

# Import

```
In [ ]: import glob
import pandas as pd
from pycaret.classification import *
```

## Data Preprocessing

Combine training .tsv files into a Pandas DataFrame. Merge them on column **PATIENTID**.

```
In [ ]: path_train = '/home/kevin/Code/precisionFDA/Data/Brain-Cancer-Data/Training-
all_files = glob.glob(path_train + '/*.tsv')

df_train = pd.DataFrame()

for file in all_files:
    df_current_train = pd.read_csv(file, sep='\t')

    if df_train.empty:
        df_train = df_current_train
    else:
        df_train = pd.merge(df_train, df_current_train, how='outer', on='PAT
```

```
In [ ]: df_train.head()
```

```
Out[ ]:
```

	PATIENTID	SURVIVAL_STATUS	SEX	RACE	WHO_GRADING	CANCER_TYPE	A1BC
0	patient_290	1		NaN	II	ASTROCYTOMA	6.557793
1	patient_394	1		NaN	NaN	GBM	6.323015
2	patient_81	1		NaN	III	ASTROCYTOMA	6.669421
3	patient_307	1		NaN	NaN	UNCLASSIFIED	6.502573
4	patient_14	1		NaN	NaN	GBM	6.624505

5 rows × 19341 columns

Find columns that have NaN or empty values.

```
In [ ]: list_empty_null = df_train.columns[df_train.isna().any()].tolist()
print (list_empty_null)
```

```
['SEX', 'RACE', 'WHO_GRADING']
```

Replace empty values with NaN and then drop all rows that have NaN. Check for nulls.

```
In [ ]: df_train.replace(' ', pd.NA, inplace=True)
df_train.dropna(subset=['SEX', 'RACE', 'WHO_GRADING'], inplace=True)
```

```
df_train[['SEX', 'RACE', 'WHO_GRADING']].isnull().sum()
```

```
Out[ ]: SEX          0
        RACE        0
        WHO_GRADING  0
        dtype: int64
```

In the `CANCER_TYPE` column, drop rows with `UNKNOWN` and `UNCLASSIFIED` values.

```
In [ ]: df_train['CANCER_TYPE'].replace({'UNKNOWN':pd.NA}, inplace=True)
df_train['CANCER_TYPE'].replace({'UNCLASSIFIED':pd.NA}, inplace=True)
df_train.dropna(subset=['CANCER_TYPE'], inplace=True)
```

Reset DataFrame index.

```
In [ ]: df_train.reset_index(drop=True, inplace=True)
```

## Train Model

In `setup()`, set the `target` to `SURVIVAL_STATUS` and ignore `PATIENTID` column.

```
In [ ]: s = setup(
        df_train,
        target='SURVIVAL_STATUS',
        ignore_features=['PATIENTID'],
        session_id=1)
```

	Description	Value
0	Session id	1
1	Target	SURVIVAL_STATUS
2	Target type	Binary
3	Original data shape	(165, 19341)
4	Transformed data shape	(165, 19349)
5	Transformed train set shape	(115, 19349)
6	Transformed test set shape	(50, 19349)
7	Ignore features	1
8	Numeric features	19335
9	Categorical features	4
10	Preprocess	True
11	Imputation type	simple
12	Numeric imputation	mean
13	Categorical imputation	mode
14	Maximum one-hot encoding	25
15	Encoding method	None
16	Fold Generator	StratifiedKFold
17	Fold Number	10
18	CPU Jobs	-1
19	Use GPU	False
20	Log Experiment	False
21	Experiment Name	clf-default-name
22	USI	3bd9

Find the best model and save it.

```
In [ ]: best_model = compare_models()
```

	Model	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC	TT (Sec)
<b>rf</b>	Random Forest Classifier	0.8886	0.0000	1.0000	0.8861	0.9388	0.2866	0.3016	35.8340
<b>et</b>	Extra Trees Classifier	0.8879	0.0000	1.0000	0.8855	0.9384	0.2871	0.3019	36.1710
<b>lda</b>	Linear Discriminant Analysis	0.8795	0.7839	0.9800	0.8921	0.9327	0.2987	0.3226	25.0900
<b>lightgbm</b>	Light Gradient Boosting Machine	0.8788	0.0000	0.9900	0.8855	0.9332	0.2491	0.2690	57.3890
<b>ridge</b>	Ridge Classifier	0.8629	0.6800	0.9589	0.8890	0.9211	0.2760	0.2857	25.4010
<b>ada</b>	Ada Boost Classifier	0.8629	0.8044	0.9600	0.8921	0.9232	0.2516	0.2646	26.3610
<b>dummy</b>	Dummy Classifier	0.8530	0.0000	1.0000	0.8530	0.9203	0.0000	0.0000	37.0920
<b>lr</b>	Logistic Regression	0.8455	0.7783	0.9378	0.8858	0.9088	0.2528	0.2644	25.6820
<b>gbc</b>	Gradient Boosting Classifier	0.8455	0.7028	0.9178	0.9011	0.9085	0.3233	0.3280	30.7820
<b>nb</b>	Naive Bayes	0.8447	0.0000	0.8878	0.9302	0.9054	0.3945	0.4110	37.3830
<b>knn</b>	K Neighbors Classifier	0.8273	0.0000	0.9700	0.8491	0.9046	-0.0350	-0.0370	36.7930
<b>svm</b>	SVM - Linear Kernel	0.8189	0.7867	0.9500	0.8557	0.8973	0.0271	0.0313	25.6790
<b>dt</b>	Decision Tree Classifier	0.7841	0.0000	0.8567	0.8871	0.8691	0.2044	0.2186	36.9220
<b>qda</b>	Quadratic Discriminant Analysis	0.6394	0.4739	0.6644	0.8842	0.7419	0.0483	0.0628	24.7500

```
In [ ]: save_model(best_model, 'best_model_v3')
```

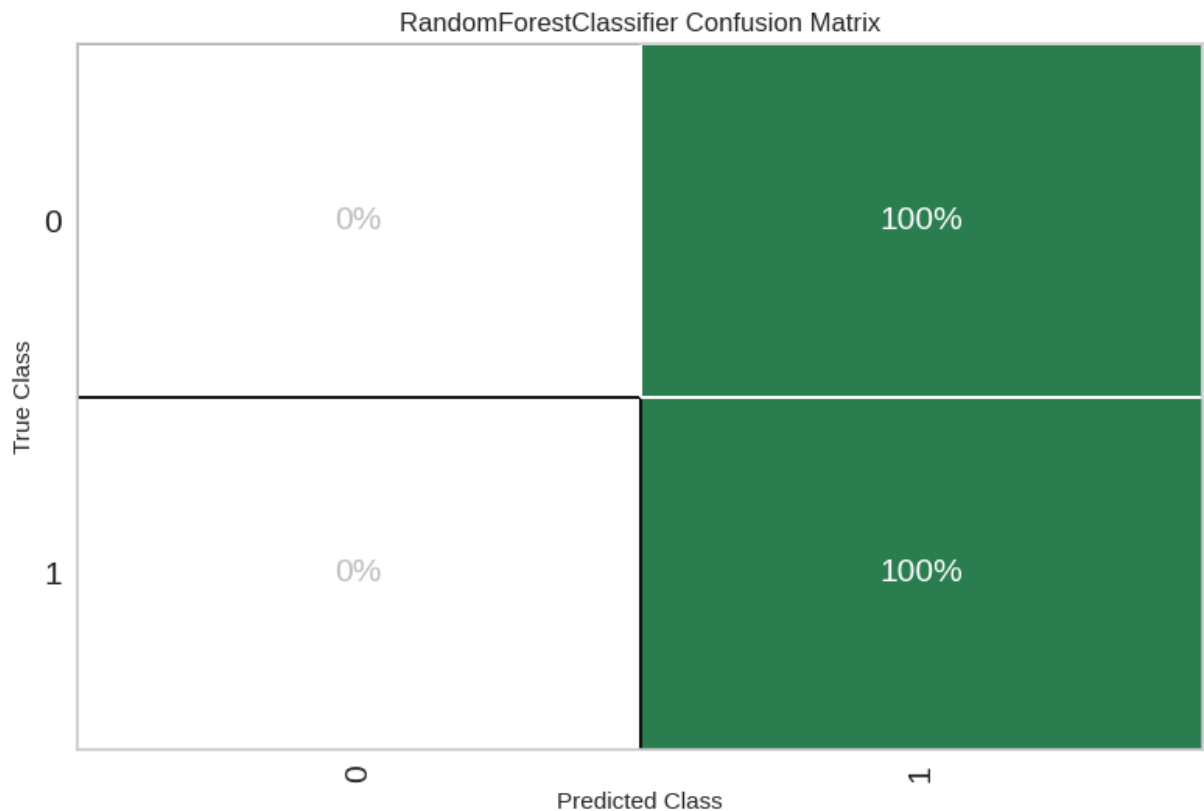
```
In [ ]: my_model = load_model('best_model_v3')
```

Evaluate the model.

```
In [ ]: evaluate_model(my_model)
```

```
interactive(children=(ToggleButtons(description='Plot Type:', icons=('',)), options= (('Pipeline Plot', 'pipelin...
```

```
In [ ]: plot_model(my_model, plot='confusion_matrix', plot_kwargs={'percent':True})
```



## Test Model

## Training Dataset

Predict on the training dataset.

```
In [ ]: predict_train = predict_model(my_model)
```

	Model	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
0	Random Forest Classifier	0.8400	0.4673	1.0000	0.8400	0.9130	0.0000	0.0000

## Test Dataset

Combine test .tsv files into a Pandas DataFrame. Merge them on column `PATIENTID`.

```
In [ ]: path_test = '/home/kevin/Code/precisionFDA/Data/Brain-Cancer-Data/Test-Datas
all_files = glob.glob(path_test + '/*.tsv')
df_test = pd.DataFrame()
for file in all_files:
```

```
df_current_test = pd.read_csv(file, sep='\t')

if df_test.empty:
    df_test = df_current_test
else:
    df_test = df_test.merge(df_current_test, how='outer', on='PATIENTID')
```

```
In [ ]: df_test.head()
```

```
Out[ ]:
```

	PATIENTID	A1BG	A1BG.AS1	A1CF	A2M	A2M.AS1	A2ML1	A4GALT
0	patient_54	6.552369	6.516572	5.670704	12.696699	6.244980	5.494503	7.031448
1	patient_456	6.341531	6.403964	5.575675	11.667261	6.208729	5.516190	7.077214
2	patient_484	6.150328	6.452206	5.465605	12.384793	5.971820	5.339407	6.787843
3	patient_441	6.569596	6.428329	5.404905	12.918034	5.915066	5.295160	6.975057
4	patient_370	6.902578	6.343173	5.243564	13.215173	6.058236	5.203713	6.786196

5 rows × 19340 columns

```
In [ ]: df_test.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 96 entries, 0 to 95
Columns: 19340 entries, PATIENTID to CANCER_TYPE
dtypes: float64(19335), object(5)
memory usage: 14.2+ MB
```

Predict on the test dataset.

```
In [ ]: predict_test = predict_model(my_model, df_test)
predict_test['prediction_score'].describe()
```

```
Out[ ]: count    96.000000
mean      0.830417
std       0.115375
min       0.520000
25%      0.780000
50%      0.850000
75%      0.922500
max       0.990000
Name: prediction_score, dtype: float64
```