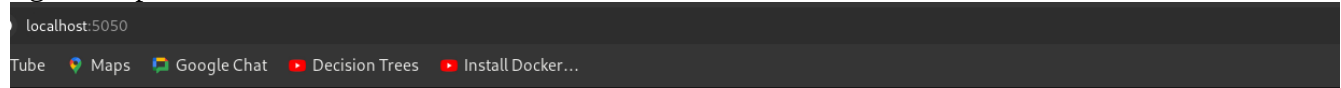


- git clone [git@github.com:trungphap/innovant.git](https://github.com:trungphap/innovant.git)
- cd innovant
- vagrant up
- set VAGRANT_PREFER_SYSTEM_BIN=0
- vagrant ssh
- cd /vagrant
- docker-compose up -d

In the browser of the host :

- go to <http://localhost:5050> : there is no result



Breast Cancer Analysis Result

Correlation between attributs



Distribution of attribut 1



Distribution of attribut 2



Distribution of attribut 5




Distribution of attribut 6



- go to <http://localhost:8899>

localhost:8899/login?next=%2Ftree%3F

es gmail.com Paris 8 Ent Pari1 Yahoo Mail IED Contacts AI Cours bdd/insert_movies.py VS Code jupyter neural network us



Password or token:

Log in

Token authentication is enabled

If no password has been configured, you need to open the server with its login token in the URL, or paste it above. This requirement will be lifted if you [enable a password](#).

The command:

```
jupyter server list
```

will show you the URLs of running servers with their tokens, which you can copy and paste into your browser. For example:

```
Currently running servers:
http://localhost:8888/?token=c8de56fa... :: /Users/you/notebooks
```

or you can paste just the token value into the password field on this page.

See [the documentation on how to enable a password](#) in place of token authentication, if you would like to avoid dealing with random tokens.

Cookies are required for authenticated access to the Jupyter server.

Setup a Password

You can also setup a password by entering your token and a new password on the fields below:

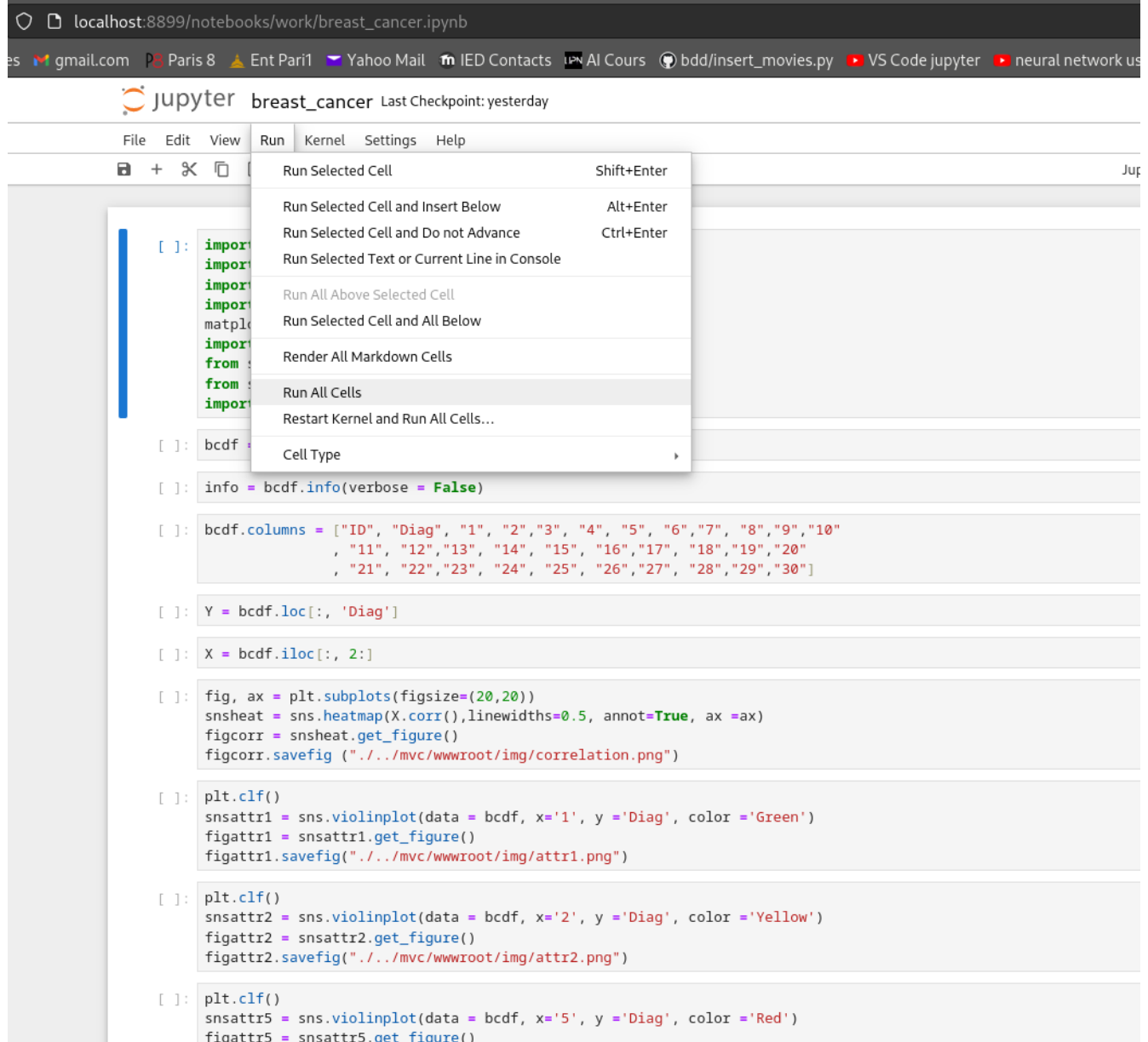
Token

New Password

Log in and set new password

- enter password in the case Password or token, then login

- click on work, click on breast_cancer.ipynb, click Run, Run All cells



The screenshot shows a web browser at localhost:8899/notebooks/work/breast_cancer.ipynb. The Jupyter interface has a top bar with the notebook name 'breast_cancer' and 'Last Checkpoint: yesterday'. Below is a menu bar with 'File', 'Edit', 'View', 'Run', 'Kernel', 'Settings', and 'Help'. The 'Run' menu is open, displaying several options. The option 'Run All Cells' is highlighted in grey. Other options include 'Run Selected Cell', 'Run Selected Cell and Insert Below', 'Run Selected Cell and Do not Advance', 'Run Selected Text or Current Line in Console', 'Run All Above Selected Cell', 'Run Selected Cell and All Below', 'Render All Markdown Cells', 'Restart Kernel and Run All Cells...', and 'Cell Type'. The notebook content consists of several code cells. The first cell contains import statements for pandas, numpy, matplotlib, and seaborn. Subsequent cells define 'bcdf.info(verbose=False)', set 'bcdf.columns' to a list of 31 feature names, and extract 'Y' and 'X' variables. The final three cells create subplots: a heatmap of correlations, and three violin plots for features '1', '2', and '5' against the 'Diag' variable, each saved as a PNG file.

```
[ ]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import train_test_split
import os

[ ]: bcdf = pd.read_csv('breast_cancer.csv')

[ ]: info = bcdf.info(verbose = False)

[ ]: bcdf.columns = ["ID", "Diag", "1", "2", "3", "4", "5", "6", "7", "8", "9", "10",
                  "11", "12", "13", "14", "15", "16", "17", "18", "19", "20",
                  "21", "22", "23", "24", "25", "26", "27", "28", "29", "30"]

[ ]: Y = bcdf.loc[:, 'Diag']

[ ]: X = bcdf.iloc[:, 2:]

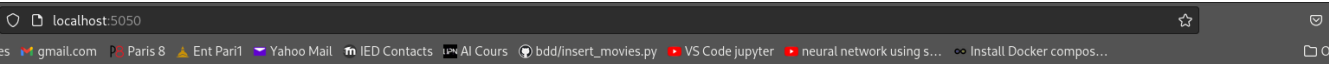
[ ]: fig, ax = plt.subplots(figsize=(20,20))
snsheat = sns.heatmap(X.corr(),linewidths=0.5, annot=True, ax =ax)
figcorr = snsheat.get_figure()
figcorr.savefig("../mvc/wwwroot/img/correlation.png")

[ ]: plt.clf()
snsattr1 = sns.violinplot(data = bcdf, x='1', y = 'Diag', color = 'Green')
figattr1 = snsattr1.get_figure()
figattr1.savefig("../mvc/wwwroot/img/attr1.png")

[ ]: plt.clf()
snsattr2 = sns.violinplot(data = bcdf, x='2', y = 'Diag', color = 'Yellow')
figattr2 = snsattr2.get_figure()
figattr2.savefig("../mvc/wwwroot/img/attr2.png")

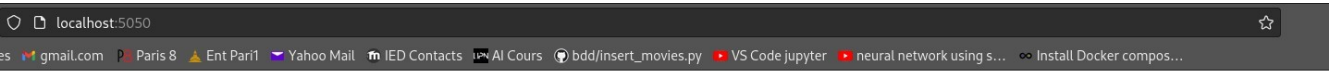
[ ]: plt.clf()
snsattr5 = sns.violinplot(data = bcdf, x='5', y = 'Diag', color = 'Red')
figattr5 = snsattr5.get_figure()
```

- go to <http://localhost:5050> : there is result, example

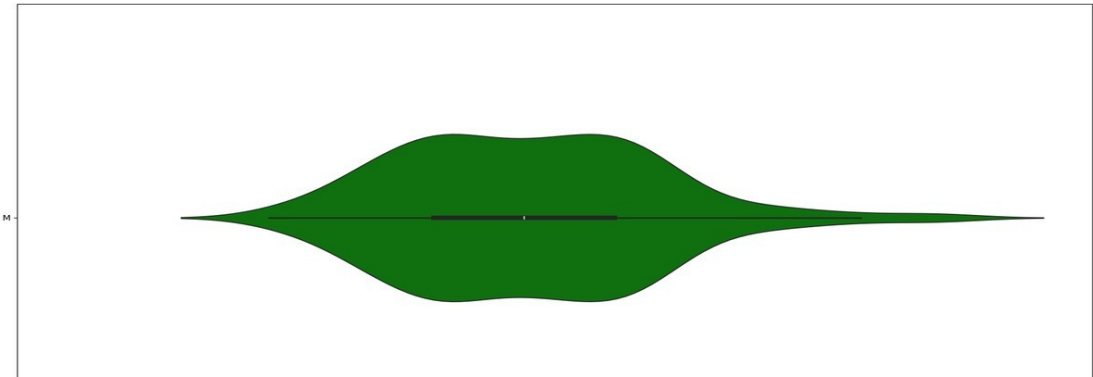


Breast Cancer Analysis Result

Correlation between attributs



Distribution of attribut 1



Classification Report for Decision_Tree_1

	Precision	Recall	F1 Score	Support
Malignant	0.95	0.94	0.95	121
Benign	0.9	0.91	0.9	67
Accuracy			0.9	
Macro Avg	0.92	0.93	0.92	188
Weighted Avg	0.93	0.93	0.93	188

Classification Report for Decision_Tree_2

	Precision	Recall	F1 Score	Support
Malignant	0.93	0.93	0.93	121
Benign	0.88	0.88	0.88	67
Accuracy			0.88	
Macro Avg	0.91	0.91	0.91	188
Weighted Avg	0.91	0.91	0.91	188