NeVOmics

Description

NeVOmics is a functional enrichment analysis tool developed in programming language Python and R that integrates ORA methodology and network-based visualization. It applies appropriate statistical methods to identify significantly enriched GO terms or pathways in a given list of genes/proteins. It provides several types of graphical visualization to show enrichment results. NeVOmics supports all organisms deposited in UniProtKB and KEGG databases.

Citation:
NeVOmics: an enrichment tool for gene ontology and functional network analysis and visualization of data from OMICs technologies

Compatibility with: **Windows** and **Linux**

Run NeVOmics

1. **Download NeVOmics**

2. Unzip **NeVOmics.zip**

3. Open your terminal window:
Windows: press the **Win+R** keys on your keyboard. Then, type **cmd** or **cmd.exe** and press **Enter** or click/tap **OK**. **Linux**: press **Ctrl+Alt+T** on your keyboard.
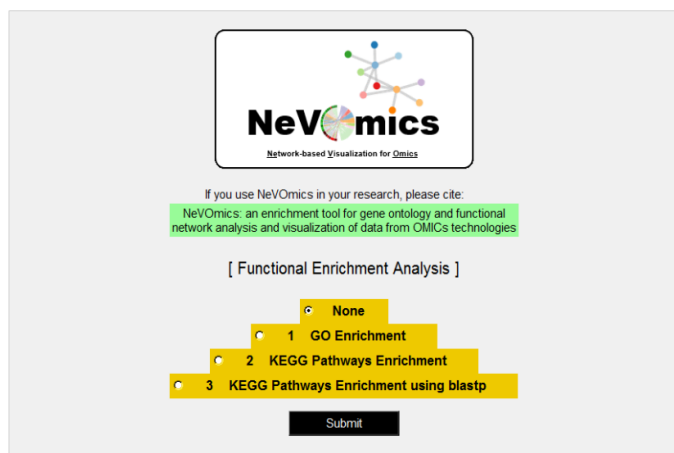
4. Change directory in **Windows** and **Linux**:

```
cd Download\NeVOmics  # On Windows
cd Download/NeVOmics  # On Linux
```
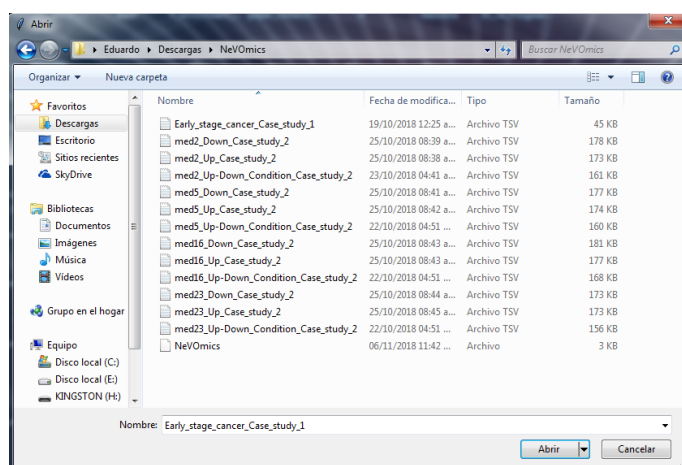
5. Type the next command to run NeVOmics:

```
python NeVOmics
```

6. Select one of the three available analyzes:

---

7. Upload protein list (must be UniProtKB identifiers):

---

8. Selection of a method p-value correction:

```
[ Step 2: Choose a correction method (e.g., FDR / Bonferroni) ]
=====> : FDR    # type any method
```

9. Choose a significance value for the analysis:

```
[ Step 3: Choose a Value (e.g., 0.05) ]
=====> : 0.05   # type a significance value
```

10. Optional creation of networks and plots:

The creation of networks and plots may take several minutes (> 5 min).

System requirements

- **Linux Operating System**
  Ubuntu 14.04
  Ubuntu 16.04
- **Windows Operating System**
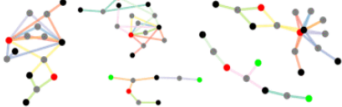 Windows 7
  Windows 8
  Windows 10
- **Internet Requirements**
  Updated Browser Google Chrome
  Minimun Internet speed of 10 MB/sec and ideally 20 MB/sec or more
- **Minimum Hardware Requirements**
  Minimun 4GB RAM
  Minimum of 500MB of hard-drive
  Minimum Screen Resolution of 1024×768

Operating Systems

Windows

> (Tested on Windows 7 and 10)

Install Anaconda (Python)

1. Download python 3.6 version

2. Double-click the `.exe` file.

3. To test your installation, in your `Anaconda Prompt`, run the command:

```
conda list  ##
           ## Name                    Version                   Build  Channel
           # _ipyw_jlab_nb_ext_conf   0.1.0              py36he6757f0_0
           # alabaster                0.7.10             py36hcd07829_0
           # anaconda                 5.2.0                      py36_3
           # anaconda-client          1.6.14                     py36_0
           # anaconda-navigator       1.8.7                      py36_0
           # anaconda-project         0.8.2              py36hfad2e28_0
           # ...
```

More detailed information about the installation of Anaconda on Windows here

4. Adding python.exe to the Windows environment:

- Open *Control Panel* > *System and Security* > *System*
- *Advanced System Settings* > *Enviroment Variables*
- Find Path in *System Variables* then click on Edit
- At the end of the row add a semicolon and then copy the **python.exe** location
- Click on OK

Install blast

1. Download BLAST software

2. Double-click the `.exe` file to install.

3. To test your installation run the command:

```
blastp -h   # USAGE
           #  blastp [-h] [-help] [-import_search_strategy filename]
           #    [-export_search_strategy filename] [-task task_name] [-db
database_name]
           #    [-dbsize num_letters] [-gilist filename] [-seqidlist filename]
           #    [-negative_gilist filename] [-negative_seqidlist filename]
           #    ...
```

Install R

1. Download R for Windows

2. Double-click the `.exe` file.
Important: change destination location to *Documents* **during installing:**
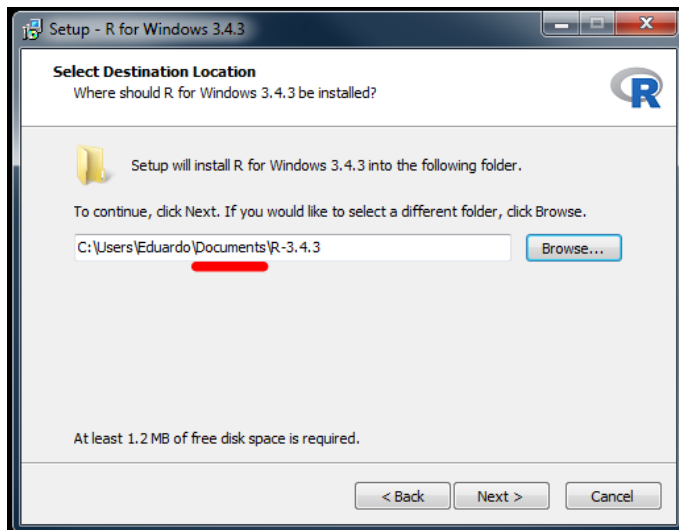
More detailed information about of R installation on Windows here

3. Adding `R.exe` to the Windows environment:

> - Open *Control Panel* > *System and Security* > *System*
> - *Advanced System Settings* > *Enviroment Variables*
> - Find Path in *System Variables* then click on Edit
> - At the end of the row add a semicolon and then copy the `R.exe` location
> - Click on OK

4. To test your R installation, open your terminal window and run the command:

```
R   # R version 3.5.1 (2018-07-02) -- "Feather Spray"
    # Copyright (C) 2018 The R Foundation for Statistical Computing
    # Platform: x86_64-w64-mingw32/x64 (64-bit)
    # ...
```

> Installation of R packages required for NeVOmics:
>
> - tidyverse
> - tidygraph
> - ggraph
> - viridis
> - circlize
> - RColorBrewer
> - cowplot
> - networkD3
> - UpSetR
> - gridBase
> - ComplexHeatmap

5. After verifying of R installation, in the same terminal, run each of the following commands to install R packages:

```r
install.packages("tidyverse", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("tidygraph", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("ggraph", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("viridis", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("circlize", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("RColorBrewer", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("cowplot", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("networkD3", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("UpSetR", dependencies = TRUE,repos='http://cran.us.r-
project.org')
install.packages("gridBase"),dependencies = TRUE,repos='http://cran.us.r-
project.org')
source("http://bioconductor.org/biocLite.R")
biocLite("ComplexHeatmap")
```

🐧 Linux

> (Tested on Ubuntu 14.04 and 16.04)

Install Anaconda (Python)

1. Download python 3.6 version

2. Open your terminal window (Ctrl+Alt+T) and enter the command:

```
bash ~/Downloads/Anaconda3-5.2.0-Linux-x86_64.sh
```

3. Close and open your terminal window for the installation to take effect, or you can enter the command:

```
source ~/.bashrc
```

4. To test your installation run the command:

```
conda list
```

More detailed information about the installation of Anaconda on Linux here

Install blast

1. Open your terminal window (Ctrl+Alt+T) and enter the command:

```
sudo apt-get install ncbi-blast+
```

2. To test your installation run the command:

```
blastp -h
```

Install R

1. [Download R for Linux]

2. To test your R installation, open your terminal window and run the command:

```
R   # R version 3.5.1 (2018-07-02) -- "Feather Spray"
    # Copyright (C) 2018 The R Foundation for Statistical Computing
    # Platform: x86_64-w64-mingw32/x64 (64-bit)
    # ...
```

> Installation of R packages required for NeVOmics:
>
> - tidyverse
> - tidygraph
> - ggraph
> - viridis
> - circlize
> - RColorBrewer
> - cowplot
> - networkD3
> - UpSetR
> - gridBase
> - ComplexHeatmap

3. After verifying of R installation, in the same terminal, run each of the following commands to install R packages:

```
install.packages("tidyverse", dependencies = TRUE,repos='http://cran.us.r-
project.org')
```

```r
install.packages("tidygraph", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("ggraph", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("viridis", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("circlize", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("RColorBrewer", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("cowplot", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("networkD3", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("UpSetR", dependencies = TRUE,repos='http://cran.us.r-project.org')
install.packages("gridBase"),dependencies = TRUE,repos='http://cran.us.r-project.org')
source("http://bioconductor.org/biocLite.R")
biocLite("ComplexHeatmap")
```