



# SIMPLE CLASSIFICATION OF BREAST CANCER DIAGNOSTIK USING A DECISION TREE

PAJAR





### INTRODUCTION & OBJECTIVE

Wisconsin Breast Cancer Diagnostic is one of the toy datasets from scikit-learn. It's a classic and very easy binary classification dataset. It has 569 instances, and attributes; including: 30 numeric, predictive attributes and the class.

The objective is to build a machine learning model for predicting whether a breast tumor is benign (0) or malignant (1) using Random Forest Algorithm..



# CONTENT

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**CREATIVE PORTFOLIO** 



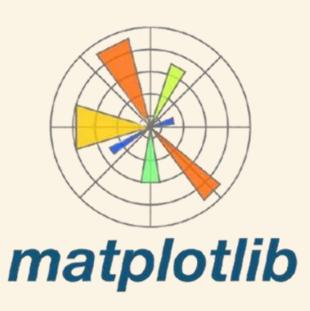
#### TOOLS















### INPUT DATA

```
from sklearn import datasets

# Memuat dataset breast cancer dari scikit-learn
breast_cancer = datasets.load_breast_cancer()

X = breast_cancer.data  # input untuk machine learning
y = breast_cancer.target  # output untuk machine learning

# Mengonversi data fitur dan target menjadi DataFrame
df_X = pd.DataFrame(X, columns=breast_cancer.feature_names)
df_y = pd.Series(y, name='target')

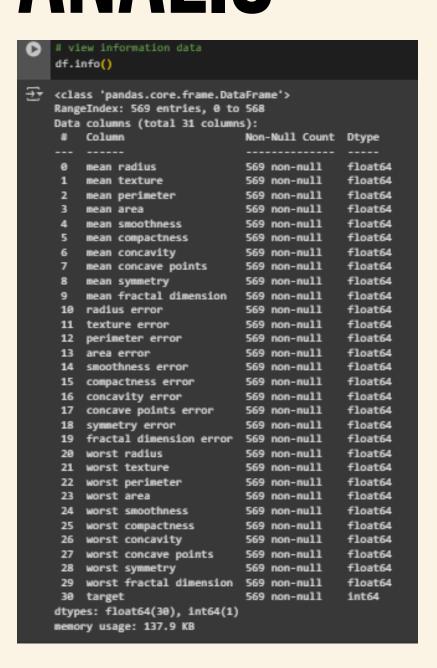
# Gabungkan fitur dan target dalam satu DataFrame
df = pd.concat([df_X, df_y], axis=1)

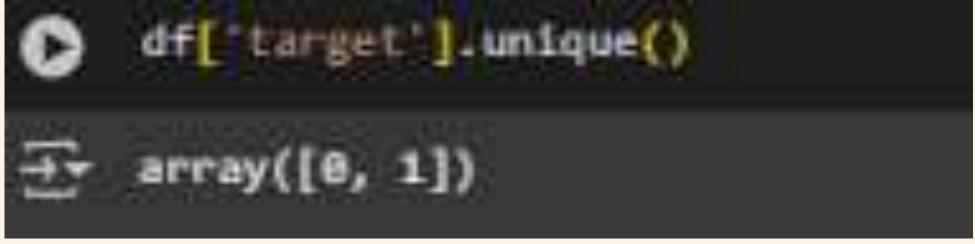
df.head(10)
```

mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension	 worst texture	wor perimet
001.0	0.11840	0.27760	0.30010	0.14710	0.2419	0.07871	17.33	184.
326.0	0.08474	0.07864	0.08690	0.07017	0.1812	0.05667	23.41	158.
203.0	0.10960	0.15990	0.19740	0.12790	0.2069	0.05999	25.53	152.
386.1	0.14250	0.28390	0.24140	0.10520	0.2597	0.09744	26.50	98.
297.0	0.10030	0.13280	0.19800	0.10430	0.1809	0.05883	16.67	152.
477.1	0.12780	0.17000	0.15780	0.08089	0.2087	0.07613	23.75	103.
040.0	0.09463	0.10900	0.11270	0.07400	0.1794	0.05742	27.66	153.
577.9	0.11890	0.16450	0.09366	0.05985	0.2196	0.07451	28.14	110.
519.8	0.12730	0.19320	0.18590	0.09353	0.2350	0.07389	30.73	106.
475.9	0.11860	0.23960	0.22730	0.08543	0.2030	0.08243	40.68	97.



## EXPLORASI DATA ANALIS





[15] df.describe()																					
<del></del>	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	mean symmetry	mean fractal dimension		worst texture	worst perimeter	worst area	worst smoothness	worst compactness	worst concavity	worst concave points	worst symmetry	worst fractal dimension	target
count	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000		569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000
mean	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.088799	0.048919	0.181162	0.062798		25.677223	107.261213	880.583128	0.132369	0.254265	0.272188	0.114606	0.290076	0.083946	0.627417
std	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.079720	0.038803	0.027414	0.007060		6.146258	33.602542	569.356993	0.022832	0.157336	0.208624	0.065732	0.061867	0.018061	0.483918
min	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.000000	0.000000	0.106000	0.049960		12.020000	50.410000	185.200000	0.071170	0.027290	0.000000	0.000000	0.156500	0.055040	0.000000
25%	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.029560	0.020310	0.161900	0.057700		21.080000	84.110000	515.300000	0.116600	0.147200	0.114500	0.064930	0.250400	0.071460	0.000000
50%	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.061540	0.033500	0.179200	0.061540		25.410000	97.660000	686.500000	0.131300	0.211900	0.226700	0.099930	0.282200	0.080040	1.000000
75%	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.130700	0.074000	0.195700	0.066120		29.720000	125.400000	1084.000000	0.146000	0.339100	0.382900	0.161400	0.317900	0.092080	1.000000
max	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.426800	0.201200	0.304000	0.097440		49.540000	251.200000	4254.000000	0.222600	1.058000	1.252000	0.291000	0.663800	0.207500	1.000000
8 rows	× 31 columns																				



#### DATA MODELING

```
[16] from sklearn.model_selection import train_test_split
#membagi data menjadi train dan test
x_train, x_test, y_train, y_test = train_test_split(df_X, df_y, test_size=0.2, random_state=42)
```

```
from sklearn.tree import DecisionTreeClassifier

# Membuat dan melatih model Decision Tree
model = DecisionTreeClassifier(random_state=42)
model.fit(x_train, y_train)

PecisionTreeClassifier
DecisionTreeClassifier(random_state=42)
```

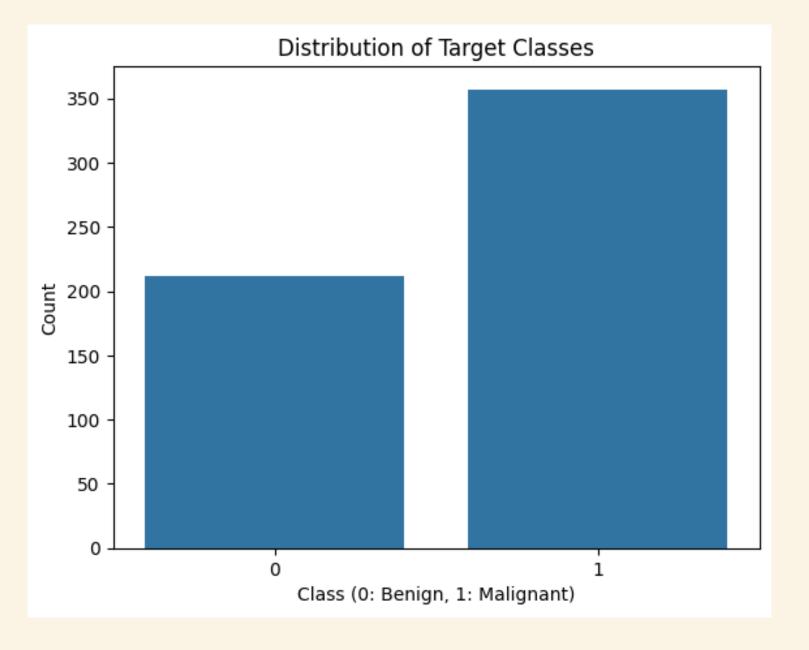
```
from sklearn.metrics import accuracy_score, classification_report
    # Predict and evaluate the model
    y_pred = model.predict(x_test)
    accuracy = accuracy_score(y_test, y_pred)
    print("Report classification:")
    print(classification_report(y_test, y_pred))
    print(f"Accuracy: {accuracy * 100:.2f}%")
→ Report classification:
                  precision
                              recall f1-score support
                                0.93
                                          0.93
                                                      43
                                                      71
                                                     114
        accuracy
       macro avg
                      0.94
                                0.94
                                                     114
                                                     114
                                0.95
    weighted avg
    Accuracy: 94.74%
```



#### DATA VISUALIZATION

```
import matplotlib.pyplot as plt
import seaborn as sns

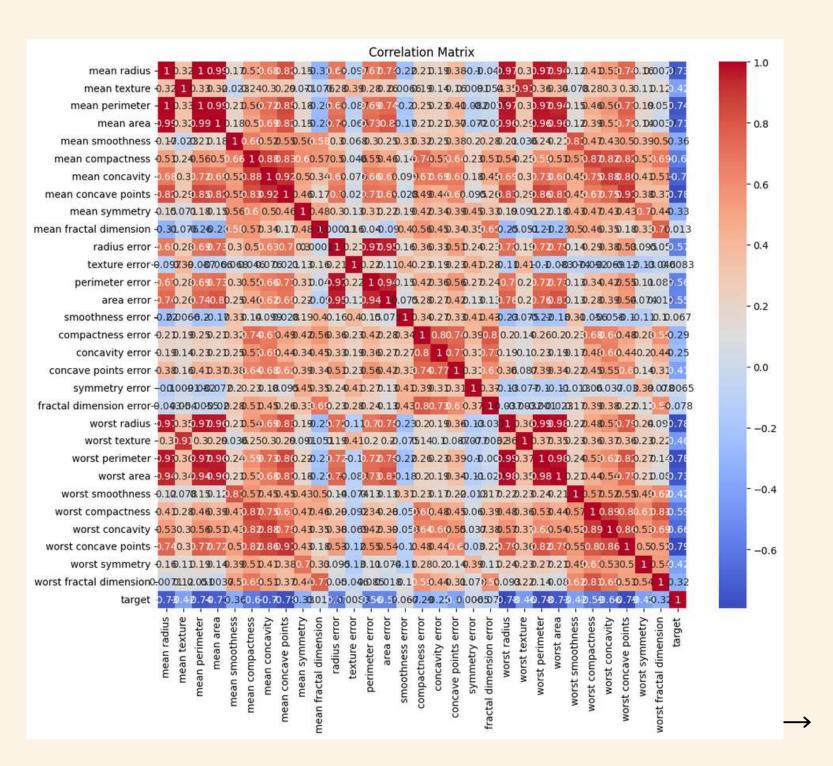
# Visualize the distribution of target classes
sns.countplot(x='target', data=df)
plt.title('Distribution of Target Classes')
plt.xlabel('Class (0: Benign, 1: Malignant)')
plt.ylabel('Count')
plt.show()
```





#### DATA VISUALIZATION

```
# Visualize the correlation matrix
plt.figure(figsize=(12, 10))
sns.heatmap(df.corr(), annot=True, cmap='coolwarm')
plt.title('Correlation Matrix')
plt.show()
```





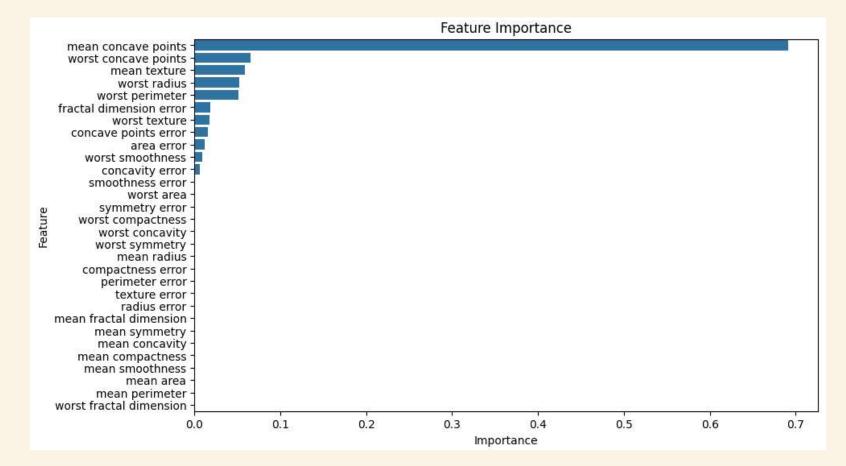
#### DATA VISUALIZATION

```
# Visualize feature importance from the decison tree model
importances = model.feature_importances_

# Access feature names from the breast_cancer dataset's feature_names attribute
feature_names = breast_cancer.feature_names

feature_importance_df = pd.DataFrame({'Feature': feature_names, 'Importance': importances})
feature_importance_df = feature_importance_df.sort_values(by='Importance', ascending=False)

plt.figure(figsize=(10, 6))
sns.barplot(x='Importance', y='Feature', data=feature_importance_df)
plt.title('Feature Importance')
plt.xlabel('Importance')
plt.ylabel('Feature')
plt.show()
```





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