		ty of the BBDD ty of inputs X ty of inputs Y	(299, 11)						
	anaemia creatinine_ph diabetes ejection_frac high_blood_pr platelets serum_creatin serum_sodium sex smoking time DEATH_EVENT	ction ressure nine	int64 int64 int64 int64 int64 float64 float64 int64 int64 int64						
:[3]:			582 7861 146 111 160	tes ejection_ 0 0 0 1	fraction high_blood_ 20 38 20 20 20	pressure plat	0.000 8.030 0.000 0.000	1.900 1.100 1.300 1.900 2.700	um_
	the following info .Age:Floa .anemia:I .creatini .diabetes	rmation: t indicating t nteger indicat ne_phosphokina :Integer to ir	the person's a ting whether o ase:Integer to ndicate whethe	ge. r not the indicate r or not y	person has anem the amount of cou have diabete or not you have	nia. Ereatine phos			clud
	<pre>.high_blo .platelet .Serum_cr .Serum_so .sex:Inte .Smoking: .Time:Int</pre>	od_pressure:Ir s:Float to ind eatinine:Float dium:Integer t ger to indicat Integer to ind eger that indi	nteger to indidicate the number indicating to that indicates the if you are dicated if you icates the time.	cate wheth ber of pla he amount the amoun a man or a smoke or n e of follo	er or not you hatelets. of serum creating to f serum soding woman.	nave diabetes ne. .um.		d.	
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	min 40.000 25% 51.000 50% 60.000 75% 70.000 max 95.000 Now that we hav	0.000 0.000 0.000 1.000 1.000	23.000 116.500 250.000 582.000 7861.000	0.000 0.000 0.000 1.000 1.000	14.000 30.000 38.000 45.000 80.000 the target, that is to s	0.000 2 1.000 3 1.000 8	25100.000 212500.000 262000.000 303500.000 350000.000	0.500 0.900 1.100 1.400 9.400 the amount of nu)))
[5]:	<pre>nulls = data: n_categories print("The of print("The of)</pre> The quantity	set['DEATH_EVE = dataset['DE quantity of nu		.sum() unique() ls)					
[6]:	<pre>dataset['DEA' f, ax = plt.: ax = sns.cour plt.show()</pre>	TH_EVENT'].val subplots(figsi ntplot(y="DEAT	ue_counts() ze=(8, 4))	a=dataset,	palette="Set1" t))*100				
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	DEATH_EVENT	25	50 75	100	125 15	50 1 7 5	200		
:[6]:	0 67.893 1 32.107 Name: DEATH_E	EVENT, dtype: 67.89% of the peop	float64	cou				ext we will observ	ve t
[7]:	heatmap = sn: min=-1, vmax	=1, annot= True	aset.corr()[["I e, cmap='BrBG'])	T"]].sort_value size':17}, pad=		EVENT", a	ascending= Fal	Lse
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	e_phosphokinase - diabetes - sex -			-0.0019 -0.0043				- 0.00	
	smoking - platelets - serum_sodium -			-0.013 -0.049				0.25 0.50	
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	diabetes ejection_frace high_blood_preplatelets serum_creatine serum_sodium sex smoking time DEATH_EVENT	ction ressure	0 0 0 0 0 0 0						
[9]:	As we can see in very different ran ranks. Thanks to	ges. In this case we this process, what	e no nulls in the da ve will use the mea t we achieve is to e	n normalization	ve are going to normation, since it is the mosoroll and the numer	st appropriate fo ical difference of	r cases with the data.	n different numer	ica
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[13]: [13]: [16]:	The first thing we into account five into accoun	ection Phave to do is to so models which are: regression ors Tree orest Tree orest mese five into account we have database. That is signer precision account we have databased and	unt because in this re to select one and why we are going to re, since the data is nodels, what we ha ze']=15,6 -1] -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1	ve can consider the consideration of the consideration of the construction of the cons	dealing with a super we are going to comm deet the time/precipit favor of the negal see what are the more well use to the see what are the more well use to the see will use to the see will use to the see will use to the see well use the see well use to the see well use the see well use the see well use to	dels. ut the classification ratio they provide them accorditions are significant atterated by the cases (death ost significant atterated by the cases (death os	part, radion and in the roblem. One ding to how provide us we have a second or a second of the roblem. It is a second of the r	ce we have chose good they can be with. As a scoring and the case of case we state = 0) state = 0) andom_state = 0) andom_state = 0) andom_state = 0)	en e
[13]: [13]: [16]:	The first thing we into account five	ection Phave to do is to so models which are: regression ors Tree orest Tree orest resefive into acco to account we have database. That is uge precision_sco to account we have database. That is uge precision_sco to account we have database. That is uge precision_sco to account we have database. That is uge precision_sco to comparison of m ['figure.figsi to ("darkgrid") aset.iloc[; -: a	ee which models we the which models we the select one and the select one and why we are going to re, since the data is nodels, what we had ze']=15,6 -1] columns)): l, model2.feath columns)): l, model2.feath 22 .069483117540(26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 2259619794396: 34 26884423035 27 2884423035 289734454 2882008 11 29 20 21 22 23 24 25 26 26 27 28 28 28 28 28 28 28 28 28	ve can consider the case we are defined in the case we are defined in the case we are defined in the case which is the case we to do is to consider the case we are defined in the case which is the case which is the case which is the case which is the case we are the case which is t	dealing with a super we are going to com, not see the time/prec in favor of the negal see what are the mo ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) pred) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) pred) e) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) pred) e) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) pred) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) pred) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) pred) ances_[i]) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) ances_[i]) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) ances_[i]) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) ances_[i]) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) ances_[i]) ances_[i]) erum_creatine, serun ones we will use to tinine', 'serum_ it(x_t, y, test) ances_[i]) ances_[i]) ances_[i])	dels. ut the classification ratio they provide them accordision ratio they provide the cases (death ost significant attention and aperform the modes accuracy of 38.3 accuracy	part, radionard, random_s format (10) ge as it could be study. In the study. In the study. In the study is a study in the study. In the study is a study in the study. In the study is a study in the study is a study in the study is a study in the study in the study is a study in the study in the study is a study in the study in	ce we have chose good they can be good to be considered asset of case we good they can be good to be considered asset of case we good they can be good to be good t	en e
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[13]: [13]: [16]:	The first thing we into account five	ection Phave to do is to so models which are: regression OTS Tree Orest Tree Orest Dese five into accook to account we have database. That is to ge precision_scot to account we have database. That is to ge precision_scot to account we have database. That is to ge precision_scot to account we have database. That is to ge precision_scot to account we have database. That is to ge precision_scot to account we have database. That is to ge precision_scot to account we have database. That is to ge precision account we have database. That is to ge precision account we have database. That is to ge precision account we have database. That is to ge precision account we have database. That is to ge precision account we have database. That is to get a control to account we have database. That is to get a control to account we have database. That is to get a control to account we have database. That is to get a control to account we have database. That is to get a control to account we have database. That is to get a control to account we have database. That is to get a control to account we have database. That is to get a control to account we have database. The to get account we h	unt because in this the to select one and why we are going to re, since the data is nodels, what we had ze', =15,6 -1] -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1 -1	ve can considerate ve can considerate ve to do so to the standard ve to do is to the standard ve to do is to the standard ve to do so to the standard ve considerate ve con	dealing with a super we are going to comm deset the time/precipitation of the negation of the	dels. ut the classification of the classification of the models of train_size and train_size an	part, random_s part, random_s	ce we have chose good they can be good they can be gith. As a scoring a state of case we have a state of case of case	en e

specified subset of the hyperparameter space of a learning algorithm while the second replaces the exhaustive enumeration of all the selected combinations at random. In terms of computational cost, it should be noted that these two forms are computationally expensive, since they have to perform exhaustive tasks that take a long time. As for other more efficient search methods, we have the Scikit-Optimize library which contains a hyperparameter optimization method called BayesSearchCV. This method is a direct replacement of GridSearchCV.

It uses Bayesian Optimization where a predictive model called "surrogate" is used to model the search space thus arriving at a good

combination of parameter values as early as possible.

'max_depth': [10, 20, 30, 40],
'max_features': ['auto'],

'min_samples_leaf': [1, 2, 5,10],
'min_samples_split': [2, 5, 10],

'n_estimators': [200, 400, 600, 800, 1000]

grid_search = GridSearchCV(estimator = Bosc, param_grid = param_grid, cv = 5)

BayesSearchCV = BayesSearchCV(cv=5,estimator=Bosc, search_spaces = param_grid)

random = RandomizedSearchCV(cv=5,estimator=Bosc, param distributions = param grid)

ax2 = sns.barplot(x='Hiperparametre', y='Temps', data = data, palette='winter')

ax2.set_ylabel('average_precision_score', fontsize=13, color=color)

model_data = {'Hiperparametre': ['GridSearchCV', 'BayesSearchCV', 'RandomizedSearchCV'], 'average_precisio

ax2 = sns.lineplot(x='Hiperparametre', y='average_precision_score', data = data, sort=False, color=colo

Hyperparameter Random Forest

BayesSearchCV

Hiperparametre

As we can observe the GridSearchCV gives us the best accuracy, but it also has the highest time cost. As for the BayesSearchCV we can observe that it provides us with the best accuracy, but its time cost is low. Finally we can observe that the RandomizedSearchCV gives us a

.The best attributes to perform the prediction are time, ejection_fraction,serum_creatine,serum_

.The best model for this problem in terms of computational cost compared to the results obtained

.The best parameters that can be used for the model are those obtained with the RandomizedSearch

0.749

0.748

0.747

average_precision_score

0.744

0.743

RandomizedSearchCV

Bosc=RandomForestClassifier()

'bootstrap': [True],

scl=(grid_search.best_score_)
parl=(grid_search.best_params_)
resl=(grid_search.cv_results_)

'bootstrap': [True],

'max_depth': [10, 20, 30, 40],
'max_features': ['auto'],

'min_samples_leaf': [1, 2, 5,10],
'min_samples_split': [2, 5, 10],

'n_estimators': [200, 400, 600, 800, 1000]

GridSearchCV:

param_grid = {

t0=time.time()

BayesSearchCV:

param_grid = {

t0=time.time()

BayesSearchCV.fit(x,y)
t2=time.time()-t0

RandomizedSearchCV:

param_grid = {

t0=time.time()
random.fit(x, y)
t3=time.time()-t0

temps=[t1,t2,t3]

color = 'tab:blue'

ax2 = ax1.twinx()
color = 'tab:red'

ax1.tick_params(axis='y')

700

600 -

500 -

Temps 400

300 -

200 -

100 -

par3

Out[28]: {'n_estimators': 600,

'min_samples_split': 2,
'min_samples_leaf': 10,
'max_features': 'auto',

'max_depth': 20,
'bootstrap': True}

6. Conclusions

sodium and age.

CV.

Webgraphy

In []:

is the random forest.

.Datauab: https://datauab.github.io

GridSearchCV

In [28]: print("In conclusion the best parameters found are: ")

In conclusion the best parameters found are:

good accuracy with a very low time cost and therefore we will use its parameters.

After solving this problem using Deep Learning we have reached the following conclusions:

.Leave-one-out: https://machinelearningmastery.com/loocv-for-evaluating-machine-learning-algorithms/

.Kaggle: https://www.kaggle.com/andrewmvd/heart-failure-clinical-data

.Curves ROC i PR: https://medium.com/bluekiri/curvas-pr-y-roc-1489fbd9a527

.Warnings: https://stackoverflow.com/questions/9031783/hide-all-warnings-in-ipython

.Models i hiperparametres: https://scikit-learn.org/stable/

sc3=(random.best_score_)
par3=(random.best_params_)
res3=random.cv_results_

data = pd.DataFrame(model_data)

In [26]:

In [27]:

sc2=(BayesSearchCV.best_score_)
par2=(BayesSearchCV.best_params_)
res2=(BayesSearchCV.cv_results_)

Bosc=RandomForestClassifier()

'bootstrap': [True],

'max_depth': [10, 20, 30, 40],
'max_features': ['auto'],

'min_samples_leaf': [1, 2, 5,10],
'min_samples_split': [2, 5, 10],

average_precision_score = [sc1 , sc2, sc3]

fig, ax1 = plt.subplots(figsize=(12,10))

ax2.tick_params(axis='y', color=color)

ax1.set_xlabel('Hiperparametre', fontsize=13)
ax1.set_ylabel('Temps', fontsize=13, color=color)

n_score': average_precision_score,'Temps': temps}

ax1.set_title('Hyperparameter Random Forest', fontsize=13)

'n estimators': [200, 400, 600, 800, 1000]

In [25]: Bosc=RandomForestClassifier()

grid_search.fit(x,y)
t1=time.time()-t0

In [24]:

Heart Failure Prediction

.matplotlib : Graph generation.

Before starting with data analysis, these are the main libraries used:

from sklearn.tree import DecisionTreeClassifier
from sklearn.model_selection import LeaveOneOut

from sklearn.linear_model import LogisticRegression
from sklearn.neighbors import KNeighborsClassifier
from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import classification report

from sklearn.model_selection import GridSearchCV

from sklearn.datasets import make_regression

from matplotlib import pyplot as plt

from sklearn.metrics import r2_score

import warnings; warnings.simplefilter('ignore')

from sklearn.linear_model import LinearRegression

from sklearn.model_selection import train_test_split

from sklearn.model_selection import cross_val_score

from sklearn.model_selection import RandomizedSearchCV

from sklearn.metrics import confusion_matrix, accuracy_score

from sklearn.metrics import f1_score, precision_recall_curve, average_precision_score, roc_curve, auc

from sklearn.model_selection import KFold

from sklearn.metrics import roc_curve
from sklearn.metrics import roc_auc_score

from skopt import BayesSearchCV

import ipywidgets as widgets

.Pandas and numpy : Data vector and matrix operations.

.sklearn : Models, metrics and data set partitioning.

1. Imported booksellers

from sklearn.svm import SVC

In [1]: #Models

#Metriques

#Hiperparametres

import numpy as np
import pandas as pd

matplotlib notebook

import scipy.stats
import seaborn as sns

import numpy as np
import random