GNC – User Guide

Using graph theory to analyze gene networks coherenceV 1.1

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Ilustration and Figures

1 Introduction

This manual aims to provide basic knowledge for any user, regardless of their computer skills, to be able to use the GNC.

GNC is an app that allows the user to obtain a coherence measure of a gene network. This approach analyzes the networks based on graph theory and calculates a quantitative measure of its coherence based on well-known stored data.

GNC is distributed as one .jar application. This file is the main executable to run our app.

2 Requirements and installation

In order to run the app, it is necessary to install an updated version of Java which can be downloaded from their website (*http://www.java.com*).

GNC is compressed as a ".zip" file. It is necessary an app to decompress it.

On the other hand, GNC software is parallelized using threads. If your computer allows multi-threading operation, result will be showed in a shorter period of time.
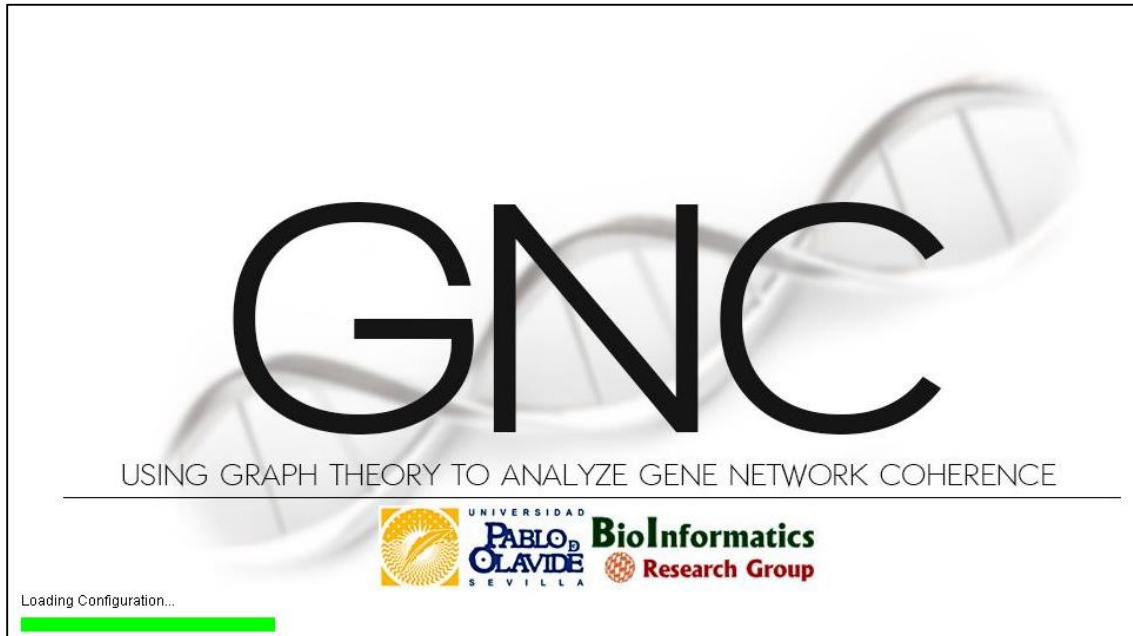
2.1 GENERAL REQUIREMENTS

- ❖ CPU: 2 GHz at least.
- ❖ RAM Memory: Mínimum 2 GB.
- ❖ HDD: Minimum 300MB.
- ❖ Minimum screen resolution 1024 x 768 pixels.

3 Use of GNC

To launch the app you must do a double click on "GNC.jar". The next splash screen will be opened:

Ilustration 1 - Splash Screen

This first screen is displayed at application startup and is as a decorated window containing the current process of the program. At the bottom of this screen appear a progress bar showing the current progress.

GNC app works with few folders grouped in one called "GNC". This folder have to be in the same directory that jar file. These files are checked every time before launch the app:
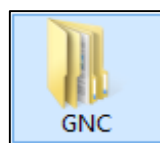
Ilustration 2 - GNC Folder
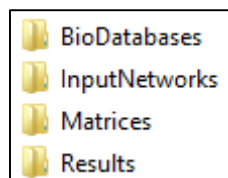
Ilustration 3 – Inside GNC Folder

Remember, do not handle or manipulate these files. The main function of the app is grouped by four folders. Each folder save previous biological databases, input networks, distance matrices or results used by the app as a record. This idea, help to reduce the waiting time.

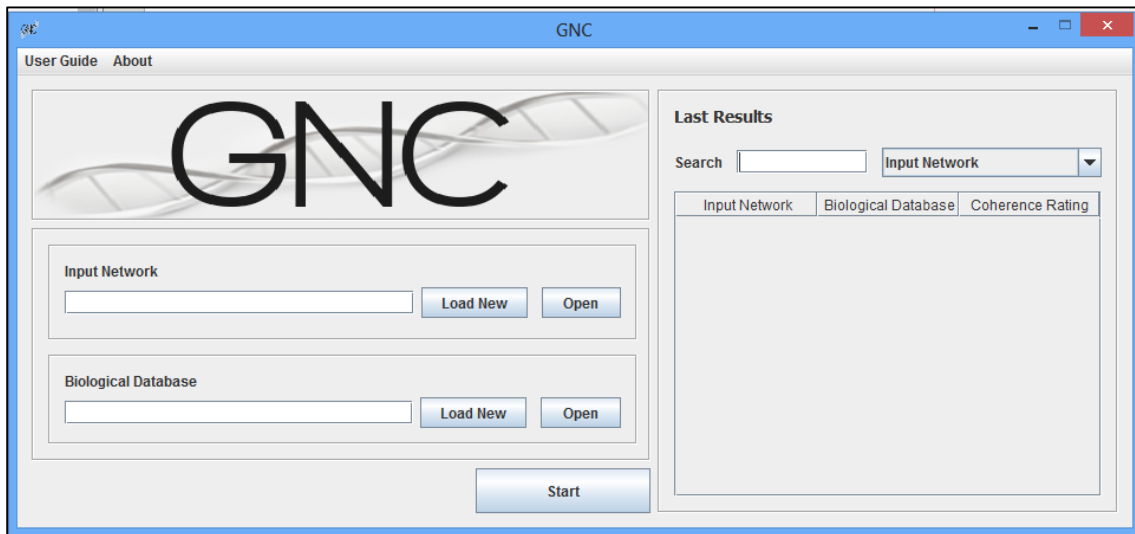## 3.1 MAIN MENU

This is the previous view of the main menu:

Ilustration 4 - Main menu

It can be divided in several parts:

❖ Top Part:
  o At the top a menu bar is located. This menu have two principal functions:
    ▪ Provide a quick access to the user guide. (User Guide)
    ▪ Information about the team developer. (About)

*Ilustration 5 - About the authors*

❖ Middle Part:
  o Evaluation Part:
    ▪ Exclusive zone to rate the coherence of an input network.
  o Last Results Part:
    ▪ Provide a quick reference of previous results calculated.

"Evaluation" and "Last Results" will be described in detail among the next chapters.

4 Evaluation Part

This is the main part of the app. The evaluation part is located in the main menu:
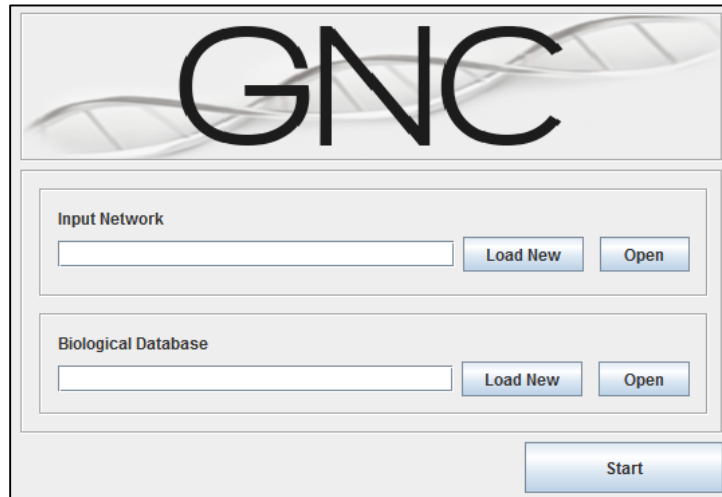
Ilustration 6 – Rating coherence sub menu

At the top, we can choose the input network that will be measured. To choose it, you must click on and find in your computer the file. **Please, ensure that input network file is built correctly** (More info in Troubleshooting). At this point the text area is filling with the absolute path of the selected file. On the other hand, if you have used the app before, the app has stored the previous used networks. To find one, you have to click on and it.

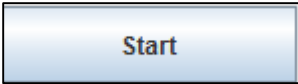The same process is used to choose the biological database.
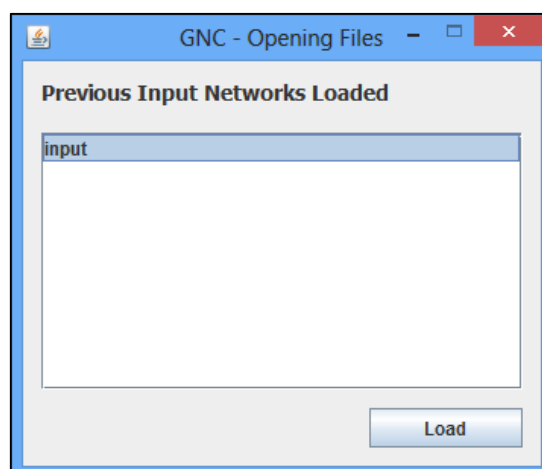
Ilustration 7 - Finding an input network

Ilustration 8 - An example of paths

Once the paths have been chosen, it is time to rating step. To start, click on

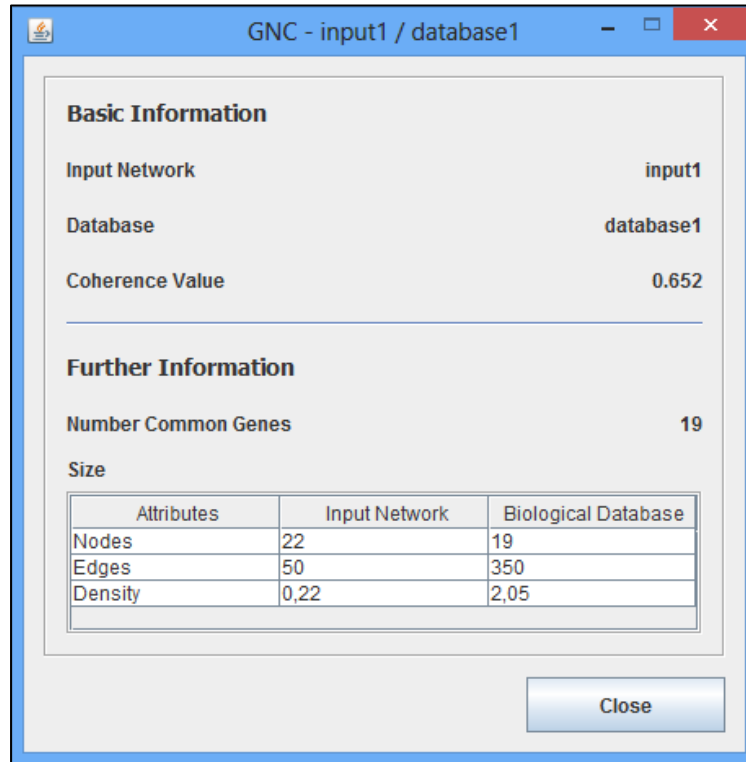 and wait to the **_"Information about the comparison"_** (More info in the next chapter).

Finally, if you use networks (input or database) that it have not been used before, the app will stored it automatically for the next time. Furthermore, if a comparison between an input and database have been done it previously, the app will detect that and it will show the next screen:

5 Information about the comparison

This section provides a description about the screen which offer information about one rating:

Ilustration 9 - Information about the comparison

At the top of the screen, it can be seen the "***Basic Information***" of the rating step. The basic information about the rating are:

- ❖ Input and database used.
- ❖ Coherence obtained of this comparison.

On the bottom, we can find "***Further Information***". As their name implies, this section provides more information about the rating step. This information consists of:

- ❖ Common genes between input and database networks.
- ❖ Information about the size of the used networks:
  - o Number of nodes for each networks.
  - o Number of edges for each networks.
  - o Density of both networks.

6 Last Results

Last Results are located in the Main Menu. This section allow to know the previous results. It is composed of table which rows notify each operations:

Ilustration 10 - An example of last result generated by GNC

Also, these result can be filter by Input Network or Biological Database used. This can be done choosing this option in the combo ( ) and typing the name of the network/database in . Dynamically, the table only show values relating to the search:

Ilustration 11 - An example of search inside last results

On the other hand, columns can be sorted alphabetically / numerically pushing in the header:

Input Network ▲	Biological Database	Coherence Rating
input1	database1	0,65200
input1	database1	0,60000
input1	database3	0,52000
input1	database4	0,15200
input2	database2	0,50000
input2	database3	0,20000

Input Network	Biological Datab... ▼	Coherence Rating
input1	database4	0,15200
input1	database3	0,52000
input2	database3	0,20000
input2	database2	0,50000
input1	database1	0,65200
input1	database1	0,60000

Ilustration 12 - Different Types of sorting

Finally, we can obtain more information about one row doing double click on it. As a result, a new window will be displayed. This windows offer several information about the comparison. For more information about this screen, visit *"Information about the comparison"* chapter.
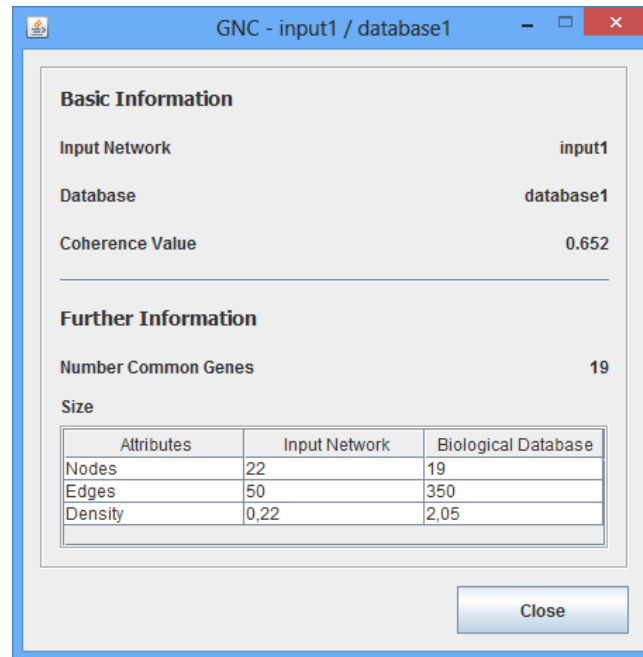

Ilustration 13 - Information about the comparison

7 Troubleshooting and F.A.Q.

Below is a list of common user mistakes when using the app as well as tips on how to avoid them:

- ❖ Be patient. Although this program is fully optimized, usually it takes a long time.
- ❖ Input network and biological databases files must be a ".txt" file and it must have the following aspect:
  - o Node1,Node2
  - o Node1,Node3
  - o …
  - o Node 1,Node N
  - o …
  - o NodeN,Node M

```
YLR210W,YDR054C
YLR210W,YGR109C
YLR210W,YAL040C
YPR120C,YPL256C
YPR120C,YGL116W
YGR109C,YMR199W
YGR109C,YPR119W
YGR109C,YPL256C
YMR043W,YPL256C
YMR043W,YGL116W
```

Ilustration 14 - An example of input network and biological database file format

8 COPYRIGHT

8.1 SOFTWARE CO - AUTORS AND DEVELOPMENT

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