
limix-genetics Documentation

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Genetic related tools for Limix.

CHAPTER 1

Install

The recommended way of installing it is via `conda`

```
conda install -c conda-forge limix-genetics
```

An alternative way would be via `pip`

```
pip install limix-genetics
```


Genetic-related tools for Limix..

`limix_genetics.maf(X)`
Compute minor allele frequencies.

It assumes that X encodes 0, 1, and 2 representing the number of alleles.

Parameters \mathbf{x} (*array_like*) – Genotype matrix.

Returns minor allele frequencies.

Return type *array_like*

`limix_genetics.qqplot(df, figure=None, colors=None, show=True, tools=None, nmax_points=1000, at_least_points=0.01, significance_level=0.01, paper_settings=False, **kwargs)`

Plot number of significant hits across p-value thresholds.

Parameters \mathbf{df} (*pandas.DataFrame*) – Columns *label* and *p-value* define labeled curves.

Example

```
from limix_genetics import qqplot
import pandas as pd
import numpy as np
random = np.random.RandomState(0)

snp_ids = np.arange(1000)

data1 = np.stack(['method1']*1000, random.rand(1000)),
            axis=1)
df1 = pd.DataFrame(data1, columns=['label', 'p-value'],
                  index=snp_ids)

data2 = np.stack(['method2']*1000, random.rand(1000)),
```

```
        axis=1)
df2 = pd.DataFrame(data2, columns=['label', 'p-value'],
                   index=snp_ids)

df = pd.concat([df1, df2])

qqplot(df)
```

`limix_genetics.hitsplot(df, figure=None, colors=None, show=True, tools=None, min_threshold=1e-05, max_threshold=0.01, paper_settings=False, perc=False, **kwargs)`

Plot number of significant hits across p-value thresholds.

Parameters `df` (pandas.DataFrame) – Columns *label* and *p-value* define labeled curves.

Example

```
from limix_genetics import hitsplot
import pandas as pd
import numpy as np
random = np.random.RandomState(0)

snp_ids = np.arange(1000)

data1 = np.stack(['method1']*1000, random.rand(1000) * 0.1),
            axis=1)
df1 = pd.DataFrame(data1, columns=['label', 'p-value'],
                   index=snp_ids)

data2 = np.stack(['method2']*1000, random.rand(1000) * 0.05),
            axis=1)
df2 = pd.DataFrame(data2, columns=['label', 'p-value'],
                   index=snp_ids)

df = pd.concat([df1, df2])

hitsplot(df)
```

CHAPTER 3

Comments and bugs

You can get the source and open issues on [Github](#).

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