QQPlots_notebook

March 11, 2024

[1]:
```
# Necessary Imports

from qqman import qqman
import pandas as pd
import matplotlib.pyplot as plt
```

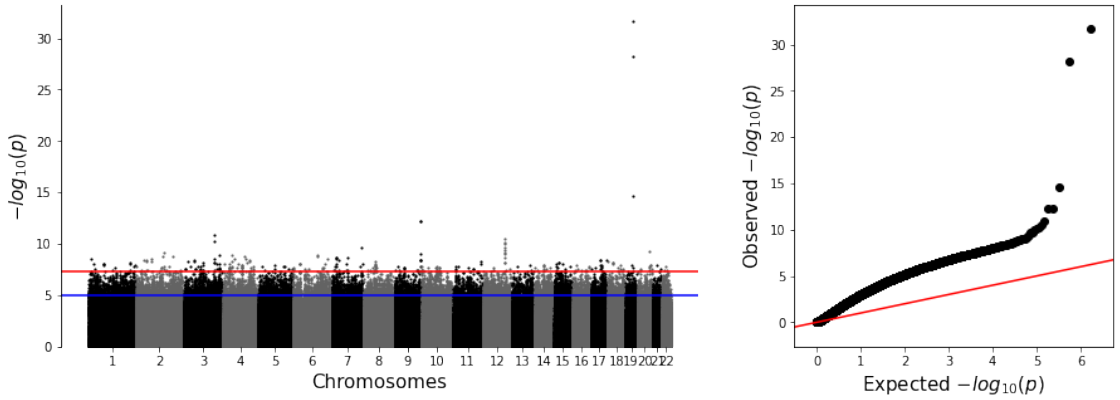
[2]:
```
# Importing plink data

plink_data = pd.read_csv("ps3_gwas.assoc.linear", delim_whitespace=True)
plink_data.head()
```

[2]:

	CHR	SNP	BP	A1	TEST	NMISS	BETA	STAT	P
0	10	rs11252127	98087	T	ADD	207	-0.20430	-1.6060	0.1097
1	10	rs7909677	111955	G	ADD	207	0.19160	0.9108	0.3635
2	10	rs11591988	126070	T	ADD	207	-0.14700	-0.6690	0.5043
3	10	rs12768206	134767	A	ADD	207	-0.05717	-0.6032	0.5471
4	10	rs10904561	135656	G	ADD	207	-0.17850	-1.4710	0.1429

[3]:
```
# QQ PLOTS for PLINK
fig, (ax0, ax1) = plt.subplots(1, 2, gridspec_kw={'width_ratios': [2, 1]})
fig.set_size_inches((15, 5))
qqman.manhattan(plink_data, ax=ax0)
qqman.qqplot(plink_data, ax=ax1)
```



[4]:
```
## Getting data, and adding necessary columns (that were previously dropped )␣
↪by merging

data = pd.read_csv("linRegResults.csv")

data = data.merge(plink_data[['SNP', 'CHR']], on='SNP', how='left')

# Now merged_data should have the chromosomes matched with SNPs from the data␣
↪dataframe

data = data.merge(plink_data[['SNP', 'BP']], on='SNP', how='left')

data.rename(columns={'p-value': 'P'}, inplace=True)

# Now merged_data should have the BP matched with SNPs from the data dataframe.
data.head()
```

[4]:

	Unnamed: 0	SNP	P	beta	CHR	BP
0	728239	rs1319484	0.999994	9.697146e-07	7	85650771
1	660203	rs3131012	0.999990	1.178195e-06	6	31115441
2	660201	rs2240063	0.999990	1.178195e-06	6	31114745
3	660200	rs2240064	0.999990	1.178195e-06	6	31114573
4	797823	rs7041298	0.999990	1.605079e-06	9	8649429

[6]:
```
# QQ plots for our analysis

fig, (ax0, ax1) = plt.subplots(1, 2, gridspec_kw={'width_ratios': [2, 1]})
fig.set_size_inches((15, 5))
qqman.manhattan(data, ax=ax0)
qqman.qqplot(data, ax=ax1)
```