df.corr()	s corrélations s avec la cible	0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 1 0	0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 0 0 0 0 1 0 0 0 0 ariables. Generation of the second of the s	0 0 0 0 0 0 0 0 0 0 0 0 0 0	o	
chronic_disease_binary (asymptomatic -(cough (fatigue (fever -(headache -(malaise (malaise (pneumonia (respiratory problems (runny nose -(diabetes (hypertension (outcome -(import seaborn as %matplotlib inline # calculate the cocorr = df.corr() # plot the heatman sns.heatmap(corr, xticklabe; yticklabe;	0.269721 0.070941 0.092924 -0.015488 0.024976 -0.024624 0.075835 -0.028209 0.036621 0.017434 0.075039 -0.020835 0.042810 0.049048 0.182647 0.063021 0.151409 0.022867 0.088150 -0.047703 0.071339 -0.054563 0.191144 0.060789 0.246387 0.046194 0.296449 -0.082325 sns e orrelation matrix	1.000000 -0.053872 -0.052710 -0.030147 -0.172809 -0.050477 -0.052212 0.518432 0.482077 -0.047538 -0.016424 0.656456 0.757860 -0.728110	1.000000 -0.130809 -0.039694 -0.194426 -0.038509 -0.032391 -0.048326 -0.043363 -0.029492 -0.050060 -0.036671 -0.041982 0.056613	-0.130809 -0. 1.000000 -00.019657 1. 0.168018 0. 0.015364 -00.001978 -00.156608 -00.127954 -0. 0.055013 -0. 0.046038 00.067095 -0.	038471 -0.099 057397 -0.188 051502 -0.201 035028 0.030 036587 -0.026 011836 -0.127	809 -0.050477 -0.426 -0.038509 -0.018
Ariable cible de no 2. Visualisez le en composan Nous allons comme X = df[['age', 'sex Y = df['outcome']] #cols = df.column: #X = df[cols[0:15] #Y = df[cols[15:1]] from sklearn.decom from sklearn.disc: pca = PCA(n_compon princ_pca = pca.fx) lda = LinearDiscr: princ_lda = lda.fx Pour la méthode LD colonnes que nous obtiendrons un max principal_Df_PCA = principal_Df_PCA = principal_Df_PCA = principal_Df_PCA.fx	que les variables 'outcome'), cela signotre jeu de données es données entes principale encer par ACP x', 'chronic_disease s.tolist()]] 6]] mposition import PO riminant_analysis in nents=2) it(X).transform(X) iminantAnalysis(n_o it(X, Y).transform(X) OA, elle utilise au m voulons obtenir. Da ximum de 1 colonn = pd.DataFrame(data , columns = ['r head() 1 principal component 2	n deux dines). Pouvez a_binary', 'asymptonic components=1) (X) naximum (n_classans notre cas, note. a = princ_pca principal components=1 principal components=1 principal components=1	nensions of vous util	en pass iser und ugh', 'fati lysis	ant par e autre	I'ACP (and méthode '
1 5.26039 2 25.26026 3 5.25975 4 -34.73866 principal_Df_LDA.1 principal component 0 -0.48658 1 0.47950 2 0.95799 3 0.53784 4 0.09856 import matplotlib plt.figure() plt.figure(figsize plt.xticks(fontsi: plt.yticks(fontsi: plt.yticks(fonts	-0.179588 -0.684727 -0.684727 -0.725729 -0.279784 -0.279	<pre> /, fontsize=20) /, fontsize=20) /, fontsize=20) ysis of Dataset lors, [0, 1, 2]], princ_pca[Y = 0.0] /, scatterpoints: // scatterp</pre>	, [0, 1]): == i, 1], cole =1)			w=lw,
1.0 -0.5 -0.5 -0.5 -0.5 -0.5 -0.5 -0.5 -0	-20		20	Discha died	ged	
Créer une foncti from sklearn.mode. import numpy as ny import random from tqdm import from sklearn.neigh def bestK_KNN(X_t: Ks = 50 mean_acc = np for n in tqdm neigh = Ki mean_acc[n plt.plot(range plt.ylabel('Ac plt.xlabel('Ac	ts obtenus do me l'erreur de omme Rappe x','chronic_disease Neighbours ton qui cherche l_selection import tqdm hbors import KNeigh rain, y_train, X_te .zeros((Ks-1)) (range(1,Ks)): NeighborsClassifier n-1] = neigh.score e(1,Ks),mean_acc,'g Accuracy ', '+/- 3x ccuracy ') umber of neighbors out() est accuracy was ",	pivent être e prédictio I, F-Measu e binary', 'asym s (K-NN) le meilleur k train_test_spl aborsClassifier est, y_test): r (n_neighbors = (X_test, y_test g') kstd')) (K)') mean_acc.max(en données de	validés er n (matrice re, ptomatic','com it n).fit(X_trans) e test et d'a	n utilisa e de co ugh', 'fati mean_acc. apprentis	nt certanfusion gue','fever ssage	et précision de la company de
best_K = bestK_KNI 100% 100	20 30 Number of neighbors (Was 0.962025316453) lassifier (n_neighborict (X_test) n squared error of y_test) ** 2).sum (tage d'erreur pour	Accuracy Accuracy 40 K) 56962 with k= 5 ors = best_K).f our prediction ()) / len(y_prediction) () / len (y_prediction) le modèle KNN	it (X_train, y_ s. d) est :", mse*1	train)	random_stat	e=random.seed
res_knn = knn.scor print("Accuracy por Accuracy pour le m import pandas as r import seaborn as import matplotlib from sklearn.metro disp = plot_confus disp.axset_title plt.show() #%matplotlib.inlin Confusion 1 1	our le modèle KNN e odèle KNN est : 96 pd sn .pyplot as plt ics import plot_cor sion_matrix(knn, X_ e ("Confusion Matrix ne 11 285	est:", res_knn .20253164556962 nfusion_matrix _test, y_test,c	*100 ,'%') %			
print("Accuray score from sklearn.metrom sklearn.me	ics import accuracy ore: \t\t",accuracy ics import f1_score \t\t",f1_score(y_t ics import precision score: \t",precision ics import recall_s re: \t\t",recall_sc	y_score(y_test, e) test, y_pred, avenuest score on_score(y_test, y_) 4556962 6494845 918919 9184149 ication_report y_pred)) 1-score suppo 0.76 0.98 2 0.96 0.87 3	erage='macro' , y_pred, ave pred, average	rage='macr		
disp = plot_confus disp.axset_title plt.show() #%matplotlib.inlin Confusion O Predicte from sklearn.metr: print("Accuray sco from sklearn.metr: print("F-Measure: from sklearn.metr: print("Precision sklearn.metr: print("Precision sklearn.metr: print("Precision sklearn.metr: print("Precision sklearn.metr:	.pyplot as plt ics import plot_corsion_matrix(clf, X_ e("Confusion Matrix ne Matrix 8	250 200 200 150 100 50 y_score y_score(y_test, e) test, y_pred2, a on_score on_score(y_test score(y_test, y_j) 5316456 8763667 968254	<pre>y_pred2)) verage='macro , y_pred2, ave</pre>	')) erage='mac		
print(classificat: prec 0 1 accuracy macro avg weighted avg Classificate from sklearn.naive clf_CB = Multinom: clf_CB.fit(X_train pred = clf_CB.prec import matplotlib from sklearn.metr: disp = plot_confus	ics import classification_report(y_test, ision recall fill 0.79 0.73 0.97 0.98 0.88 0.86 0.95 0.96 Ur Bayes e_bayes import MultialNB() n, y_train) dict(X_test) .pyplot as plt ics import plot_corsion_matrix(clf_CB, e("Confusion Matrix n Matrix	<pre>y_pred2)) 1-score suppo 0.76 0.98 2 0.96 3 0.87 3 0.96 3 tinomialNB afusion_matrix X_test, y_tes</pre>	30 86 16 16 16	.Blues)		
print ("Accuray score from sklearn.metroprint ("F-Measure: from sklearn.metroprint ("Precision strom sklearn.metroprint ("Recall score: Accuray score: F-Measure: Precision score: Recall score: # Classification strom sklearn.metroprint (classification sklearn.metroprint (classification sklearn.metroprint (classification sklearn.metroprint sklearn.met	ics import accuracy ore: \t\t",accuracy ics import fl_score \t\t",fl_score(y_t ics import precision score: \t",precision ics import recall_s re: \t\t",recall_s 0.9778481012 0.9279173593 0.9880546073 0.8833333333 report ics import classificition_report(y_test, ision recall fill 1.00 0.77 0.98 1.00 0.99 0.88 0.98 0.98 ression pour pre	y_score(y_test, e) test, pred, average test, pred, average pn_score pn_score(y_test) score core(y_test, pred) 2658228 1423079 5085324 3333333 ication_report pred)) 1-score suppo 0.87 0.99 2 0.98 3 0.98 3 6dire l'âge (a	rt 30 86 16 16 16 16 16	sonnes e	n fonctio	n d'autres
<pre>rester sur tous les v X2 = df[['sex','cl' Y2 = df['age'] X_train2, X_test2, from sklearn.linearegres reg.fit(X_train2) LinearRegression() y2_pred = reg.pred from sklearn.metr: MSE = mean_squared print('l\'erreur MSE : 32 Jtiliser RFE pour sé from sklearn.featus electeur = RFE(es sel = selecteur.f: print(sel.n_featus print(sel.support) 7 [False False False False True</pre> # get the feature rfe_mask = sel.sup # reduce the data.	hronic_disease_bina , y_train2, y_test2 ar_model import Lir ssion() , y_train2) dict(X_test2) dict(X_test2) ics import mean_squ d_error(y_test2, y2 MSE : ',MSE) 1.6017646906366 electionner les varia ure_selection import stimator = reg) it(X_test2, y_test2 res_) _) False True True] support boolean line	e la prédictio ary', 'asymptoma 2 = train_test_ nearRegression alared_error 2_pred) ables explicative rt RFE 2) False False Fa	n à l'aide de tic', 'cough', split(X2, Y2,	e l'erreur 'fatigue', test_size	MSE (Me	ean Squared
cough fatigue 0 0 1 0 2 1 3 1 4 0 0 0 3 1 0 0 1572 1 0 0 1573 0 0 0 1574 1 0 0 1575 1 0 0 577 rows × 7 columns X2_RFE = X2_RFE = df['age']	pneumonia respiratory 1 0 0 0 0 0 0 0 0 0 0 1	problems runny no 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0	C. Y2 RFE.	test size=0.2
reg_RFE = LinearRereg_RFE.fit(X_trained print(X_trained print) from sklearn.metrom sklearn.metrom sklearn.metrom sklearn.metrom sklearn.metrom sklearn.metrom sklearn.metrom sklearn.clusted print(X_trained print) from sklearn.metrom sklearn.clusted print(X_trained print) from sklearn.metrom sklearn.clusted print(X_trained print) from sklearn.clusted print(X_trained print) from sklearn.metrom sklearn.clusted print(X_trained print) from sklearn.clusted print(X_trained print) from sklearn.metrom sklearn.metrom sklearn.clusted print(X_trained	egression() in_RFE , y_train_RFRFE.predict(X_test_ ics import mean_squd_error(y_test_RFE, MSE : ',MSE) 2.0825627294294 is méthodes de egmenter les pe e meilleur nomb ics import silhouet ter import KMeans cients = [] clusters pour le control	clustering (Korsonnes en de cluste	-means, NN ifférents gr rs.	ΛF et CA	H) sur l'e	nsemble de
silhouette_coe if score > sil silh_score best_clust plt.style.use("fir plt.plot(range(2, plt.xticks(range(2, plt.xlabel("Number plt.ylabel("Silhou plt.show() print('D\'après 1') 0.60 0.58 0.56 0.54 2 3 4 5 D'après l'index de 3 from sklearn impor kmeans = kMeans(n y_kmeans = kmeans labels = kmeans.la	<pre>uette_score(princ_p efficients.append(s lh_score: e = score ters = k vethirtyeight") 21), silhouette_cd 2, 21)) r of Clusters") uette Coefficient") \'index de Silhouet rt metrics _clusters= best_clu .predict(princ_pca) abels_ e_score(princ_pca,</pre>	Defficients) Litte, le meilleu Listers	p 20 e clusters es _state=0).fit	t: 18 ave	c un score	
<pre>from sklearn.decor import sklearn.pre best_clusters_nmf silh_score_nmf = (silhouette_coeffic) # assurer que tour X_scaled = skprep: # On commence à 2 for k in range(2,</pre>	cients = [] tes les données ne roc.minmax_scale(pr clusters pour le d 21): (n_components=k, ir it_transform(X_scal omponents_ np.argmax(D, axis=1 uette_score(X_scale efficients.append(s lh_score_nmf: e_nmf = score ters_nmf = k vethirtyeight") 21), silhouette_cd 2, 21))	sont pas négat rinc_pca) coefficient de nit='random', m led) l) ed, NMF_labels) score)	r nombre de c	lusters es	c:',best_cl	usters_nmf,' a
plt.xticks(range(2 plt.xlabel("Number plt.ylabel("Silhon plt.show() print('D\'après 1') 0.3 0.2 0.1 0.0 -0.1 -0.2	6 7 8 9 10 11 12 1			t: 2 avec		
plt.plot(range(2, plt.xticks (range(2) plt.xticks plt.xticks (range(2) plt.xticks plt.xti	Number of Clu Silhouette, le me: nents= best_cluster form(X) s_ decimals = 2) decimals = 2) 00e-02 3.0000e-02 2 0e+00 1.0000e-02 2 0e-02 2.0000e-02] 0e+01 0.0000e+00 0 0e+00 0.0000e+00 0 0e+00 0.0000e+00]	illeur nombre d rs_nmf , init=' 1.0000e-02 0.00 .0000e-02 2.000 .0000e+00 2.199 .0000e+00 0.000 X_e , decimals = 7.000e-02 3.000 8.000e-02 3.000 8.000e-02 1.000 8.000e-02 4.000	random', rand 00e+00 1.0000 0e-02 0.0000e 0e+01 9.0000e 0e+01 1.1700e = 2)}') 0e-02 8.000e-0 e-02 6.000e-0 e-02 3.000e-0 e-02 9.000e-0	e-02 +00 -02 +00		

600 500 400 300	
100 0	(96) (71) (60) (70) (16) (27) (50) (129) (84) (212) (146) (170) (9) (91) (115) (2) (130) (
kme y_k lab cen plt plt	ans_sc = KMeans(n_clusters= 2 , random_state=0).fit(princ_pca) means = kmeans_sc.predict(princ_pca) els_sc = kmeans_sc.labels_ troids = kmeans_sc.cluster_centers_ .title('Scatter Plot for Kmeans', fontsize = 16) .scatter(df['age'], Y, c=labels_sc) .scatter(centroids[:,0], centroids[:,1], marker='x', c='black')
_	Scatter Plot for Kmeans Scatter Plot for Kmeans
	0 20 40 60 80 100
plt	
0.0 0.0 -0.0 CAH	ol
mod mod plt plt plt	<pre>.title('Scatter Plot for CAH', fontsize = 16) el_cah2 = AgglomerativeClustering(n_clusters=2, affinity='euclidean', linkage='average') el_cah2 = model_cah2.fit(X) .scatter(X['age'], Y, c=model_cah2.labels_, marker='o', edgecolors='black') .xlabel("X", fontsize = 14) .ylabel("Y", fontsize = 14) .show()</pre> <pre> Scatter Plot for CAH 0</pre>
>- 0.	es données sont déséquilibrées. Vous pouvez les équilibrer en réduisant
aléa pré 70]: from from # A pri.	atoirement la classe majoritaire. Supposons que vous extrayez atoirement des échantillons équilibrés. Comment les résultats de la diction changeront-ils? m collections import Counter m imblearn.under_sampling import RandomUnderSampler fficher la distribution des classes nt (Counter(Y)) éfinir la méthode 'undersample' ersample = RandomUnderSampler (sampling strategy='majority')
# a X_o # 1 pri Coun Coun Si la g	juster et appliquer la transformation ver, y_over = undersample.fit_resample(X, Y) a distribution des classes après la transformation nt(Counter(y_over)) ter({1: 1439, 0: 138}) ter({0: 138, 1: 138}) rande majorité des observations appartient à la même catégorie, on risque d'avoir un modèle peu intelligent qui va toujours re la classe dominante.
Une to de la comieux modè 9. F Gre	Comment pouvez-vous mieux gérer ce déséquilibre entre les classes ? echnique consiste tout simplement à rééquilibrer le jeu de données. Soit en faisant de l'undersampling, en enlevant des données classe majoritaire, soit en faisant de l'oversampling, en rajoutant des nouvelles données dans la classe minoritaire. Aussi il vaut d'utiliser des métriques plus adaptées, comme : La précision , Le rappel , Le F1-Score et La matrice de confusion afin d'avoir un le performant. Pour trouver les meilleurs paramètres pour les modèles, l'algorithme sedy Search peut être utilisé, disponible dans la bibliothèque scikit-learn pliquez l'algorithme et utilisez-le pour les modèles d'apprentissage chois de trouver les meilleurs paramètres
pour l choix object chaqu optim Cas (rithme Greedy Search automatise la recherche d'un optimum parmi les hyperparamètre afin de trouver les meilleurs paramètres es modèles, L'algorithme Greedy Search fait toujours le choix qui semble être le meilleur à ce moment-là. Cela signifie qu'il fait de localement optimal dans l'espoir que ce choix conduira à une solution globalement optimale. Supposons qu'on a une fonction tive qui doit être optimisée (maximisée ou minimisée) à un moment donné. L'algorithme Greedy fait des choix gourmands à le étape pour s'assurer que la fonction objectif est optimisée. L'algorithme Greedy n'a qu'un seul coup pour calculer la solution ale afin qu'il ne revienne jamais en arrière et annule la décision. **Metann.model_selection import GridSearchCV** **Mameters = {'n neighbors': list(range(1,30))}
grigri gri Fitt [Par [CV] [CV] [CV] [CV] [CV]	d = GridSearchCV(knn, parameters, verbose=2, return_train_score=True) d.fit(X_train, y_train) ing 5 folds for each of 29 candidates, totalling 145 fits allel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent workers. n_neighbors=1
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=2, total= 0.0s n_neighbors=2</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=3</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=4 n_neighbors=4, total= 0.0s n_neighbors=4 n_neighbors=4, total= 0.0s n_neighbors=5 n_neighbors=5, total= 0.0s
[cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=6, total= 0.0s n_neighbors=6 n_neighbors=6, total= 0.0s n_neighbors=6 n_neighbors=6, total= 0.0s n_neighbors=6 n_neighbors=6, total= 0.0s n_neighbors=6 n_neighbors=6, total= 0.0s n_neighbors=7 n_neighbors=7, total= 0.0s n_neighbors=7 n_neighbors=7, total= 0.0s n_neighbors=7 n_neighbors=7, total= 0.0s
[cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=7</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=9</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=11</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=12, total= 0.0s n_neighbors=12 n_neighbors=12, total= 0.0s n_neighbors=13 n_neighbors=13, total= 0.0s n_neighbors=13 n_neighbors=13, total= 0.0s n_neighbors=13
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=13
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=15</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=16, total= 0.0s n_neighbors=16 n_neighbors=16, total= 0.0s n_neighbors=16 n_neighbors=16, total= 0.0s n_neighbors=17 n_neighbors=17, total= 0.0s n_neighbors=17
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=18</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=19, total= 0.0s n_neighbors=19 n_neighbors=19, total= 0.0s n_neighbors=19 n_neighbors=19, total= 0.0s n_neighbors=20 n_neighbors=20, total= 0.0s
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=21</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=23</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	n_neighbors=24
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=25</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=27</pre>
[cv] [cv] [cv] [cv] [cv] [cv] [cv] [cv]	<pre>n_neighbors=28</pre>
[Par 71]: Grid 72]: res k = tra	<pre>allel(n_jobs=1)]: Done 145 out of 145 elapsed: 11.1s finished SearchCV(estimator=KNeighborsClassifier(),</pre>
ax.	<pre>score = pd.DataFrame(dict(k=k, test=test_score, train=train_score)) = df_score.plot(x='k', y='train', figsize=(6, 4)) score.plot(x='k', y='test', ax=ax, grid=True) set_title("Evolution de la performance sur\nles bases d'apprentissage et de test" +</pre>
2 0	0.96 0.95 0.94 0.93 0.92 5 10 15 20 25 k
en qu 92]: pri bes Les Cas (6 voisins, la pertinence du modèle décroît fortement, ce qui paraît normal car plus il y a de voisins, moins la prédiction est local elque sorte. nt ('Les meilleurs paramètres sont :',grid.best_estimator_) t_n_neighbors = grid.best_params_['n_neighbors'] meilleurs paramètres sont : KNeighborsClassifier(n_neighbors=3) d'arbre de decision ams = {'max_leaf_nodes': list(range(2, 100)), 'min_samples_split': [2, 3, 4]}
gri gri Fitt [Par	<pre>d_search_cv = GridSearchCV(clf, params, verbose=1, cv=3) d_search_cv.fit(X_train, y_train) ing 3 folds for each of 294 candidates, totalling 882 fits allel(n_jobs=1)]: Using backend SequentialBackend with 1 concurrent workers. allel(n_jobs=1)]: Done 882 out of 882 elapsed: 5.3s finished SearchCV(cv=3, estimator=DecisionTreeClassifier(),</pre>
acc 30]: 0.96 bes bes pri	<pre>red = grid_search_cv.predict(X_test) uracy_score(y_test, y_pred) 51898734177216 t_max_leaf_nodes = grid_search_cv.best_params_['max_leaf_nodes'] t_min_samples_split = grid_search_cv.best_params_['min_samples_split'] nt ('Les meilleurs paramètres sont :',grid_search_cv.best_estimator_) meilleurs paramètres sont : DecisionTreeClassifier(max_leaf_nodes=12, min_samples_split=3)</pre>
par clf clf clf	<pre>de classificateur Bayes ameters = {'alpha':[0.01, 0.05, 0.1, 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60] } _CB_GS = GridSearchCV(clf_CB, parameters, scoring='f1') _CB_GS.fit(X_train, y_train) SearchCV(estimator=MultinomialNB(),</pre>
0.98 108 pri bes Les 10.	_CB_GS.score(X_test, y_test) 79101899827288 nt ('Les meilleurs paramètres sont :',clf_CB_GS.best_estimator_) t_alpha = clf_CB_GS.best_params_['alpha'] meilleurs paramètres sont : MultinomialNB(alpha=0.05) Présentez et expliquez le formalisme algorithmique et mathématique de néthode qui donne les meilleurs résultats. Expliquez tous les paramètres
Nous KNN 95]: bes 95]: 3	t_n_neighbors Nearest Neighbors
y_p knn pri knn pri knn pri	<pre>2 = KNeighborsClassifier(n_neighbors = best_n_neighbors).fit(X_train,y_train) red_KNN = knn2.predict(X_test) _Accuracy = accuracy_score(y_test, y_pred_KNN) nt("Accuray score: \t\t", knn_Accuracy) _F1_Score = f1_score(y_test, y_pred_KNN,average='macro') nt("F-Measure: \t\t", knn_F1_Score) _Precision = precision_score(y_test, y_pred_KNN, average='macro') nt("Precision score: \t", knn_Precision) Recall = recall score(y test, y pred_KNN, average='macro')</pre>
Accu F-Me Prec Reca 98]: fro knn	<pre>Recall = recall_score(y_test, y_pred_knn, average='macro') nt("Recall score: \t\t", knn_Recall) ray score:</pre>
pri The	<pre>auc = roc_auc_score(y_test, knn_pred_test_prob) nt("The AUC score: \t\t", knn_auc) AUC score:</pre>
	<pre>plt.ylabel('True Positive Rates', fontsize=15) plt.legend(loc='best') plt.show() t_roc_curve(fpr=fpr, tpr=tpr, label="AUC = %.3f" % knn_auc) ROC Curve AUC = 0.841</pre>
True Positive Rates	.6
Arb	0
103 3	<pre>t_min_samples_split ad = tree.DecisionTreeClassifier(max_leaf_nodes= best_max_leaf_nodes , min_samples_split= best_min_s ad.fit(X_train,y_train) red_ad = clf_ad.predict(X_test)</pre>
pri ad_ pri ad_ pri ad_ ad_ pri	Accuracy = accuracy_score(y_test, y_pred_ad) nt("Accuray score: \t\t", ad_Accuracy) F1_Score = f1_score(y_test, y_pred_ad, average='macro') nt("F-Measure: \t\t", ad_F1_Score) Precision = precision_score(y_test, y_pred_ad, average='macro') nt("Precision score: \t", ad_Precision) Recall = recall_score(y_test, y_pred_ad, average='macro') nt("Recall score: \t\t", ad_Recall)
F-Me Prec Reca 106 ad_ #Tr fpr ad_	ray score: 0.9651898734177216 asure: 0.886727278652198 ision score: 0.9411633773556907 ll score: 0.8465034965034965 pred_test_prob = clf_ad.predict_proba(X_test)[:, 1] ue Positive Rate and False Positive Rate. , tpr, threshold = roc_curve(y_test, ad_pred_test_prob) auc = roc_auc_score(y_test, ad_pred_test_prob) nt("The AUC score: \t\t", ad_auc)
The 107 plo	AUC score: 0.8123543123543124 t_roc_curve(fpr=fpr, tpr=tpr, label="AUC = %.3f" % ad_auc) ROC Curve .0 AUC = 0.812
True Positive	.6
Cla	.0 00 00 00 00 00 00 00 00 00 00 00 00 0
clf y_p 111 nb_, pri nb_ pri	<pre>_nb = MultinomialNB(alpha=best_alpha) _nb.fit(X_train, y_train) red_nb = clf_nb.predict(X_test) Accuracy = accuracy_score(y_test, y_pred_nb) nt("Accuray score: \t\t", nb_Accuracy) F1_Score = f1_score(y_test, y_pred_nb, average='macro') nt("F-Measure: \t\t", nb_F1_Score)</pre>
nb_pri nb_i pri Accu F-Me Prec Reca	Precision = precision_score(y_test, y_pred_nb, average='macro') nt("Precision score: \t", nb_Precision) Recall = recall_score(y_test, y_pred_nb, average='macro') nt("Recall score: \t\t", nb_Recall) ray score:
#Tr fpr nb_pri The plo	<pre>ue Positive Rate and False Positive Rate. , tpr, threshold = roc_curve(y_test, nb_pred_test_prob) auc = roc_auc_score(y_test, nb_pred_test_prob) nt("The AUC score: \t\t", nb_auc) AUC score: 0.896969696969697 t_roc_curve(fpr=fpr, tpr=tpr, label="AUC = %.3f" % nb_auc) ROC Curve </pre>
ates	.6
e Posi	.2
0	.0 — AUC = 0.897
0 0 1114 res	0.00 0.00 0.10 0.10 0.10 0.10 0.10 0.10

current_count += counts[child_idx - n_samples]

counts[i] = current_count

Plot the corresponding dendrogram
dendrogram(linkage_matrix, **kwargs)