

Timeline

The first step was understand, clean and analyse the dataset

Then four different algorithms have been applied through cross-validation

EXPLORATION FEATURE ENGINEERING MODELS APPLICATION MODEL TUNING

Then external knowledge deriving from academic articles and studies has been used in order to create new features, which are used to get the best results out of the dataset

Finally, the best model is tuned in order to improve the final results

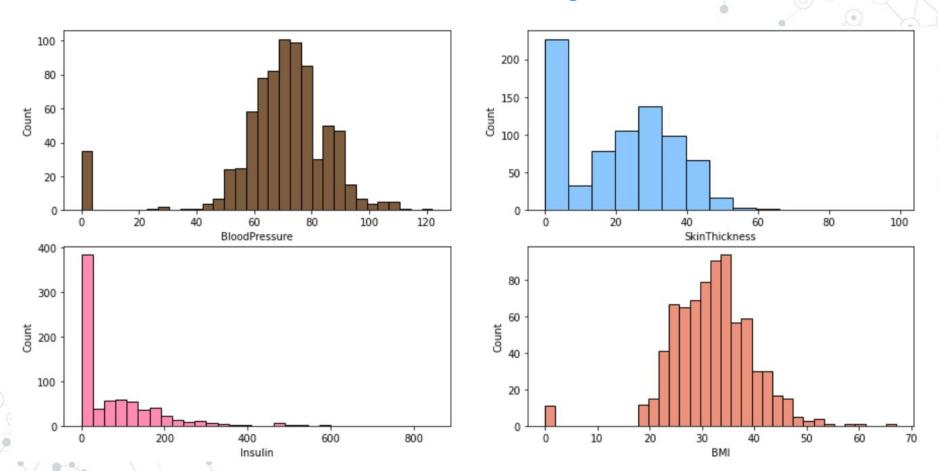


Dataset Exploration

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	вмі	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.850000	120.890000	69.110000	20.540000	79.800000	31.990000	0.470000	33.240000	0.350000
std	3.370000	31.970000	19.360000	15.950000	115.240000	7.880000	0.330000	11.760000	0.480000
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.080000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.240000	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.370000	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.600000	0.630000	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000
-	- 1		V23						

Dataset Cleaning



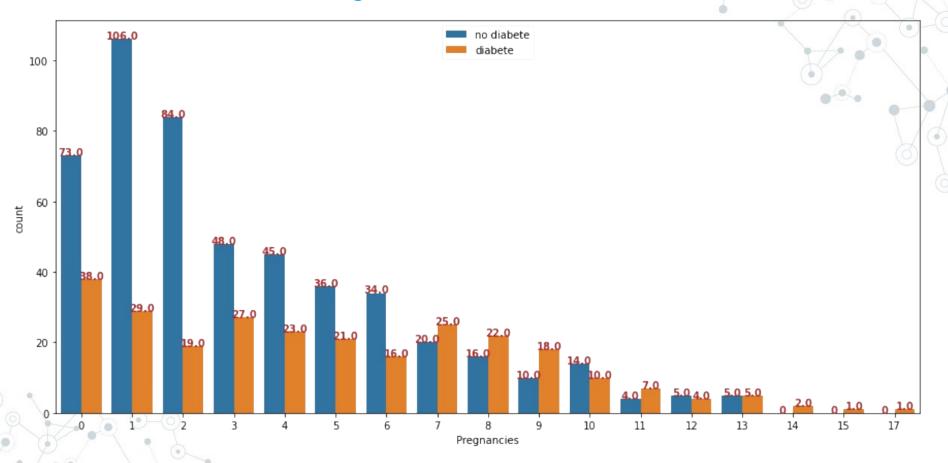
Feature Analysis

Some interesting correlations can be noticed, in particular observing the **Outcome column**.

These are reported in the following table of correlations:

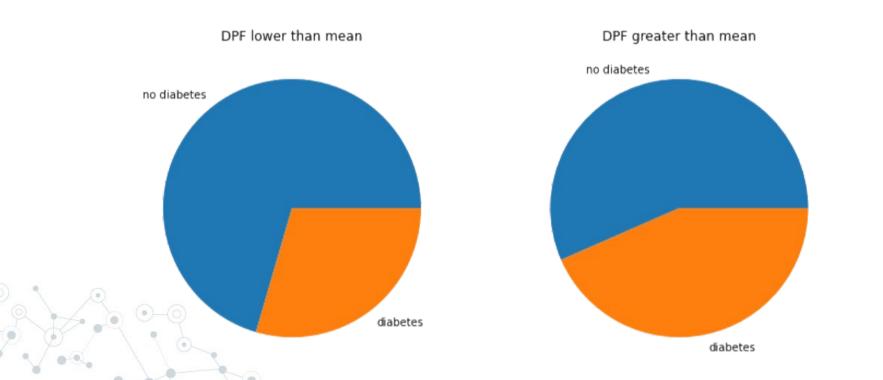
	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
Pregnancies	1.000000	0.130155	0.209151	0.089028	0.058767	0.023890	-0.033523	0.544341	0.221898
Glucose	0.130155	1.000000	0.225141	0.229289	0.490015	0.236171	0.138353	0.268910	0.495990
BloodPressure	0.209151	0.225141	1.000000	0.199349	0.070128	0.286399	-0.001443	0.325135	0.174469
SkinThickness	0.089028	0.229289	0.199349	1.000000	0.200129	0.566086	0.106280	0.129537	0.295138
Insulin	0.058767	0.490015	0.070128	0.200129	1.000000	0.238443	0.146878	0.123629	0.377081
ВМІ	0.023890	0.236171	0.286399	0.566086	0.238443	1.000000	0.152771	0.027849	0.315577
DiabetesPedigreeFunction	-0.033523	0.138353	-0.001443	0.106280	0.146878	0.152771	1.000000	0.033561	0.173844
Age	0.544341	0.268910	0.325135	0.129537	0.123629	0.027849	0.033561	1.000000	0.238356
Outcome	0.221898	0.495990	0.174469	0.295138	0.377081	0.315577	0.173844	0.238356	1.000000

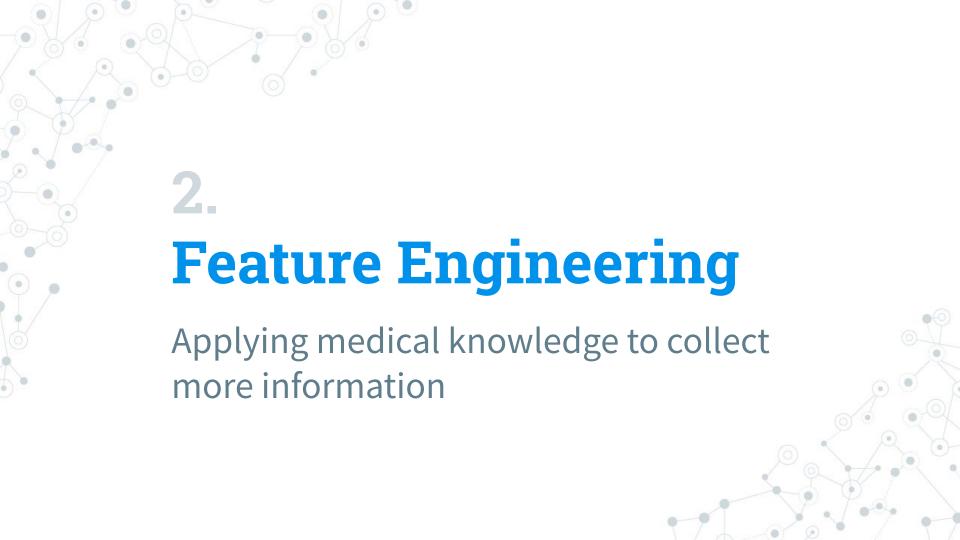
Pregnancies and Outcome



Diabetes Pedigree Function and Outcome

Diabetes Pedigree is the function which indicates likelihood of diabetes based on **family history**: these plots analyze the percentage of cases of diabetes for the classes which contains a value under or over the mean for this metric.





The Idea

BMI Glucose Blood Skin
Pressure Thickness





Classify Features

Explore and analyse medical academic articles in order to get a classification for these features.



Transform the new columns in matrices

Take the new categorical features and make them numerical through the creation of matrices, which contain a column for each class of each feature.



Use the new features in the *Outcome* Prediction

Append these new matrices to the dataset in order to exploit the information and achieve more accurate predictions.

Feature Engineering

ВМІ						
Underweight	BMI <= 18.5					
Normal	18.5 < BMI <= 24.9					
Overweight	24.9 < BMI <= 29.9					
Obesity 1	29.9 < BMI <= 34.9					
Obesity 2	34.9 < BMI <= 39.9					
Obesity 3	BMI > 39.9					

Glucose						
Glucose <= 140	Normal					
140 < Glucose <= 199	Prediabetes					
Glucose > 199	Diabetes					

Feature Engineering

Blood Pressure					
BP <= 80	Normal				
80 < BP <= 89	Prehypertension				
BP > 89	Hypertension				

Skin Thickness							
16.1 <= TSF <= 31.1	Normal						
TSF < 16.1 or TSF > 31.1	Abnormal						

Feature Engineering

The new categorical features are then converted into matrices, in order to fit the *RobustScaler* function used in the dataset preprocessing before model application.

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI Di	abetesPedigreeFunction	Age	Outcome	NewBMI	NewGlucose	NewBP	NewTSF
0	6	148.0	72.0	35.0	169.5	33.6	0.627	50	1	Obesity 1	Prediabetes	Normal	Abnormal
1	1	85.0	66.0	29.0	102.5	26.6	0.351	31	0	Overweight	Normal	Normal	Normal
2	8	183.0	64.0	32.0	169.5	23.3	0.672	32	1	Normal	Prediabetes	Normal	Abnormal
3	1	89.0	66.0	23.0	94.0	28.1	0.167	21	0	Overweight	Normal	Normal	Normal
4	0	137.0	40.0	35.0	168.0	43.1	2.288	33	1	Obesity 3	Normal	Normal	Abnormal
	NewBMI_Obe	sity New	BMI_Obesity Ne 2	wBMI_Obesity 3	NewBMI_0	Overweigl	nt NewBMI_Underweight	New	vGlucose_N	ormal NewC	Glucose_Predia	ibetes N	ewBP_Norm
0		1	0	0			0 0			0		1	
1		0	0	0			1 0			1		0	
2		0	0	0			0 0			0		1	
3		0	0	0			1 0	0		1		0	
4	2.	0	0) 1 e			0 0	1		1	00	00	

Outcome Prediction The application and tune of Supervised Learning algorithms

Supervised Learning Algorithms

Logistic Regression

is a model for analyzing a dataset in which there are one or more independent variables that determine an outcome.

Random Forest

is a model that uses multiple decision trees and aggregates their individual predictions to produce a final output.

KNeighbors Classifier

is an algorithm that classifies data points based on their proximity to their k nearest neighbors in the feature space.

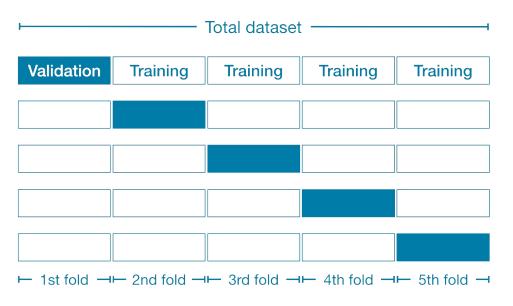
SVM

is an algorithm that classifies data by finding the optimal hyperplane that maximally separates the data into classes.

Cross Validation

Splits the data in *k* bins and runs *k* separate experiments, where each:

- Picks a bin as validation set
- Uses the other bins as training set
- Trains the model



Then collects the chosen metrics as **the average** of the results from those *k* experiments.

Chosen Metrics

Balanced Accuracy

Is similar to accuracy, but it takes into account the imbalance in the dataset by calculating the average of recall for each class.

Recall

it is the number of true positive predictions divided by the sum of the true positive predictions and false negative predictions.

ROC/AUC

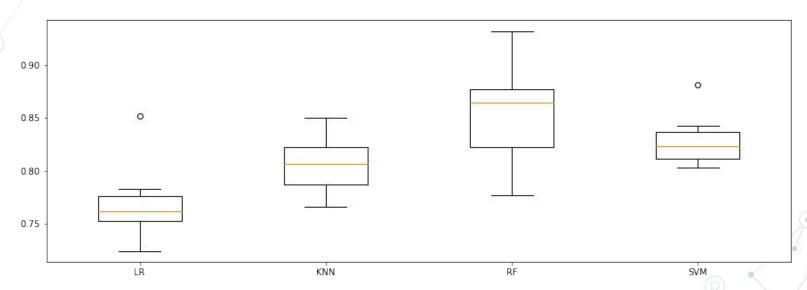
It indicates how much the model is able to distinguishing between positive and negative cases.

F1

Is the harmonic mean of precision and recall, often used when data is unbalanced.

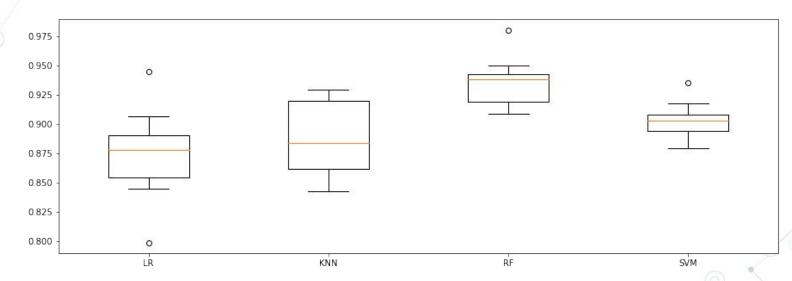
Balanced Accuracy

balanced_accuracy - algorithm comparison



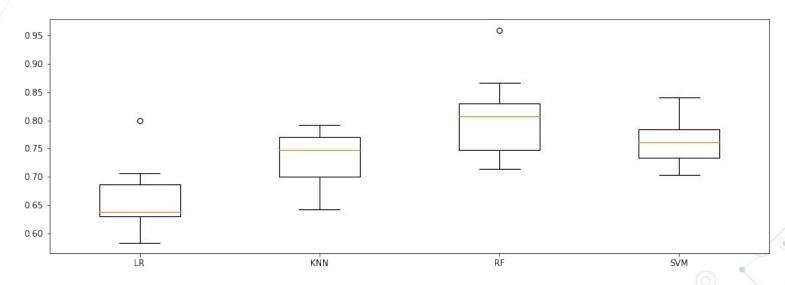
ROC/AUC



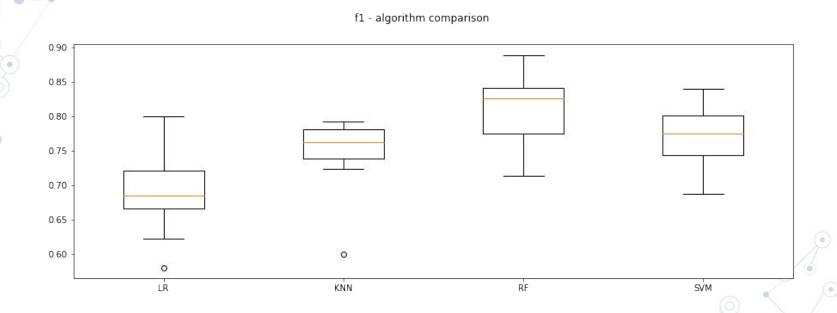


Recall









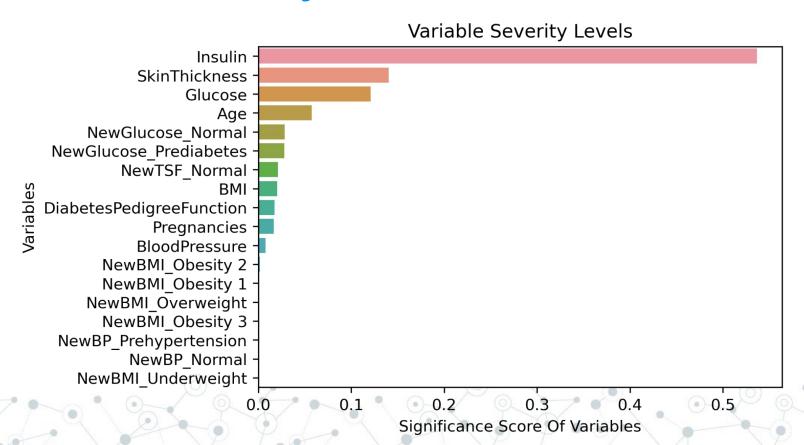
Random Forest Tuning

Hyperparameter	Description	Possible Values	Selected Value	
n_estimators	number of trees in the forest	[100, 500, 1000]	100	
max_features	max number of features considered for splitting a node	[2, 5, 7]	7	
min_samples_split	minimum number of data points placed in a node before it's split	[2, 5, 10]	2	
max_depth	max number of levels in each decision tree	[None, 5, 25]	None	
min_samples_leaf	minimum number of data points allowed in a leaf node	[1, 5, 15]	5	

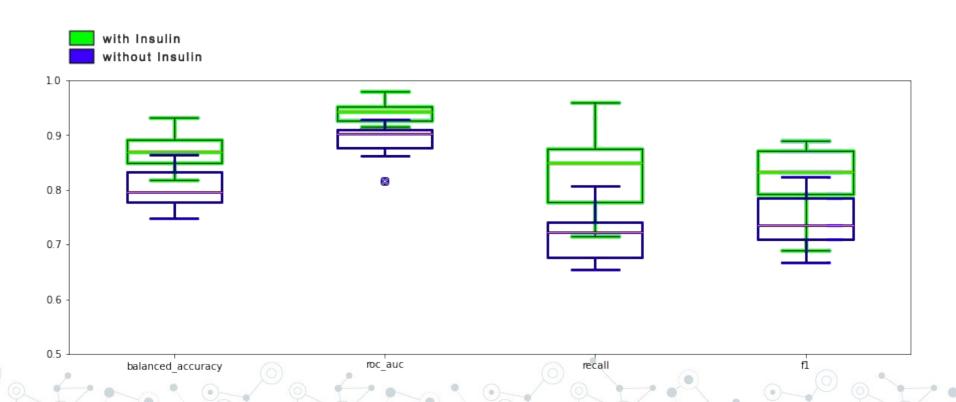
Final Results

Metric	Score Before Tuning	Score After Tuning	Improvement
Accuracy	0.853605	0.862414	0.008809
ROC/AUC	0.935069	0.945228	0.010159
Recall	0.804767	0.811582	0.006815
F1	0.808100	0.818264	0.010164

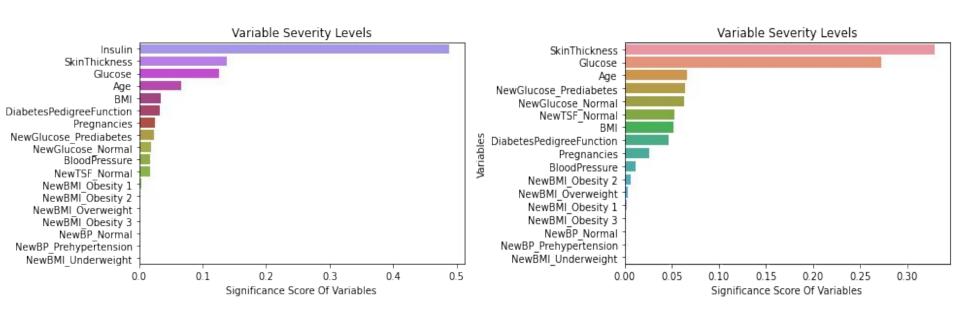
Variable Severity Levels



Final Results with and without Insulin



Severity Levels with and without Insulin



Thanks!



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