main_py

August 18, 2021

1 Pie chart of samples

```
[1]: import pandas as pd
    import matplotlib.pyplot as plt
[2]: %matplotlib inline
[3]: df = pd.read_csv("../../input/phenotypes/merged/_m/merged_phenotypes.csv", __
     →index_col=0)

¬"Schizo"]))].copy()
    df.Race = df.Race.astype("category").cat.rename_categories({'CAUC': 'EA'})
    df.head()
[3]:
             BrNum
                     RNum
                           Region RIN
                                         Age Sex Race
                                                          Dx mitoRate
    R12864 Br1303 R12864
                          Caudate
                                   9.6
                                        42.98
                                               F
                                                       Schizo 0.032654
                                                   AA
    R12865 Br1320 R12865
                           Caudate 9.5
                                        53.12
                                               М
                                                   AA
                                                       Schizo 0.019787
    R12866 Br1321 R12866
                           Caudate
                                   9.1
                                        57.13
                                               F
                                                   AA
                                                      Schizo 0.013006
    R12867
           Br1326
                           Caudate
                                   9.2
                                        74.56
                                                       Schizo
                                                              0.032594
                   R12867
                                               Μ
                                                   AA
    R12868 Br1418 R12868
                           Caudate 9.5
                                        43.35
                                               М
                                                   AA Schizo 0.052347
            rRNA_rate
                     overallMapRate
    R12864
             0.000087
                            0.909350
    R12865
             0.000070
                            0.873484
    R12866
             0.000040
                            0.905505
    R12867
             0.000038
                            0.910551
    R12868
             0.000056
                           0.748659
[4]: df.groupby("Region").size()
[4]: Region
    Caudate
                   420
    DLPFC
                   434
    DentateGyrus
                   161
    HIPPO
                   447
    dtype: int64
```

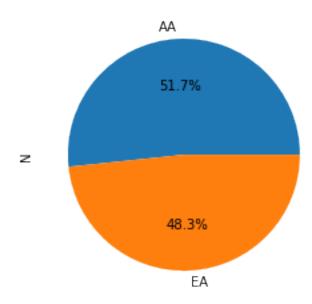
```
[5]: data = df.groupby(["Region", "Race"]).size().reset_index().rename(columns={0:

□"N"})

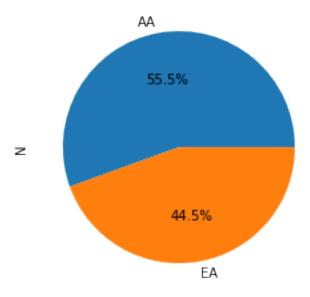
data
```

```
[5]:
             Region Race
                            N
                      AA 217
            Caudate
            Caudate
    1
                      ΕA
                         203
    2
              DLPFC
                      AA 241
    3
              DLPFC
                      EA 193
    4 DentateGyrus
                          78
                      AA
    5 DentateGyrus
                      ΕA
                           83
    6
              HIPPO
                      AA 248
    7
              HIPPO
                          199
                      EΑ
```

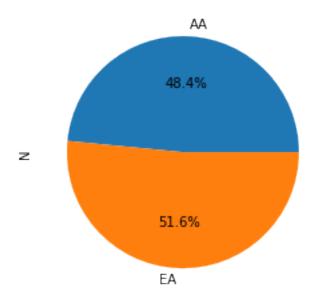
```
[7]: caudate.N.plot.pie(autopct="%.1f%%")
plt.savefig('caudate_pie.pdf')
```



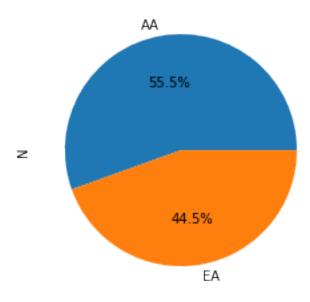
```
[8]: dlpfc.N.plot.pie(autopct="%.1f%%");
plt.savefig('dlpfc_pie.pdf')
```







[10]: hippocampus.N.plot.pie(autopct="%.1f%%")
plt.savefig('hippocampus_pie.pdf')



[]:[