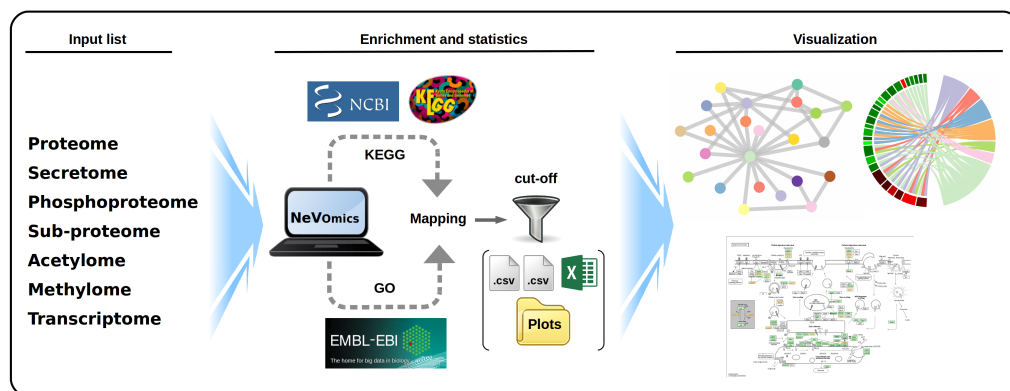


NeVOmics

Description

NeVOmics is a functional enrichment analysis tool developed in programming language Python and R that integrates Over-representation analysis (ORA) methodology and network-based visualization. It applies appropriate statistical methods to identify significantly enriched Gene Ontology (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 UniProt Knowledgebase (UniProtKB) and Kyoto Encyclopedia of Genes and Genomes (KEGG) databases.



Citation:

NeVOmics: An Enrichment Tool for Gene Ontology and Functional Network Analysis and Visualization of Data from OMICS Technologies. doi.org/10.3390/genes9120569

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

Download **NeVOmics** for 

Download **NeVOmics** for 

Run NeVOmics



Before running **NeVOmics** you need to install **Python** (See Operating Systems section).
If your input file is **.fasta**, you need to install **BLAST** (See Operating Systems section).
If you want to get all the networks you need to install **R** (See Operating Systems section).

1. Download NeVOmics for Windows or Linux

2. Unzip NeVOmics_[Windows/Linux].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 Downloads\NeVOmics_Windows
```



```
cd Downloads/NeVOmics_Linux
```

5. Type the next command to run NeVOmics:



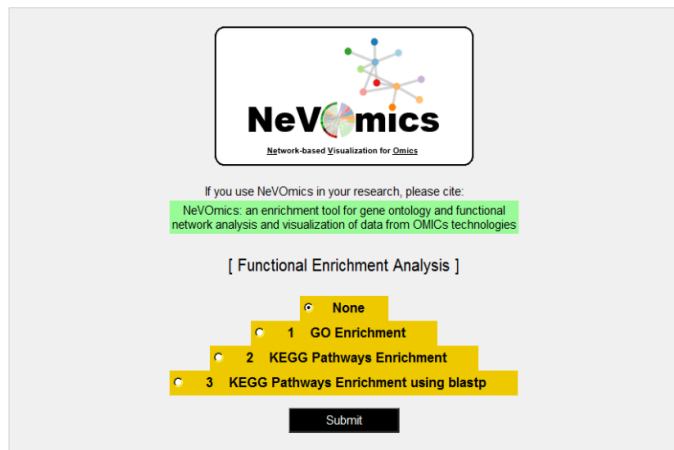
```
python NeVOmics
```

Or double-click on **NeVOmics.exe** (**Only for Windows**) included in **NeVOmics.zip**.

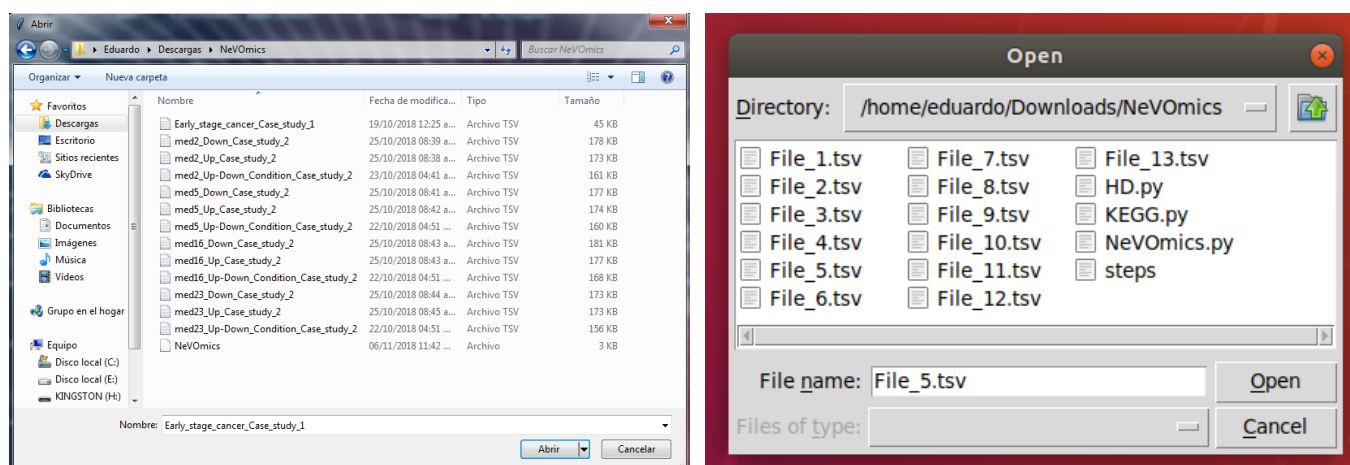


```
python3 NeVOmics.py
```

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:

If you use NeVOmics in your research, please cite:
NeVOmics: an enrichment tool for gene ontology and functional
network analysis of data from OMICs technologies


[You want to create the network visualizations]

☐ None
☒ **KEGG PATHWAYS**


!!!! It may take several minutes !!!!

Submit

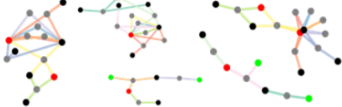
Chord Plot



Bar Plot



Networks



The creation of networks and plots may take several minutes (5 - 20 min).

System requirements

- **Linux (64-bit) Operating System**
[Ubuntu 18.04 LTS \(Bionic Beaver\)](#)
 - **Windows Operating System**
Windows 7
Windows 10
 - **Internet Requirements**
Minimum Internet speed of 10 MB/sec and ideally 20 MB/sec or more
 - **Minimum Hardware Requirements**
Minimum 4GB RAM
Minimum of 500MB of hard-drive
Minimum Screen Resolution of 1024×768
-

Operating Systems



(Tested on Windows 7 and 10)

Install Python

1. [Download python 3.6.7 version](#)
2. Double-click the **.exe** file.

- Click on **Run**



- Select the option **Add Python 3.6 to PATH** and then **Install Now**



- Click on **Close**



3. To test your installation, open your terminal window and type:

```
python --version
```

- It should show something like this:

```
C:\Users\Eduardo>python --version
Python 3.6.7
```

More detailed information about the installation of Python on Windows [here](#)

4. Download `install_python_modules.exe`

5. Go to downloads and to find `install_python_modules.exe`, right click and Run as administrator.

Install blast

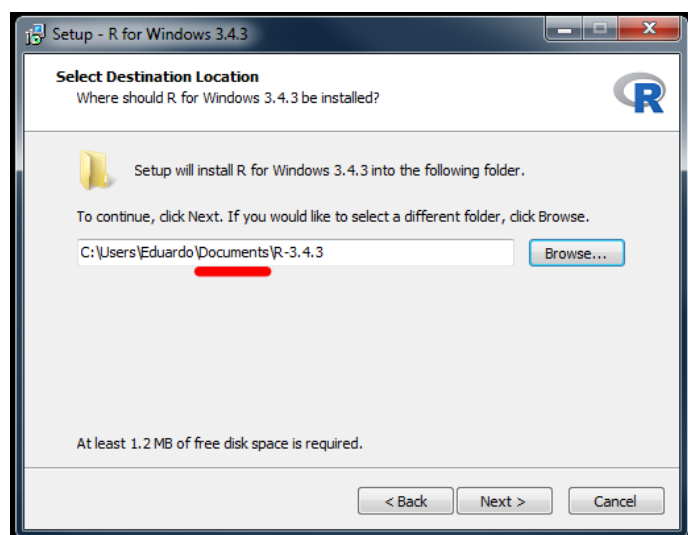
1. Download **BLAST** software
2. Double-click the **.exe** file to install.
3. To test your installation run the command:

```
blastp -h
```

Install R

1. Download [R for Windows](#)
2. Double-click the **.exe** file.

****Important:** change installation location to **Documents**.



More detailed information about of R installation on Windows [here](#)

3. Install R Packages required by NeVOmics:

Download [install_R_packages.exe](#)

- Go to downloads and to find **install_R_packages.exe**, right click and Run as administrator.

R packages needed to build networks and plots with NeVOmics:

- **GetoptLong**, **tidyverse**, **tidygraph**, **ggraph**, **viridis**, **circlize**, **RColorBrewer**, **cowplot**, **networkD3**, **UpSetR**, **gridBase**, **reshape2** and **ComplexHeatmap**



Linux

NeVOmics was updated to work with Ubuntu 18.04 LTS (Bionic Beaver)

Python

1. Python3 (v3.6.7) is included by default in Ubuntu 18.04

```
eduardo@eduardo-Lenovo-IdeaPad-Y480:~$ python3 -V -V
Python 3.6.7 (default, Oct 22 2018, 11:32:17)
[GCC 8.2.0]
eduardo@eduardo-Lenovo-IdeaPad-Y480:~$ |
```

2. NeVOmics requires complementary python3 modules:

Open your terminal and type the next commands to download and run the next python3 script

`Python3_mod_Ubuntu.py` to install the modules:

```
wget -q
https://raw.githubusercontent.com/bioinfproject/bioinfo/master/Folder/Python3_mod_Ubuntu.py
```

```
python3 Python3_mod_Ubuntu.py
```

```
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ wget -q https://raw.githubusercontent.com/bioinfproject/bioinfo/master/Folder/Python3_mod_Ubuntu.py
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ python3 Python3_mod_Ubuntu.py

Installation of modules used by NeVOmics

Administrator permissions are required to install the following modules:
MODULE: pip, tkinter, requests, pandas, scipy and openpyxl
https://docs.python.org/3/installing/index.html [Ctrl+click]

Type your password
[sudo] password for eduardo: |

Collecting openpyxl
Collecting jdcal (from openpyxl)
  Using cached https://files.pythonhosted.org/packages/a0/38/dcf83532480f25284f3ef13f8ed63e03c58a65c9d3ba2a6a894ed9497207/jdcal-1.4-py2.py3-none-any.whl
Collecting et-xmlfile (from openpyxl)
Installing collected packages: jdcal, et-xmlfile, openpyxl
Successfully installed et-xmlfile-1.0.1 jdcal-1.4 openpyxl-2.6.1

Modules have been installed successfully

eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ |
```

3. To test modules installation run the next commands:

```
python3
```

```
help('pandas')
```

```

eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ python3
Python 3.6.7 (default, Oct 22 2018, 11:32:17)
[GCC 8.2.0] on linux
Type "help", "copyright", "credits" or "license()" for more information.
>>> help('pandas')

Help on package pandas:

NAME
  pandas

DESCRIPTION
  pandas - a powerful data analysis and manipulation library for Python
  =====

  **pandas** is a Python package providing fast, flexible, and expressive data
  structures designed to make working with "relational" or "labeled" data both
  easy and intuitive. It aims to be the fundamental high-level building block for
  doing practical, **real world** data analysis in Python. Additionally, it has
  the broader goal of becoming **the most powerful and flexible open source data
  analysis / manipulation tool available in any language**. It is already well on
  its way toward this goal.

  :|

```

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
```

```

eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ blastp -h
USAGE
  blastp [-h] [-help] [-import_search_strategy filename]
  [-export_search_strategy filename] [-task task_name] [-db database_name]
  [-dbsize num_letters] [-glist filename] [-seqidlist filename]
  [-negative_glist filename] [-entrez_query entrez_query]
  [-db_soft_mask filtering_algorithm] [-db_hard_mask filtering_algorithm]
  [-subject subject input_file] [-subject_loc range] [-query input_file]
  [-out output_file] [-evalue evalue] [-word_size int_value]
  [-gapopen open_penalty] [-gapextend extend_penalty]
  [-qcov_hsp_perc float_value] [-max_hsps int_value]
  [-xdrop_ungap float_value] [-xdrop_gap float_value]
  [-xdrop_gap_final float_value] [-searchsp int_value]
  [-sum_stats bool_value] [-seg SEG_options] [-soft_masking soft_masking]
  [-matrix matrix_name] [-threshold float_value] [-culling_lmit int_value]
  [-best_hit_overhang float_value] [-best_hit_score_edge float_value]
  [-window_size int_value] [-lcase_masking] [-query_loc range]
  [-parse_deflines] [-outfmt format] [-show_gls]
  [-num_descriptions int_value] [-num_alignments int_value]
  [-line_length line_length] [-html] [-max_target_seqs num_sequences]
  [-num_threads int_value] [-ungapped] [-remote] [-comp_based_stats compo]
  [-use_sw_tback] [-version]

DESCRIPTION
  Protein-Protein BLAST 2.6.0+

```

Install R

1. Open your terminal and type the next command:

```
sudo apt-get install r-base
```

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

```
R
```



```

eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ R
R version 3.4.4 (2018-03-15) -- "Someone to Lean On"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> |

```

3. Preparation of a suitable environment for R

R packages needed to build networks and plots with NeVOmics:

- **GetoptLong**, **tidyverse**, **tidygraph**, **ggraph**, **viridis**, **circlize**, **RColorBrewer**, **cowplot**, **networkD3**, **UpSetR**, **gridBase**, **reshape2** and **ComplexHeatmap**

4. Installing of Libraries and local R Packages:

Open your terminal and type the next commands to download and run the next python3 script **R-Libs-Packs-Ubuntu.py** to install the libraries and packages:

```

wget -q
https://raw.githubusercontent.com/bioinfproject/bioinfo/master/Folder/R-
Libs-Packs-Ubuntu.py

```

```
python3 R-Libs-Packs-Ubuntu.py
```

```

eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ wget -q https://raw.githubusercontent.com/bioinfproject/bioinfo/master/Folder/R-Libs-Packs-Ubuntu.py
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ python3 R-Libs-Packs-Ubuntu.py

Preparing the environment for R

*** 1. Install Libraries

Permissions are needed to install the following libraries
for the operation of R in your system:

LIBRARY: libxml2-dev
INFORMATION DETAILS: https://packages.debian.org/es/std/libxml2-dev [Ctrl+click]

LIBRARY: libcurl4-openssl-dev
INFORMATION DETAILS: https://packages.debian.org/es/std/libcurl4-openssl-dev [Ctrl+click]

LIBRARY: libssl-dev
INFORMATION DETAILS: https://packages.debian.org/es/std/libssl-dev [Ctrl+click]

Type your password
[sudo] password for eduardo: |

0 upgraded, 0 newly installed, 0 to remove and 0 not upgraded.
Reading package lists... Done
Building dependency tree
Reading state information... Done
libssl-dev is already the newest version (1.1.0g-2ubuntu4.3).
0 upgraded, 0 newly installed, 0 to remove and 0 not upgraded.

*** 2. Install R Packages

Running: Rscript

trying URL 'http://cran.us.r-project.org/src/contrib/xml2 1.2.0.tar.gz'
Content type 'application/x-gzip' length 251614 bytes (245 KB)
=====
downloaded 245 KB

* installing *source* package 'xml2' ...
** package 'xml2' successfully unpacked and MD5 sums checked
Found pkg-config cflags and libs!
Using PKG_CFLAGS=-I/usr/include/libxml2
Using PKG_LIBS=-lxml2
** libs

```

```
* installing *source* package 'ComplexHeatmap' ...
** R
** inst
** preparing package for lazy loading
** help
*** installing help indices
** building package indices
** installing vignettes
** testing if installed package can be loaded
* DONE (ComplexHeatmap)

The downloaded source packages are in
  '/tmp/RtmpCSPobj/downloaded_packages'

!!! All packages have been installed successfully!!!
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$
```

5. Setting the local R library path:

Open your terminal and type the next commands:

- To define the R library path create a file `.Renviron` in your home directory:
- Open the text editor:

```
nano ~/.Renviron
```

```
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ nano ~/.Renviron
```

- Add the following line to the file:

```
R_LIBS=~/.R-NeVOmics
```

```
GNU nano 2.9.3 /home/eduardo/.Renviron Modified
R_LIBS=~/.R-NeVOmics
^G Get Help ^O Write Out ^M Where Is ^K Cut Text ^J Justify ^C Cur Pos
^X Exit ^R Read File ^\ Replace ^U Uncut Text ^T To Spell ^_ Go To Line
```

- Save file (Ctrl+O), then enter and then exit (Ctrl+x) of text editor:

```
GNU nano 2.9.3 /home/eduardo/.Renviron Modified
R_LIBS=~/.R-NeVOmics
File Name to Write: /home/eduardo/.Renviron
^G Get Help ^M-D DOS Format ^M-A Append ^M-B Backup File
^C Cancel ^M-M Mac Format ^M-P Prepend ^T To Files
```

```
GNU nano 2.9.3 /home/eduardo/.Renviron
R_LIBS=~/.R-NeVOmics
[ Wrote 1 line ]
^G Get Help ^O Write Out ^M Where Is ^K Cut Text ^J Justify ^C Cur Pos
^X Exit ^R Read File ^\ Replace ^U Uncut Text ^T To Spell ^_ Go To Line
```

```
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$ nano ~/.Renviron
eduardo@eduardo-Lenovo-IdeaPad-Y480:~/Downloads$
```

6. With this settings the directory `~/R-NeVOmics` is added to the list of places to look for R packages. Verify the location of the library and packages with the next commands:

```
.libPaths()
```

```
eduardo@eduardo-Lenovo-IdeaPad-Y480:~$ R

R version 3.4.4 (2018-03-15) -- "Someone to Lean On"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> .libPaths()
[1] "/home/eduardo/R-NeVOmics"      "/usr/local/lib/R/site-library"
[3] "/usr/lib/R/site-library"      "/usr/lib/R/library"
> |
```

library()

```
Packages in library '/home/eduardo/R-NeVOmics':

askpass           Safe Password Entry for R, Git, and SSH
assertthat        Easy Pre and Post Assertions
backports         Reimplementations of Functions Introduced Since
                  R-3.0.0
base64enc         Tools for base64 encoding
BH               Boost C++ Header Files
broom            Convert Statistical Analysis Objects into Tidy
                  Tibbles
callr            Call R from R
cellranger       Translate Spreadsheet Cell Ranges to Rows and
                  Columns
circlize         Circular Visualization
cli             Helpers for Developing Command Line Interfaces
clipr           Read and Write from the System Clipboard
colorspace       A Toolbox for Manipulating and Assessing Colors
                  and Palettes
ComplexHeatmap   Making Complex Heatmaps
cowplot         Streamlined Plot Theme and Plot Annotations for
:|
```