
                          param_grid=log_reg_grid,  
                          cv=5,  
                          verbose=True)  
  
gs_log_reg.fit(X_train, y_train);
```

Fitting 5 folds for each of 30 candidates, totalling 150 fits

```
[79]: gs_log_reg.best_params_
```

```
[79]: {'C': 0.008531678524172805, 'solver': 'liblinear'}
```

```
[80]: gs_log_reg.score(X_test, y_test)
```

```
[80]: 0.75
```

```
[82]: y_preds = gs_log_reg.predict(X_test)  
y_preds
```

```
[82]: array([0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 0, 0, 0,  
        0, 1, 1, 0, 0, 0, 0, 0, 1, 0, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0,  
        0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1], dtype=int64)
```

```
[96]: print(confusion_matrix(y_test, y_preds))
```

```
[[33  2]  
 [13 12]]
```

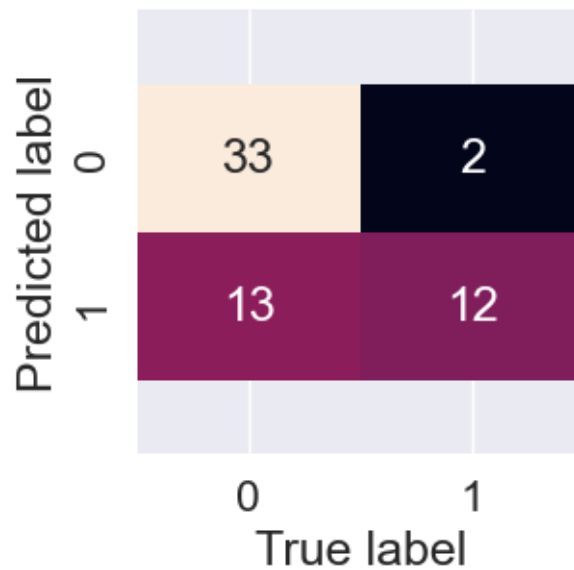
```
[97]: sns.set(font_scale=1.5)  
  
def plot_conf_mat(y_test, y_preds):  
  
    fig, ax = plt.subplots(figsize=(3, 3))  
    ax = sns.heatmap(confusion_matrix(y_test, y_preds),  
                    annot=True,  
                    cbar=False)
```



```
plt.xlabel("True label")
plt.ylabel("Predicted label")

bottom, top = ax.get_ylim()
ax.set_ylim(bottom + 0.5, top - 0.5)

plot_conf_mat(y_test, y_preds)
```



```
[98]: print(classification_report(y_test, y_preds))
```

	precision	recall	f1-score	support
0	0.72	0.94	0.81	35
1	0.86	0.48	0.62	25
accuracy			0.75	60
macro avg	0.79	0.71	0.72	60
weighted avg	0.78	0.75	0.73	60

```
[100]: clf = LogisticRegression(C=0.008531678524172805,
                                solver="liblinear")
```

```
[110]: cv_acc = cross_val_score(clf,
                                X,
                                y,
                                cv=5,
                                scoring="accuracy")
```

```

cv_acc = np.mean(cv_acc)
cv_acc

cv_precision = cross_val_score(clf,
                                X,
                                y,
                                cv=5,
                                scoring="precision")
cv_precision=np.mean(cv_precision)
cv_precision

cv_recall = cross_val_score(clf,
                             X,
                             y,
                             cv=5,
                             scoring="recall")
cv_recall = np.mean(cv_recall)
cv_recall

cv_f1 = cross_val_score(clf,
                        X,
                        y,
                        cv=5,
                        scoring="f1")
cv_f1 = np.mean(cv_f1)
cv_f1

cv_metrics = pd.DataFrame({"Accuracy": cv_acc,
                           "Precision": cv_precision,
                           "Recall": cv_recall,
                           "F1": cv_f1},
                           index=[0])

cv_metrics.T.plot.bar(title="Cross-validated classification metrics",
                      legend=False);

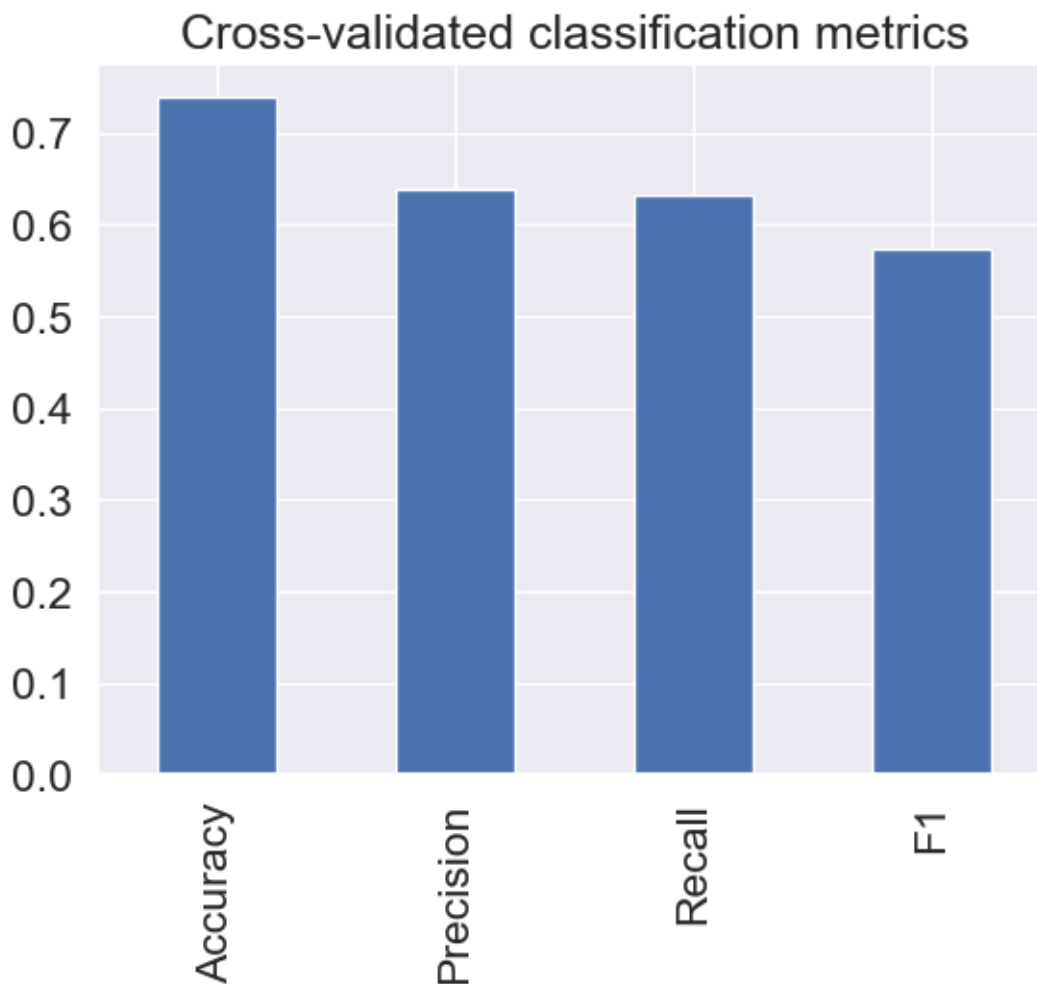
```

C:\Users\vidus\anaconda3.1\Lib\site-packages\sklearn\metrics_classification.py:1469: UndefinedMetricWarning: Precision is ill-defined and being set to 0.0 due to no predicted samples. Use `zero_division` parameter to control this behavior.

```

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

```



```
[111]: clf = LogisticRegression(C=0.008531678524172805,  
                                solver="liblinear")
```

```
clf.fit(X_train, y_train);
```

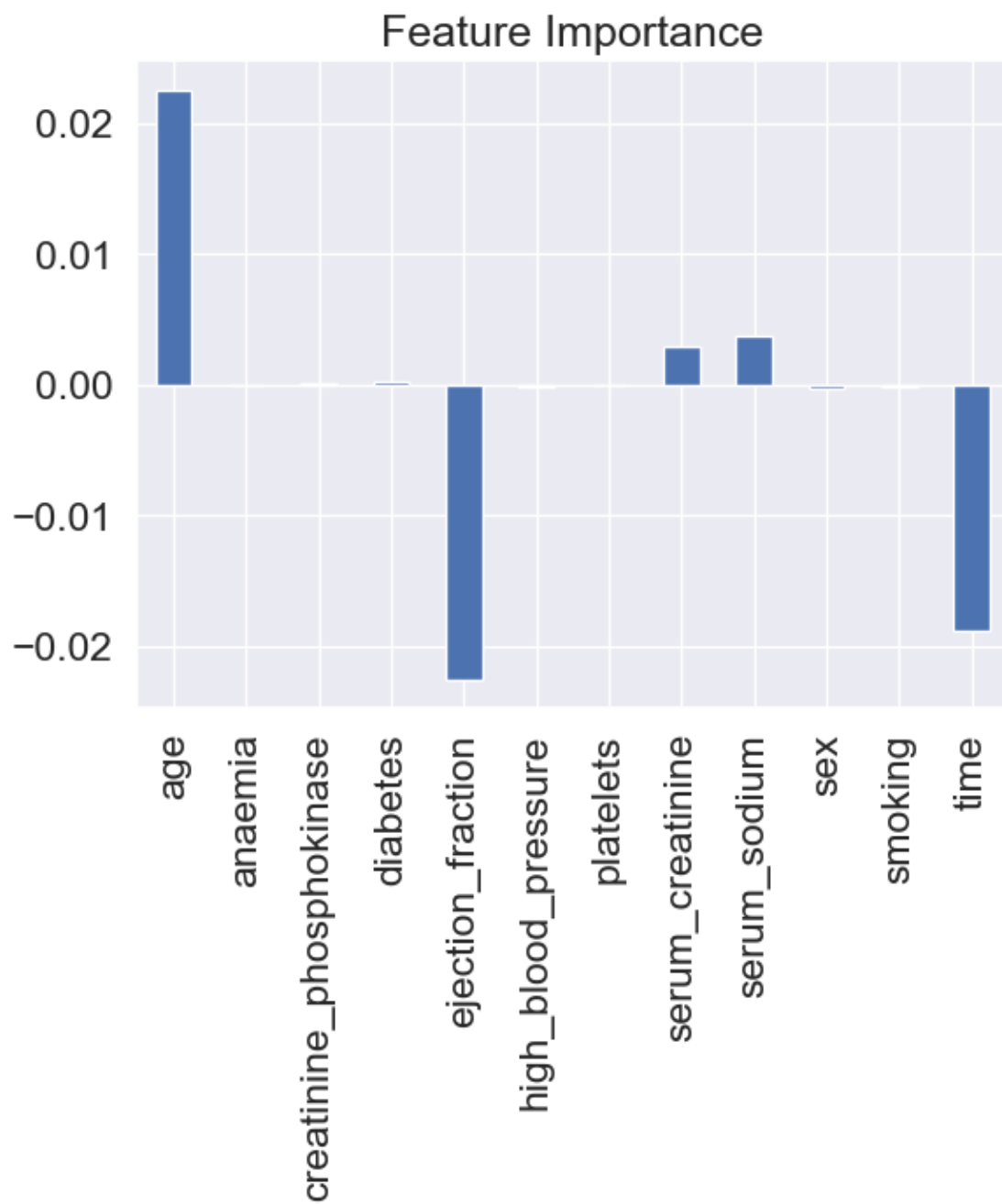
```
[106]: clf.coef_
```

```
[106]: array([[ 2.25664095e-02, -1.32373957e-05,  1.11736658e-04,  
              2.12224031e-04, -2.25512363e-02, -1.64240711e-04,  
              1.44950743e-07,  2.93717113e-03,  3.74278962e-03,  
             -2.93417830e-04, -1.29592144e-04, -1.87936576e-02]])
```

```
[107]: feature_dict = dict(zip(df.columns, list(clf.coef_[0])))  
feature_dict
```

```
[107]: {'age': 0.02256640949058526,  
        'anaemia': -1.3237395694908342e-05,  
        'creatinine_phosphokinase': 0.0001117366583958865,  
        'diabetes': 0.00021222403098543558,  
        'ejection_fraction': -0.0225512363385351,  
        'high_blood_pressure': -0.00016424071054663595,  
        'platelets': 1.4495074316257639e-07,  
        'serum_creatinine': 0.0029371711289282337,  
        'serum_sodium': 0.0037427896151338,  
        'sex': -0.00029341783017448317,  
        'smoking': -0.0001295921442812619,  
        'time': -0.018793657590705382}
```

```
[108]: feature_df = pd.DataFrame(feature_dict, index=[0])  
feature_df.T.plot.bar(title="Feature Importance", legend=False);
```



[]: