

theAwesome_PredModel

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1 Prediction Model

- **Course:** Data Mining
- **Name:** Enes Kemal Ergin

Dataset from Breast Cancer UCI Machine Learning Repo

Attribute Information:

1. ID number
2. Diagnosis (M = malignant, B = benign)

3-32: Ten real-valued features are computed for each cell nucleus:

- radius (mean of distances from center to points on the perimeter)
- texture (standard deviation of gray-scale values)
- perimeter
- area
- smoothness (local variation in radius lengths)
- compactness ($\text{perimeter}^2 / \text{area} - 1.0$)
- concavity (severity of concave portions of the contour)
- concave points (number of concave portions of the contour)
- symmetry
- fractal dimension ("coastline approximation" - 1)

The mean, standard error and "worst" or largest (mean of the three largest values) of these features were computed for each image, resulting in 30 features. For instance, field 3 is Mean Radius, field 13 is Radius SE, field 23 is Worst Radius.

All feature values are recoded with four significant digits.

Missing attribute values: none

Class distribution: 357 benign, 212 malignant

1.1 Step 0: Data Preparation and Cleaning

```
In [19]: import pandas as pd
```

```
In [20]: # Read CSV data into df
df = pd.read_csv('./theAwesome_PredModel.csv')
# delete id column no need
```

```
df.drop('id',axis=1,inplace=True)
# delete unnamed column at the end
df.drop('Unnamed: 32',axis=1,inplace=True)
df.head()
```

```
Out[20]:
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	M	17.99	10.38	122.80	1001.0	
1	M	20.57	17.77	132.90	1326.0	
2	M	19.69	21.25	130.00	1203.0	
3	M	11.42	20.38	77.58	386.1	
4	M	20.29	14.34	135.10	1297.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.3001	0.14710	
1	0.08474	0.07864	0.0869	0.07017	
2	0.10960	0.15990	0.1974	0.12790	
3	0.14250	0.28390	0.2414	0.10520	
4	0.10030	0.13280	0.1980	0.10430	

	symmetry_mean	...	radius_worst	texture_worst	\
0	0.2419	...	25.38	17.33	
1	0.1812	...	24.99	23.41	
2	0.2069	...	23.57	25.53	
3	0.2597	...	14.91	26.50	
4	0.1809	...	22.54	16.67	

	perimeter_worst	area_worst	smoothness_worst	compactness_worst	\
0	184.60	2019.0	0.1622	0.6656	
1	158.80	1956.0	0.1238	0.1866	
2	152.50	1709.0	0.1444	0.4245	
3	98.87	567.7	0.2098	0.8663	
4	152.20	1575.0	0.1374	0.2050	

	concavity_worst	concave points_worst	symmetry_worst	\
0	0.7119	0.2654	0.4601	
1	0.2416	0.1860	0.2750	
2	0.4504	0.2430	0.3613	
3	0.6869	0.2575	0.6638	
4	0.4000	0.1625	0.2364	

	fractal_dimension_worst
0	0.11890
1	0.08902
2	0.08758
3	0.17300
4	0.07678

[5 rows x 31 columns]

```
In [8]: # Learn the unique values in diagnosis column
df.diagnosis.unique()
# M: Malign (Yes Cancer)
# B: Benign (No Cancer)

# I can also map M and B as 1 and 0 for more numerical
# approach
df['diagnosis'] = df['diagnosis'].map({'M':1, 'B':0})
```

1.2 Step 1: Data Information and Descriptive Statistics

Generate the information about your dataset: number of columns and rows, names and data types of the columns, memory usage of the dataset.

Hint: Pandas data frame info() function.

Generate descriptive statistics of all columns (input and output) of your dataset. Descriptive statistics for numerical columns include: count, mean, std, min, 25 percentile (Q1), 50 percentile (Q2, median), 75 percentile (Q3), max values of the columns. For categorical columns, determine distinct values and their frequency in each categorical column.

Hint: Pandas, data frame describe() function.

```
In [9]: df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
diagnosis                569 non-null int64
radius_mean              569 non-null float64
texture_mean             569 non-null float64
perimeter_mean           569 non-null float64
area_mean                569 non-null float64
smoothness_mean          569 non-null float64
compactness_mean         569 non-null float64
concavity_mean           569 non-null float64
concave points_mean      569 non-null float64
symmetry_mean            569 non-null float64
fractal_dimension_mean   569 non-null float64
radius_se                569 non-null float64
texture_se               569 non-null float64
perimeter_se             569 non-null float64
area_se                  569 non-null float64
smoothness_se            569 non-null float64
compactness_se           569 non-null float64
concavity_se             569 non-null float64
concave points_se        569 non-null float64
symmetry_se              569 non-null float64
fractal_dimension_se     569 non-null float64
```

```

radius_worst          569 non-null float64
texture_worst         569 non-null float64
perimeter_worst       569 non-null float64
area_worst            569 non-null float64
smoothness_worst      569 non-null float64
compactness_worst     569 non-null float64
concavity_worst       569 non-null float64
concave points_worst  569 non-null float64
symmetry_worst        569 non-null float64
fractal_dimension_worst 569 non-null float64
dtypes: float64(30), int64(1)
memory usage: 137.9 KB

```

```
In [10]: df.describe()
```

```

Out[10]:
      diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean \
count  569.000000   569.000000   569.000000   569.000000   569.000000
mean    0.372583    14.127292    19.289649    91.969033   654.889104
std     0.483918     3.524049     4.301036    24.298981   351.914129
min     0.000000     6.981000     9.710000    43.790000   143.500000
25%     0.000000    11.700000    16.170000    75.170000   420.300000
50%     0.000000    13.370000    18.840000    86.240000   551.100000
75%     1.000000    15.780000    21.800000   104.100000   782.700000
max     1.000000    28.110000    39.280000   188.500000  2501.000000

      smoothness_mean  compactness_mean  concavity_mean  concave points_mean \
count  569.000000      569.000000      569.000000      569.000000
mean    0.096360        0.104341        0.088799        0.048919
std     0.014064        0.052813        0.079720        0.038803
min     0.052630        0.019380        0.000000        0.000000
25%     0.086370        0.064920        0.029560        0.020310
50%     0.095870        0.092630        0.061540        0.033500
75%     0.105300        0.130400        0.130700        0.074000
max     0.163400        0.345400        0.426800        0.201200

      symmetry_mean  ...  radius_worst  texture_worst \
count  569.000000    ...      569.000000   569.000000
mean    0.181162    ...      16.269190   25.677223
std     0.027414    ...       4.833242    6.146258
min     0.106000    ...       7.930000   12.020000
25%     0.161900    ...      13.010000   21.080000
50%     0.179200    ...      14.970000   25.410000
75%     0.195700    ...      18.790000   29.720000
max     0.304000    ...      36.040000   49.540000

      perimeter_worst  area_worst  smoothness_worst  compactness_worst \
count  569.000000   569.000000   569.000000      569.000000

```

mean	107.261213	880.583128	0.132369	0.254265
std	33.602542	569.356993	0.022832	0.157336
min	50.410000	185.200000	0.071170	0.027290
25%	84.110000	515.300000	0.116600	0.147200
50%	97.660000	686.500000	0.131300	0.211900
75%	125.400000	1084.000000	0.146000	0.339100
max	251.200000	4254.000000	0.222600	1.058000

	concavity_worst	concave points_worst	symmetry_worst	\
count	569.000000	569.000000	569.000000	
mean	0.272188	0.114606	0.290076	
std	0.208624	0.065732	0.061867	
min	0.000000	0.000000	0.156500	
25%	0.114500	0.064930	0.250400	
50%	0.226700	0.099930	0.282200	
75%	0.382900	0.161400	0.317900	
max	1.252000	0.291000	0.663800	

	fractal_dimension_worst
count	569.000000
mean	0.083946
std	0.018061
min	0.055040
25%	0.071460
50%	0.080040
75%	0.092080
max	0.207500

[8 rows x 31 columns]

1.3 Step 2: Train Test Split

Split your data into Training and Test data set by randomly selecting; use 70% for training and 30 % for testing. Generate descriptive statistics of all columns (input and output) of Training and Test datasets. Review the descriptive statistics of input output columns in Train, Test and original Full (before the splitting operation) datasets and compare them to each other. Are they similar or not? Do you think Train and Test dataset are representative of the Full datasets ? why ?

Hint: Scikit learn, data train_test_split(), stratified function.

```
In [11]: df["diagnosis"].value_counts(df["diagnosis"].unique()[0])
```

```
Out[11]: 0    0.627417
         1    0.372583
         Name: diagnosis, dtype: float64
```

```
In [12]: # Splitting train and test data
         # .7 and .3
         import numpy as np # Linear algebra and numerical apps
```

```

msk = np.random.rand(len(df)) < 0.7
train_df = df[msk]
test_df = df[~msk]

```

```
In [15]: train_df.describe()
```

```

Out[15]:
      diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean \
count  422.000000    422.000000    422.000000    422.000000    422.000000
mean     0.383886     14.184332     19.225924     92.302227    663.239100
std      0.486908      3.650024      4.335877     25.114122    365.713579
min      0.000000      6.981000      9.710000     43.790000    143.500000
25%      0.000000     11.602500     16.162500     74.262500    412.550000
50%      0.000000     13.415000     18.760000     86.210000    555.900000
75%      1.000000     16.167500     21.575000    106.525000    812.200000
max      1.000000     28.110000     39.280000    188.500000   2501.000000

      smoothness_mean  compactness_mean  concavity_mean  concave points_mean \
count      422.000000      422.000000      422.000000      422.000000
mean         0.096341         0.103223         0.086774         0.048537
std          0.013840         0.051327         0.076341         0.038415
min          0.052630         0.019380         0.000000         0.000000
25%          0.086688         0.062370         0.028973         0.020195
50%          0.096530         0.091705         0.061745         0.033285
75%          0.105375         0.130200         0.123275         0.073580
max          0.163400         0.345400         0.426800         0.201200

      symmetry_mean  ...      radius_worst  texture_worst \
count      422.000000  ...      422.000000      422.000000
mean         0.180788  ...      16.405773      25.683531
std          0.027480  ...       5.027512       6.185842
min          0.120300  ...       7.930000      12.020000
25%          0.161900  ...      12.842500      20.992500
50%          0.178750  ...      14.975000      25.465000
75%          0.195225  ...      19.792500      30.100000
max          0.304000  ...      36.040000      47.160000

      perimeter_worst  area_worst  smoothness_worst  compactness_worst \
count      422.000000    422.000000      422.000000      422.000000
mean      108.022346    900.204976         0.132793         0.252230
std        34.791385    594.827452         0.022765         0.155543
min         50.410000    185.200000         0.071170         0.027290
25%         83.535000    507.425000         0.117275         0.144425
50%         98.115000    685.550000         0.132650         0.211750
75%        129.075000   1216.000000         0.146075         0.341175
max        251.200000   4254.000000         0.222600         0.937900

      concavity_worst  concave points_worst  symmetry_worst \
count      422.000000      422.000000      422.000000

```

mean	0.268960	0.114119	0.290083
std	0.205858	0.065442	0.062144
min	0.000000	0.000000	0.164800
25%	0.108950	0.064945	0.250250
50%	0.229800	0.098330	0.280600
75%	0.385300	0.162725	0.316875
max	1.252000	0.286700	0.663800

fractal_dimension_worst	
count	422.000000
mean	0.083759
std	0.017556
min	0.055210
25%	0.071572
50%	0.079460
75%	0.092082
max	0.173000

[8 rows x 31 columns]

1.4 Step 3: Analysis of the Output Column

Analyze the output columns in Train and Test dataset. If the output column is numerical then calculate the IQR (inter quartile range, Q3-Q1) and Range (difference between max and min value). If your output column is categorical then determine if the column is nominal or ordinal, why?. Is there a class imbalance problem? (check if there is big difference between the number of distinct values in your categorical output column)

```
In [13]: print(train_df["diagnosis"].value_counts(train_df["diagnosis"].unique()[0]))
         print(len(train_df))
         train_df.describe()
```

```
0    0.616114
1    0.383886
Name: diagnosis, dtype: float64
422
```

```
Out[13]:
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
count	422.000000	422.000000	422.000000	422.000000	422.000000	
mean	0.383886	14.184332	19.225924	92.302227	663.239100	
std	0.486908	3.650024	4.335877	25.114122	365.713579	
min	0.000000	6.981000	9.710000	43.790000	143.500000	
25%	0.000000	11.602500	16.162500	74.262500	412.550000	
50%	0.000000	13.415000	18.760000	86.210000	555.900000	
75%	1.000000	16.167500	21.575000	106.525000	812.200000	
max	1.000000	28.110000	39.280000	188.500000	2501.000000	

	smoothness_mean	compactness_mean	concavity_mean	concave	points_mean	\
--	-----------------	------------------	----------------	---------	-------------	---

count	422.000000	422.000000	422.000000	422.000000
mean	0.096341	0.103223	0.086774	0.048537
std	0.013840	0.051327	0.076341	0.038415
min	0.052630	0.019380	0.000000	0.000000
25%	0.086688	0.062370	0.028973	0.020195
50%	0.096530	0.091705	0.061745	0.033285
75%	0.105375	0.130200	0.123275	0.073580
max	0.163400	0.345400	0.426800	0.201200

	symmetry_mean	...	radius_worst	texture_worst	\
count	422.000000	...	422.000000	422.000000	
mean	0.180788	...	16.405773	25.683531	
std	0.027480	...	5.027512	6.185842	
min	0.120300	...	7.930000	12.020000	
25%	0.161900	...	12.842500	20.992500	
50%	0.178750	...	14.975000	25.465000	
75%	0.195225	...	19.792500	30.100000	
max	0.304000	...	36.040000	47.160000	

	perimeter_worst	area_worst	smoothness_worst	compactness_worst	\
count	422.000000	422.000000	422.000000	422.000000	
mean	108.022346	900.204976	0.132793	0.252230	
std	34.791385	594.827452	0.022765	0.155543	
min	50.410000	185.200000	0.071170	0.027290	
25%	83.535000	507.425000	0.117275	0.144425	
50%	98.115000	685.550000	0.132650	0.211750	
75%	129.075000	1216.000000	0.146075	0.341175	
max	251.200000	4254.000000	0.222600	0.937900	

	concavity_worst	concave points_worst	symmetry_worst	\
count	422.000000	422.000000	422.000000	
mean	0.268960	0.114119	0.290083	
std	0.205858	0.065442	0.062144	
min	0.000000	0.000000	0.164800	
25%	0.108950	0.064945	0.250250	
50%	0.229800	0.098330	0.280600	
75%	0.385300	0.162725	0.316875	
max	1.252000	0.286700	0.663800	

	fractal_dimension_worst
count	422.000000
mean	0.083759
std	0.017556
min	0.055210
25%	0.071572
50%	0.079460
75%	0.092082
max	0.173000

[8 rows x 31 columns]

```
In [14]: print(test_df["diagnosis"].value_counts(test_df["diagnosis"].unique()[0]))
print(len(test_df))
test_df.describe()
```

0 0.659864

1 0.340136

Name: diagnosis, dtype: float64

147

```
Out[14]:
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
count	147.000000	147.000000	147.000000	147.000000	147.000000	
mean	0.340136	13.963544	19.472585	91.012517	630.918367	
std	0.475374	3.140310	4.208618	21.842541	308.798010	
min	0.000000	8.950000	10.380000	56.360000	245.200000	
25%	0.000000	11.940000	16.570000	77.080000	439.300000	
50%	0.000000	13.170000	19.220000	86.870000	537.300000	
75%	1.000000	14.995000	22.215000	98.570000	696.250000	
max	1.000000	24.630000	33.560000	165.500000	1841.000000	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
count	147.000000	147.000000	147.000000	147.000000	
mean	0.096415	0.107551	0.094612	0.050017	
std	0.014738	0.056924	0.088731	0.040008	
min	0.064290	0.026750	0.000000	0.000000	
25%	0.085130	0.067720	0.032380	0.022085	
50%	0.094620	0.095090	0.060150	0.035280	
75%	0.105100	0.130900	0.133350	0.074435	
max	0.139800	0.311400	0.426400	0.182300	

	symmetry_mean	...	radius_worst	texture_worst	\
count	147.000000	...	147.000000	147.000000	
mean	0.182235	...	15.877095	25.659116	
std	0.027291	...	4.217536	6.052036	
min	0.106000	...	9.414000	14.100000	
25%	0.162050	...	13.220000	21.380000	
50%	0.181300	...	14.960000	25.210000	
75%	0.196850	...	17.375000	29.125000	
max	0.255600	...	31.010000	49.540000	

	perimeter_worst	area_worst	smoothness_worst	compactness_worst	\
count	147.000000	147.000000	147.000000	147.000000	
mean	105.076190	824.253741	0.131149	0.260109	
std	29.931954	486.390633	0.023061	0.162776	
min	60.900000	270.000000	0.085670	0.050360	

25%	86.160000	532.000000	0.114150	0.152400
50%	97.170000	686.500000	0.130100	0.216400
75%	115.800000	926.950000	0.144050	0.327600
max	206.800000	2944.000000	0.190900	1.058000

	concavity_worst	concave points_worst	symmetry_worst	\
count	147.000000	147.000000	147.000000	
mean	0.281458	0.116004	0.290055	
std	0.216822	0.066766	0.061277	
min	0.000000	0.000000	0.156500	
25%	0.131700	0.064410	0.251350	
50%	0.224100	0.101500	0.292900	
75%	0.379200	0.153000	0.320400	
max	1.105000	0.291000	0.488200	

	fractal_dimension_worst
count	147.000000
mean	0.084481
std	0.019493
min	0.055040
25%	0.071370
50%	0.081130
75%	0.091870
max	0.207500

[8 rows x 31 columns]

Our output/classification label is diagnosis(M(1)/B(0)), which is nominal categorical data.

The ratios between Benign and Malignant outputs in train and test are pretty similar to what we had in the full data.

1.5 Step 4: Scale Training and Test Dataset

Using one of the scaling method (max, min-max, standard or robust), create a scaler object and scale the numerical input columns of the Training dataset. Using the same scaler object, scale the numerical input columns of the Test set. Generate the descriptive statistics of the scaled input columns of Training and Test set.

If some of the input columns are categorical then convert them to binary columns using one-hotencoder() function (scikit learn) or dummy() function (Pandas data frame).

Hint: <http://scikit-learn.org/stable/modules/preprocessing.html#preprocessing>

```
In [13]: # I am going to apply min-max scaling for my data.
from sklearn import preprocessing
# Fitting the minmax scaled version for training data
minmax_scale = preprocessing.MinMaxScaler().fit(train_df.iloc[:, 1:])
# Now actually scale train and test data
train_df.iloc[:, 1:] = minmax_scale.transform(train_df.iloc[:, 1:])
test_df.iloc[:, 1:] = minmax_scale.transform(test_df.iloc[:, 1:])
```

```
/Users/eneskemalergin/anaconda3/lib/python3.5/site-packages/pandas/core/indexing.py:477: Setting
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead
```

```
See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html#
self.obj[item] = s
```

```
In [11]: train_df.head()
```

```
Out[11]:
```

	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
1	1	0.643144	0.272574	0.615783	0.501591	
2	1	0.601496	0.390260	0.595743	0.449417	
3	1	0.210090	0.360839	0.233501	0.102906	
5	1	0.258839	0.202570	0.267984	0.141506	
8	1	0.284869	0.409537	0.302052	0.159618	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
1	0.277910	0.181768	0.203799	0.366806	
2	0.588699	0.431017	0.462946	0.668583	
3	1.000000	0.811361	0.566135	0.549922	
5	0.816227	0.461996	0.370075	0.422844	
8	0.809976	0.533157	0.435976	0.488918	

	symmetry_mean	...	radius_worst	texture_worst	\
1	0.407367	...	0.606901	0.324132	
2	0.546587	...	0.556386	0.384462	
3	0.832611	...	0.248310	0.412066	
5	0.556338	...	0.268232	0.333808	
8	0.698808	...	0.268943	0.532442	

	perimeter_worst	area_worst	smoothness_worst	compactness_worst	\
1	0.539818	0.435214	0.301026	0.148757	
2	0.508442	0.374508	0.446763	0.381154	
3	0.241347	0.094008	0.909445	0.812734	
5	0.263908	0.136748	0.692253	0.479232	
8	0.277852	0.136183	0.629996	0.494080	

	concavity_worst	concave points_worst	symmetry_worst	\
1	0.192971	0.639175	0.233590	
2	0.359744	0.835052	0.403706	
3	0.548642	0.884880	1.000000	
5	0.427716	0.598282	0.477035	
8	0.430511	0.707904	0.554504	

	fractal_dimension_worst
1	0.222878
2	0.213433

```

3          0.773711
5          0.454939
8          0.342123

```

```
[5 rows x 31 columns]
```

```
In [12]: test_df.head()
```

```

Out[12]:      diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0           1      0.521037      0.022658      0.545989      0.363733
4           1      0.629893      0.156578      0.630986      0.489290
6           1      0.533343      0.347311      0.523875      0.380276
7           1      0.318472      0.376057      0.320710      0.184263
17          1      0.433007      0.370984      0.444406      0.277964

      smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
0          0.698712      0.792037      0.703799      0.768949
4          0.472434      0.347893      0.464353      0.545217
6          0.401550      0.274891      0.264306      0.386827
7          0.704963      0.445126      0.219653      0.312859
17         0.681210      0.560763      0.403846      0.537376

      symmetry_mean  ...      radius_worst  texture_worst  \
0          0.736186  ...      0.620776      0.151110
4          0.405742  ...      0.519744      0.132328
6          0.397616  ...      0.531839      0.445077
7          0.615385  ...      0.324795      0.458736
17         0.598050  ...      0.463536      0.553785

      perimeter_worst  area_worst  smoothness_worst  compactness_worst  \
0          0.668310      0.450698      0.572692      0.616677
4          0.506948      0.341575      0.397241      0.166732
6          0.511928      0.349194      0.445348      0.218115
7          0.299766      0.174941      0.595331      0.326157
17         0.430251      0.277674      0.690838      0.379982

      concavity_worst  concave points_worst  symmetry_worst  \
0          0.568610      0.912027      0.598462
4          0.319489      0.558419      0.157500
6          0.302236      0.663918      0.295289
7          0.213898      0.534708      0.321506
17         0.382109      0.712371      0.422038

      fractal_dimension_worst
0          0.418864
4          0.142595
6          0.187853
7          0.393939

```

17

0.388036

[5 rows x 31 columns]

1.6 Step 5: Build Predictive Model

Using one of the methods (K-Nearest Neighbor, Naïve Bayes, Neural Network, Support Vector Machines, Decision Tree), build your predictive model using the scaled input columns of Training set. You can use any value for the model parameters, or use the default values. In building your model, use k-fold crossvalidation.

Hint: - http://scikit-learn.org/stable/supervised_learning.html#supervised-learning
-, - http://scikit-learn.org/stable/modules/cross_validation.html

```
In [15]: # Input and Output
```

```
inp_train = train_df.iloc[:, 1:]
out_train = train_df["diagnosis"]
inp_test = test_df.iloc[:, 1:]
out_test = test_df["diagnosis"]
```

```
In [16]: # Naive Bayes:
```

```
from sklearn.naive_bayes import GaussianNB
from sklearn.model_selection import cross_val_score
nb_model = GaussianNB()
nb_model.fit(inp_train, out_train)
```

```
# Cross validation score of my model
```

```
nb_model_scores = cross_val_score(nb_model, inp_train, out_train, cv=10, scoring='accuracy')
print(nb_model_scores)
```

```
[ 0.95      0.875      0.9       0.9       0.925      0.925      0.95
 0.925      0.94871795  0.94736842]
```

1.7 Step 6. Model Predictions on Training Dataset

Apply your model to input (scaled) columns of Training dataset to obtain the predicted output for Training dataset. If your model is regression then plot actual output versus predicted output column of Training dataset. If your model is classification then generate confusion matrix on actual and predicted columns of Training dataset.

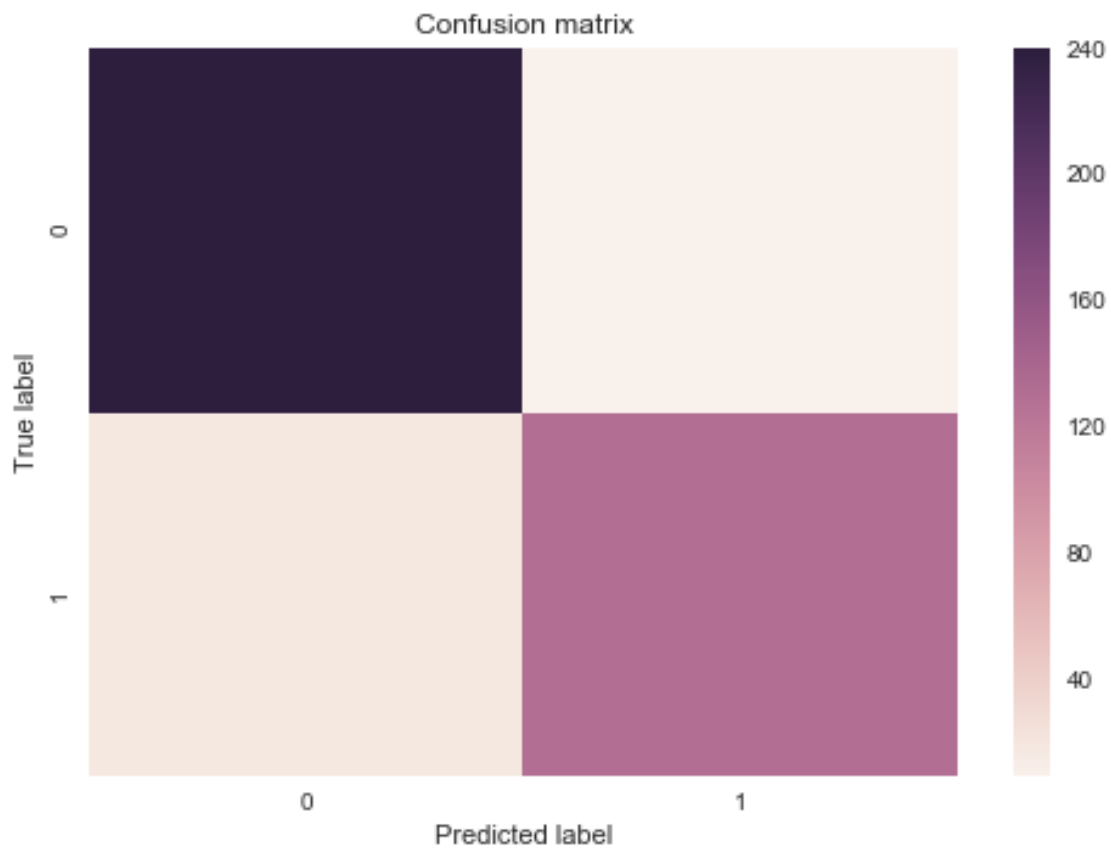
Hint: Matplotlib, Seaborn, Bokeh scatter(), plot() functions - http://scikit-learn.org/0.15/auto_examples/plot_confusion_matrix.html - http://scikit-learn.org/stable/auto_examples/model_selection/plot_confusion_matrix.html

```
In [17]: # importing libraries for plotting
```

```
# Importing library for confusion matrix
from sklearn.metrics import confusion_matrix
import matplotlib.pyplot as plt
import seaborn as sns
sns.set(style='darkgrid')
```

```
In [18]: # train prediction for train data
out_train_pred = nb_model.predict(inp_train)
# Compute confusion matrix for prediction of train
cm = confusion_matrix(out_train, out_train_pred)
print(cm)
# Show confusion matrix in a separate window
sns.heatmap(cm)
plt.title('Confusion matrix')
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()
```

```
[[240   9]
 [ 18 130]]
```



1.8 Step 7. Model Predictions on Test Dataset

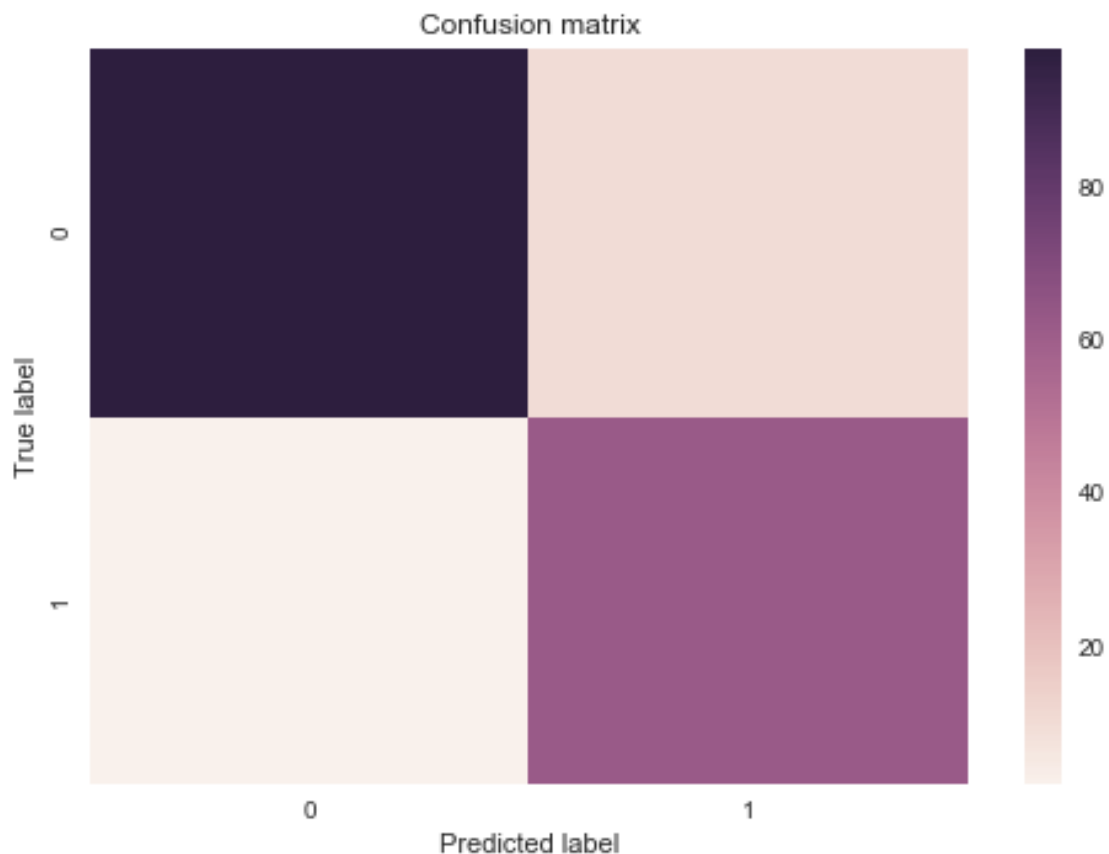
Apply your model to input (scaled) columns of Test dataset to obtain the predicted output for Test dataset. If your model is regression then plot actual output versus predicted output column of

Test dataset. If your model is classification then generate confusion matrix on actual and predicted columns of Test dataset.

Hint: Matplotlib, Seaborn, Bokeh scatter(), plot() functions - http://scikit-learn.org/0.15/auto_examples/plot_confusion_matrix.html - http://scikit-learn.org/stable/auto_examples/model_selection/plot_confusion_matrix.html

```
In [19]: # train prediction for train data
out_test_pred = nb_model.predict(inp_test)
# Compute confusion matrix for prediction of train
cm = confusion_matrix(out_test, out_test_pred)
print(cm)
# Show confusion matrix in a separate window
sns.heatmap(cm)
plt.title('Confusion matrix')
plt.ylabel('True label')
plt.xlabel('Predicted label')
plt.show()
```

```
[[98 10]
 [ 2 62]]
```



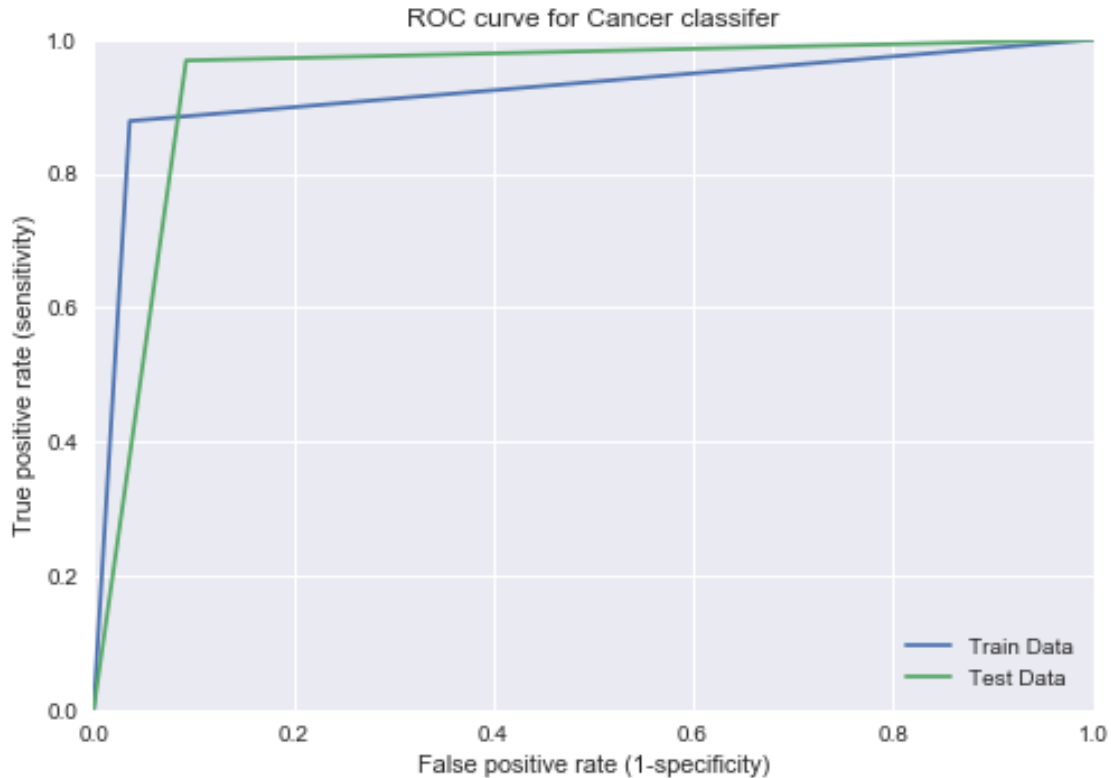
1.9 Step 8. Model Performance

Using one of the error (evaluation) metrics (classification or regression), calculate the performance of the model on Training set and Test set. Compare the performance of the model on Training and Test set. Which one (Training or Testing performance) is better, is there an overfitting case, why ?. Would you deploy (Productionize) this model for using in actual usage in your business system? why ?

Classification Metrics: Accuracy, Precision, Recall, F-score, Recall, AUC, ROC etc Regression Metrics: RMSE, MSE, MAE, R2 etc

- http://scikit-learn.org/stable/model_selection.html#model-selection
- http://scikit-learn.org/stable/modules/model_evaluation.html#classification-report

```
In [20]: # I would like to use ROC
         # Area under ROC Curve (or AUC for short) is
         # a performance metric for binary classification problems.
         from sklearn.metrics import roc_curve
         # ROC curve for train data
         fpr,tpr,thresholds = roc_curve(out_train, out_train_pred)
         # plot the curve
         plt.plot(fpr, tpr, label="Train Data")
         # ROC curve for test data
         fpr, tpr, thresholds = roc_curve(out_test, out_test_pred)
         # Plotting the curves
         plt.plot(fpr, tpr, label="Test Data")
         plt.xlim([0.0,1.0])
         plt.ylim([0.0,1.0])
         plt.title('ROC curve for Cancer classifier')
         plt.xlabel('False positive rate (1-specificity)')
         plt.ylabel('True positive rate (sensitivity)')
         plt.legend(loc=4,)
         plt.show()
```

As it seems clear in the plot we created, the Test data is better than the Train data. Which is not expected. **I do not see the traces of overfitting since the test data is also performing well.**

But there is also another chance that Test data is also overfitting... ??

Naive bayes on this particular data set works really good. It might be good for fast prototyping and usage.

1.10 Step 9. Update the Model

Go back to Step5, and choose different values of the model parameters and re-train the model. Repeat Steps: 6 and 7. Using the same error metric, generate the accuracy of the model on Training and Test dataset. Did you get a better performance on Training or Test set? Explain why the new model performs better or worse than the former model.

Let's try to calibrate the GaussianNB(); I will be using isotonic, sigmoid calibration for Gaussian Naive Bayes:

```
In [19]: # For Training Data:
          # Let's remember we have GaussianNB model with
          # no calibration called out_train_pred
```

```

from sklearn.calibration import CalibratedClassifierCV
# Gaussian Naive-Bayes with isotonic calibration
nb_model_isotonic = CalibratedClassifierCV(nb_model, cv=2, method='isotonic')
nb_model_isotonic.fit(inp_train, out_train)
out_train_isotonic = nb_model_isotonic.predict_proba(inp_train)[:, 1]
out_test_isotonic = nb_model_isotonic.predict_proba(inp_test)[:, 1]

In [20]: # Gaussian Naive-Bayes with sigmoid calibration
nb_model_sigmoid = CalibratedClassifierCV(nb_model, cv=2, method='sigmoid')
nb_model_sigmoid.fit(inp_train, out_train)
out_train_sigmoid = nb_model_sigmoid.predict_proba(inp_train)[:, 1]
out_test_sigmoid = nb_model_sigmoid.predict_proba(inp_test)[:, 1]

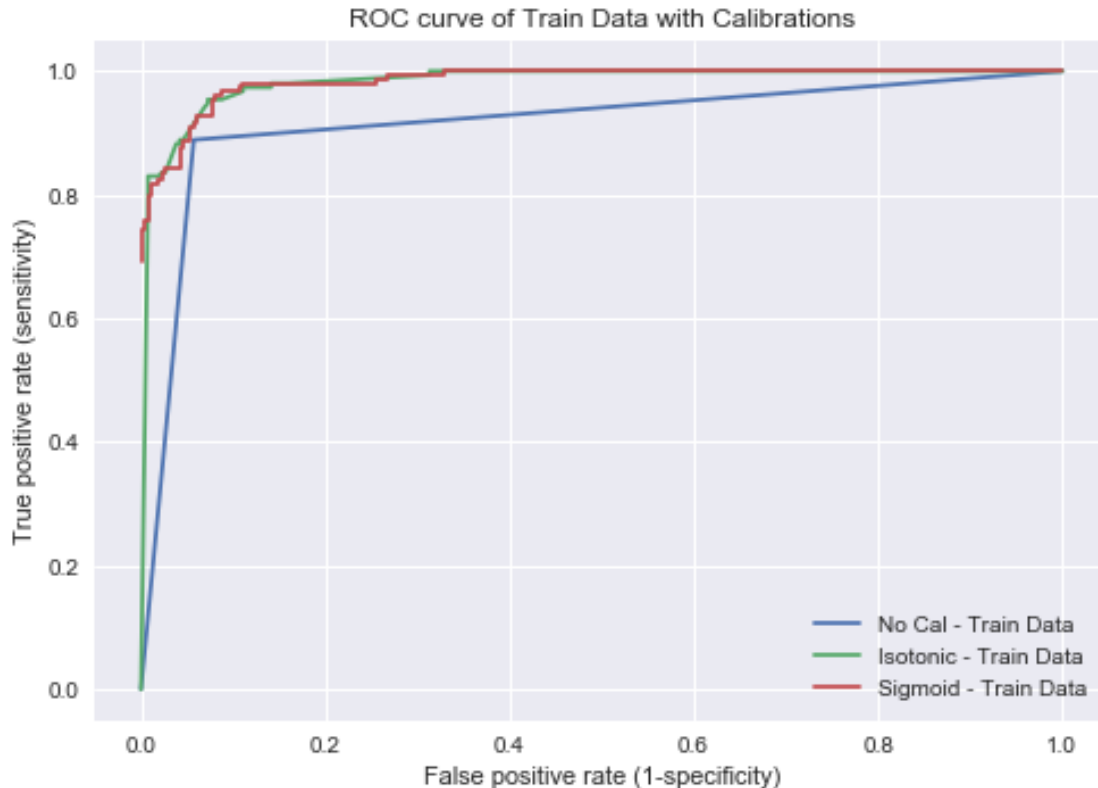
In [21]: ## Plotting the comparison of train Data roc_curves
# ROC curve for train data no calibration
fpr,tpr,thresholds = roc_curve(out_train, out_train_pred)
# plot the curve
plt.plot(fpr, tpr, label="No Cal - Train Data")

# ROC curve for train data isotonic calibration
fpr,tpr,thresholds = roc_curve(out_train, out_train_isotonic)
# plot the curve
plt.plot(fpr, tpr, label="Isotonic - Train Data")

# ROC curve for train data sigmoid calibration
fpr,tpr,thresholds = roc_curve(out_train, out_train_sigmoid)
# plot the curve
plt.plot(fpr, tpr, label="Sigmoid - Train Data")

plt.xlim([-0.05,1.05])
plt.ylim([-0.05,1.05])
plt.title('ROC curve of Train Data with Calibrations')
plt.xlabel('False positive rate (1-specificity)')
plt.ylabel('True positive rate (sensitivity)')
plt.legend(loc=4,)
plt.show()

```

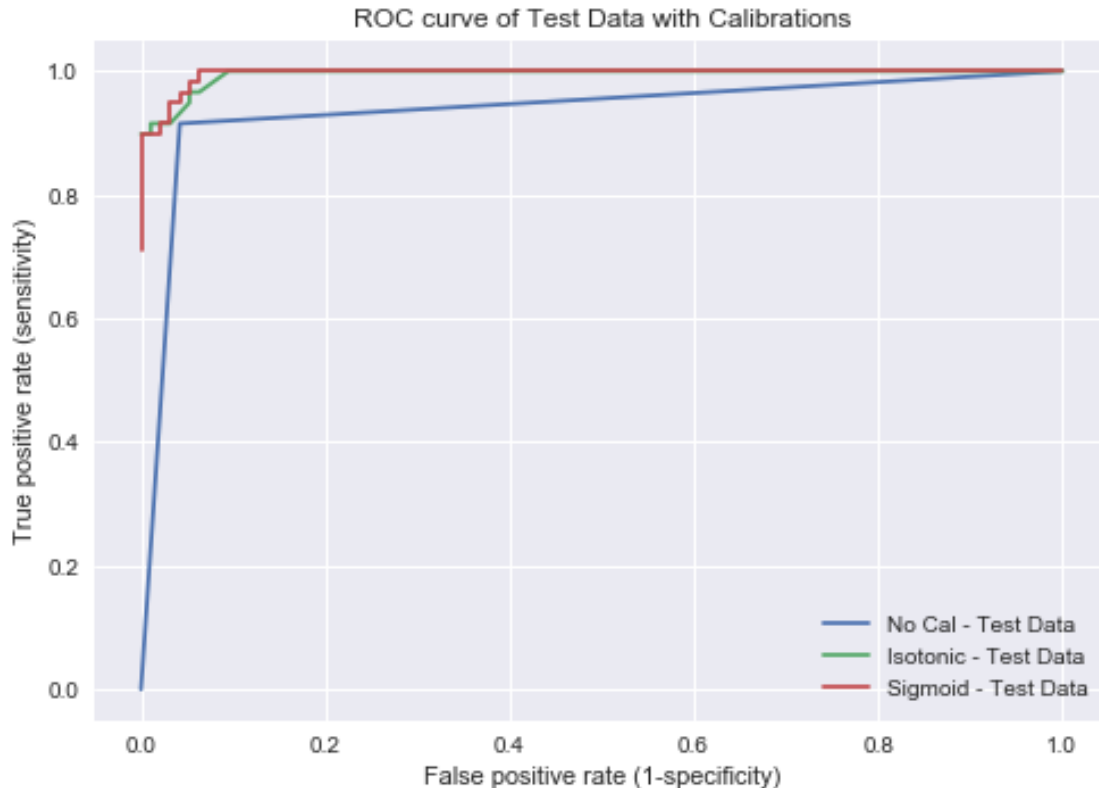


```
In [22]: # ROC curve for test data no calibration
fpr, tpr, thresholds = roc_curve(out_test, out_test_pred)
# Plotting the curves
plt.plot(fpr, tpr, label="No Cal - Test Data")

# ROC curve for test data isotonic calibration
fpr,tpr,thresholds = roc_curve(out_test, out_test_isotonic)
# plot the curve
plt.plot(fpr, tpr, label="Isotonic - Test Data")

# ROC curve for test data sigmoid calibration
fpr,tpr,thresholds = roc_curve(out_test, out_test_sigmoid)
# plot the curve
plt.plot(fpr, tpr, label="Sigmoid - Test Data")

plt.xlim([-0.05,1.05])
plt.ylim([-0.05,1.05])
plt.title('ROC curve of Test Data with Calibrations')
plt.xlabel('False positive rate (1-specificity)')
plt.ylabel('True positive rate (sensitivity)')
plt.legend(loc=4,)
plt.show()
```



Extra calibration which add one more layer above the GaussianNB() works better than no calibration. Isotonic and Sigmoid calibrations are performed better than the initial no calibration version.

1.11 Step 10. Change the Error Metric

Choose another error metric other than you used in Step 8 and evaluate the performance of the model on Training and Test dataset by generating the accuracy of the model based on the new metric. Compare the results and explain which error metric is better for your modeling and why?

```
In [23]: # Checking the error metric to Brier scores
from sklearn.metrics import brier_score_loss

# Checking for only test data predictions

print("Brier scores: (the smaller the better)")
mdl_score = brier_score_loss(out_test, out_test_pred)
print("No calibration: %1.3f" % mdl_score)
mdl_isotonic_score = brier_score_loss(out_test, out_test_isotonic)
print("With isotonic calibration: %1.3f" % mdl_isotonic_score)
mdl_sigmoid_score = brier_score_loss(out_test, out_test_sigmoid)
print("With sigmoid calibration: %1.3f" % mdl_sigmoid_score)
```

Brier scores: (the smaller the better)

No calibration: 0.058

With isotonic calibration: 0.026

With sigmoid calibration: 0.037

```
In [24]: # Applying other metrics
from sklearn import metrics
print("Printing the different metric results for Not calibrated test data")
print("-"*60)
print("Precision score: %1.3f" %
      metrics.precision_score(out_test, out_test_pred))
print("Recall score on: %1.3f" %
      metrics.recall_score(out_test, out_test_pred))
print("F1 score on: %1.3f" %
      metrics.f1_score(out_test, out_test_pred) )
print("Fbeta score with b=0.5 on: %1.3f" %
      metrics.fbeta_score(out_test, out_test_pred, beta=0.5))
print("Fbeta score with b=1.0 on: %1.3f" %
      metrics.fbeta_score(out_test, out_test_pred, beta=1))
print("Fbeta score with b=2.0 on: %1.3f" %
      metrics.fbeta_score(out_test, out_test_pred, beta=2))
```

Printing the different metric results for Not calibrated test data

```
-----
Precision score: 0.931
Recall score on: 0.915
F1 score on: 0.923
Fbeta score with b=0.5 on: 0.928
Fbeta score with b=1.0 on: 0.923
Fbeta score with b=2.0 on: 0.918
```

When it comes to selecting a way to show how well my models are working I always use both error and accuracy together. In this specific task I had an opportunity to try different metrics available in scikit-learn. In terms of showing a better results, for this model, I would go with Recall score. However I usually go with precision_score.

As the ending remarks for the project I would like to emphasize that Naive Bayes is working suprisingly good for this particular dataset (Breast Cancer from UCI ML website). I am suspecting that my model overfitted because for both test and train data is produced ~92-98% precision, which is quite impossible with ~30 or so features and 500 data points.

I could use more data and selected features to get more real results. For the Final project I am planning to use some techniques that will allow me to select features and only work with them.

-Enes K. Ergin-