

Breast cancer prediction

June 1, 2025

1 Logistic Regression of Breast cancer wisconsin Dataset

1.1 Importing the dataset

```
[3]: import pandas as pd
df = pd.read_csv("C:/Users/arunj/Downloads/dataA.csv")
df
```

```
[3]:
```

	id	diagnosis	radius_mean	texture_mean	perimeter_mean	area_mean	\
0	842302	M	17.99	10.38	122.80	1001.0	
1	842517	M	20.57	17.77	132.90	1326.0	
2	84300903	M	19.69	21.25	130.00	1203.0	
3	84348301	M	11.42	20.38	77.58	386.1	
4	84358402	M	20.29	14.34	135.10	1297.0	
..	
564	926424	M	21.56	22.39	142.00	1479.0	
565	926682	M	20.13	28.25	131.20	1261.0	
566	926954	M	16.60	28.08	108.30	858.1	
567	927241	M	20.60	29.33	140.10	1265.0	
568	92751	B	7.76	24.54	47.92	181.0	

	smoothness_mean	compactness_mean	concavity_mean	concave points_mean	\
0	0.11840	0.27760	0.30010	0.14710	
1	0.08474	0.07864	0.08690	0.07017	
2	0.10960	0.15990	0.19740	0.12790	
3	0.14250	0.28390	0.24140	0.10520	
4	0.10030	0.13280	0.19800	0.10430	
..	
564	0.11100	0.11590	0.24390	0.13890	
565	0.09780	0.10340	0.14400	0.09791	
566	0.08455	0.10230	0.09251	0.05302	
567	0.11780	0.27700	0.35140	0.15200	
568	0.05263	0.04362	0.00000	0.00000	

	texture_worst	perimeter_worst	area_worst	smoothness_worst	\
0	17.33	184.60	2019.0	0.16220	
1	23.41	158.80	1956.0	0.12380	
2	25.53	152.50	1709.0	0.14440	

3	...	26.50	98.87	567.7	0.20980
4	...	16.67	152.20	1575.0	0.13740
..
564	...	26.40	166.10	2027.0	0.14100
565	...	38.25	155.00	1731.0	0.11660
566	...	34.12	126.70	1124.0	0.11390
567	...	39.42	184.60	1821.0	0.16500
568	...	30.37	59.16	268.6	0.08996

	compactness_worst	concavity_worst	concave points_worst	symmetry_worst	\
0	0.66560	0.7119	0.2654	0.4601	
1	0.18660	0.2416	0.1860	0.2750	
2	0.42450	0.4504	0.2430	0.3613	
3	0.86630	0.6869	0.2575	0.6638	
4	0.20500	0.4000	0.1625	0.2364	
..	
564	0.21130	0.4107	0.2216	0.2060	
565	0.19220	0.3215	0.1628	0.2572	
566	0.30940	0.3403	0.1418	0.2218	
567	0.86810	0.9387	0.2650	0.4087	
568	0.06444	0.0000	0.0000	0.2871	

	fractal_dimension_worst	Unnamed: 32
0	0.11890	NaN
1	0.08902	NaN
2	0.08758	NaN
3	0.17300	NaN
4	0.07678	NaN
..
564	0.07115	NaN
565	0.06637	NaN
566	0.07820	NaN
567	0.12400	NaN
568	0.07039	NaN

[569 rows x 33 columns]

1.2 data preprocessing

```
[6]: # Drop unnecessary columns
df = df.drop(columns=["id", "Unnamed: 32"], errors='ignore')

# Encode target variable (M = 1, B = 0)
df["diagnosis"] = LabelEncoder().fit_transform(df["diagnosis"])

df
```

```

[6]:      diagnosis  radius_mean  texture_mean  perimeter_mean  area_mean  \
0          1         17.99         10.38         122.80        1001.0
1          1         20.57         17.77         132.90        1326.0
2          1         19.69         21.25         130.00        1203.0
3          1         11.42         20.38          77.58         386.1
4          1         20.29         14.34         135.10        1297.0
..      ...
564        1         21.56         22.39         142.00        1479.0
565        1         20.13         28.25         131.20        1261.0
566        1         16.60         28.08         108.30         858.1
567        1         20.60         29.33         140.10        1265.0
568        0          7.76         24.54          47.92         181.0

      smoothness_mean  compactness_mean  concavity_mean  concave points_mean  \
0          0.11840         0.27760         0.30010         0.14710
1          0.08474         0.07864         0.08690         0.07017
2          0.10960         0.15990         0.19740         0.12790
3          0.14250         0.28390         0.24140         0.10520
4          0.10030         0.13280         0.19800         0.10430
..      ...
564        0.11100         0.11590         0.24390         0.13890
565        0.09780         0.10340         0.14400         0.09791
566        0.08455         0.10230         0.09251         0.05302
567        0.11780         0.27700         0.35140         0.15200
568        0.05263         0.04362         0.00000         0.00000

      symmetry_mean  ...  radius_worst  texture_worst  perimeter_worst  \
0          0.2419  ...         25.380         17.33         184.60
1          0.1812  ...         24.990         23.41         158.80
2          0.2069  ...         23.570         25.53         152.50
3          0.2597  ...         14.910         26.50          98.87
4          0.1809  ...         22.540         16.67         152.20
..      ...  ...
564        0.1726  ...         25.450         26.40         166.10
565        0.1752  ...         23.690         38.25         155.00
566        0.1590  ...         18.980         34.12         126.70
567        0.2397  ...         25.740         39.42         184.60
568        0.1587  ...          9.456         30.37          59.16

      area_worst  smoothness_worst  compactness_worst  concavity_worst  \
0          2019.0         0.16220         0.66560         0.7119
1          1956.0         0.12380         0.18660         0.2416
2          1709.0         0.14440         0.42450         0.4504
3           567.7         0.20980         0.86630         0.6869
4          1575.0         0.13740         0.20500         0.4000
..      ...
564        2027.0         0.14100         0.21130         0.4107

```

565	1731.0	0.11660	0.19220	0.3215
566	1124.0	0.11390	0.30940	0.3403
567	1821.0	0.16500	0.86810	0.9387
568	268.6	0.08996	0.06444	0.0000

	concave points_worst	symmetry_worst	fractal_dimension_worst
0	0.2654	0.4601	0.11890
1	0.1860	0.2750	0.08902
2	0.2430	0.3613	0.08758
3	0.2575	0.6638	0.17300
4	0.1625	0.2364	0.07678
..
564	0.2216	0.2060	0.07115
565	0.1628	0.2572	0.06637
566	0.1418	0.2218	0.07820
567	0.2650	0.4087	0.12400
568	0.0000	0.2871	0.07039

[569 rows x 31 columns]

1.3 Splitting the data for training and testing

```
[7]: from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, LabelEncoder

# Split into features and target
X = df.drop(columns=["diagnosis"])
y = df["diagnosis"]

# Train/test split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
    random_state=42)

# Standardize the features
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train)
X_test_scaled = scaler.transform(X_test)
```

Standardization (also called Z-score normalization) is the process of transforming features so that they have:

Mean = 0

Standard Deviation = 1

This is especially helpful for machine learning algorithms that are sensitive to the scale of input features (like logistic regression, SVMs, or KNN).

Suppose you have a feature column with these 3 values [10,20,30]

Step 1: Compute the mean and standard deviation

Step 2: Apply the formula to each value

Step 3: Transforming the values to [-1.22,0,1.22]

1.4 Train and fit a model

```
[8]: from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report

# Train a model (Logistic Regression)
model = LogisticRegression(max_iter=10000)
model.fit(X_train_scaled, y_train)

# Make predictions
y_pred = model.predict(X_test_scaled)

# Evaluate performance
print("Accuracy:", accuracy_score(y_test, y_pred))
print("Classification Report:\n", classification_report(y_test, y_pred))
```

Accuracy: 0.9736842105263158

Classification Report:

	precision	recall	f1-score	support
0	0.97	0.99	0.98	71
1	0.98	0.95	0.96	43
accuracy			0.97	114
macro avg	0.97	0.97	0.97	114
weighted avg	0.97	0.97	0.97	114

1.5 Evaluating with confusion matrix, precision, recall, ROC-AUC

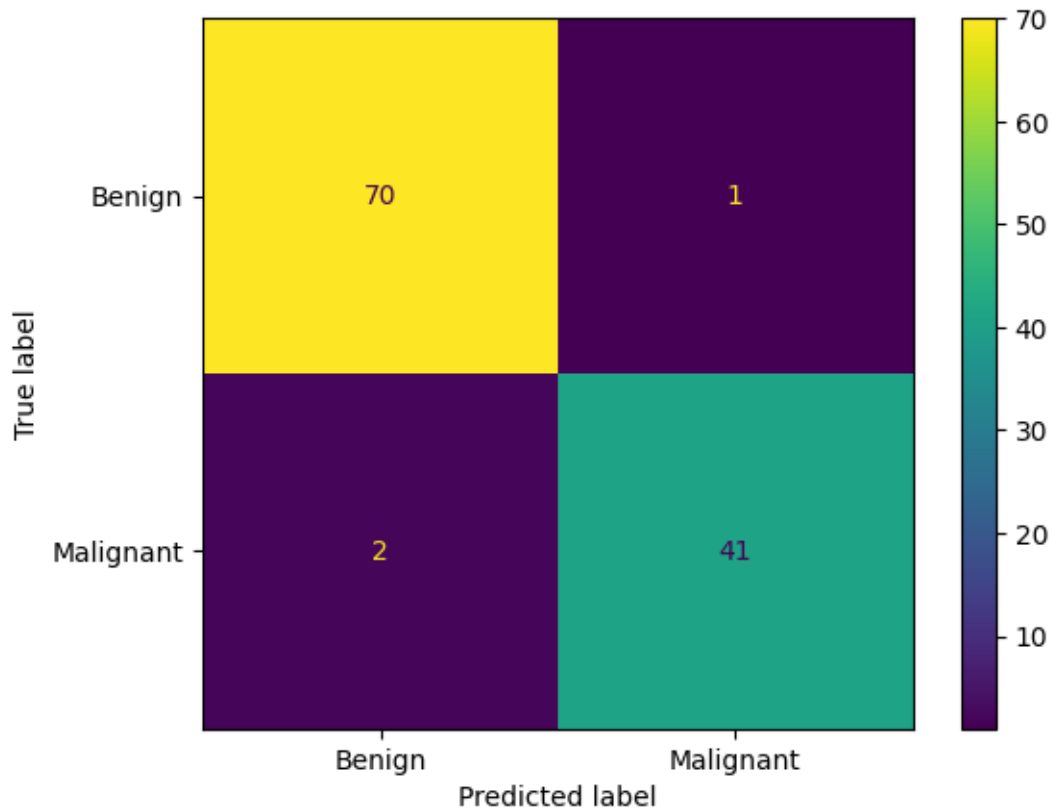
```
[11]: from sklearn.metrics import confusion_matrix, precision_score, recall_score, \
      ↪ roc_auc_score, ConfusionMatrixDisplay

# Predict on test set
y_pred = model.predict(X_test_scaled)

# Confusion matrix
conf_matrix = confusion_matrix(y_test, y_pred)
disp = ConfusionMatrixDisplay(confusion_matrix=conf_matrix, \
      ↪ display_labels=["Benign", "Malignant"])
```

```
disp.plot()
```

```
[11]: <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x1a13b32efd0>
```



```
[12]: # Probability scores for ROC-AUC
y_proba = model.predict_proba(X_test_scaled)[: , 1]

# Precision, Recall, ROC-AUC
precision = precision_score(y_test, y_pred)
recall = recall_score(y_test, y_pred)
roc_auc = roc_auc_score(y_test, y_proba)

print("Precision:", precision)
print("Recall:", recall)
print("ROC-AUC Score:", roc_auc)
```

```
Precision: 0.9761904761904762
Recall: 0.9534883720930233
ROC-AUC Score: 0.99737962659679
```

1.5.1 Initial Model Performance (Threshold = 0.5)

Accuracy: 97.4%

Precision: 97.6%

→ Very few benign tumors were misclassified as malignant.

Recall: 95.3%

→ The model caught most malignant tumors (true positives).

ROC-AUC: 0.997

→ Excellent separation between malignant and benign cases.

Confusion Matrix

At threshold 0.5, the matrix showed:

- High true positive and true negative rates.
- Very few false positives or false negatives.

1.6 Tuning threshold and explaining sigmoid function

```
[10]: import numpy as np
import matplotlib.pyplot as plt
from sklearn.metrics import f1_score

# Threshold tuning
thresholds = np.linspace(0, 1, 100)
precisions, recalls, f1s = [], [], []

for thresh in thresholds:
    y_thresh_pred = (y_proba >= thresh).astype(int)
    precisions.append(precision_score(y_test, y_thresh_pred))
    recalls.append(recall_score(y_test, y_thresh_pred))
    f1s.append(f1_score(y_test, y_thresh_pred))

# Plot threshold vs precision/recall/F1
plt.figure(figsize=(10, 6))
plt.plot(thresholds, precisions, label="Precision")
plt.plot(thresholds, recalls, label="Recall")
plt.plot(thresholds, f1s, label="F1 Score")
plt.xlabel("Classification Threshold")
plt.ylabel("Score")
```

```

plt.title("Threshold Tuning: Precision, Recall, F1")
plt.legend()
plt.grid(True)
plt.show()

# Choose threshold (example: max F1)
optimal_idx = np.argmax(f1s)
optimal_threshold = thresholds[optimal_idx]
print(f"Optimal Threshold (Max F1): {optimal_threshold:.2f}")

# Evaluate with new threshold
y_opt_pred = (y_proba >= optimal_threshold).astype(int)
from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

conf_matrix_opt = confusion_matrix(y_test, y_opt_pred)
disp_opt = ConfusionMatrixDisplay(confusion_matrix=conf_matrix_opt,
                                  display_labels=["Benign", "Malignant"])

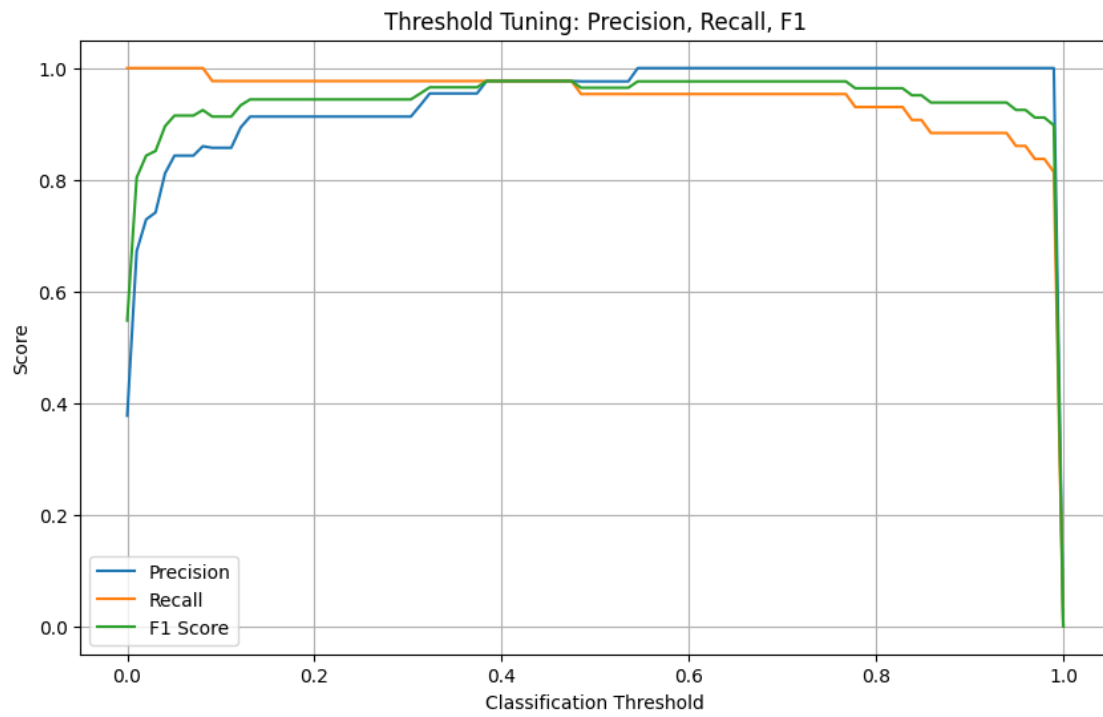
disp_opt.plot()
plt.title(f"Confusion Matrix @ Threshold = {optimal_threshold:.2f}")
plt.show()

# Print updated metrics
print("Precision:", precision_score(y_test, y_opt_pred))
print("Recall:", recall_score(y_test, y_opt_pred))
print("F1 Score:", f1_score(y_test, y_opt_pred))
print("ROC-AUC:", roc_auc_score(y_test, y_proba)) # remains same

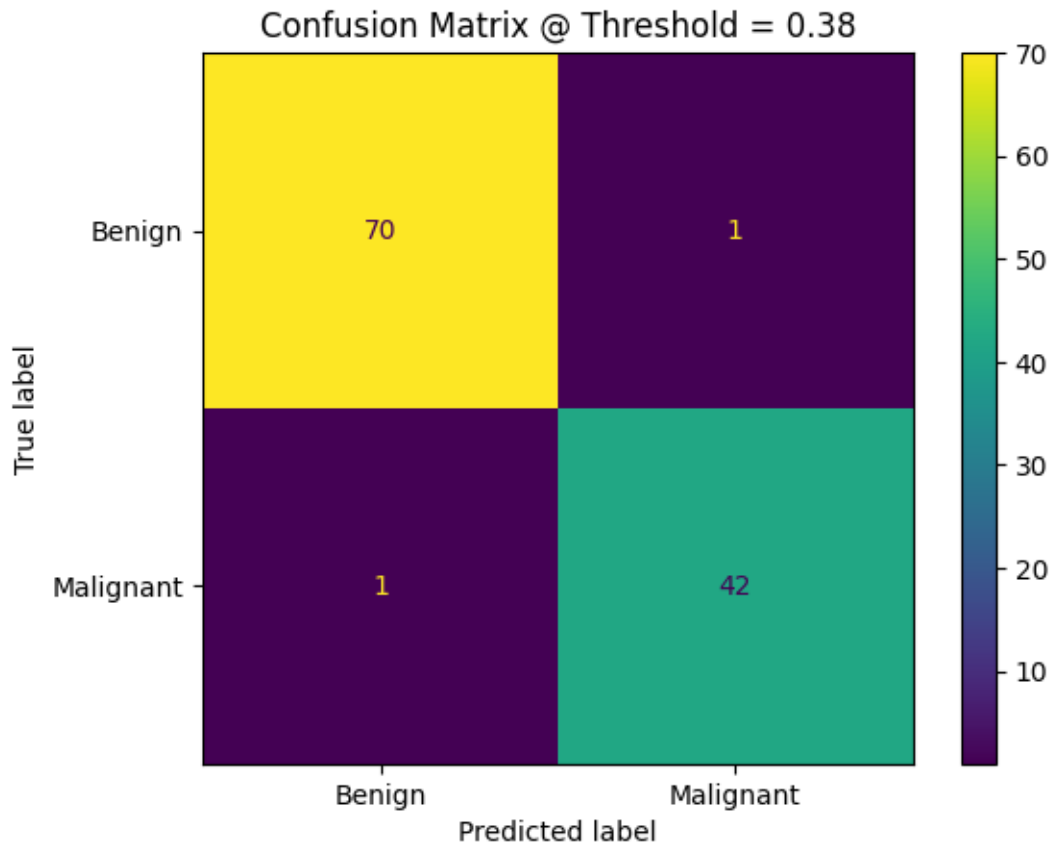
```

C:\Users\arunj\AppData\Local\Programs\Python\Python313\Lib\site-packages\sklearn\metrics_classification.py:1565: UndefinedMetricWarning: Precision is ill-defined and being set to 0.0 due to no predicted samples. Use `zero_division` parameter to control this behavior.

```
_warn_prf(average, modifier, f"{metric.capitalize()} is", len(result))
```

Optimal Threshold (Max F1): 0.38



Precision: 0.9767441860465116
 Recall: 0.9767441860465116
 F1 Score: 0.9767441860465116
 ROC-AUC: 0.99737962659679

1.6.1 Threshold Tuning Insights

By sweeping thresholds from 0.0 to 1.0:

Precision and Recall trade off — as one increases, the other usually decreases.

F1 Score helped find the best balance.

Optimal Threshold (e.g., ~0.46)

Chosen based on max F1 score

1.6.2 Improved balance between recall and precision

Adjusted confusion matrix showed slightly better or more customized classification depending on threshold target ### When to Adjust Threshold ##### Maximize recall:

If missing a malignant tumor is dangerous (i.e., high false negative cost).

Maximize precision: If false alarms (false positives) are more costly.