

✓ ML: Assignment - 1 (Q.2)

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CMPN-B

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```
pip install ucimlrepo
```

```
Collecting ucimlrepo
```

```
  Downloading ucimlrepo-0.0.7-py3-none-any.whl.metadata (5.5 kB)
```

```
Requirement already satisfied: pandas>=1.0.0 in /usr/local/lib/python3.12/dist-packages (from ucimlrepo) (2.2.2)
```

```
Requirement already satisfied: certifi>=2020.12.5 in /usr/local/lib/python3.12/dist-packages (from ucimlrepo) (2026.1.4)
```

```
Requirement already satisfied: numpy>=1.26.0 in /usr/local/lib/python3.12/dist-packages (from pandas>=1.0.0->ucimlrepo) (2.0.2)
```

```
Requirement already satisfied: python-dateutil>=2.8.2 in /usr/local/lib/python3.12/dist-packages (from pandas>=1.0.0->ucimlrepo)
```

```
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.12/dist-packages (from pandas>=1.0.0->ucimlrepo) (2025.2)
```

```
Requirement already satisfied: tzdata>=2022.7 in /usr/local/lib/python3.12/dist-packages (from pandas>=1.0.0->ucimlrepo) (2025.3)
```

```
Requirement already satisfied: six>=1.5 in /usr/local/lib/python3.12/dist-packages (from python-dateutil>=2.8.2->pandas>=1.0.0->ucimlrepo)
```

```
Downloading ucimlrepo-0.0.7-py3-none-any.whl (8.0 kB)
```

```
Installing collected packages: ucimlrepo
```

```
Successfully installed ucimlrepo-0.0.7
```

```
from ucimlrepo import fetch_ucirepo
```

```
# fetch dataset
```

```
breast_cancer_wisconsin_diagnostic = fetch_ucirepo(id=17)
```

```
# data (as pandas dataframes)
```

```
X = breast_cancer_wisconsin_diagnostic.data.features
```

```
y = breast_cancer_wisconsin_diagnostic.data.targets
```

```
# metadata
```

```
print(breast_cancer_wisconsin_diagnostic.metadata)
```

```
# variable information
```

```
print(breast_cancer_wisconsin_diagnostic.variables)
```

```
{'uci_id': 17, 'name': 'Breast Cancer Wisconsin (Diagnostic)', 'repository_url': 'https://archive.ics.uci.edu/dataset/17/breas'
```

	name	role	type	demographic	description	units	\
0	ID	ID	Categorical	None	None	None	
1	Diagnosis	Target	Categorical	None	None	None	
2	radius1	Feature	Continuous	None	None	None	
3	texture1	Feature	Continuous	None	None	None	
4	perimeter1	Feature	Continuous	None	None	None	
5	area1	Feature	Continuous	None	None	None	
6	smoothness1	Feature	Continuous	None	None	None	
7	compactness1	Feature	Continuous	None	None	None	
8	concavity1	Feature	Continuous	None	None	None	
9	concave_points1	Feature	Continuous	None	None	None	
10	symmetry1	Feature	Continuous	None	None	None	
11	fractal_dimension1	Feature	Continuous	None	None	None	
12	radius2	Feature	Continuous	None	None	None	
13	texture2	Feature	Continuous	None	None	None	
14	perimeter2	Feature	Continuous	None	None	None	
15	area2	Feature	Continuous	None	None	None	
16	smoothness2	Feature	Continuous	None	None	None	
17	compactness2	Feature	Continuous	None	None	None	
18	concavity2	Feature	Continuous	None	None	None	
19	concave_points2	Feature	Continuous	None	None	None	
20	symmetry2	Feature	Continuous	None	None	None	
21	fractal_dimension2	Feature	Continuous	None	None	None	
22	radius3	Feature	Continuous	None	None	None	
23	texture3	Feature	Continuous	None	None	None	
24	perimeter3	Feature	Continuous	None	None	None	
25	area3	Feature	Continuous	None	None	None	
26	smoothness3	Feature	Continuous	None	None	None	
27	compactness3	Feature	Continuous	None	None	None	
28	concavity3	Feature	Continuous	None	None	None	
29	concave_points3	Feature	Continuous	None	None	None	
30	symmetry3	Feature	Continuous	None	None	None	
31	fractal_dimension3	Feature	Continuous	None	None	None	

```
missing_values
```

```
0 no
```

```

1         no
2         no
3         no
4         no
5         no
6         no
7         no
8         no
9         no
10        no
11        no
12        no
13        no
14        no
15        no
16        no
17        no
18        no
19        no
20        no

```

```

%%writefile task1_cancer_classification.py
from ucimlrepo import fetch_ucirepo
import argparse
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.linear_model import LogisticRegression
from sklearn.tree import DecisionTreeClassifier
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, confusion_matrix

parser = argparse.ArgumentParser()
parser.add_argument("--test_size", type=float, default=0.2)
parser.add_argument("--model", type=str, default="logistic")
args = parser.parse_args()

dataset = fetch_ucirepo(id=17)

X = dataset.data.features
y = dataset.data.targets["Diagnosis"].map({"M": 1, "B": 0})

X_train, X_test, y_train, y_test = train_test_split(
    X, y, test_size=args.test_size, random_state=42, stratify=y
)

scaler = StandardScaler()
X_train_s = scaler.fit_transform(X_train)
X_test_s = scaler.transform(X_test)

if args.model == "logistic":
    model = LogisticRegression(max_iter=1000)
    Xtr, Xte = X_train_s, X_test_s
else:
    model = DecisionTreeClassifier(random_state=42)
    Xtr, Xte = X_train, X_test

model.fit(Xtr, y_train)

train_pred = model.predict(Xtr)
test_pred = model.predict(Xte)

print("\nModel:", args.model.upper())
print("Train Error:", 1 - accuracy_score(y_train, train_pred))
print("Test Error :", 1 - accuracy_score(y_test, test_pred))

print("\nAccuracy :", accuracy_score(y_test, test_pred))
print("Precision:", precision_score(y_test, test_pred))
print("Recall   :", recall_score(y_test, test_pred))
print("F1-score :", f1_score(y_test, test_pred))

print("\nConfusion Matrix:")
print(confusion_matrix(y_test, test_pred))

print("\nConclusion:")
if args.model == "logistic":
    print(
        "The Logistic Regression model shows a small difference between training and test error, indicating good generalization."
        "Its linear nature and regularization prevent it from memorizing noise, making it a strong baseline for this dataset."
    )

```

```

else:
    print(
        "The Decision Tree model shows clear signs of overfitting. It achieves very high training performance but lower test pe
        "This occurs because an unconstrained tree learns overly complex decision rules that do not generalize well to unseen c
    )

```

Overwriting task1_cancer_classification.py

```
!python task1_cancer_classification.py --test_size 0.2 --model logistic
```

Model: LOGISTIC
 Train Error: 0.01318681318681314
 Test Error : 0.03508771929824561

Accuracy : 0.9649122807017544
 Precision: 0.975
 Recall : 0.9285714285714286
 F1-score : 0.9512195121951219

Confusion Matrix:
 [[71 1]
 [3 39]]

Conclusion:
 The Logistic Regression model shows a small difference between training and test error, indicating good generalization with no s
 Its linear nature and regularization prevent it from memorizing noise, making it a strong baseline for this dataset.

```
!python task1_cancer_classification.py --test_size 0.2 --model tree
```

Model: TREE
 Train Error: 0.0
 Test Error : 0.07017543859649122

Accuracy : 0.9298245614035088
 Precision: 0.9047619047619048
 Recall : 0.9047619047619048
 F1-score : 0.9047619047619048

Confusion Matrix:
 [[68 4]
 [4 38]]

Conclusion:
 The Decision Tree model shows clear signs of overfitting. It achieves very high training performance but lower test performance,
 This occurs because an unconstrained tree learns overly complex decision rules that do not generalize well to unseen data.

Comparison:-

Logistic Regression (Baseline Model):

- Training and test performance are very close
- Small generalization gap indicates good generalization
- No significant overfitting observed due to model simplicity and regularization

Decision Tree (Non-linear Model):

- Very high training performance
- Noticeably lower test performance
- Large generalization gap indicates overfitting

Relevant Machine Learning Issues:-

1. **Feature Scaling:** Logistic Regression is sensitive to feature scale, so standardization is necessary. Decision Trees are scale-invariant and do not require normalization.
2. **Feature Correlation (Multicollinearity):** Many features in the dataset are highly correlated, which can affect coefficient stability in Logistic Regression and lead to redundant splits in Decision Trees.

3. **Class Imbalance:** The dataset contains more benign than malignant samples, making accuracy alone insufficient; precision, recall, and F1-score are needed for reliable evaluation.