main

July 12, 2021

1 Enrichment in DE genes

[1]:

```
import functools
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from scipy.stats import fisher_exact
from statsmodels.stats.multitest import multipletests
```

1.1 Functions

1.1.1 Cached functions

[2]:

```
@functools.lru_cache()
def get_wgcna_modules():
    return pd.read_csv("../../_m/modules.csv", index_col=0)


@functools.lru_cache()
def get_degs():
    return set(pd.read_csv('../../../../differential_analysis/'+\
                           'dlpfc/_m/genes/diffExpr_EAvsAA_FDR05.txt',
                           sep='\t', usecols=[0], index_col=0).index)


@functools.lru_cache()
def get_mhc_genes():
    return set(pd.read_csv('../../../../input/counts/mhc_region_genes/'+\
                           '_m/mhc_genes.csv')['gene_id'])
```

1.1.2 Simple functions

[3]:

```
def fet(a, b, u):
    # a, b, u are sets
    # u is the universe
    yes_a = u.intersection(a)
    yes_b = u.intersection(b)
    no_a = u - a
    no_b = u - b
    m = [[len(yes_a.intersection(yes_b)), len(no_a.intersection(yes_b)) ],
         [len(yes_a.intersection(no_b)), len(no_a.intersection(no_b))]]
    return fisher_exact(m)


def enrichment_rows():
    mod = get_wgcna_modules().module.unique()
    u = set(get_wgcna_modules().index)
    for ii in range(len(mod)): # for each module
        a = set(get_wgcna_modules()[(get_wgcna_modules().module) == mod[ii]].
 ↪index)
        b = set(get_wgcna_modules()[(get_wgcna_modules().module) == mod[ii]].
 ↪index) - get_mhc_genes()
        yield (mod[ii],
               len(a),
               *fet(a, get_degs(), u),
               *fet(b, get_degs() - get_mhc_genes(), u),
               )
```

1.2 Main

1.2.1 Enrichment

[4]:
```
edf = pd.DataFrame.from_records(enrichment_rows(),
                                 columns=['Module_ID', 'N_Genes', 'DEG_OR',␣
 ↪'DEG_P',
                                          'DEG_noMHC_OR', 'DEG_noMHC_P'],
                                 index='Module_ID')
edf['DEG_FDR'] = multipletests(edf['DEG_P'], method='fdr_bh')[1]
edf['DEG_noMHC_FDR'] = multipletests(edf['DEG_noMHC_P'], method='fdr_bh')[1]
edf = edf.loc[:, ['N_Genes', 'DEG_OR', 'DEG_P', 'DEG_FDR', 'DEG_noMHC_OR',␣
 ↪'DEG_noMHC_P', 'DEG_noMHC_FDR']]
```

[5]:
```
print(edf[(edf["DEG_FDR"] < 0.05)].shape)
edf[(edf["DEG_FDR"] < 0.05)]
```

```
(20, 7)
```

[5]:
```
               N_Genes    DEG_OR         DEG_P       DEG_FDR  DEG_noMHC_OR  \
Module_ID
grey              9301  1.381842  2.557465e-15  2.109908e-14      1.413304
cyan               387  2.641789  1.448431e-14  7.966372e-14      2.620217
blue              1086  0.623003  1.019720e-05  4.807252e-05      0.631043
pink               498  0.667243  1.057143e-02  1.744287e-02      0.669036
purple             423  0.518651  3.136625e-04  8.625719e-04      0.512765
darkgrey           185  0.361765  1.000292e-03  2.539203e-03      0.371172
```

```
turquoise         2005  0.464224  1.675530e-19  1.843083e-18      0.465871
royalblue          236  0.345246  8.895660e-05  2.736170e-04      0.352893
darkturquoise      188  4.507851  8.189218e-20  1.351221e-18      4.626529
red                590  0.524307  1.971498e-05  7.228825e-05      0.528745
magenta            482  0.621041  3.206185e-03  6.223772e-03      0.629198
greenyellow        418  0.565068  1.532203e-03  3.526794e-03      0.575902
darkred            218  3.426856  1.168969e-14  7.715196e-14      3.456068
black              545  2.666836  5.515621e-20  1.351221e-18      2.626515
lightgreen         250  0.355950  9.120566e-05  2.736170e-04      0.358929
brown              996  0.723479  3.042612e-03  6.223772e-03      0.729723
lightcyan          344  0.388879  1.427514e-05  5.888497e-05      0.400892
salmon             401  1.544866  1.603088e-03  3.526794e-03      1.558055
darkgreen          214  1.696614  4.467483e-03  8.190385e-03      1.710942
grey60             336  0.592925  9.257342e-03  1.607854e-02      0.597913

                DEG_noMHC_P  DEG_noMHC_FDR
Module_ID
grey           3.656371e-17   3.016506e-16
cyan           3.604968e-14   1.982733e-13
blue           1.787571e-05   8.427120e-05
pink           1.184407e-02   1.954272e-02
purple         2.712386e-04   7.459062e-04
darkgrey       1.339033e-03   3.156293e-03
turquoise      3.160914e-19   5.215508e-18
royalblue      1.693397e-04   5.080192e-04
darkturquoise  2.639454e-20   8.710198e-19
red            3.183431e-05   1.167258e-04
magenta        4.730019e-03   8.671702e-03
greenyellow    2.357781e-03   5.187117e-03
darkred        8.093031e-15   5.341400e-14
black          7.585462e-19   8.344009e-18
lightgreen     8.977488e-05   2.962571e-04
brown          4.059547e-03   7.880298e-03
lightcyan      2.479156e-05   1.022652e-04
salmon         1.207110e-03   3.064203e-03
darkgreen      3.189378e-03   6.578091e-03
grey60         9.203549e-03   1.598511e-02
```

[6]:

```
print(edf[(edf["DEG_noMHC_FDR"] < 0.05)].shape)
set(edf[(edf["DEG_FDR"] < 0.05)].index) - set(edf[(edf["DEG_noMHC_FDR"] < 0.
 ↪05)].index)
```

```
(20, 7)
```

[6]:

```
set()
```

sienna3 is enriched in MHC differentially expressed genes

[7]:

```
edf.to_csv('wgcna_module_enrichment.csv')
```

1.2.2 Plot heatmap

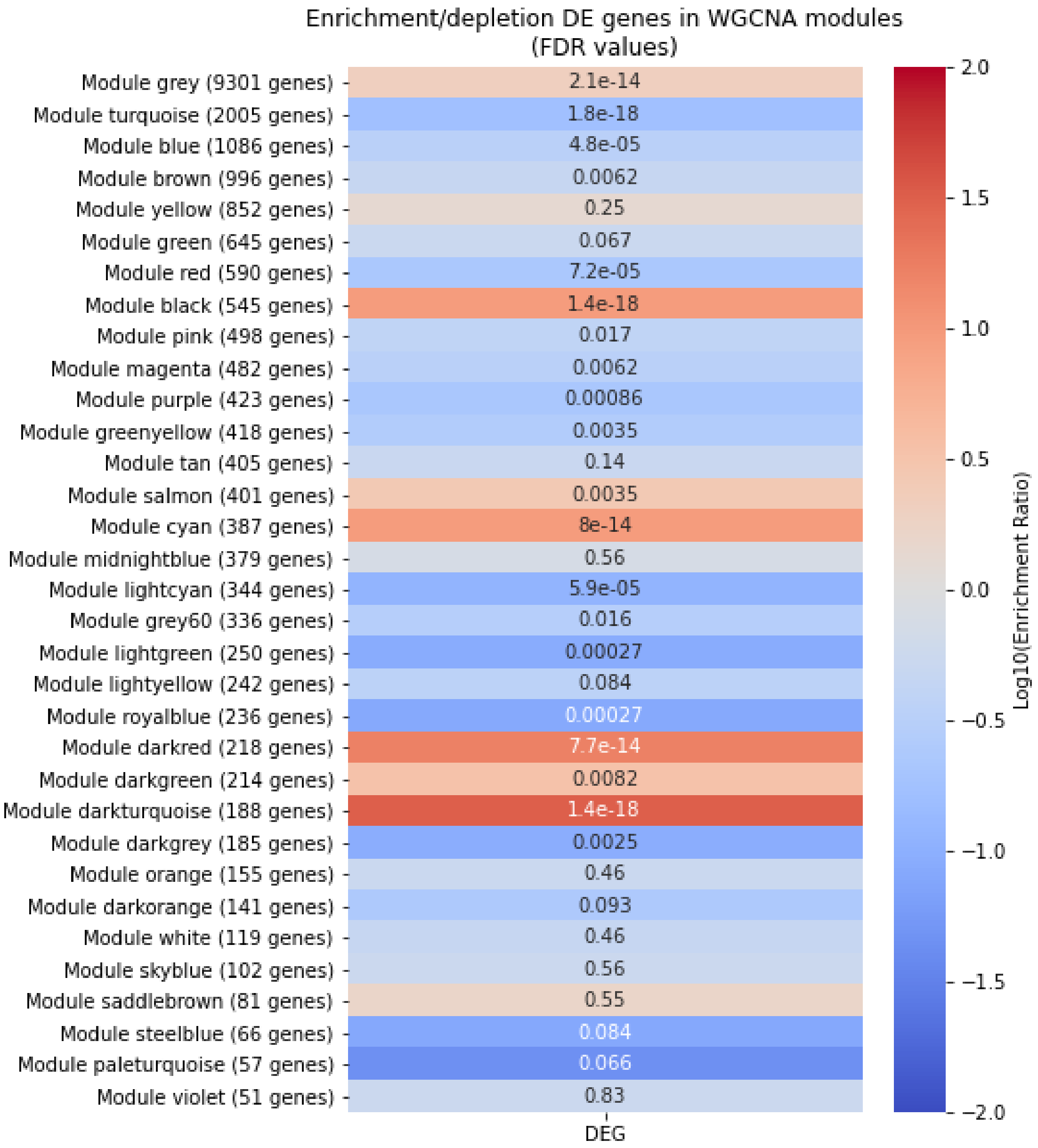
[8]:

```
df = edf.sort_values("N_Genes", ascending=False)
df2 = np.log(df.loc[:, ['DEG_OR']]).replace([np.inf, -np.inf], 0)
df2.columns = ['DEG']
df2.index = ["Module %s (%d genes)" % (x,y) for x,y in zip(df2.index,␣
 ↪df['N_Genes'])]
df3 = df.loc[:, ['DEG_FDR']]

fig, ax = plt.subplots(figsize=(6,10))
p = sns.heatmap(df2, cmap='coolwarm', annot=df3, yticklabels=df2.index,␣
 ↪center=0,
                cbar_kws={'label': 'Log10(Enrichment Ratio)'}, vmin=-2, vmax=2)
p.set_title("Enrichment/depletion DE genes in WGCNA modules\n(FDR values)")
p.get_figure().savefig('wgcna_module_enrichment.pdf', bbox_inches='tight')
p
```

[8]:

```
<AxesSubplot:title={'center':'Enrichment/depletion DE genes in WGCNA
modules\n(FDR values)'}>
```

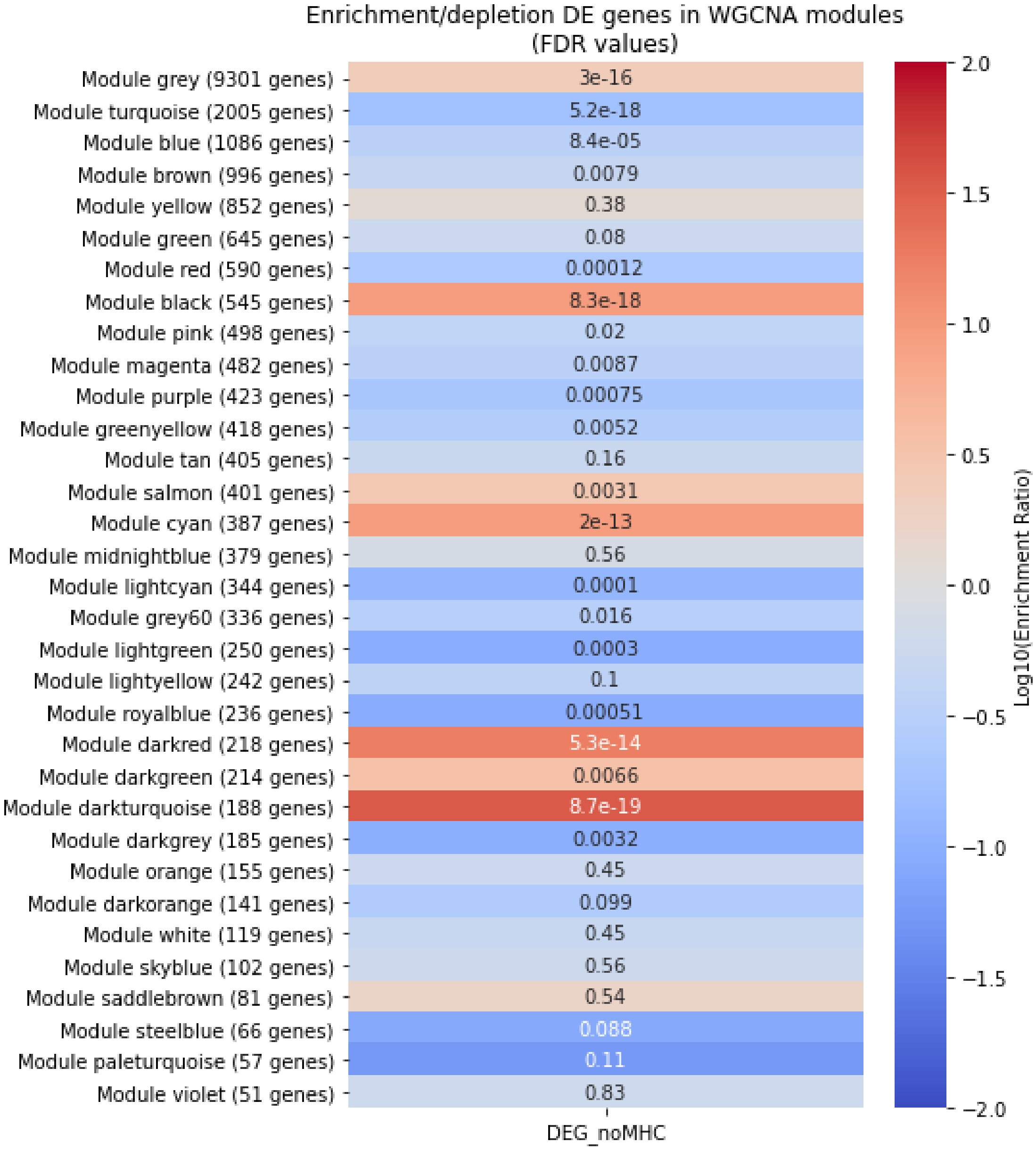


```
[9]: df = edf.sort_values("N_Genes", ascending=False)
     df2 = np.log(df.loc[:, ['DEG_noMHC_OR']]).replace([np.inf, -np.inf], 0)
     df2.columns = ['DEG_noMHC']
     df2.index = ["Module %s (%d genes)" % (x,y) for x,y in zip(df2.index,␣
      ↪df['N_Genes'])]
     df3 = df.loc[:, ['DEG_noMHC_FDR']]

     fig, ax = plt.subplots(figsize=(6,10))
```

```
p = sns.heatmap(df2, cmap='coolwarm', annot=df3, yticklabels=df2.index,␣
 ↪center=0,
                cbar_kws={'label': 'Log10(Enrichment Ratio)'}, vmin=-2, vmax=2)
p.set_title("Enrichment/depletion DE genes in WGCNA modules\n(FDR values)")
p.get_figure().savefig('wgcna_module_enrichment_noMHC.pdf', bbox_inches='tight')
p
```

```
[9]: <AxesSubplot:title={'center':'Enrichment/depletion DE genes in WGCNA
     modules\n(FDR values)'}>
```



```
[ ]:
```