

OmicsX: a web server for integrated OMICS analysis

Manual (version 1.0, Nov 2019)

1. Required Python Packages

Package name	Version
python	version >= 3.5
numpy	version >= 1.13.0
sklearn	version >= 0.19.0
pandas	version >= 0.21.0
matplotlib	version >= 2.1.0
scipy	version >= 1.3.1
gseapy	version >= 0.9.16
catheat	0.2.0

2. Working Procedure

Put the downloaded python files and input data in a directory. Open the command prompt and type the following commands. Below are the editorial part of the commands:

omics1.txt: file name of 1st omics matrix

omics2.txt: file name of 2nd omics matrix

annotation.txt: filename of the sample annotation

long: group1 name

short: group2 name

2.1 Gene correlation

```
python genecorrelation.py omics1.txt omics2.txt
```

2.2 Sample correlation

Option 1: `python samplecorrelation.py omics1.txt omics2.txt`

Option 2: `python samplecorrelation.py omics1.txt omics2.txt annotation.txt`

2.3 Sample clustering

Option 1: `python clustering.py omics1.txt omics2.txt`

Option 2: `python clustering.py omics1.txt omics2.txt annotation.txt`

2.4 Group difference

`python difference.py long short omics1.txt omics2.txt annotation.txt`