main

October 25, 2021

1 Fine-mapped eQTL comparison across brain regions

[1]:
```
import numpy as np
import pandas as pd
from venn import venn
from matplotlib import pyplot as plt
```

1.1 Prepare data

[2]:
```
def get_data(feature):
    cc = pd.read_csv("../../_m/caudate/eqtl_%s.Caudate.EA_AA.NC_SZ" % feature+\
                     ".age13.fm.index_q0.05.log10bf_2.csv.gz")
    dg = pd.read_csv("../../_m/dentateGyrus/eqtl_%s.DG.EA_AA.NC_SZ" % feature+\
                     ".age13.fm.index_q0.05.log10bf_2.csv.gz")
    dd = pd.read_csv("../../_m/dlpfc/eqtl_%s.DLPFC.EA_AA.NC_SZ" % feature+\
                     ".age13.fm.index_q0.05.log10bf_2.csv.gz")
    hh = pd.read_csv("../../_m/hippocampus/eqtl_%s.HIPPO.EA_AA.NC_SZ" %␣
 ↪feature+\
                     ".age13.fm.index_q0.05.log10bf_2.csv.gz")
    return cc, dg, dd, hh
```

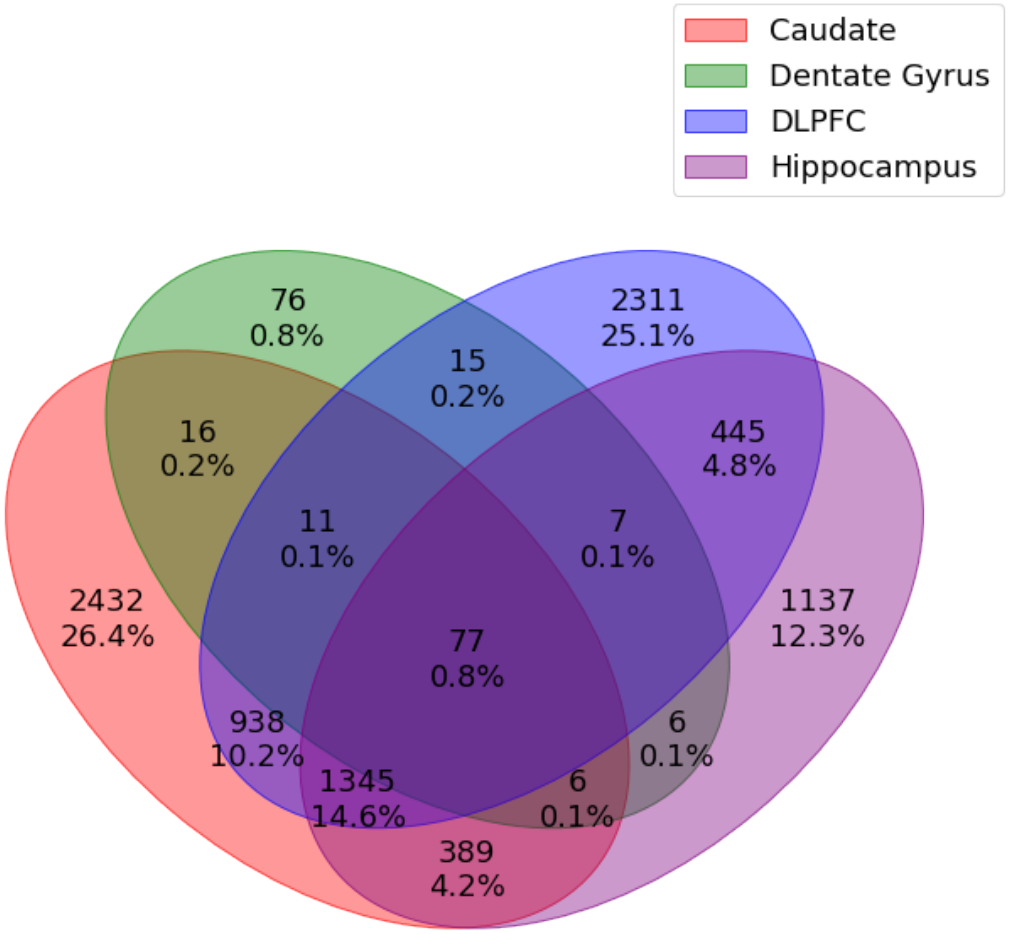
1.2 Venn diagrams

1.2.1 Genes

[3]:
```
feature = "gene"
cc, dg, dd, hh = get_data(feature)
tissues = {
    'Caudate': set(cc.gene),
    'Dentate Gyrus': set(dg.gene),
    'DLPFC': set(dd.gene),
    'Hippocampus': set(hh.gene),
}
```

[4]:
```
venn(tissues, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('eqtl_finemap_%s.png' % feature)
plt.savefig('eqtl_finemap_%s.pdf' % feature)
```

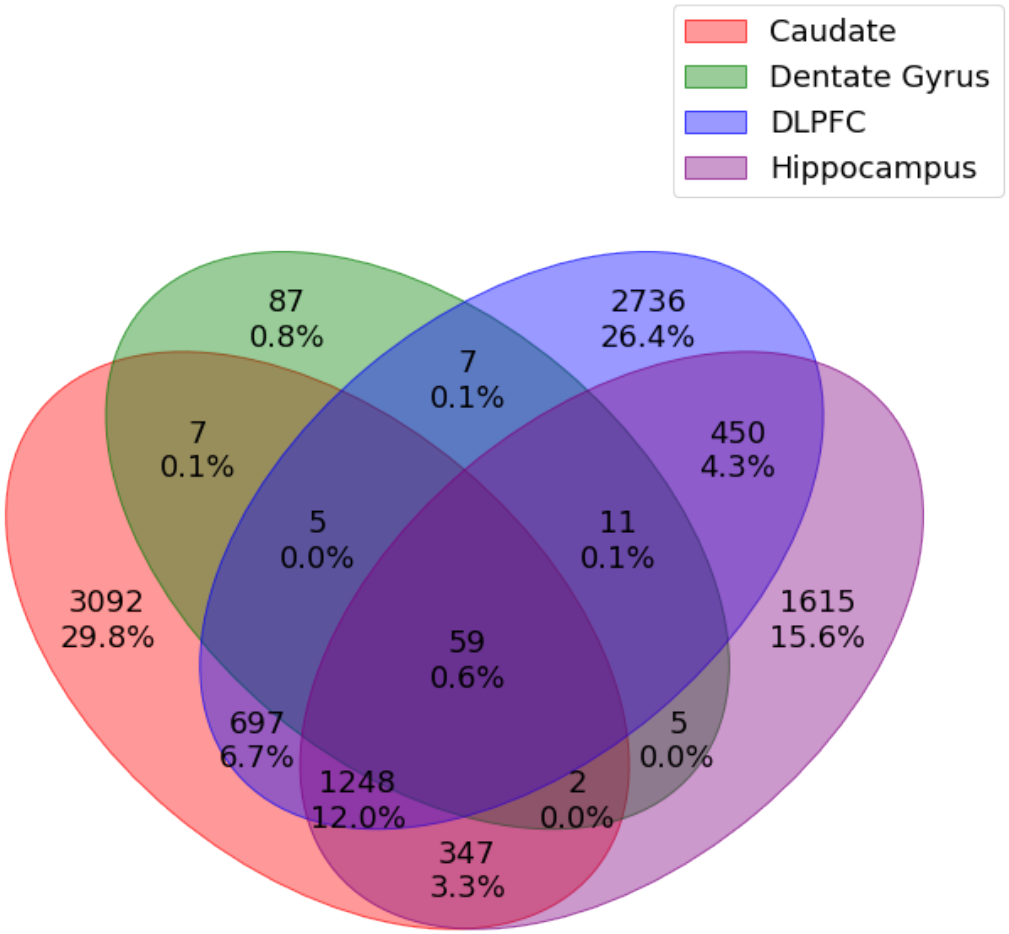
```
plt.show()
```



1.2.2 Transcripts

[5]:
```
feature = "tx"
cc, dg, dd, hh = get_data(feature)
tissues = {
    'Caudate': set(cc.gene),
    'Dentate Gyrus': set(dg.gene),
    'DLPFC': set(dd.gene),
    'Hippocampus': set(hh.gene),
}
```

[6]:
```
venn(tissues, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('eqtl_finemap_%s.png' % feature)
plt.savefig('eqtl_finemap_%s.pdf' % feature)
plt.show()
```

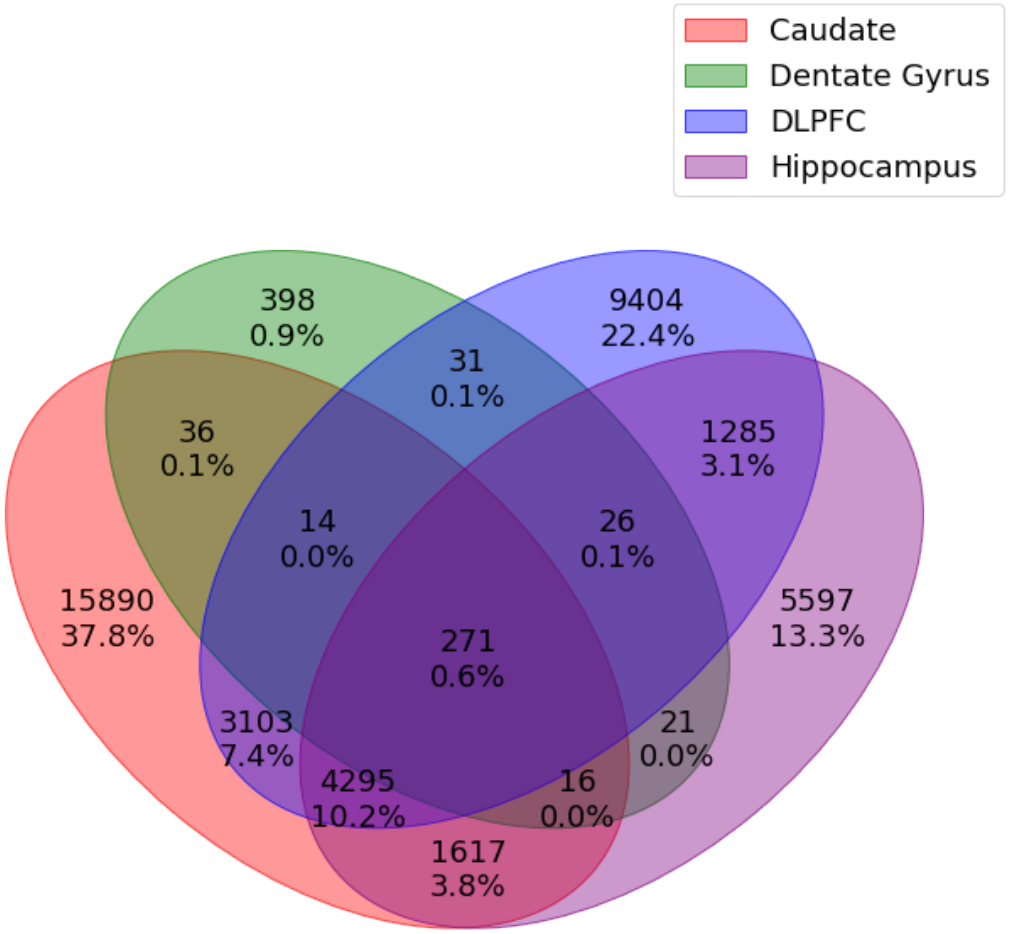


1.2.3 Exons

[7]:
```
feature = "exon"
cc, dg, dd, hh = get_data(feature)
tissues = {
    'Caudate': set(cc.gene),
    'Dentate Gyrus': set(dg.gene),
```

```
    'DLPFC': set(dd.gene),
    'Hippocampus': set(hh.gene),
}
```

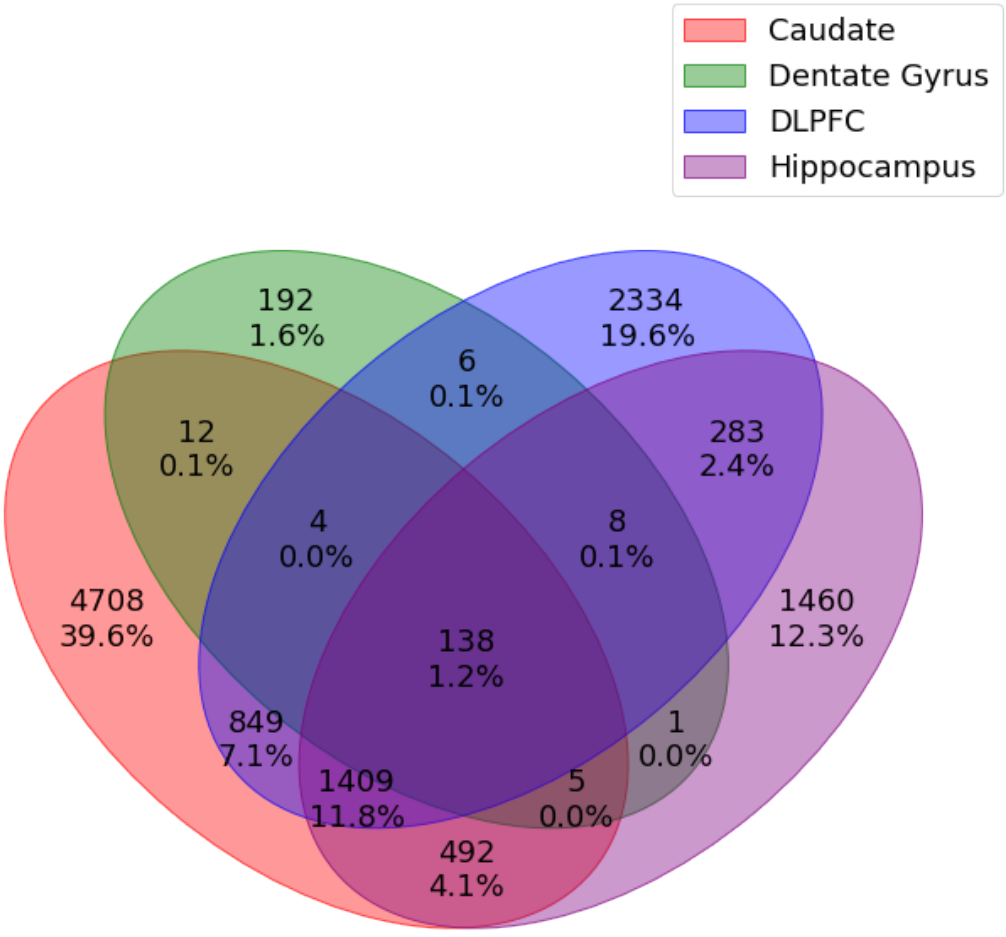
[8]:
```
venn(tissues, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('eqtl_finemap_%s.png' % feature)
plt.savefig('eqtl_finemap_%s.pdf' % feature)
plt.show()
```



1.2.4 Junctions

[9]:
```
feature = "jxn"
cc, dg, dd, hh = get_data(feature)
tissues = {
    'Caudate': set(cc.gene),
    'Dentate Gyrus': set(dg.gene),
    'DLPFC': set(dd.gene),
    'Hippocampus': set(hh.gene),
}
```

[10]:
```
venn(tissues, fmt="{size}\n{percentage:0.1f}%", fontsize=18, legend_loc="best",
     figsize=(12, 12), cmap=['red', 'green', 'blue', 'purple'])
plt.savefig('eqtl_finemap_%s.png' % feature)
plt.savefig('eqtl_finemap_%s.pdf' % feature)
plt.show()
```



1.3 Session Information

[11]:
```
import types
from IPython import sys_info

def imports():
    for name, val in globals().items():
        if isinstance(val, types.ModuleType):
            yield val.__name__

#exclude all modules not listed by `!pip freeze`
excludes = ['__builtin__', 'types', 'IPython.core.shadowns', 'sys', 'os']
function_modules = ["venn", "matplotlib"]
imported_modules = [module for module in imports() if module not in excludes] +␣
 ↪function_modules
pip_modules = !pip freeze #you could also use `!conda list` with anaconda
pip_modules = [item for item in pip_modules if "@" not in item]
```

[12]:
```
print(sys_info())
#print the names and versions of the imported modules
print("\nImported Modules:")
for module in pip_modules:
    name, version = module.split('==')
    if name in imported_modules:
        print(name + ':\t' + version)
```

```
{'commit_hash': 'e76fa004a',
 'commit_source': 'installation',
 'default_encoding': 'utf-8',
 'ipython_path': '/usr/lib/python3.9/site-packages/IPython',
 'ipython_version': '7.28.0',
 'os_name': 'posix',
 'platform': 'Linux-5.12.10-arch1-1-x86_64-with-glibc2.33',
 'sys_executable': '/usr/bin/python3',
 'sys_platform': 'linux',
 'sys_version': '3.9.7 (default, Oct 10 2021, 15:13:22) \n[GCC 11.1.0]'}

Imported Modules:
matplotlib:     3.3.4
numpy:  1.20.2
pandas: 1.3.3
venn:   0.1.3
```

[ ]: