**User Manual and Case Studies**

(Drivergene.net: a Cytoscape app for identification of cancer-driver genes on large molecular biology networks)

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# 1. Installation

## 1.1. Install Cytoscape

- Drivergene.net-1.0 can run on Cytoscape 3.7.1 (or later) platform, which has Automation features, therefore the user should download this version at <http://cytoscape.org/>

- Cytoscape needs JRE to run, therefore download JRE version 8. x or later from

<http://www.oracle.com/technetwork/java/index.html>and install it.

- Install Cytoscape to the root folder (e.g., /Applications/Cytoscape\_v3.7.1).

## 1.2. Install the Drivergene.net app

Download the Drivergene.net-1.0.jar file from https://github.com/tinhpd80/Drivergene.net.

Then, install it by going to Apps →App Manager…. After that, choose Install from file…, then browse the downloaded Drivergene.net-1.0.jar file. (Figure 1).

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| **Figure 1**. Install Drivergene.net app |

***Note that***: Drivergene.net-1.0 can work on Windows, Ubuntu and Mac OS. The following manual was prepared when running Drivergene.net on Windows.

After installing, Drivergene.net will be automatically loaded in the App menu of Cytoscape. (Figure 2)

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| **Figure 2**. Drivergene.net loaded in the App menu of Cytoscape |

# 2. Import example data

The example data are made available at https://github.com/tinhpd80/Drivergene.net.

**Step 1**. Open Cytoscape

**Step 2**: Load data sets (target gene interactions network)

- From the Cytoscape menu, select submenu File -> Import -> Network from file ( Figure 3)

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| **Figure 3.** Load data sets |

- Select file → Open. (Figure 4)

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| **Figure 4**. Select and open file |

- Next, specify the Start and End columns for the data. (Figure 5)

|  |  |
| --- | --- |
|  |  |
| **Figure 5**. Specify the Start and End columns for the data | |

# 3. Compute total support by Drivergene.net

**Step 1**. Select an example data set from the left panel

**Step 2**. Select Apps menu of Cytoscape→ submenu Drivergene.net → 1) Compute Loyal Point. (Figure 6)

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| **Figure 6**. Drivergene.net loaded in the App menu of Cytoscape |

**Step 3**. Choose an execution mode. (Figure 7)

Drivergene.net provides three execution modes

- Sequence: sequence execute on the CPU

- Parallel: parallel execute on multi-core CPU or GPU

- Multi-Parallel: choose one or many combined parallel execution on CPU and GPU

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| **Figure 7**. Choose execution modes |

**Step 4.** Click execute for computing

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| **Figure 8.** Computing the total support of nodes on the network to each network node. |

The actual computing time for the entire network is displayed after the computing is finished. (Figure 9).

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| **Figure 9.** The actual computing time for the entire network is displayed |

# 4. Output computation results

After the computing is finished, click Node table tap → Export Table to file. (Figure 10)

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| **Figure 10**. Export computation results |

Select the path and set the file name, the default file name is the import data file name with the extension is csv. (Figure 11)

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| **Figure 11**. Set the path and file name |

# 5. Output data processing

**Step 1**. Open file .csv

**Step 2**. Split data into columns: Select column data → select menu Data → Text to columns → Dilimited → Next → Other → input ‘;’ →Next → Finish

**Step 3**. Sort data descesding by total support columns values

|  |  |  |
| --- | --- | --- |
|  |  |  |
| **A** | **B** | **C** |
| **Figure 13**. Sort data descesding by total support values | | |

A) Molecule signal network. B) Protein-protein interaction network. C) Gene Regulatory Network