

main

July 10, 2021

1 Cell type enrichment analysis

```
[1]: import os, errno
import functools
import numpy as np
import pandas as pd
from matplotlib_venn import venn3
from matplotlib import 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_deg(tissue):
    fn = '../.../differential_expression/%s/_m/genes/
    ↪diffExpr_maleVfemale_full.txt' % tissue
    return pd.read_csv(fn, sep='\t', index_col=0)

@functools.lru_cache()
def get_xci():
    return pd.read_csv('../.../xci_status_hg19.txt', sep='\t')
```

1.1.2 Simple functions

```
[3]: def tissue_annotation(tissue):
    return {'caudate': "Caudate", "dlpfc": "DLPFC",
            "hippocampus": "Hippocampus"}[tissue]

def mkdir_p(directory):
    try:
        os.makedirs(directory)
    except OSError as e:
        if e.errno != errno.EEXIST:
```

```

        raise

def cal_fishers(status, tissue):
    deg = get_deg(tissue)
    xci = get_xci()
    xci['ensemblID'] = xci['Gene ID'].str.replace("\\\\..*", "", regex=True)
    df = deg.merge(xci, on='ensemblID', how='left')
    table = [[np.sum((df['adj.P.Val']<0.05) & (df['Combined XCI status'] ==_
↪status)),
               np.sum((df['adj.P.Val']<0.05) & (df['Combined XCI status'] !=_
↪status))),
               [np.sum((df['adj.P.Val']>0.05) & (df['Combined XCI status'] ==_
↪status)),
               np.sum((df['adj.P.Val']>0.05) & (df['Combined XCI status'] !=_
↪status))]]
    #print(table)
    return fisher_exact(table)

def cal_fishers_direction(status, direction, tissue):
    deg = get_deg(tissue)
    if direction == 'Up':
        deg = deg[(deg['t'] > 0)].copy()
    else:
        deg = deg[(deg['t'] < 0)].copy()
    xci = get_xci()
    xci['ensemblID'] = xci['Gene ID'].str.replace("\\\\..*", "", regex=True)
    df = deg.merge(xci, on='ensemblID', how='left')
    table = [[np.sum((df['adj.P.Val']<0.05) & (df['Combined XCI status'] ==_
↪status)),
               np.sum((df['adj.P.Val']<0.05) & (df['Combined XCI status'] !=_
↪status))),
               [np.sum((df['adj.P.Val']>0.05) & (df['Combined XCI status'] ==_
↪status)),
               np.sum((df['adj.P.Val']>0.05) & (df['Combined XCI status'] !=_
↪status))]]
    #print(table)
    return fisher_exact(table)

def cal_fisher_by_xci_status(tissue):
    xci_status = xci = get_xci().loc[:, 'Combined XCI status'].unique()
    xci_lt = []; pval_lt = []; oddratio_lt = []; dir_lt = [];
    for status in xci_status:
        odd_ratio, pval = cal_fishers(status, tissue)

```

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        xci_lt.append(status); pval_lt.append(pval);
        oddratio_lt.append(odd_ratio); dir_lt.append('All')
        if pval < 0.05:
            print("There is a significant enrichment (p-value < %.1e) of %s!" %
                  (pval, status))

    for status in xci_status:
        odd_ratio, pval = cal_fishers_direction(status, "Up", tissue)
        xci_lt.append(status); pval_lt.append(pval);
        oddratio_lt.append(odd_ratio); dir_lt.append('Male Bias')
        if pval < 0.05:
            print("There is a significant enrichment of male bias genes_
→(p-value < %.1e) of %s!" %
                  (pval, status))

    for status in xci_status:
        odd_ratio, pval = cal_fishers_direction(status, "Down", tissue)
        xci_lt.append(status); pval_lt.append(pval);
        oddratio_lt.append(odd_ratio); dir_lt.append('Female Bias')
        if pval < 0.05:
            print("There is a significant enrichment of female bias genes_
→(p-value < %.1e) of %s!" %
                  (pval, status))
    return pd.DataFrame({"Tissue": tissue_annotation(tissue),
                        'XCI status': xci_lt, 'OR': oddratio_lt,
                        'PValue': pval_lt, 'Direction': dir_lt})

```

1.2 Gene set overlaps

```

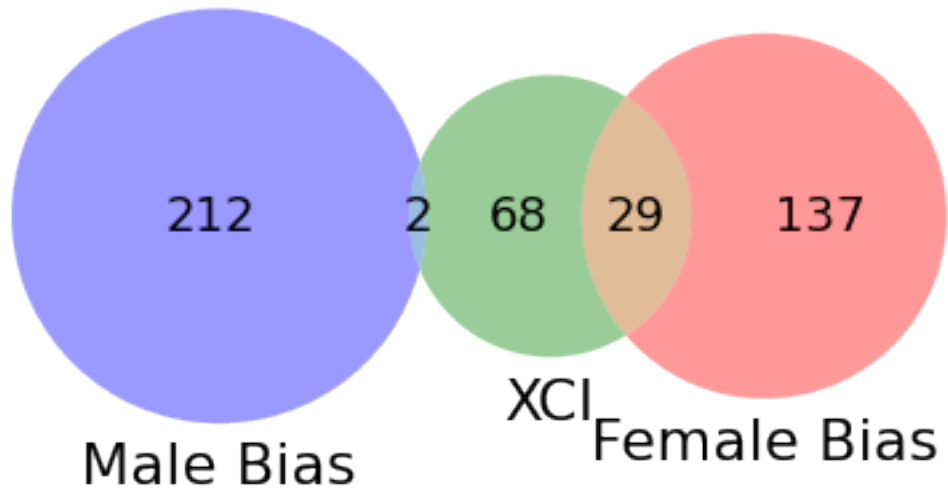
[4]: for tissue in ["caudate", "dlpfc", "hippocampus"]:
    mkdir_p(tissue)
    print(tissue_annotation(tissue))
    deg = get_deg(tissue)
    xci = get_xci()
    xci['ensemblID'] = xci['Gene ID'].str.replace("\\.*", "", regex=True)
    xci_status = get_xci().loc[:, 'Combined XCI status'].unique()
    ## Plot venn diagram
    for status in xci_status:
        setA = set(deg[(deg["adj.P.Val"] < 0.05) & (deg['t'] < 0)].ensemblID)
        setB = set(xci[(xci["Combined XCI status"] == status)].ensemblID)
        setC = set(deg[(deg["adj.P.Val"] < 0.05) & (deg['t'] > 0)].ensemblID)
        plt.rcParams.update({'font.size': 18})
        plt.figure(figsize=(7,7))
        v = venn3([setA, setB, setC], ("Female Bias", "XCI", "Male Bias"))
        plt.title(status.title())
        fn = '%s/venn_DEGs_%s' % (tissue, status)
        for ext in ['png', 'pdf', 'svg']:

```

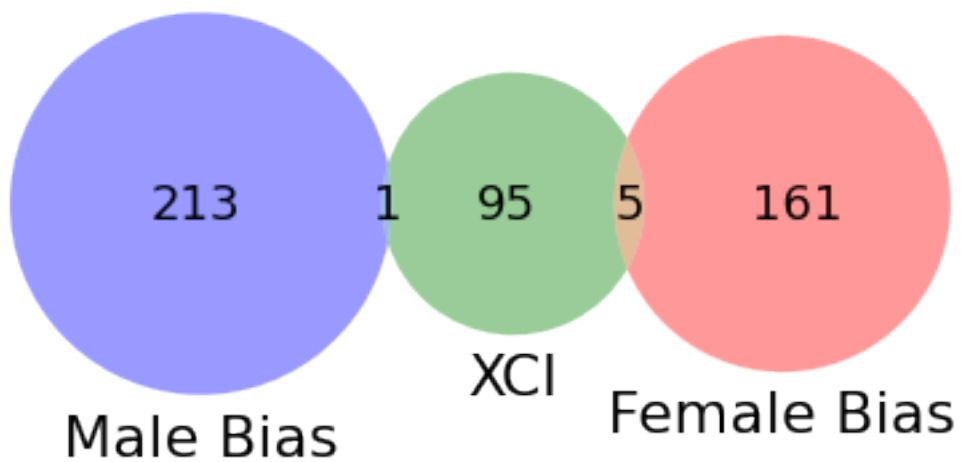
```
plt.savefig(fn + '.' + ext)
plt.show()
```

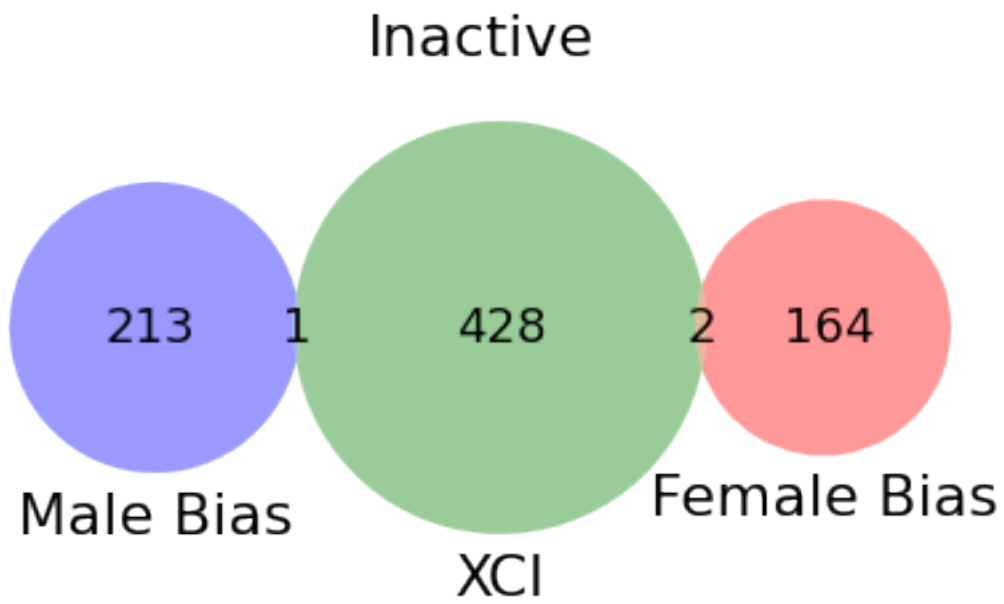
Caudate

Escape

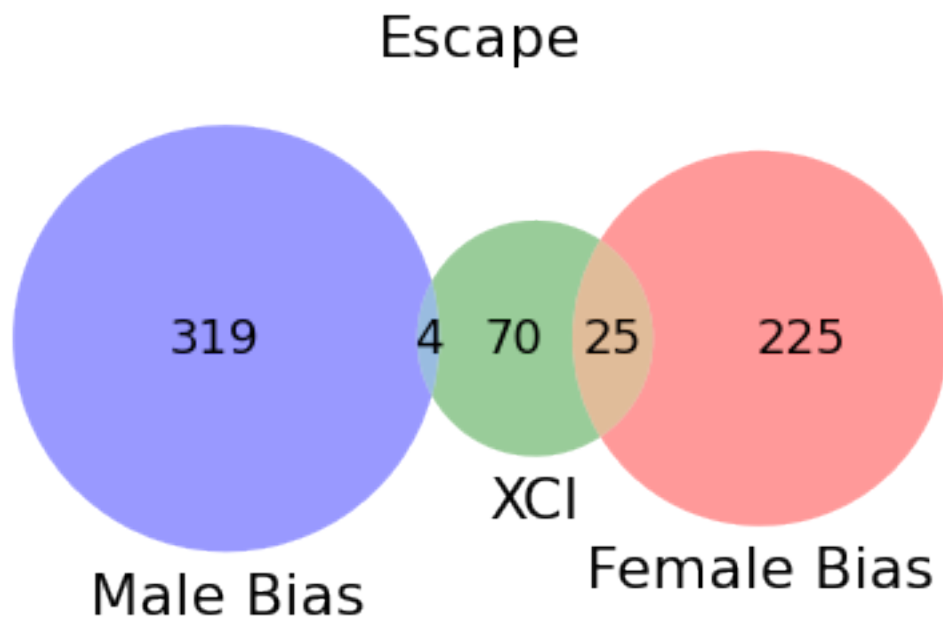


Variable

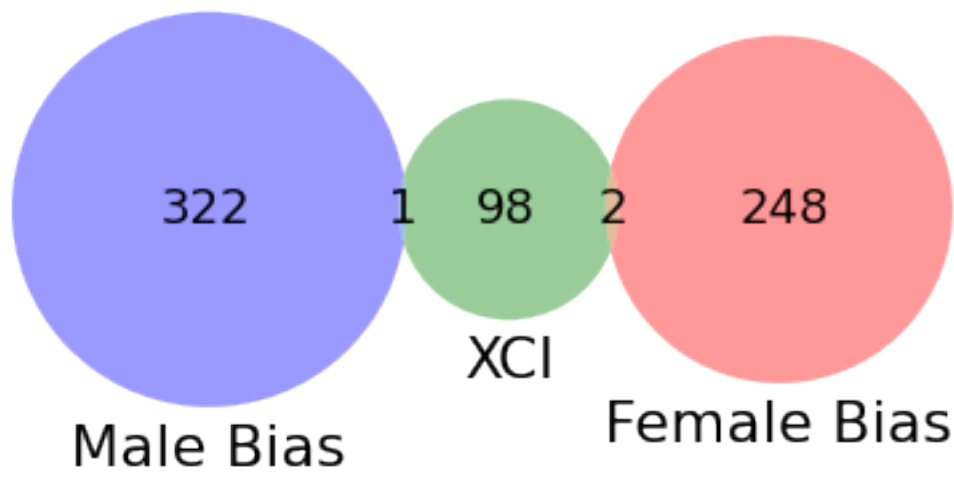




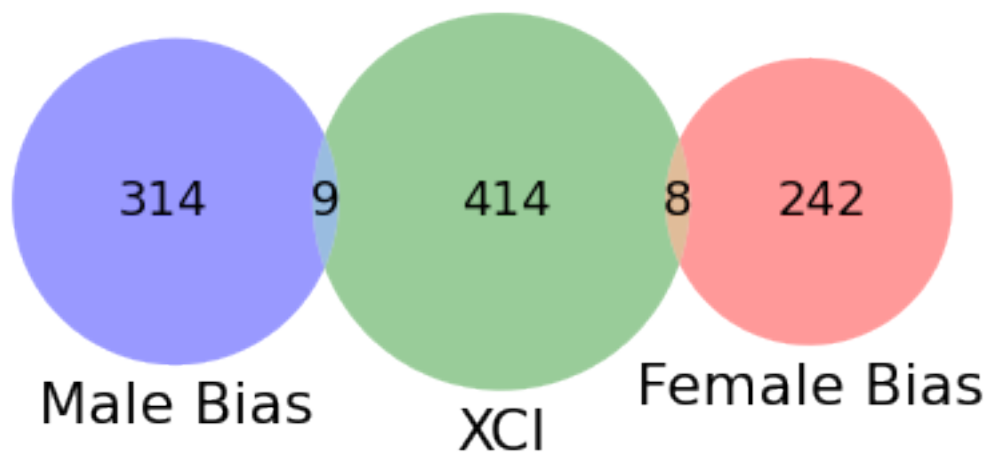
DLPFC



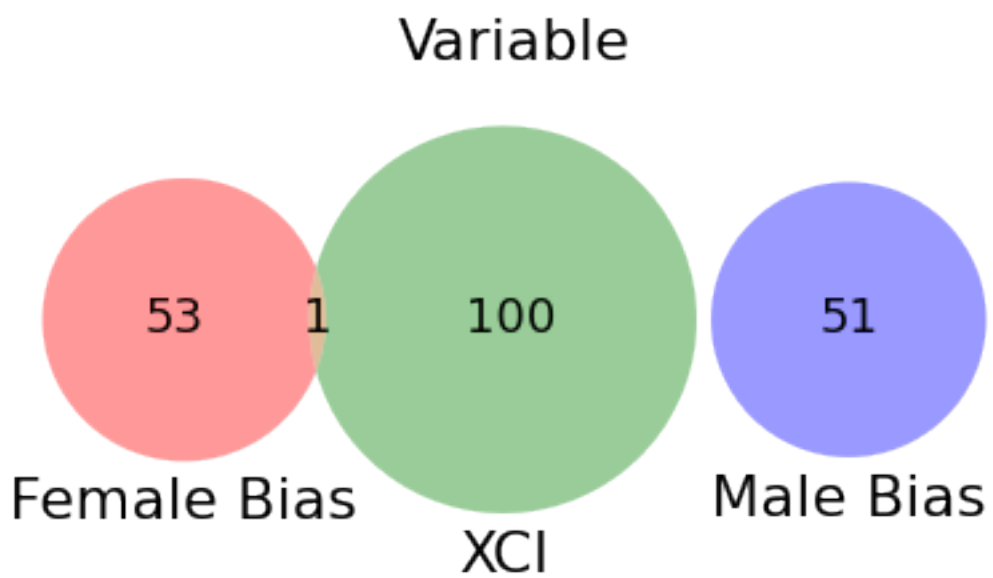
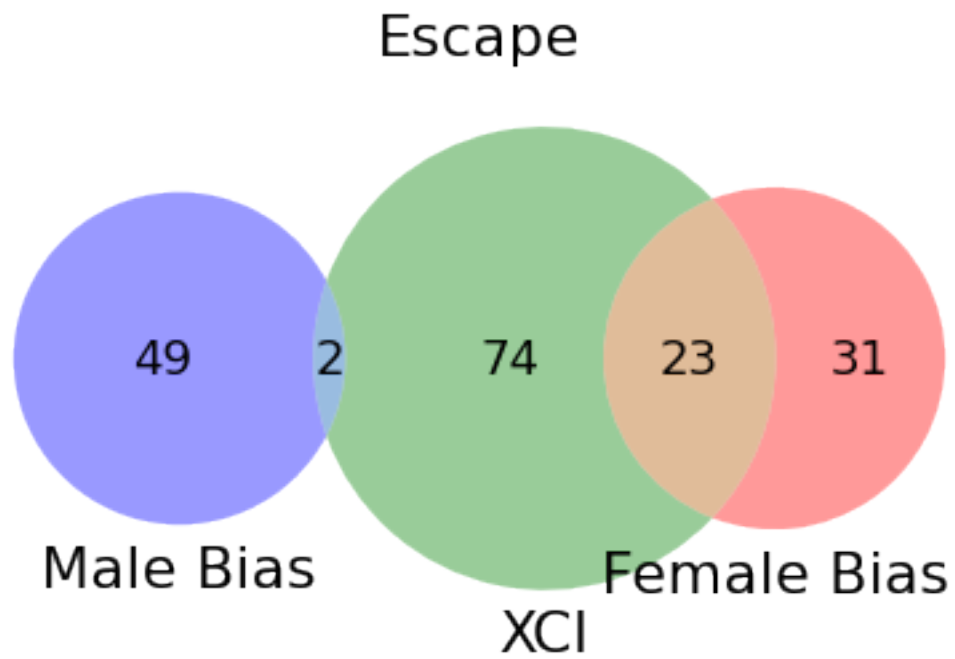
Variable

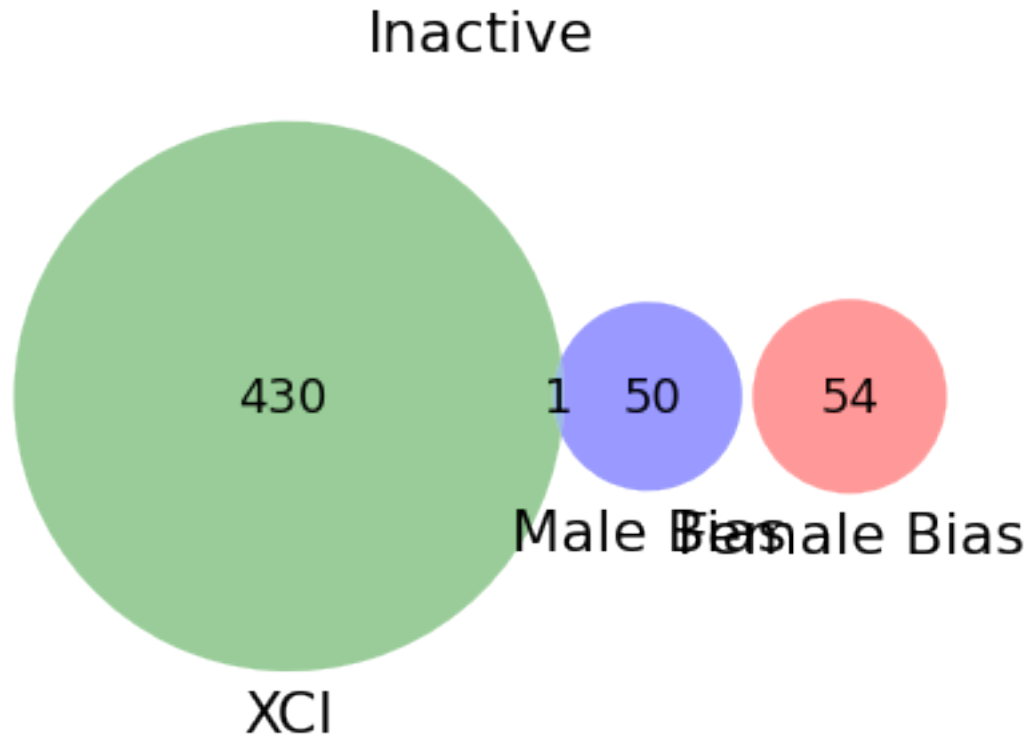


Inactive



Hippocampus





1.3 Calculated fisher's exact for each XCI status

```
[5]: d = dict()
for tissue in ["caudate", "dlpfc", "hippocampus"]:
    print(tissue_annotation(tissue))
    df = cal_fisher_by_xci_status(tissue)
    _, fdr, _, _ = multipletests(df.PValue, method='bonferroni')
    df['Bonferroni'] = fdr
    d[tissue] = df
```

Caudate

There is a significant enrichment (p-value < 3.5e-37) of escape!

There is a significant enrichment (p-value < 1.0e-03) of variable!

There is a significant enrichment of female bias genes (p-value < 1.2e-42) of escape!

There is a significant enrichment of female bias genes (p-value < 8.6e-05) of variable!

DLPFC

There is a significant enrichment (p-value < 2.3e-28) of escape!

There is a significant enrichment (p-value < 2.0e-02) of inactive!

There is a significant enrichment of male bias genes (p-value < 3.8e-03) of escape!

There is a significant enrichment of female bias genes (p-value < 6.5e-30) of


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escape!
Hippocampus
There is a significant enrichment (p-value < 2.8e-41) of escape!
There is a significant enrichment of male bias genes (p-value < 2.4e-03) of
escape!
There is a significant enrichment of female bias genes (p-value < 2.9e-41) of
escape!

```

```

[6]: dft = pd.concat(d.values(), axis=0)
     dft[(dft.Bonferroni <= 0.05)]

```

```

[6]:
      Tissue XCI status      OR      PValue  Direction  Bonferroni
0   Caudate  escape  52.541253  3.525156e-37         All  3.172640e-36
1   Caudate  variable  5.687289  1.018592e-03         All  9.167329e-03
6   Caudate  escape  136.346071  1.182377e-42  Female Bias  1.064139e-41
7   Caudate  variable  13.068562  8.613979e-05  Female Bias  7.752581e-04
0     DLPFC  escape  29.157326  2.319487e-28         All  2.087538e-27
3     DLPFC  escape   7.182445  3.797823e-03   Male Bias  3.418041e-02
6     DLPFC  escape  58.037037  6.541881e-30  Female Bias  5.887693e-29
0  Hippocampus  escape  148.678385  2.768297e-41         All  2.491467e-40
3  Hippocampus  escape  32.317784  2.362670e-03   Male Bias  2.126403e-02
6  Hippocampus  escape  256.447818  2.873171e-41  Female Bias  2.585853e-40

```

```

[7]: df.to_csv('xci_enrichment_analysis_3brainRegions.txt', sep='\t', index=False)

```

```

[ ]:

```