

# EDA & DEV.

# PIPELINE

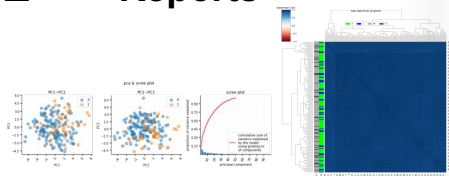
## Notebook 1

- ☐ EDA
- ☐ Feature Selection
- ☐ Testing Pre-processing Steps



## Notebook 2

- Development of:
  - ☐ Custom transformers
  - ☐ QC methods
  - ☐ Differential Gene Expr Reports



Patient Data

Tpm Data

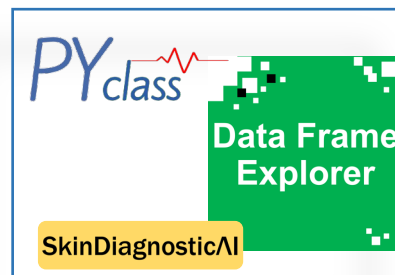


Data



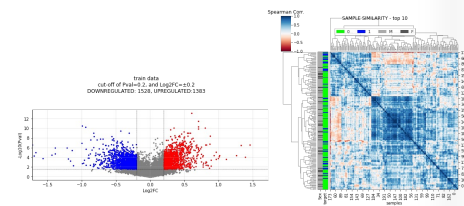
ML Models

External  
recourses  
+  
My  
recourses



## Notebook 3

- ☐ Cleaning
- ☐ Outlier removal
- ☐ Scaling
- ☐ Differential Gene expression



## Notebook 4

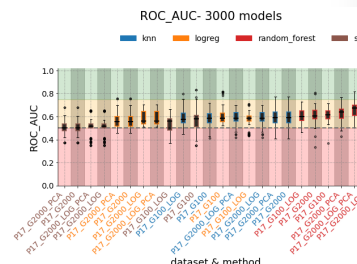
- ☐ Model Training
- ☐ Prediction saving
- ☐ GridSearch

~3000 models

model_name	dataset_name	id	ROC_AUC	precision	recall	FI	FI	event	count	model_params
560	svm	P12_0100_1790	0.740	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
578	svm	P12_0100_1802	0.736	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
538	random_forest	P12_0100_1808	0.733	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
540	random_forest	P12_0100_1809	0.737	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
526	random_forest	P12_0100_1806	0.724	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
498	random_forest	P12_0100_1801	0.718	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
584	svm	P12_0100_1788	0.717	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
536	random_forest	P12_0100_1803	0.714	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
576	svm	P12_0100_1800	0.701	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
588	svm	P12_0100_1792	0.689	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
341	logit	P12_0100_1803	0.686	0.778	0.006	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
338	logit	P12_0100_1801	0.686	0.778	0.006	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
337	logit	P12_0100_1804	0.684	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
336	logit	P12_0100_1806	0.682	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
335	logit	P12_0100_1805	0.680	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
187	svm	P12_0100_1803	0.680	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
313	svm	P12_0100_1801	0.680	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
146	svm	P12_0100_1803	0.680	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
303	svm	P12_0100_1803	0.680	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')
149	svm	P12_0100_1803	0.680	0.000	0.000	0.00	0.0	(D: 38, 5: 1)	(D: 30)	(C1: 0.5, gamma: 0.05, kernel: 'rbf')

## Notebook 5

- ☐ ROC analysis
- ☐ Model Selection
- ☐ Threshold calibration



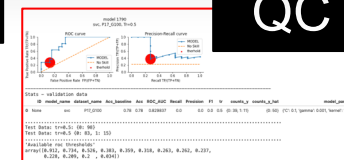
Results

Predictions

1	prediciton_test			
	y_hat	y_hat_probs	trhreshhold	
0	0	0.078297	0.5	
1	0	0.123569	0.5	
2	1	0.729784	0.5	

In Ardigen/data/results

QC report



In Notebook 05



# Early-Stage Design Choices

## TO CREATE A PIPELINE

*For running & selection of thousands of models  
with different datasets & parameters*

- 
- Divide the work into smaller pieces
  - Use parameters for controlling design choices
  - Consistent naming conventions,
  - Ability to add new steps and conditions, ,
  - QC data collected at each step
  - the same functions used in EDA, pipeline dev. and data analysis

# MAKE IT USER FRIENDLY

- Panel A: Similarity scores**

Heatmap showing similarity scores (0 to 1) between columns. The color scale ranges from blue (0) to red (1). The columns are grouped into three main categories: Clinical, Genomic, and Molecular. The rows are grouped into three main categories: Clinical, Genomic, and Molecular.

**Panel B: Missing data percentages**

Heatmap showing the percentage of missing data for various variables. The color scale ranges from blue (0%) to red (100%). The variables are grouped into three main categories: Clinical, Genomic, and Molecular.

**Panel C: Percentage of missing data**

Bar chart showing the percentage of missing data for each variable. The x-axis represents the percentage of missing data (0% to 100%). The y-axis lists the variables. The color scale ranges from blue (0%) to red (100%).

**Panel D: Percentage of missing data**

Bar chart showing the percentage of missing data for each variable. The x-axis represents the percentage of missing data (0% to 100%). The y-axis lists the variables. The color scale ranges from blue (0%) to red (100%).

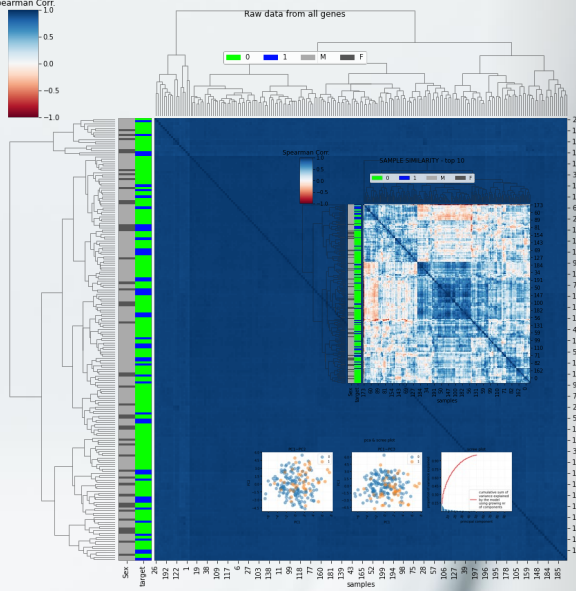
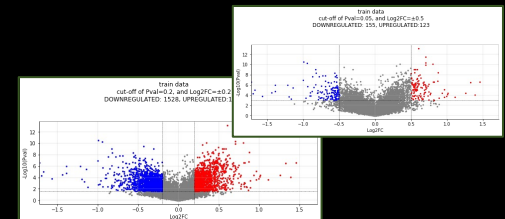
# Early-Stage Design Choices

## TO CREATE ALL THE FUNCTIONS

I used only most basic functions, from open source packages such as numpy, pandas, Matplotlib, and sklearn, to create all functions, presented in this project

That includes:

- Custom transformers,
- QC reports,
- Pipeline for differential gene expression
- And more...





# Model Training

## Notebook 04

I created large number of model (>3000) with 4 different techniques

```
1 # model
2 model = RandomForestClassifier()
3 model_name = "random_forest"
4
5 # data
6 path_in = PATH_data_interim
7 path_out = PATH_data_interim
8 dataset_name_list = ["P17_G2000", "P17_G2000_PCA",
9                     "P17_G100_LOG", "P17_G2000_LOG", "P17_G2000_LOG_PCA"] # 6 dataset variants prepared in different way,
10 rand_nr_list = [0,1,2]
11
12 # model parameters,
13 param_grid = ParameterGrid({
14     'max_depth': [4,5,6],
15     'n_estimators': [10,25,50,100,150, 200],
16     'class_weight': ['balanced'],
17 })
18
19 # train and evaluate models
20 rf_model_statistics, _, _ = train_and_evaluate_models(
21     model_name,
22     dataset_name_list,
23     rand_nr_list,
24     param_grid,
25     model,
26     path_in=path,
27     path_out=path,
28     none_at=None,
29     verbose=False,
30     b_verbose=True
31 )
32
33 # display top ten performing models
34 display(rf_model_statistics.loc[:, display_in_summary_table].sort_values("ROC_AUC", ascending=False).head(10))
```

The same syntax for all different models

I USED FOUR DIFFERENT ALGORITHMS –

- **Logistic regression** – classic solution for binary classification problems
- **Random Forest** – with different tree nr, and depth
- **SVM** – to apply kernel trick, for samples mixed in feature space

and SIX DIFFERENT DATASETS with

- different number of expressed differentially genes (~100, or ~2000)
- data from potential outliers or not
- I could use only patient data or only tpm data, (I had no time to do that but there is a simple parameter in the pipeline that allows that)
- Different scaling methods ....
- And many more choices that may be introduced and tested in Notebooks 2 and 3.

# Model Performance

## Notebook 05

Because of Large number of models (~3000 in total)

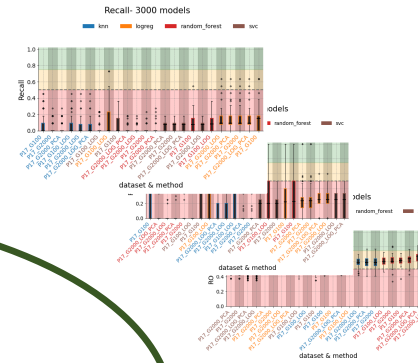
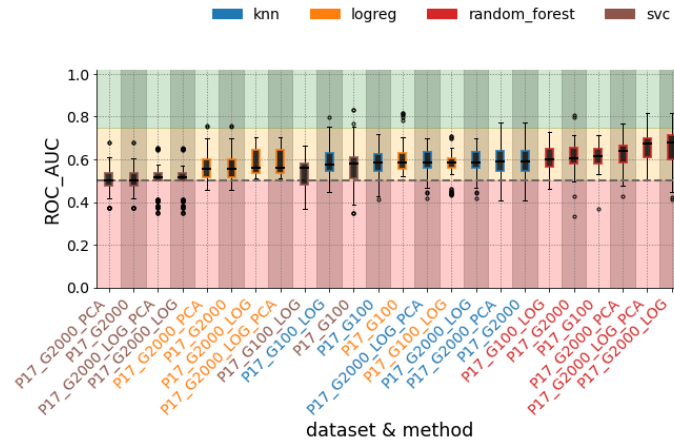
I provided three types of reports (plots and tables), to select and fine tune ML models in notebook 5

- **High Level Performance report:**
  - For tuning feature selection and data preprocessing pipeline
  - comparing methods, such as knn, svm, nn implemented
- **Intermediate Level Performance report:**
  - to select best model comparing methods, such as knn, svm, nn
- **Low High Level Performance report:**
  - Detailed examination of the best possible candidates, with large number of available statistics
  - hyperparameters, compare with similar models,
  - P threshold for classification
  - Plots, with ROC, PR curves,
  - Confusion matrices and more ....

# High Level

Compare any number of models on few plots

ROC\_AUC- 3000 models



# Intermediate Level

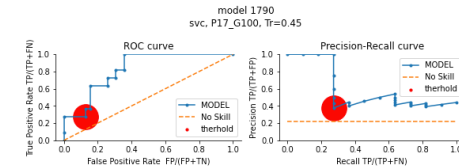
	model_name	dataset_name	ID	ROC_AUC	Precision	Recall	F1	tr	counts_y	counts_y_hat	model_params
566	svc	P17_G100	1790	0.740	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'C': 0.1, 'gamma': 0.001, 'kernel': 'rbf'}
578	svc	P17_G100	1802	0.736	0.111	0.030	0.048	0.5	{0: 39, 1: 11}	{0: 50}	{'C': 1, 'gamma': 0.001, 'kernel': 'rbf'}
518	random_forest	P17_G2000_LOG	1628	0.733	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'class_weight': 'balanced', 'max_depth': 5, '...
545	random_forest	P17_G2000_LOG_PCA	1691	0.727	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'class_weight': 'balanced', 'max_depth': 6, '...
526	random_forest	P17_G2000_LOG	1636	0.724	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'class_weight': 'balanced', 'max_depth': 6, '...
495	random_forest	P17_G2000	1461	0.718	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'class_weight': 'balanced', 'max_depth': 4, '...
564	svc	P17_G100	1788	0.717	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'C': 0.1, 'gamma': 'auto', 'kernel': 'rbf'}
536	random_forest	P17_G2000_LOG_PCA	1682	0.714	0.167	0.026	0.044	0.5	{0: 39, 1: 11}	{0: 50}	{'class_weight': 'balanced', 'max_depth': 5, '...
576	svc	P17_G100	1800	0.701	0.644	0.147	0.220	0.5	{0: 39, 1: 11}	{0: 45, 1: 5}	{'C': 1, 'gamma': 'auto', 'kernel': 'rbf'}
568	svc	P17_G100	1792	0.689	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'C': 0.1, 'gamma': 0.01, 'kernel': 'rbf'}
341	logreg	P17_G100	1053	0.666	0.778	0.086	0.151	0.5	{0: 39, 1: 11}	{0: 49, 1: 1}	{'C': 0.005994842503189409, 'class_weight': No...
339	logreg	P17_G100	1051	0.666	0.167	0.030	0.051	0.5	{0: 39, 1: 11}	{0: 50}	{'C': 0.000774263682681127, 'class_weight': No...
337	logreg	P17_G100	1049	0.664	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'C': 0.0001, 'class_weight': None, 'penalty': 'l...
336	logreg	P17_G100	1048	0.662	0.338	0.427	0.373	0.5	{0: 39, 1: 11}	{0: 34, 1: 16}	{'C': 0.0001, 'class_weight': 'balanced', 'pen...
338	logreg	P17_G100	1050	0.660	0.339	0.401	0.363	0.5	{0: 39, 1: 11}	{0: 34, 1: 16}	{'C': 0.000774263682681127, 'class_weight': 'b...
197	knn	P17_G2000_LOG	813	0.655	0.333	0.030	0.056	0.5	{0: 39, 1: 11}	{0: 49, 1: 1}	{'n_neighbors': 16, 'p': 1, 'weights': 'distan...
313	knn	P17_G2000_PCA	481	0.655	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'n_neighbors': 18, 'p': 1, 'weights': 'distan...
145	knn	P17_G2000	313	0.655	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'n_neighbors': 18, 'p': 1, 'weights': 'distan...
253	knn	P17_G2000_LOG_PCA	981	0.655	0.333	0.030	0.056	0.5	{0: 39, 1: 11}	{0: 49, 1: 1}	{'n_neighbors': 16, 'p': 1, 'weights': 'distan...
149	knn	P17_G2000	317	0.654	0.000	0.000	0.000	0.5	{0: 39, 1: 11}	{0: 50}	{'n_neighbors': 20, 'p': 1, 'weights': 'distan...

Select best candidate and compare with each other

- Consistent nomenclature
- And unique ID for each model

# Low Level

Fine tuning of model hyperparameters,



Stats - validation data												
ID	model_name	dataset_name	Acc_baseline	Acc	ROC_AUC	Recall	Precision	F1	tr	counts_y	counts_y_hat	model_params
0	None	svc	P17_G100	0.78	0.74	0.829837	0.272727	0.375	0.315789	0.45	{0: 39, 1: 11}	{0: 42, 1: 8} ('C': 0.1, 'gamma': 0.001, 'kernel': 'rbf')

.....

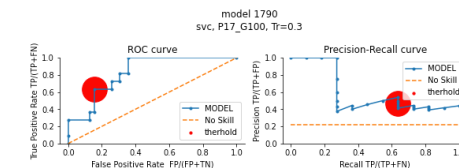
Test Data: tr=0.5: {0: 98}

Test Data: tr=0.45 {0: 81, 1: 17}

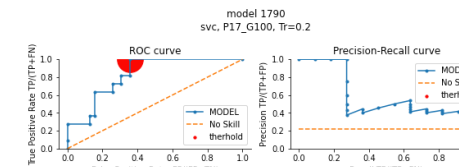
.....

'Available roc thresholds'

array([0.912, 0.734, 0.526, 0.383, 0.359, 0.318, 0.263, 0.262, 0.237, 0.228, 0.209, 0.2 , 0.034])



Stats - validation data												
ID	model_name	dataset_name	Acc_baseline	Acc	ROC_AUC	Recall	Precision	F1	tr	counts_y	counts_y_hat	model_params
0	None	svc	P17_G100	0.78	0.76	0.829837	0.636364	0.466667	0.538462	0.3	{0: 39, 1: 11}	{0: 35, 1: 15} ('C': 0.1, 'gamma': 0.001, 'kernel': 'rbf')
.....												
Test Data: tr=0.5: {0: 98}												
Test Data: tr=0.3 {0: 69, 1: 29}												
.....												
'Available roc thresholds'												
array([0.912, 0.734, 0.526, 0.383, 0.359, 0.318, 0.263, 0.262, 0.237,												
0.228, 0.209, 0.2, 0.034])												



Stats - validation data													
	ID	model_name	dataset_name	Acc_baseline	Acc	ROC_AUC	Recall	Precision	F1	tr	counts_y	counts_y_hat	model_params
0	None	svc	P17_G100	0.78	0.72	0.829837	1.0	0.44	0.611111	0.2	{0: 39, 1: 11}	{0: 25, 1: 25}	{'C': 0.1, 'gamma': 0.001, 'kernel': 'rbf'}

.....

Test Data: tr=0.5 {0: 98}

Test Data: tr=0.2 {0: 60, 1: 38}

.....

'Available roc thresholds'

array([0.912, 0.734, 0.526, 0.383, 0.359, 0.318, 0.263, 0.262, 0.237, 0.228, 0.209, 0.2, 0.034])