Jupyter Notebooks

June 30, 2020

1 Plotting Graphs in Python

This is a brief tutorial on how to plot graphs with python, we will be using the "D_mel_atlas.csv" dataset which is attached with the email containing the link to this notebook.

First we import the necessary libraries, which will include "seaborn", "matplotlib" and "pandas"

```
[1]: import pandas as pd # for dataset manipulation
import matplotlib.pyplot as plt
import seaborn as sns

from mpl_toolkits import mplot3d #a necessary import for plotting 3D graphs
```

```
[2]: sns.set(style="white") sns.set(style="whitegrid", color_codes=True) #setting stylistic choices for the → graphs
```

```
[3]: df = pd.read_csv("D_mel_atlas.csv") #importing our dataset
```

We will begin with plotting a distribution plot for the evergene.

```
[4]: columns = df.columns.to_list()
print(columns) #always look at how the genes are named in the dataset before

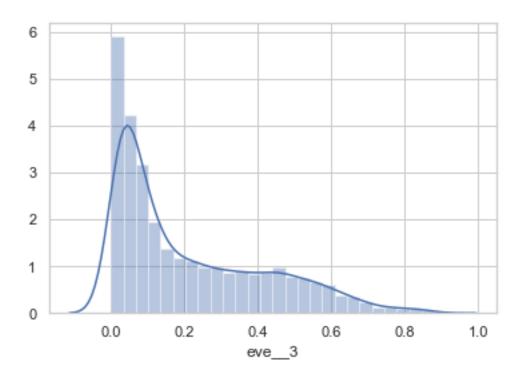
→starting
```

```
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'Cyp310a1__1', 'D__1', 'Kr__1', 'Traf1__1', 'bcd__1', 'cad__1', 'croc__1',
'eve__1', 'fkh__1', 'ftz__1', 'gt__1', 'h__1', 'hb__1', 'hkb__1', 'kni__1',
'knrl__1', 'noc__1', 'odd__1', 'prd__1', 'rho__1', 'slp1__1', 'slp2__1',
'sna__1', 'tll__1', 'trn__1', 'twi__1', 'zen__1', 'KrP__1', 'bcdP__1', 'gtP__1',
'hbP__1', 'x__2', 'y__2', 'z__2', 'Nx__2', 'Ny__2', 'Nz__2', 'CG10924__2',
'CG31607__2', 'D__2', 'Kr__2', 'Traf1__2', 'bcd__2', 'brk__2', 'cad__2',
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'slp2__2', 'sna__2', 'tll__2', 'trn__2', 'tsh__2', 'twi__2', 'zen__2', 'KrP__2',
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```

```
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'srp_3', 'term_3', 'tll_3', 'trn_3', 'tsh_3', 'twi_3', 'zen_3', 'KrP_3',
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'Nz 4', 'Alh 4', 'Ama 4', 'Ance 4', 'Blimp-1 4', 'Bsg25A 4', 'Btk29A 4',
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'Cyp310a1_4', 'D_4', 'Dfd_4', 'Doc2_4', 'Doc3_4', 'Esp_4', 'Ilp4_4',
'ImpE2__4', 'Kr__4', 'MESR3__4', 'Mdr49__4', 'Mes2__4', 'Nek2__4', 'NetA__4',
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'CG8147_5', 'CG8965_5', 'Cyp310a1_5', 'D_5', 'Dfd_5', 'Esp_5', 'HLHm5_5',
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'CG13333__6', 'CG14427__6', 'CG17724__6', 'CG17786__6', 'CG31607__6',
'CG31670_6', 'CG8147_6', 'CG8965_6', 'Cyp310a1_6', 'D_6', 'Dfd_6',
'Doc2 6', 'Doc3 6', 'Esp 6', 'HLHm5 6', 'Ilp4 6', 'ImpE2 6', 'ImpL2 6',
'Kr_6', 'MESR3_6', 'Mdr49_6', 'Mes2_6', 'Nek2_6', 'NetA_6', 'Traf1_6',
'aay__6', 'apt__6', 'bmm__6', 'brk__6', 'bun__6', 'cad__6', 'cenG1A__6',
'cnc_6', 'comm2_6', 'croc_6', 'dan_6', 'danr_6', 'dpn_6', 'edl_6',
'emc_6', 'eve_6', 'fj_6', 'fkh_6', 'ftz_6', 'gk_6', 'gt_6', 'h_6',
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'mfas_6', 'noc_6', 'nub_6', 'numb_6', 'oc_6', 'odd_6', 'peb_6', 'prd_6',
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'srp_6', 'tkv_6', 'tll_6', 'toc_6', 'trn_6', 'tsh_6', 'twi_6', 'zen_6',
'KrP_6', 'gtP_6', 'hbP_6]', 'Unnamed: 411', 'Unnamed: 412', 'Unnamed: 413',
'Unnamed: 414', 'Unnamed: 415', 'Unnamed: 416', 'Unnamed: 417', 'Unnamed: 418',
'Unnamed: 419']
```

```
[5]: sns.distplot(df["eve__3"]) # we will be using timepoint 3 for this example
```

[5]: <matplotlib.axes._subplots.AxesSubplot at 0x11a26e67e48>



As we can see, most of the cells have an eve expression ranging from 0.0 to ~ 0.2 . As eve is expressed only in 7 stripes we expect only a small number of cells to have a high eve concentration. Therefore looking at the distribution plot, we can infer that the activation threshold should range around ~ 0.2 to ~ 0.4 .

Look at the seaborns documentation for more customisation purposes and to expose yourself to the different types of graphs available for plotting.

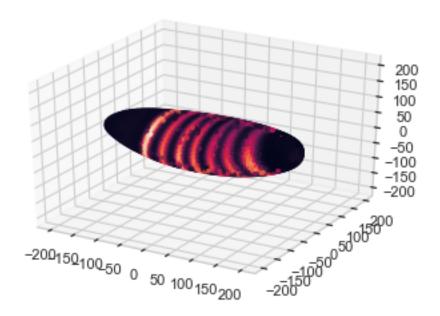
Now, we will plot a 3D model of the Drosophila embryo to visualise eve expression by using eve to colorise our points.

```
[9]: ax = plt.axes(projection="3d") # prepares the ax variable for 3D plotting

#Now we set the limits of our plots
ax.set_xlim([-220,220])
ax.set_ylim([-220,220])
ax.set_zlim([-220,220])

ax.set_zlim([-220,220])

ax.scatter(df["x__3"],df["y__3"],df["z__3"], c=df["eve__3"], s=30, marker=".")
plt.show()
```



Cells with high concentration of eve can be seen as red, producing a 3D graph with the distinct 7 stripes.

Now on your own, plot eve from the 6 different time points provided in the dataset: (i) Use a "for" loop to automate the process (ii) Set the angle so that graph outputs are consistent (iii) Remove the tick values (iv) Try using a different colormap outside of the default.