DrugComboExplorer

Version 1.0.0

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# System requirements

The minimum of system requirements for DrugComboExplorer

**Hardware:**

Processor 2GHz

Memory 4Gb

Graphics Card On board Video

Monitor XGA (1024X768)

**Software:**

Java SE Runtime Environment 7 or higher

Python 2.7.x

# Getting Started

# Install and run DrugComboExplorer on Windows OS

## Install Java JRE

DrugComboExplorer is a Java-based application. If Java is not installed on your computer, please download and install Java SE 7 or higher. The JRE package is available from:

<http://www.oracle.com/technetwork/java/javase/downloads/jre7-downloads-1880261.html>

## Install Python package 2.7.x

<https://www.python.org/downloads/release/python-2713/>

## Run DrugComboExplorer

Decompress DrugComboExplorer.zip

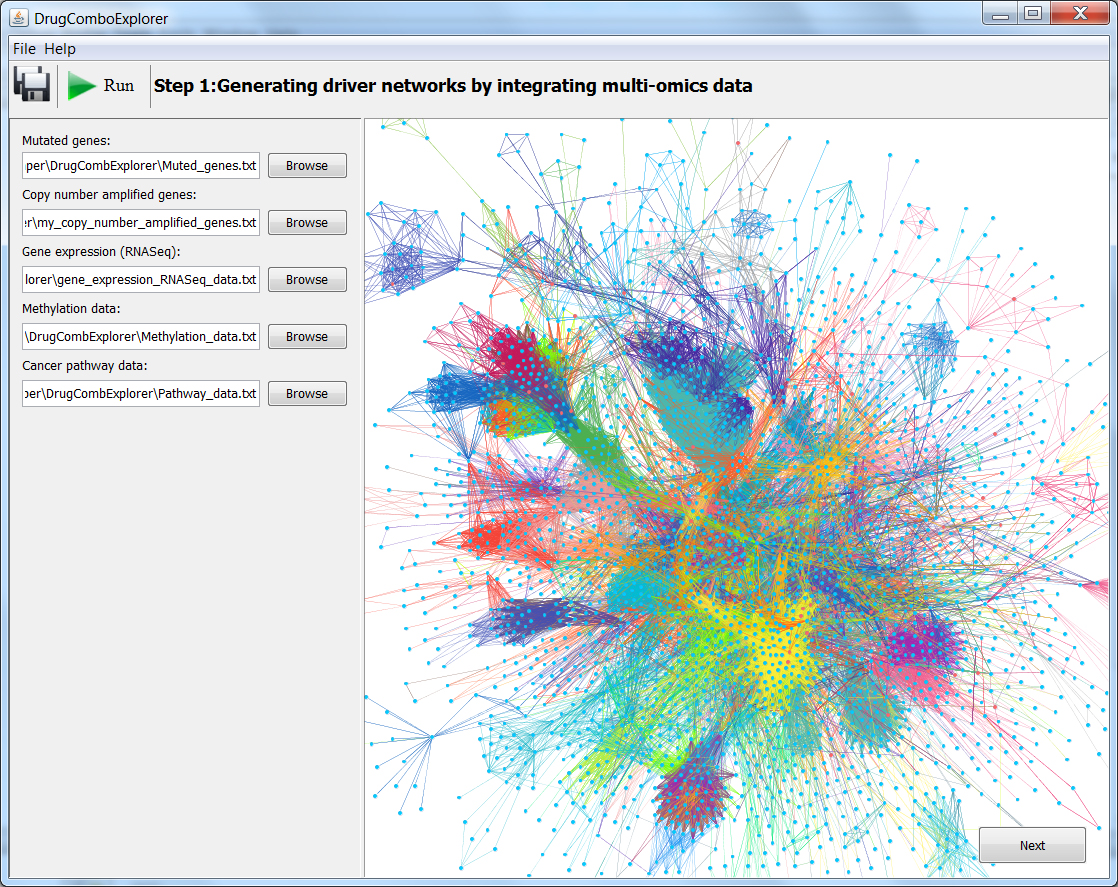
Run java –jar DrugComboExplorer.jar command in your CMD window.

There are 3 steps for DrugComboExplorer.

**Step1 : Generating driver networks by integrating multi-omics data**

To run this step, we need to load Mutated genes file, Copy number amplified genes file, Gene expression file, Methylation data file and Cancer pathway data first.

Then click on Run button, the DrugComboExplorer will run the task. When it is done, the driver networks will be displayed on the right-side window. E.g. Figure 1.

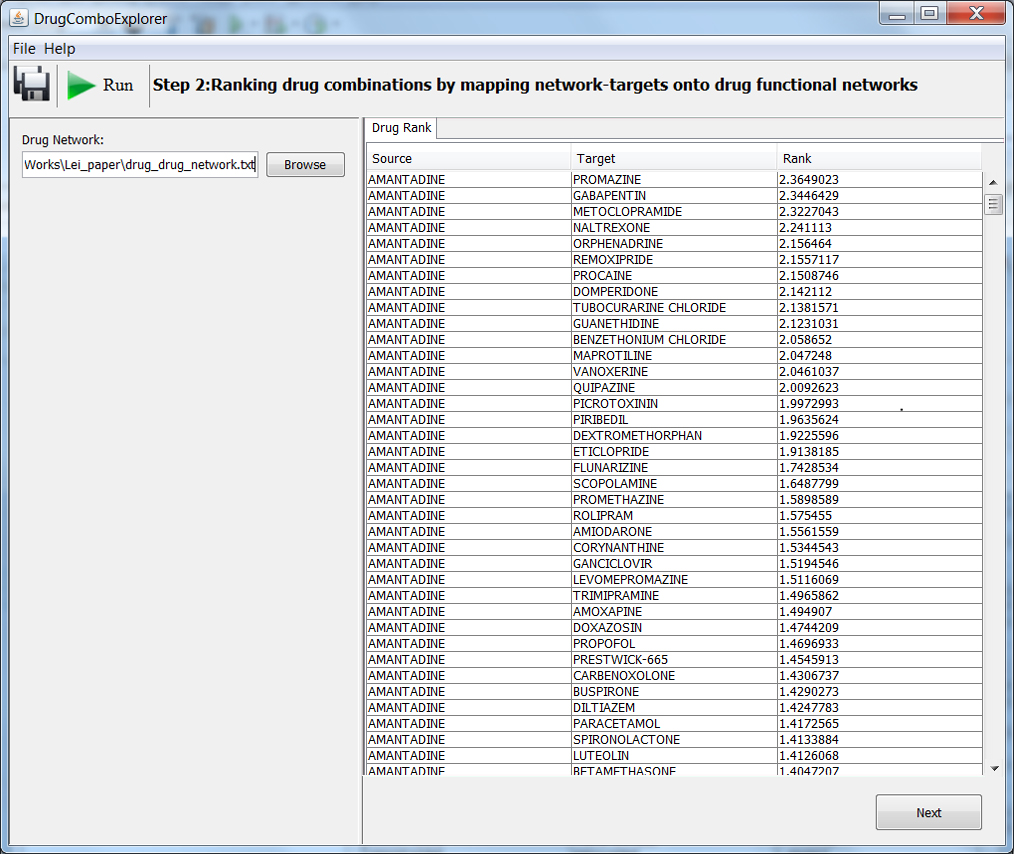


**Figure 1**

**Step 2: Ranking drug combinations by mapping network-targets onto drug functional networks.**

After you finished the step 1, click the Next button, the second step window will show up.

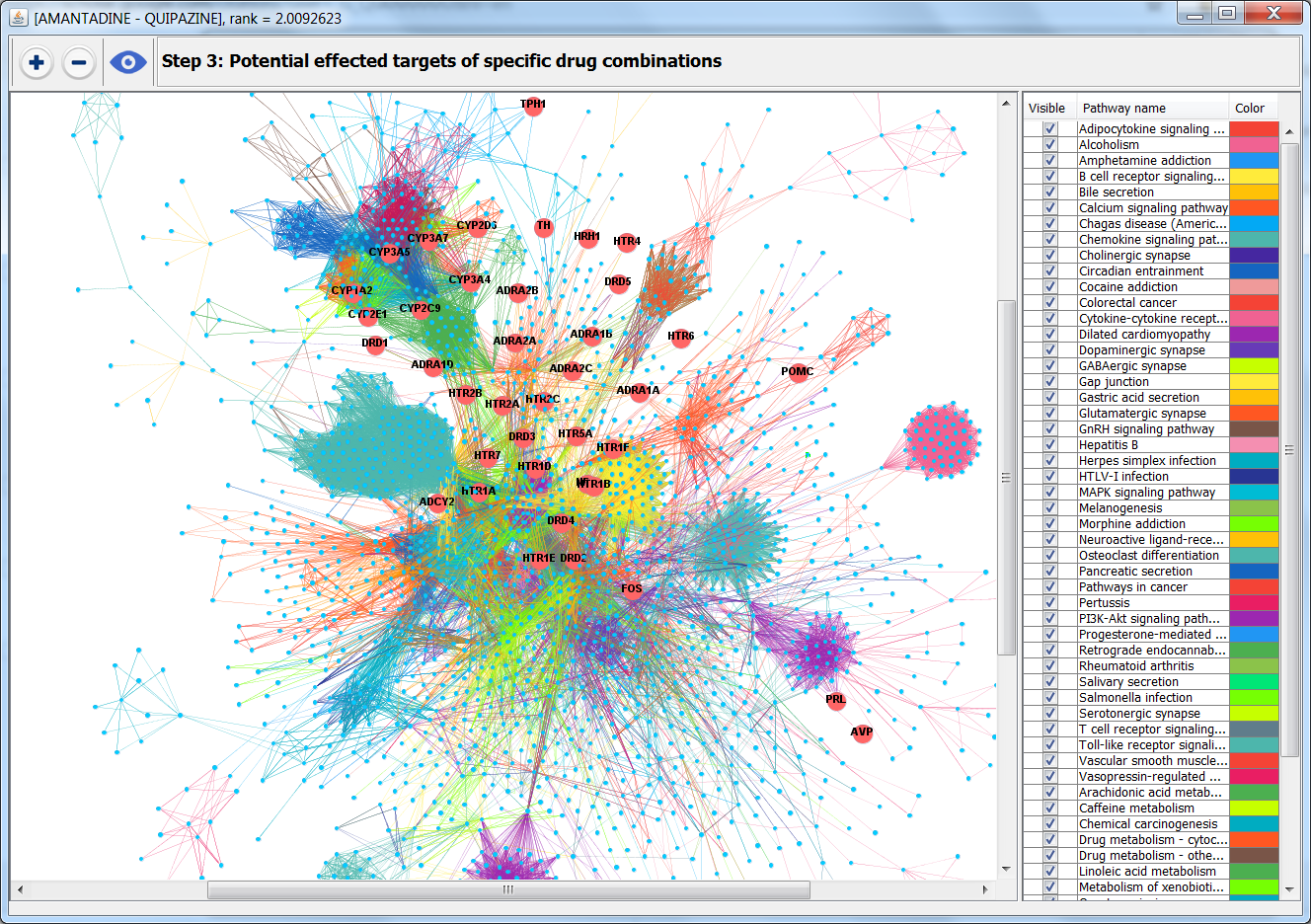
In this step, we need to load the drug network. DrugComboExplorer will generate a drug combination rank. E.g. Figure 2.

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**Figure 2**

**Step 3: Potential effected targets of specific drug combinations.**

Choose one drug combination from the drug rank list and click the next button, a window will show the pathway information of the potential effected targets of this drug combination. E.g. Figure 3.

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**Figure 3**