Liang-mmc7

June 26, 2022

[13]:
```
#AD affected
```

1 importing pandas package

[14]:
```
import pandas as pd
```

2 Reading the AD affected in Liang's databse and extracting the list of genes at different sheet

[15]:
```
AD_affected_EC=pd.read_excel('AD affected.
 ↪xlsx',sheet_name='EC',engine='openpyxl')
AD_affected_HIP=pd.read_excel('AD affected.
 ↪xlsx',sheet_name='HIP',engine='openpyxl')
AD_affected_PC=pd.read_excel('AD affected.
 ↪xlsx',sheet_name='PC',engine='openpyxl')
AD_affected_MTG=pd.read_excel('AD affected.
 ↪xlsx',sheet_name='MTG',engine='openpyxl')
AD_affected_SFG=pd.read_excel('AD affected.
 ↪xlsx',sheet_name='SFG',engine='openpyxl')
AD_affected_VCX=pd.read_excel('AD affected.
 ↪xlsx',sheet_name='VCX',engine='openpyxl')
AD_affected_EC=list(AD_affected_EC['symbol'])
AD_affected_HIP=list(AD_affected_HIP['symbol'])
AD_affected_PC=list(AD_affected_PC['symbol'])
AD_affected_MTG=list(AD_affected_MTG['symbol'])
AD_affected_SFG=list(AD_affected_SFG['symbol'])
AD_affected_VCX=list(AD_affected_VCX['symbol'])
```

3 Reading the MMC7 file with different sheet name.

[16]:
```
mmc7_Herpesvirus_virus2host=pd.read_excel('mmc7_Herpesvirus.
 ↪xlsx',sheet_name='virus2host',engine='openpyxl')
```

```
mmc7_Herpesvirus_host2virus=pd.read_excel('mmc7_Herpesvirus.
↪xlsx',sheet_name='host2virus',engine='openpyxl')
```

4 Filtering "MMC7" with sheetname "virus2host" in selecting rows with having the same gene with Liang(AD affected) in a "hostGene" column.

[17]:
```
intresect_virus2host_AD_affected_EC =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(AD_affected_EC)]
intresect_virus2host_AD_affected_HIP =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(AD_affected_HIP)]
intresect_virus2host_AD_affected_PC =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(AD_affected_PC)]
intresect_virus2host_AD_affected_MTG =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(AD_affected_MTG)]
intresect_virus2host_AD_affected_SFG=␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(AD_affected_SFG)]
intresect_virus2host_AD_affected_VCX=␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(AD_affected_VCX)]
```

5 Filtering "MMC7" with sheetname "host2virus" in selecting rows with having the same gene with Liang(AD affected) in a "hostGene" column.

[18]:
```
intresect_host2virus_AD_affected_EC =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(AD_affected_EC)]
intresect_host2virus_AD_affected_HIP =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(AD_affected_HIP)]
intresect_host2virus_AD_affected_PC =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(AD_affected_PC)]
intresect_host2virus_AD_affected_MTG =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(AD_affected_MTG)]
```

```
intresect_host2virus_AD_affected_SFG=␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(AD_affected_SFG)]
intresect_host2virus_AD_affected_VCX=␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(AD_affected_VCX)]
```

6 Saving the filtering MMC7 based on Liang(AD affected) as a CSV file

[19]:
```
writer = pd.ExcelWriter('AD-Affected.xlsx', engine='xlsxwriter')
intresect_virus2host_AD_affected_EC.to_excel(writer, 'virustohost-EC')
intresect_virus2host_AD_affected_SFG.to_excel(writer, 'virustohost-SFG')
intresect_virus2host_AD_affected_HIP.to_excel(writer, 'virustohost-HIP')
intresect_virus2host_AD_affected_PC.to_excel(writer, 'virustohost-PC')
intresect_virus2host_AD_affected_MTG.to_excel(writer, 'virustohost-MTG')
intresect_virus2host_AD_affected_VCX.to_excel(writer, 'virustohost-VCX')
intresect_host2virus_AD_affected_EC.to_excel(writer, 'host2virus-EC')
intresect_host2virus_AD_affected_HIP.to_excel(writer, 'host2virus-HIP')
intresect_host2virus_AD_affected_PC.to_excel(writer, 'host2virus-PC')
intresect_host2virus_AD_affected_MTG.to_excel(writer, 'host2virus-MTG')
intresect_host2virus_AD_affected_SFG.to_excel(writer, 'host2virus-SFG')
intresect_host2virus_AD_affected_VCX.to_excel(writer, 'host2virus-VCX')
writer.save()
```

7 Reading the Non demanted in Liang's databse and extracting the list of genes at different sheet

[20]:
```
Non_demented_EC=pd.read_excel('Liang-non-demented.xlsx',sheet_name='entorhinal␣
↪cortex',engine='openpyxl')
Non_demented_HIP=pd.read_excel('Liang-non-demented.
↪xlsx',sheet_name='hippocampus',engine='openpyxl')
Non_demented_PC=pd.read_excel('Liang-non-demented.xlsx',sheet_name='middle␣
↪temporal gyrus',engine='openpyxl')
Non_demented_MTG=pd.read_excel('Liang-non-demented.xlsx',sheet_name='posterior␣
↪cingulate corrtex',engine='openpyxl')
Non_demented_SFG=pd.read_excel('Liang-non-demented.xlsx',sheet_name='superior␣
↪frontal gyrus',engine='openpyxl')
Non_demented_VCX=pd.read_excel('Liang-non-demented.xlsx',sheet_name='primary␣
↪visual cortex',engine='openpyxl')
Non_demented_EC=list(Non_demented_EC['symbol'])
Non_demented_HIP=list(Non_demented_HIP['symbol'])
Non_demented_PC=list(Non_demented_PC['symbol'])
Non_demented_MTG=list(Non_demented_MTG['symbol'])
```

```
Non_demented_SFG=list(Non_demented_SFG['symbol'])
Non_demented_VCX=list(Non_demented_VCX['symbol'])
```

8 Filtering "MMC7" with sheetname "virus2host" in selecting rows with having the same gene with Liang(Non demented) in a "hostGene" column.

[21]:
```
intresect_virus2host_Non_demented_EC =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(Non_demented_EC)]
intresect_virus2host_Non_demented_HIP =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(Non_demented_HIP)]
intresect_virus2host_Non_demented_PC =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(Non_demented_PC)]
intresect_virus2host_Non_demented_MTG =␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(Non_demented_MTG)]
intresect_virus2host_Non_demented_SFG=␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(Non_demented_SFG)]
intresect_virus2host_Non_demented_VCX=␣
↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
↪isin(Non_demented_VCX)]
```

9 Filtering "MMC7" with sheetname "host2virus" in selecting rows with having the same gene with Liang(Non demented) in a "hostGene" column.

[22]:
```
intresect_host2virus_Non_demented_EC =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(Non_demented_EC)]
intresect_host2virus_Non_demented_HIP =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(Non_demented_HIP)]
intresect_host2virus_Non_demented_PC =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(Non_demented_PC)]
intresect_host2virus_Non_demented_MTG =␣
↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
↪isin(Non_demented_MTG)]
```

```
intresect_host2virus_Non_demented_SFG=␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Non_demented_SFG)]
intresect_host2virus_Non_demented_VCX=␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Non_demented_VCX)]
```

10 Saving the filtering MMC7 based on Liang(Non demented) as a CSV file

[62]:
```
writer = pd.ExcelWriter('Non-demented.xlsx', engine='xlsxwriter')
intresect_virus2host_Non_demented_EC.to_excel(writer, 'virustohost-EC')
intresect_virus2host_Non_demented_MTG.to_excel(writer, 'virustohost-MTG')
intresect_virus2host_Non_demented_SFG.to_excel(writer, 'virustohost-SFG')
intresect_host2virus_Non_demented_SFG.to_excel(writer, 'hosttovirus-SFG')
intresect_virus2host_Non_demented_HIP.to_excel(writer, 'virustohost-HIP')
intresect_virus2host_Non_demented_PC.to_excel(writer, 'virustohost-PC')
intresect_virus2host_Non_demented_VCX.to_excel(writer, 'virustohost-VCX')
intresect_host2virus_Non_demented_EC.to_excel(writer, 'hosttovirus-EC')
intresect_host2virus_Non_demented_HIP.to_excel(writer, 'hosttovirus-HIP')
intresect_host2virus_Non_demented_PC.to_excel(writer, 'hosttovirus-PC')
intresect_host2virus_Non_demented_MTG.to_excel(writer, 'hosttovirus-MTG')
intresect_host2virus_Non_demented_VCX.to_excel(writer, 'hosttovirus-VCX')

writer.save()
```

11 Reading the Normal aged in Liang's databse and extracting the list of genes at different sheet

[23]:
```
Normal_aged_EC=pd.read_excel('Liang-normal-aged.
 ↪xlsx',sheet_name='EC',engine='openpyxl')
Normal_aged_HIP=pd.read_excel('Liang-normal-aged.
 ↪xlsx',sheet_name='HIP',engine='openpyxl')
Normal_aged_MTG=pd.read_excel('Liang-normal-aged.
 ↪xlsx',sheet_name='MTG',engine='openpyxl')
Normal_aged_PC=pd.read_excel('Liang-normal-aged.
 ↪xlsx',sheet_name='PC',engine='openpyxl')
Normal_aged_SFG=pd.read_excel('Liang-normal-aged.
 ↪xlsx',sheet_name='SFG',engine='openpyxl')
Normal_aged_VCX=pd.read_excel('Liang-normal-aged.
 ↪xlsx',sheet_name='VCX',engine='openpyxl')
Normal_aged_EC=list(Normal_aged_EC['symbol'])
Normal_aged_HIP=list(Normal_aged_HIP['symbol'])
Normal_aged_PC=list(Normal_aged_PC['symbol'])
```

```
Normal_aged_MTG=list(Normal_aged_MTG['symbol'])
Normal_aged_SFG=list(Normal_aged_SFG['symbol'])
Normal_aged_VCX=list(Normal_aged_VCX['symbol'])
```

12 Filtering "MMC7" with sheetname "virus2host" in selecting rows with having the same gene with Liang(Normal aged) in a "hostGene" column.

[67]:
```
intresect_virus2host_Normal_aged_EC =␣
 ↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
 ↪isin(Normal_aged_EC)]
intresect_virus2host_Normal_aged_HIP =␣
 ↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
 ↪isin(Normal_aged_HIP)]
intresect_virus2host_Normal_aged_PC =␣
 ↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
 ↪isin(Normal_aged_PC)]
intresect_virus2host_Normal_aged_MTG =␣
 ↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
 ↪isin(Normal_aged_MTG)]
intresect_virus2host_Normal_aged_SFG=␣
 ↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
 ↪isin(Normal_aged_SFG)]
intresect_virus2host_Normal_aged_VCX=␣
 ↪mmc7_Herpesvirus_virus2host[mmc7_Herpesvirus_virus2host['hostGene'].
 ↪isin(Normal_aged_VCX)]
```

13 Filtering "MMC7" with sheetname "host2virus" in selecting rows with having the same gene with Liang(Normal aged) in a "hostGene" column.

[84]:
```
intresect_host2virus_Normal_aged_EC =␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Normal_aged_EC)]
intresect_host2virus_Normal_aged_HIP =␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Normal_aged_HIP)]
intresect_host2virus_Normal_aged_PC =␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Normal_aged_PC)]
intresect_host2virus_Normal_aged_MTG =␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Normal_aged_MTG)]
```

```
intresect_host2virus_Normal_aged_SFG=␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Normal_aged_SFG)]
intresect_host2virus_Normal_aged_VCX=␣
 ↪mmc7_Herpesvirus_host2virus[mmc7_Herpesvirus_host2virus['hostGene'].
 ↪isin(Normal_aged_VCX)]
```

14 Saving the filtering MMC7 based on Liang(Normal aged) as a CSV file

[91]:
```
writer = pd.ExcelWriter('Normal-aged.xlsx', engine='xlsxwriter')
intresect_virus2host_Normal_aged_MTG.to_excel(writer, 'virustohost-MTG')
intresect_host2virus_Normal_aged_MTG.to_excel(writer, 'hosttovirus-MTG')
intresect_virus2host_Normal_aged_EC.to_excel(writer, 'virustohost-EC')
intresect_virus2host_Normal_aged_HIP.to_excel(writer, 'virustohost-HIP')
intresect_virus2host_Normal_aged_PC.to_excel(writer, 'virustohost-PC')
intresect_virus2host_Normal_aged_SFG.to_excel(writer, 'virustohost-SFG')
intresect_virus2host_Normal_aged_VCX.to_excel(writer, 'virustohost-VCX')
intresect_host2virus_Normal_aged_EC.to_excel(writer, 'hosttovirus-EC')
intresect_host2virus_Normal_aged_HIP.to_excel(writer, 'hosttovirus-HIP')
intresect_host2virus_Normal_aged_PC.to_excel(writer, 'hosttovirus-PC')
intresect_host2virus_Normal_aged_SFG.to_excel(writer, 'hosttovirus-SFG')
intresect_host2virus_Normal_aged_VCX.to_excel(writer, 'hosttovirus-VCX')
writer.save()
```

[ ]:
```
```