Out[3]: Click here to toggle on/off the raw code.

# Question 4 ¶

## Loading Abalone dataset

Out[13]:
```
array([[-0.57455813, -0.43214879, -1.06442415, ..., -0.60768536,
        -0.72621157, -0.63821689],
       [-1.44898585, -1.439929  , -1.18397831, ..., -1.17090984,
        -1.20522124, -1.21298732],
       [ 0.05003309,  0.12213032, -0.10799087, ..., -0.4634999 ,
        -0.35668983, -0.20713907],
       ...,
       [ 0.6329849 ,  0.67640943,  1.56576738, ...,  0.74855917,
         0.97541324,  0.49695471],
       [ 0.84118198,  0.77718745,  0.25067161, ...,  0.77334105,
         0.73362741,  0.41073914],
       [ 1.54905203,  1.48263359,  1.32665906, ...,  2.64099341,
         1.78744868,  1.84048058]])
```

# using PCA-preprocessing on abalone dataset

Out[14]:

| | PC1 | PC2 | PC3 |
|---|---|---|---|
| **0** | -1.756019 | -0.390532 | -0.329928 |
| **1** | -3.362734 | -0.105153 | 0.252264 |
| **2** | -0.482338 | 0.252055 | -0.443918 |
| **3** | -1.509041 | 0.207608 | -0.000519 |
| **4** | -3.654006 | -0.272819 | 0.275035 |
| **...** | ... | ... | ... |
| **4172** | 0.801361 | 0.385426 | -0.064832 |
| **4173** | 0.719312 | -0.329146 | -0.293062 |
| **4174** | 2.167373 | 0.724010 | 0.402521 |
| **4175** | 1.647501 | -0.305166 | -0.306030 |
| **4176** | 4.894542 | -0.705798 | 0.550942 |

4177 rows × 3 columns

# using LDA-preprocessing on abalone dataset

Out[15]:

| Rings | 0 | 1 | 2 |
|---|---|---|---|
| **15** | -0.791003 | -0.235208 | 0.359351 |
| **7** | -2.355522 | 0.336978 | 0.214024 |
| **9** | 0.766719 | -0.246564 | 1.129422 |
| **10** | -0.611434 | 0.098075 | 0.230542 |
| **7** | -2.674301 | 0.527509 | 0.102575 |
| **...** | ... | ... | ... |
| **11** | 0.921330 | -0.612381 | -0.272399 |
| **10** | 0.425796 | -0.894428 | -0.034727 |
| **9** | 1.064523 | -0.385654 | -0.787231 |
| **10** | 0.840757 | -1.513723 | -0.864217 |
| **12** | 0.843580 | 0.352389 | -2.262564 |

4177 rows × 3 columns

# Loading wine dataset

Out[16]:

| | fixed acidity | volatile acidity | citric acid | residual sugar | chlorides | free sulfur dioxide | total sulfur dioxide | density | pH | sulphates | alcoho |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **0** | 7.0 | 0.270 | 0.36 | 20.7 | 0.045 | 45.0 | 170.0 | 1.0010 | 3.00 | 0.45 | 8. |
| **1** | 6.3 | 0.300 | 0.34 | 1.6 | 0.049 | 14.0 | 132.0 | 0.9940 | 3.30 | 0.49 | 9. |
| **2** | 8.1 | 0.280 | 0.40 | 6.9 | 0.050 | 30.0 | 97.0 | 0.9951 | 3.26 | 0.44 | 10. |
| **3** | 7.2 | 0.230 | 0.32 | 8.5 | 0.058 | 47.0 | 186.0 | 0.9956 | 3.19 | 0.40 | 9. |
| **4** | 7.2 | 0.230 | 0.32 | 8.5 | 0.058 | 47.0 | 186.0 | 0.9956 | 3.19 | 0.40 | 9. |
| **...** | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | . |
| **95** | 7.1 | 0.260 | 0.29 | 12.4 | 0.044 | 62.0 | 240.0 | 0.9969 | 3.04 | 0.42 | 9. |
| **96** | 6.0 | 0.340 | 0.66 | 15.9 | 0.046 | 26.0 | 164.0 | 0.9979 | 3.14 | 0.50 | 8. |
| **97** | 8.6 | 0.265 | 0.36 | 1.2 | 0.034 | 15.0 | 80.0 | 0.9913 | 2.95 | 0.36 | 11. |
| **98** | 9.8 | 0.360 | 0.46 | 10.5 | 0.038 | 4.0 | 83.0 | 0.9956 | 2.89 | 0.30 | 10. |
| **99** | 6.0 | 0.340 | 0.66 | 15.9 | 0.046 | 26.0 | 164.0 | 0.9979 | 3.14 | 0.50 | 8. |

100 rows × 13 columns

# using PCA-preprocessing on wine dataset

Out[17]:

| | PC1 | PC2 |
|---|---|---|
| **0** | -2.185179 | 3.529983 |
| **1** | -0.247707 | -0.553177 |
| **2** | -0.380592 | 0.365447 |
| **3** | -1.735882 | 0.929351 |
| **4** | -1.735882 | 0.929351 |
| **...** | ... | ... |
| **6492** | 2.699833 | -0.854172 |
| **6493** | 2.524458 | -1.161039 |
| **6494** | 2.775507 | -0.761733 |
| **6495** | 2.984356 | -0.767021 |
| **6496** | 1.852698 | -0.516246 |

6497 rows × 2 columns

# using LDA-preprocessing on wine dataset

```
(6497, 2)
```

Out[18]:

| | 0 | 1 |
|---|---|---|
| **quality** | | |
| **6** | 0.752078 | -1.466209 |
| **6** | 1.445150 | 0.392049 |
| **6** | -0.123015 | 0.911451 |
| **6** | 0.288961 | -0.721769 |
| **6** | 0.288961 | -0.721769 |
| **...** | ... | ... |
| **5** | 0.512278 | -0.224430 |
| **6** | -0.514707 | -0.597340 |
| **6** | -0.231160 | -0.831907 |
| **5** | 0.630811 | 0.158871 |
| **6** | -0.668993 | -2.296580 |

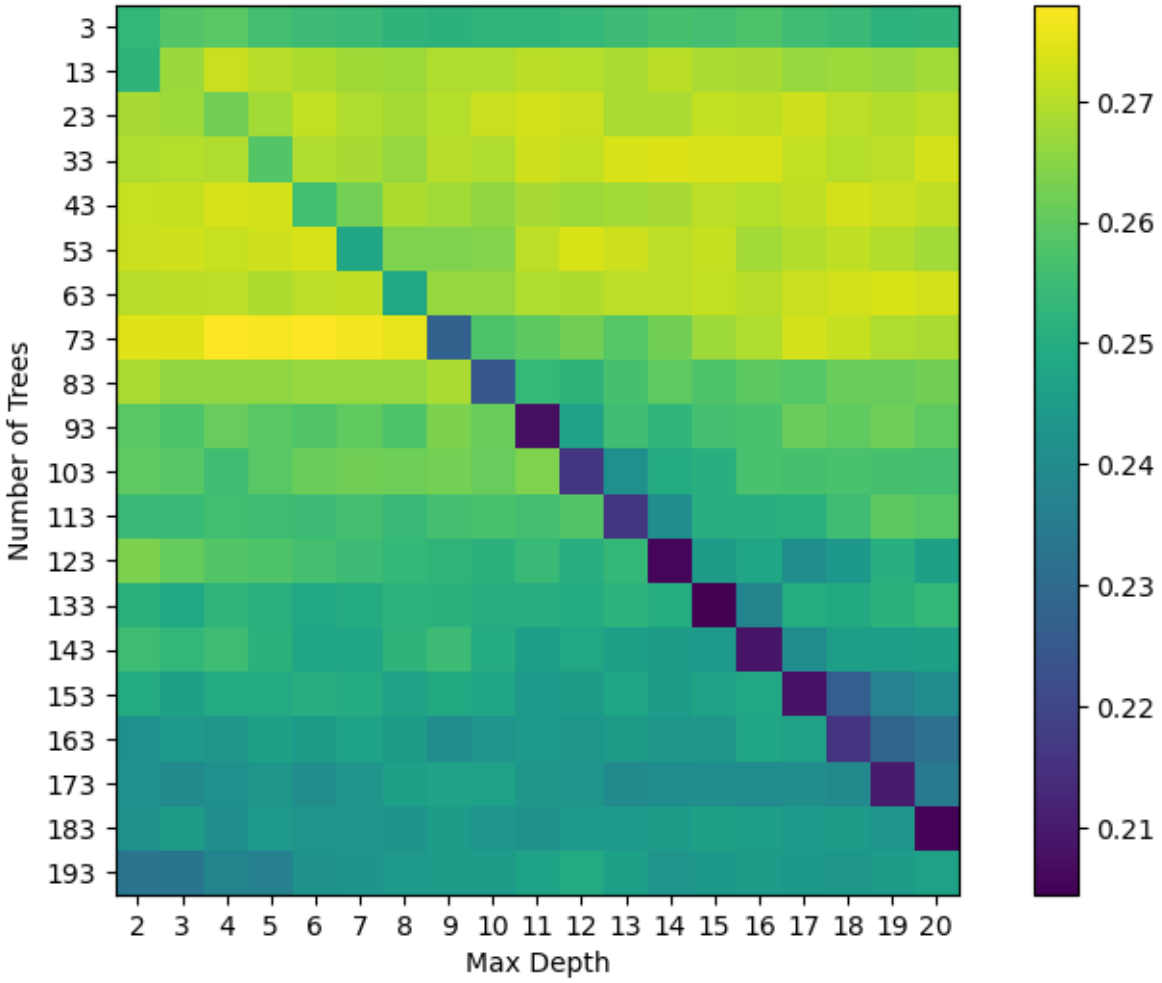
6497 rows × 2 columns

# Random Forest on Abalone dataset

**Printing accuracy and best parameter for raw abalone dataset**

```
Best Parameters: {'max_depth': 8, 'n_estimators': 153}
Mean Accuracy: 0.277958055181503
```

To produce a plot showing the mean accuracy vs. the above parameter settings, we can use the following code:

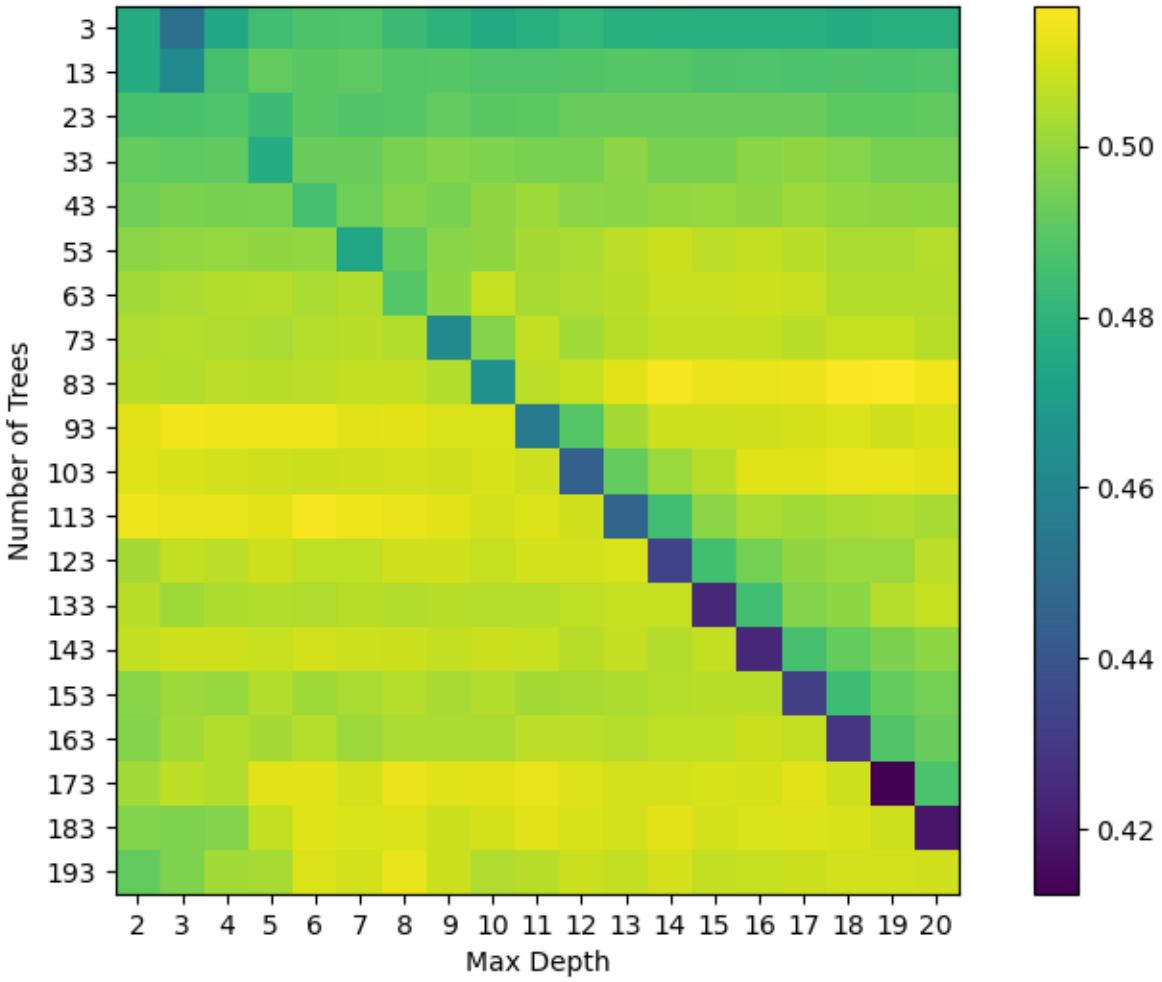



From the heat plot, we can see that the best mean accuracy is achieved with a maximum depth of 8 and 153 trees. from the above colorbar, we can see that if we go on increasing the max depth, which in turn would increase the number of trees which would result the model to overfit and the accuracy will drop. so to get the best parameters, we shall use the parameters that is best suited for the data.

# Random Forest on Wine - raw dataset:

**Printing accuracy and best parameter for raw wine dataset**

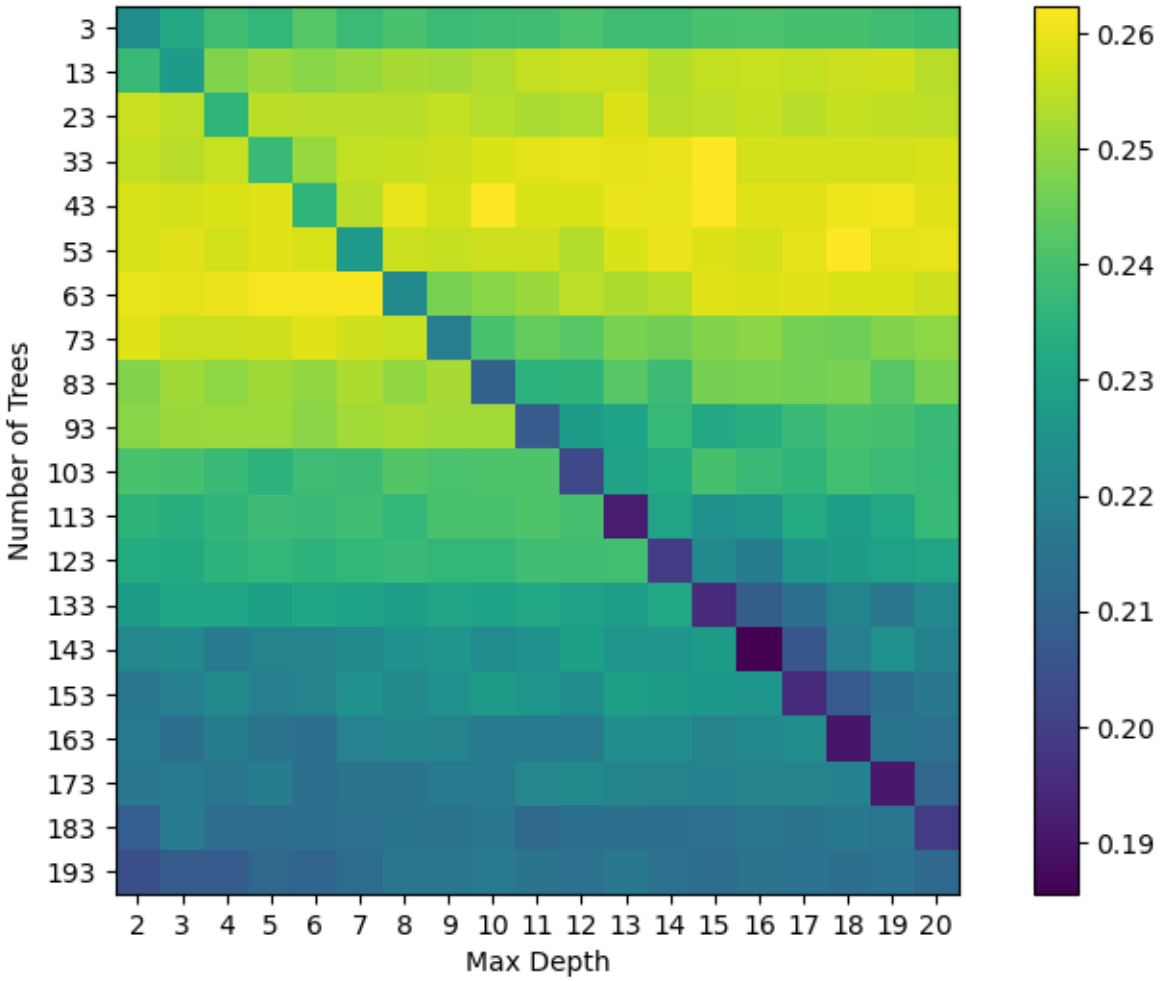
```
Best Parameters: {'max_depth': 10, 'n_estimators': 93}
Mean Accuracy: 0.5163887013679161
```




From the heat plot, we can see that the best mean accuracy is achieved with a maximum depth of 10 and 93 trees.

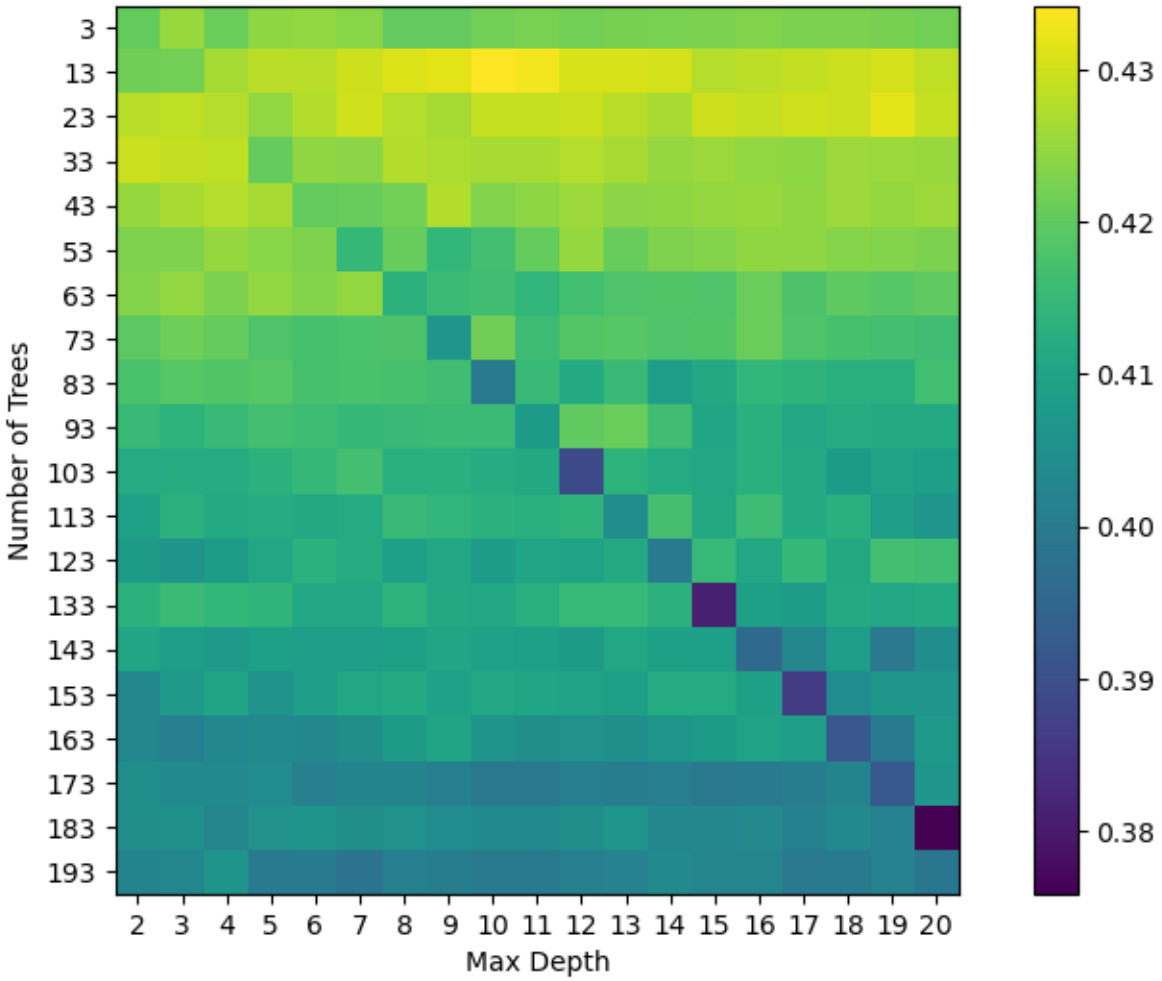
# Random Forest - Abalone PCA dataset

```
Best Parameters: {'max_depth': 6, 'n_estimators': 43}
Mean Accuracy: 0.26239606910580754
```



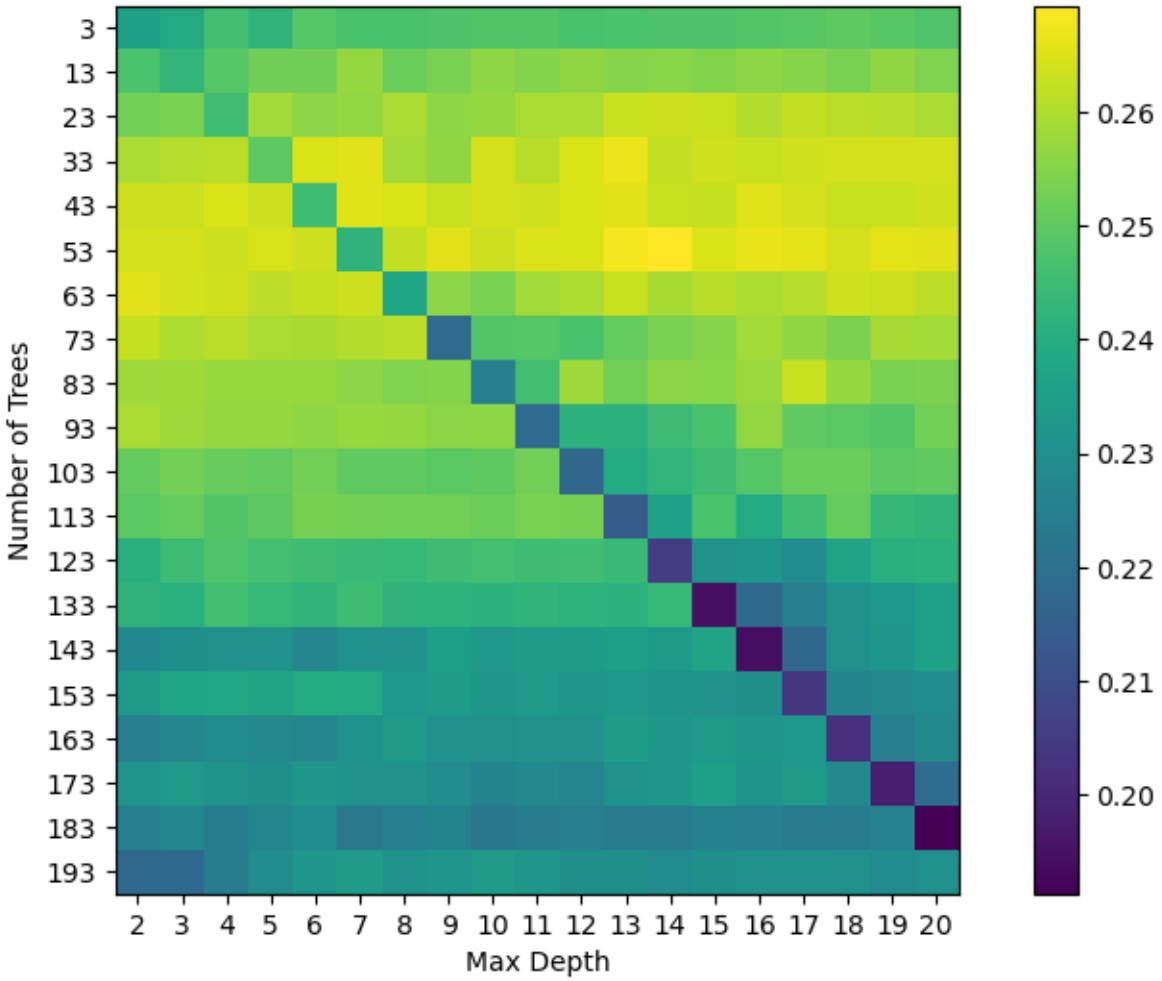

# Random Forest - Wine PCA dataset

```
Best Parameters: {'max_depth': 3, 'n_estimators': 73}
Mean Accuracy: 0.4341899686149109
```



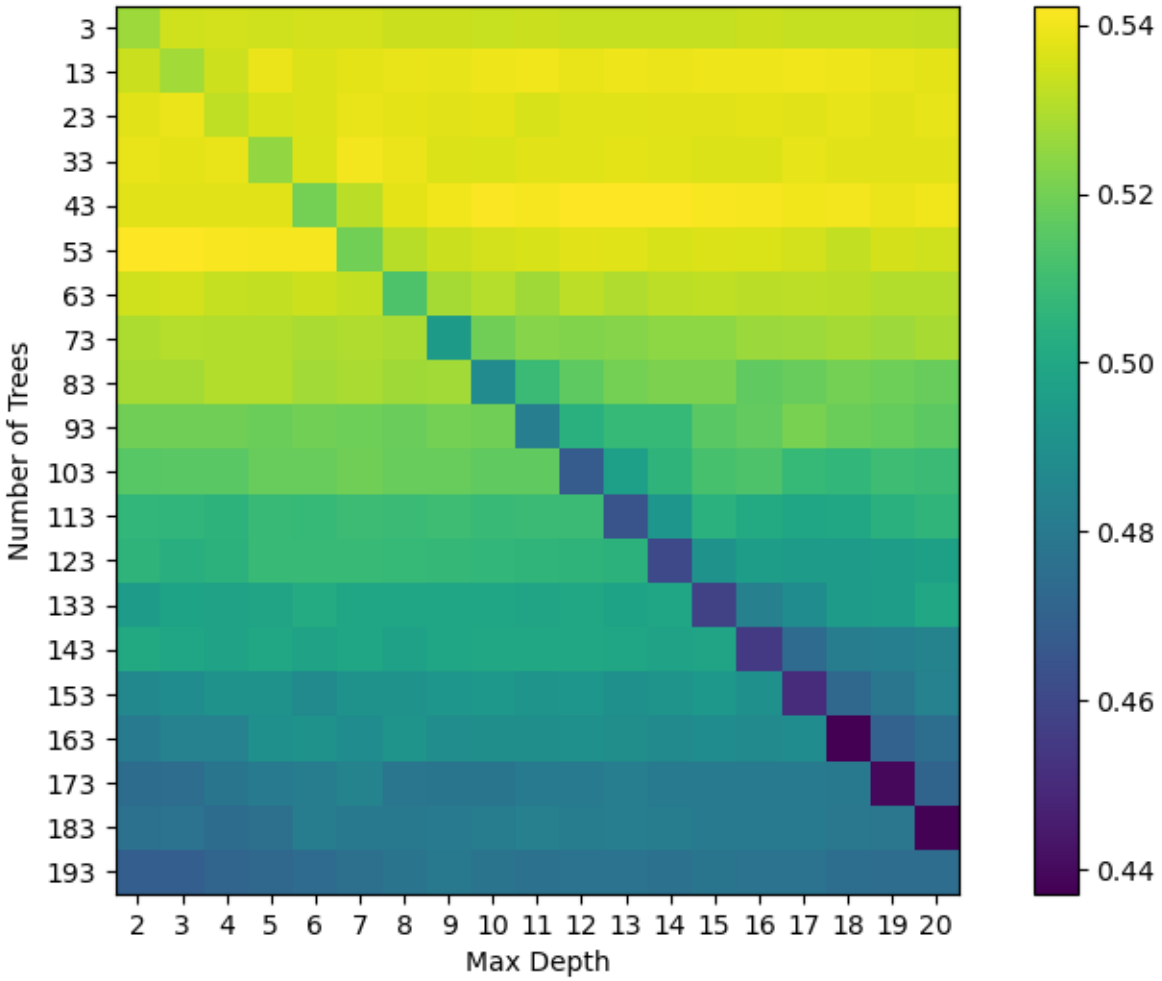

# Random Forest - Abalone LDA dataset

```
Best Parameters: {'max_depth': 7, 'n_estimators': 73}
Mean Accuracy: 0.26933701974042346
```




# Random Forest - Wine LDA dataset

```
Best Parameters: {'max_depth': 6, 'n_estimators': 73}
Mean Accuracy: 0.5422585420737845
```




## Conclusion

PCA reduces the dimensionality of the data by creating new features that capture the most important variation in the data. This can help reduce overfitting and improve the generalization performance of the model. However, in this case, we see that the accuracy is lower than the raw data setting, which could indicate that some important information was lost during the PCA transformation.

LDA is a supervised dimensionality reduction technique that can be used to project the data onto a lower-dimensional space that maximizes class separation. This can help improve the accuracy of the model by reducing the amount of noise and irrelevant features in the data. In this case, we see that the accuracy is slightly higher than the raw data setting, indicating that LDA was able to capture important discriminative information for the classification task.