Homework 3

March 12, 2018

1 Homework 3: Hyperparameter Tuning with SVMs

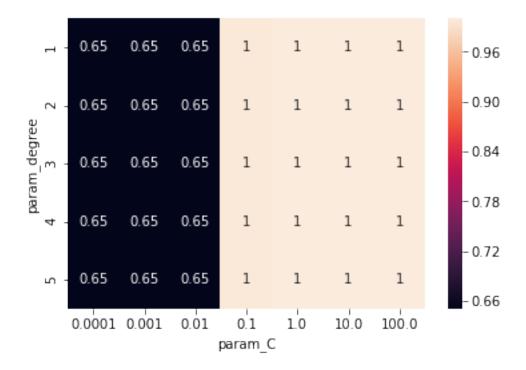
The final deliverable for this homework will be this Jupyter notebook, which should include all relevant code, markdown cells before each code block describing what the code does, and any write-ups/images/plots that you wish to include.

To add a block click on Insert > Insert Cell Below. To make a markdown cell, click the drop-down menu at the top of this page and select Markdown.

The starter code for this homework is purposely very minimal. You should get used to coding from scratch. Just follow all the instructions in the PDF you will be fine.

```
In [25]: import numpy as np
         import pandas as pd
         from sklearn.svm import SVC
         from sklearn.model_selection import train_test_split, GridSearchCV
         from sklearn import preprocessing
         from sklearn.metrics import accuracy_score
         import matplotlib.pyplot as plt
         import seaborn as sns
In [26]: cols = ['ID', 'Clump Thickness', 'Uniformity of Cell Size',
                 'Uniformity of Cell Shape', 'Marginal Adhesion',
                 'Single Epithelial Cell Size', 'Bare Nuclei',
                 'Bland Chromatin', 'Normal Nucleoli', 'Mitoses', 'Class']
         data = pd.read_csv("breast-cancer-wisconsin.data",names=cols)
In [27]: #NORMALIZE DATA
         data.set index(["ID"],inplace=True)
         data = (data-data.min())/(data.max()-data.min())
In [28]: #SPLIT DATA
         train_data, test_data = train_test_split(data)
In [29]: #PREDICT
         params = {
             "C": [.0001,.001,.01,.1,1,10,100],
```

best pair of parameters {'C': 1, 'degree': 1} General trends: degree doesn't matter, but C values do. Higher C value means higher penalty for misclassification of data and so higher the C value, the more the (over)fitting.



```
In [31]: #PREDICT
    params = {
        "C": [.0001,.001,.01,.1,1,10,100],
        "gamma": [.001,.01,.1,1,10,100]
}
```

