```
In [20]: import pandas as pd

df = pd.read_csv('prepped_diabetes_data.csv', index_col='Patient number')
```

Out[20]:

	Cholesterol	Glucose	HDL Chol	Age	Gender	Height	Weight	ВМІ	Systolic BP	Diastolic BP	wai
Patient number											
1	193	77	49	19	1	61	119	22.5	118	70	
2	146	79	41	19	1	60	135	26.4	108	58	
3	217	75	54	20	1	67	187	29.3	110	72	
4	226	97	70	20	1	64	114	19.6	122	64	
5	164	91	67	20	1	70	141	20.2	122	86	
386	227	105	44	83	1	59	125	25.2	150	90	
387	226	279	52	84	1	60	192	37.5	144	88	
388	301	90	118	89	1	61	115	21.7	218	90	
389	232	184	114	91	1	61	127	24.0	170	82	
390	165	94	69	92	1	62	217	39.7	160	82	

390 rows × 15 columns

In [21]:

In [24]:

	Description	Value
0	session_id	362
1	Target	Diabetes
2	Target Type	Binary
3	Label Encoded	0: 0, 1: 1
4	Original Data	(390, 15)
5	Missing Values	False
6	Numeric Features	13
7	Categorical Features	1
8	Ordinal Features	False
9	High Cardinality Features	False
10	High Cardinality Method	None
11	Transformed Train Set	(272, 14)

In [30]:

Out[30]:

	Cholesterol	Glucose	HDL Chol	Age	Height	Weight	ВМІ	Systolic BP	Diastolic BP	waist
Patient number										
8	164.0	71.0	63.0	20.0	72.0	145.0	19.700001	108.0	78.0	29.0
169	269.0	59.0	66.0	41.0	67.0	191.0	29.900000	130.0	73.0	38.0
51	164.0	94.0	58.0	28.0	67.0	180.0	28.200001	128.0	94.0	39.0
242	218.0	182.0	54.0	51.0	66.0	215.0	34.700001	139.0	69.0	42.0
260	216.0	79.0	46.0	54.0	65.0	138.0	23.000000	132.0	80.0	33.0
95	300.0	65.0	59.0	34.0	65.0	160.0	26.600000	120.0	60.0	40.0
137	268.0	90.0	48.0	38.0	63.0	181.0	32.099998	142.0	100.0	38.0
112	179.0	81.0	35.0	36.0	63.0	125.0	22.100000	110.0	76.0	33.0
191	244.0	101.0	39.0	44.0	71.0	168.0	23.400000	140.0	89.0	36.0
30	164.0	86.0	40.0	23.0	69.0	245.0	36.200001	126.0	75.0	44.0

118 rows × 14 columns

In [31]:

	Model	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC	TT (Sec)
lda	Linear Discriminant Analysis	0.9081	0.9132	0.5700	0.8633	0.6578	0.6111	0.6427	0.0150
knn	K Neighbors Classifier	0.9007	0.8880	0.5650	0.8067	0.6428	0.5893	0.6140	0.0340
ridge	Ridge Classifier	0.9007	0.0000	0.5050	0.7767	0.5993	0.5562	0.5805	0.0150
catboost	CatBoost Classifier	0.8937	0.9295	0.6150	0.7350	0.6548	0.5940	0.6056	1.4950
et	Extra Trees Classifier	0.8898	0.8908	0.4850	0.8133	0.5776	0.5238	0.5590	0.1300
qda	Quadratic Discriminant Analysis	0.8827	0.7754	0.5300	0.6300	0.5685	0.5120	0.5189	0.0210
lightgbm	Light Gradient Boosting Machine	0.8827	0.9178	0.5550	0.7133	0.5962	0.5337	0.5517	0.1560
xgboost	Extreme Gradient Boosting	0.8753	0.9082	0.5550	0.6855	0.5933	0.5235	0.5385	0.1870
rf	Random Forest Classifier	0.8751	0.9051	0.4900	0.7533	0.5593	0.4946	0.5246	0.1570
gbc	Gradient Boosting Classifier	0.8643	0.8919	0.5500	0.6562	0.5822	0.5034	0.5154	0.0590
nb	Naive Bayes	0.8639	0.8906	0.6100	0.6690	0.5870	0.5118	0.5401	0.0160

			mouoi	Accurac	cy A	AUC	Recall	Pre	C.	F1 I	Kappa	M	cc (s	TT ec)
	ada	Ada Boost C	Classifier	0.856	35 0.8	3254	0.5350	0.540	0.53	322 (	0.4578	0.46	611 0.07	780
	dt		ion Tree Classifier	0.834	19 0.6	6961	0.4850	0.54	58 0.50	004 (	0.4051	0.41	128 0.0°	180
In [38]:		7												
Out[38]:	sklearn.	discrimina	ant_ana	lysis.l	_inea	rDis	crimi	nantAı	nalysi	.S				
In [36]:		^ 47												
Out[36]:	(1, 15)													
In [37]:		1 7 /1			. <u>-</u>		7.							
Out[37]:		Cholesterol	Glucose	HDL Chol	Age	Gend	ler He	eight \	Weight	ВМІ	Systo	olic BP	Diastolic BP	wa
	Patient number													
	389	232	184	114	91		1	61	127	24.0		170	82	,
In [39]:	Transfor	rmation Pi	peline		del S	ucce	sfull	y Sav	ed					

Out[39]:

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```
In [11]: import pickle
         with open('LDA_model.pk', 'wb') as f:
In [12]: with open('LDA_model.pk', 'rb') as f:
In [13]: new_data = df.iloc[-2:-1].copy()
         new_data.drop('Diabetes', axis=1, inplace=True)
Out[13]: array([1])
In [41]:
         Transformation Pipeline and Model Successfully Loaded
In [42]:
Out[42]:
                Cholesterol Glucose HDL Chol Age Gender Height Weight BMI Systolic Diastolic BP BP
          Patient
         number
            389
                      232 184 114 91 1
                                                    61 127 24.0 170
                                                                             82
In [48]: from IPython.display import Code
Out[48]:
```

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Transformation Pipeline and Model Successfully Loaded predictions:

Patient number

391 Diabetes

No diabetesNo diabetes

394 No diabetes

Name: Diabetes\_prediction, dtype: object

Summary and Short Analysis

This week assignment is about automation techniques for data science with Python. First we loaded the same prepared data from week 2 where everything ha been converted to numbers. Second, we used pycart for autoML but before doing that we installed Python package with condo. Then we import the function we need. After that, we satup our autoML and we basically run the autoML to find the best model. But before we run our autoML to find the best model, we have if our datatypes of the input are correct and in our case, they were fine. This i updated in real time within the notebook as needed. Boosting algorithms such as xgboost and catboost take the longest to run. xgboost is frequently towards the top. To use xgboost and lightgbm, we must either enable preprocessing (which transforms categorical columns to numeric columns) or set our categorical columns to numeric using 'autom1 = setup(df, target='Diabetes', preprocess=False, numeric features= Gender). Our best model object now contains the highest-scoring model. We can also use the 'compare models' argument'sort' to select another metric as our scoring metric. It employs precision by default (and we can see the table above is sorted by accuracy). We may set this to'sort='Precision" to utilize precision (TP / (TP FN)), for example. we found out that our best mpdel is LDA. Third, we used our best\_model to make predictions. We selected the last row, but using the indexing [-2:-1] to make it 2D array instead of 1D. From there, we can see thi creates a new column, 'Score' with the propability of class1. It also creates 'Label' column with the predicted label, where it rounds up if score is >=0.5 (greater than or equal to 0.5). Finally, we stored our trained model so we can utilize it later in a Python file. For instance, pycaret includes a convenient method that saves the model as a pickle file. In this case, we utilize the built-in 'open' function to open a file called 'LDA model.pk,' then open it fo writing with "w" and in binary format with "b."That file object is saved in th variable 'f.'After we exit the with statement, the file is automatically closed; otherwise, we must use the method 'close' from the file object 'f'. Pickle is then used to store our data to a file. After that, we saved our code to GitHub.