main_py

August 26, 2022

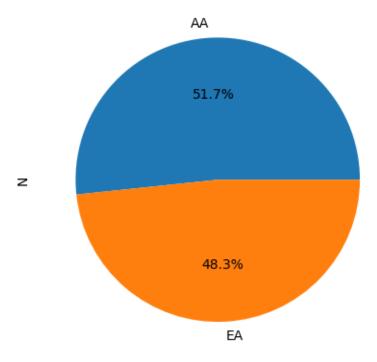
1 Pie chart of samples

```
[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)

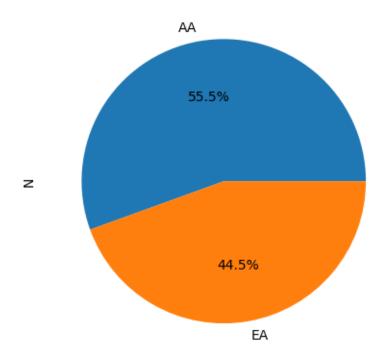
¬"Schizo"]))].copy()
    df.Race = df.Race.astype("category").cat.rename_categories({'CAUC': 'EA'})
    df.head()
[3]:
             BrNum
                     RNum
                            Region RIN
                                          Age Sex Race
                                                           Dx mitoRate
           Br1303
                  R12864
                           Caudate
    R12864
                                   9.6
                                        42.98
                                                   AA
                                                       Schizo
                                                               0.032654
    R12865
           Br1320 R12865
                           Caudate
                                   9.5
                                        53.12
                                                Μ
                                                   AA
                                                       Schizo 0.019787
    R12866 Br1321 R12866
                                        57.13
                           Caudate
                                   9.1
                                                F
                                                   AA
                                                       Schizo 0.013006
    R12867
            Br1326
                   R12867
                           Caudate
                                   9.2
                                        74.56
                                                Μ
                                                   AA
                                                       Schizo
                                                               0.032594
    R12868
            Br1418 R12868
                           Caudate 9.5
                                        43.35
                                                       Schizo 0.052347
                                                Μ
                                                   AA
            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]:
            Region Race
                          N
            Caudate
                     AA 217
            Caudate
                     EA 203
    1
    2
             DLPFC
                     AA 241
             DLPFC
                     EA 193
    3
    4 DentateGyrus
                     AA
                        78
    5 DentateGyrus
                        83
                     EΑ
    6
             HIPPO
                     AA 248
    7
             HIPPO
                     EA 199
```

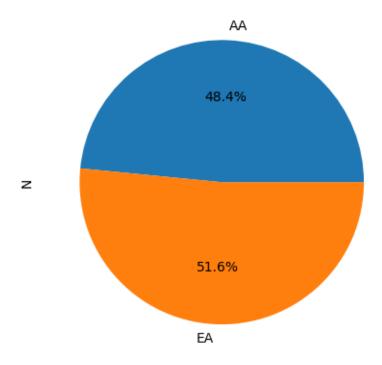
```
[7]: caudate.N.plot.pie(autopct="%.1f%%")
plt.savefig('caudate_pie.pdf')
```



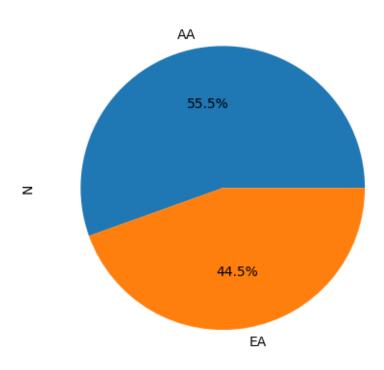
```
[8]: dlpfc.N.plot.pie(autopct="%.1f%%");
plt.savefig('dlpfc_pie.pdf')
```



```
[9]: gyrus.N.plot.pie(autopct="%.1f%%");
plt.savefig('dentate_gyrus_pie.pdf')
```



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



[]: