

# NeVOmics

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## 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** 

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## Run NeVOmics

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### 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.

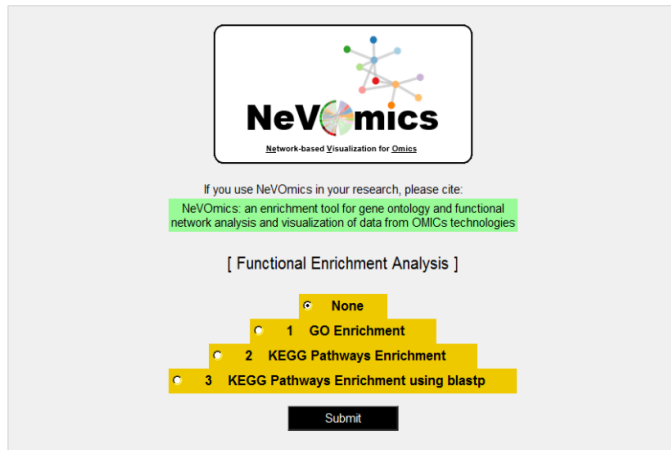
### 4. Change directory in **Windows** and **Linux**:

```
cd Downloads\NeVOmics # On Windows
cd Downloads/NeVOmics # On Linux
```

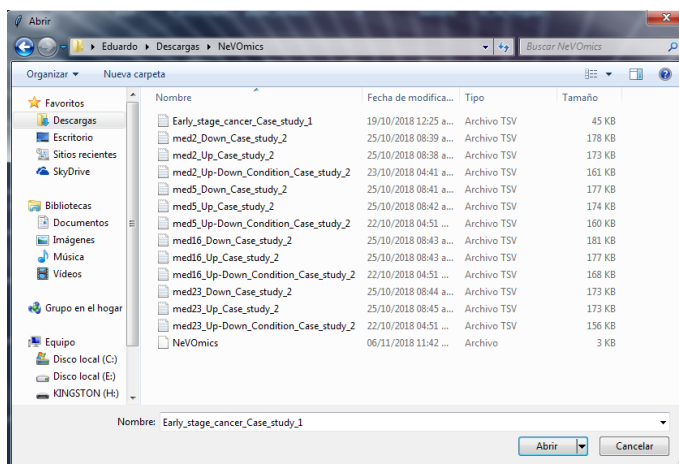
### 5. Type the next command to run NeVOmics:

```
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:

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**

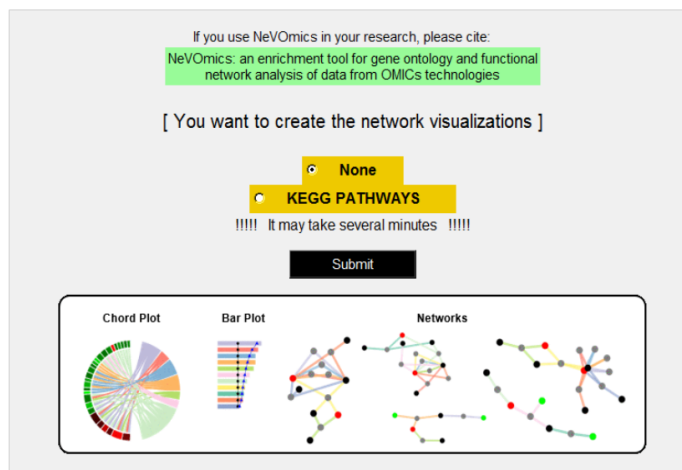
!!!! It may take several minutes !!!!

**Submit**

Chord Plot

Bar Plot

Networks

The screenshot shows the NeVOmics web interface. At the top, there is a citation instruction in a green box. Below it, a text box asks if the user wants to create network visualizations. There are two radio buttons: 'None' and 'KEGG PATHWAYS' (which is selected). A warning message '!!!! It may take several minutes !!!!' is displayed. A 'Submit' button is below the radio buttons. At the bottom, there is a preview box containing three types of visualizations: a Chord Plot, a Bar Plot, and a Networks graph.

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

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## System requirements

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- **Linux Operating System**

[Ubuntu 14.04](#)

[Ubuntu 16.04](#)

- **Windows Operating System**

Windows 7

Windows 8

Windows 10

- **Internet Requirements**

Updated Browser Google Chrome

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

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## Operating Systems

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# Windows

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(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:

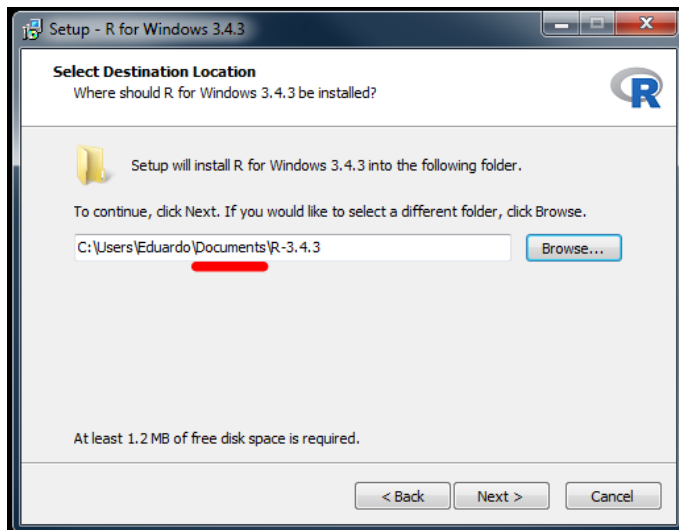
```
blastp -h # USAGE
# blastp [-h] [-help] [-import_search_strategy filename]
# [-export_search_strategy filename] [-task task_name] [-db
database_name]
# [-dbsize num_letters] [-gilist filename] [-seqidlist filename]
# [-negative_gilist filename] [-negative_seqidlist filename]
# ...
```

## 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** > **Environment 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:

```
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')
```

```
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")
```