



# ML Lab #1: Breast Cancer Classification

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# Overview

- **Prerequisite**

- Anacodna (Individual Edition)

- **Practice: Breast Cancer Classification**

- The given data
- Expected results
- Practice with the skeleton code
  - Step #1) Visualize all features and its classification results
  - Step #2) Use another classifier



[Pinkwashing](#)

- **Assignment**

- Complete the following three missions
  1. Load the data from the raw file
  2. Try at least two different classifiers
  3. Calculate balanced accuracy

# Practice: Breast Cancer Classification

- The given data: [Breast Cancer Wisconsin \(Diagnostic\) Data Set](#)
  - Classes (#: **2**): *Malignant* (M; 악성종양 in Korean), *Benign* (B; 양성종양)
  - Attributes: **30** real numbers (except ID and target class)
    - Radius
    - Texture
    - Perimeter
    - Area
    - ...
  - The number of data: **569** (M: 212, B: 357)
  - cf. Load the dataset using scikit-learn [\[API\]](#)  
`from sklearn import datasets`  
`wdbc = datasets.load_breast_cancer()`

UCI Machine Learning Repository

https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+%28Diagnostic%29

UCI Machine Learning Repository  
Center for Machine Learning and Intelligent Systems

About Citation Policy Donate a Data Set Contact

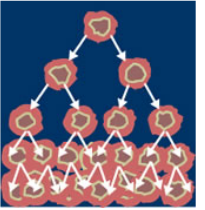
Repository Web

View ALL Data Sets

### Breast Cancer Wisconsin (Diagnostic) Data Set

Download: [Data Folder](#) [Data Set Description](#)

Abstract: Diagnostic Wisconsin Breast Cancer Database



Data Set Characteristics:	Multivariate	Number of Instances:	569	Area:	Life
Attribute Characteristics:	Real	Number of Attributes:	32	Date Donated	1995-11-01
Associated Tasks:	Classification	Missing Values?	No	Number of Web Hits:	1604079

Source:

Creators:

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Data Set Information:

Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image. A few of the images can be found at [\[Web Link\]](#)

Separating plane described above was obtained using Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree Construction Via Linear Programming," Proceedings of the 4th Midwest Artificial Intelligence and Cognitive Science Society, pp. 97-101, 1992], a classification method which uses linear programming to construct a decision tree. Relevant features were selected using an exhaustive search in the space of 1-4 features and 1-3 separating planes.

The actual linear program used to obtain the separating plane in the 3-dimensional space is that described in: [K. P. Bennett and O. L. Mangasarian: "Robust Linear Programming Discrimination of Two Linearly Inseparable Sets", Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:  
`ftp ftp.cs.wisc.edu`  
`cd math-prog/cpo-dataset/machine-learn/WDBC/`

# Practice: Breast Cancer Classification

- The given data (file: data/wdbc.data)

- File format: [CSV](#) (comma-separated values)

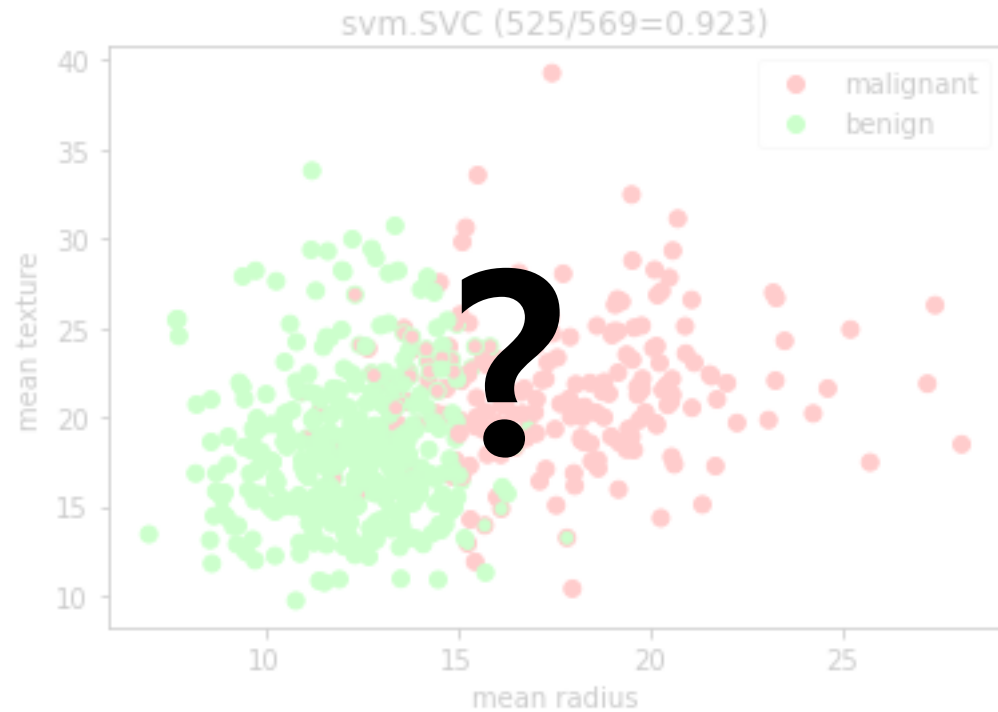
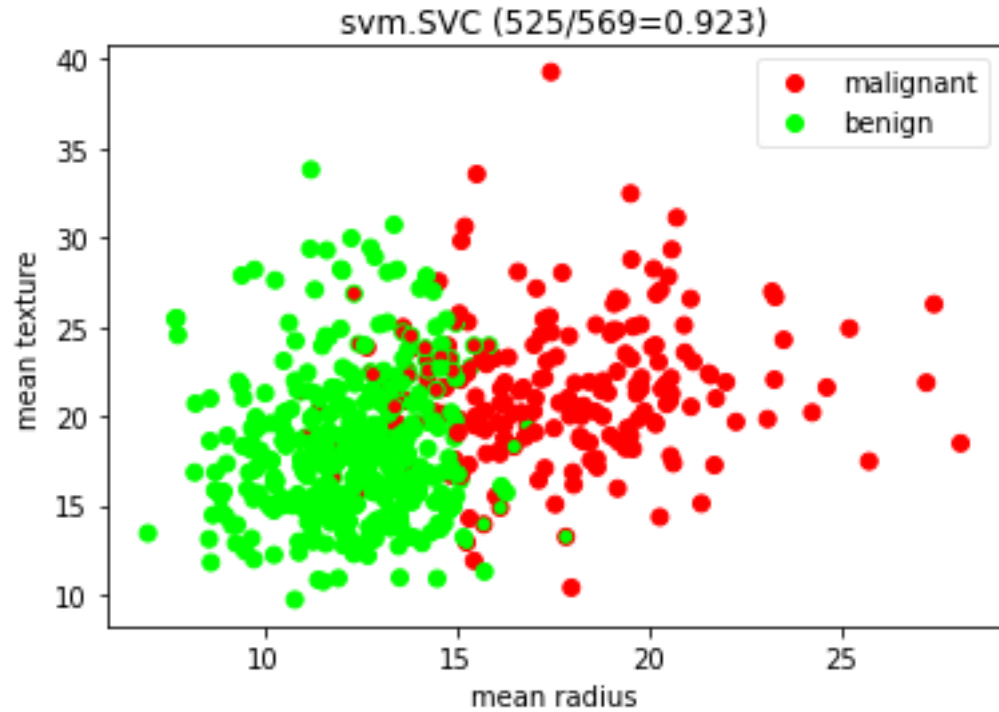
- ID, target class (M or F), radius, texture, perimeter, area, ...

- Example

```
842302,M,17.99,10.38,122.8,1001,0.1184,0.2776,0.3001,0.1471,0.2419,0.07871,1.095,0.9053,8.589,15
3.4,0.006399,0.04904,0.05373,0.01587,0.03003,0.006193,25.38,17.33,184.6,2019,0.1622,0.6656,0.711
9,0.2654,0.4601,0.1189
...
```

# Practice: Breast Cancer Classification

- Expected results
  - Our default classifier: SVM (svm.SVC)



# Practice: Breast Cancer Classification

- The given skeleton code (wdbc\_classification\_skeleton.py)

```
import numpy as np
import matplotlib.pyplot as plt
from sklearn import (datasets, svm) # Mission #2 and #3) You need to import some modules if necessary
from matplotlib.lines import Line2D # For the custom legend

def load_wdbc_data(filename):
    # TODO

# Load a dataset
wdbc = datasets.load_breast_cancer()
#wdbc = load_wdbc_data('data/wdbc.data') # Mission #1) Implement 'load_wdbc_data()'

# Train a model
model = svm.SVC() # Mission #2) Try at least two different classifiers
model.fit(wdbc.data, wdbc.target)

# Test the model
predict = model.predict(wdbc.data)
n_correct = sum(predict == wdbc.target)
accuracy = n_correct / len(wdbc.data) # Mission #3) Calculate balanced accuracy
```

# Practice: Breast Cancer Classification

- The given skeleton code (wdbc\_classification\_skeleton.py)

```
# Visualize testing results
```

```
cmap = np.array([(1, 0, 0), (0, 1, 0)])
```

```
clabel = [Line2D([0], [0], marker='o', lw=0, label=wdbc.target_names[i], color=cmap[i]) for i in range(len(cmap))]
```

```
for (x, y) in [(0, 1)]: # Not mandatory, but try [(i, i+1) for i in range(0, 30, 2)]
```

```
plt.title(f'svm.SVC ({n_correct}/{len(wdbc.data)}={accuracy:.3f})')
```

```
plt.scatter(wdbc.data[:,x], wdbc.data[:,y], c=cmap[wdbc.target], edgecolors=cmap[predict])
```

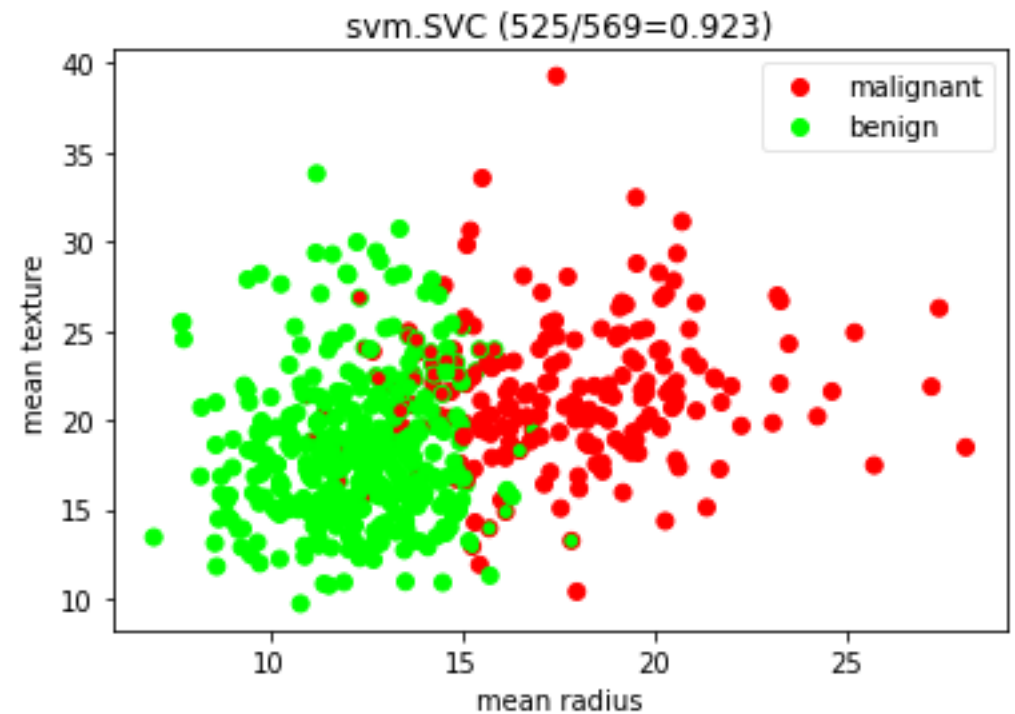
```
plt.xlabel(wdbc.feature_names[x])
```

```
plt.ylabel(wdbc.feature_names[y])
```

```
plt.legend(handles=clabel, framealpha=0.5)
```

```
plt.show()
```

- Practice
  - Step #1) Visualize all features and its classification results
  - Step #2) Use another classifier



# Assignment

- Mission
  - Complete the following three missions using the given skeleton code (`wdbc_classification_skeleton.py`)
    1. Load the data from the raw file (10 points)
    2. Try at least two different classifiers (5 points)
    3. Calculate balanced accuracy (5 points)
  - Submit your code (`wdbc_classification.py`) and its two result images (`wdbc_classification_???.png`)
- Condition
  - Please follow the above filename convention.
  - You **can** start from scratch (without using the given skeleton code).
    - However, you **should** use the given data.
  - You **can** freely change the given skeleton code if necessary.
- Submission
  - Deadline: **November 24, 2021 23:59** (**firm deadline**; no extension)
  - Where: e-Class > Assignments
  - Score: Max 20 points