Comorbidity-Viewer

User Manual

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Overview

The Comorbidity-Viewer is a software to visualize Human Disease Networks. It was developed by students in a course at the Department of Computer Science of the University of Leipzig.

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1 System requirements

To use our software you will need the following software packages:

  – a up-to-date JRE (1.6x)

  – a MySQL-database most likely running on your localhost.

If you are running the program as a runnable .jar file you only need a Java Runtime Environment from Java.com.
You should install a MySQL database. You will find manuals and help at MySQL.com. A MySQL-Community-Server is all you need, but you can also install a database within a XAMPP-Distribution. You will benefit from a guided install process and will be able to use the database managment tool *phpadmin*.

If you are in pocession of our source code we recommend that you make an Eclipse project. In order to run the program you will need to include the Prefuse-Toolkit and the BorderFlow libary to your build path.
Please make sure you have the right JDBC-driver for MySQL darabases: You will need the one prefuse is using: *mysql-connector-java-3.1.12.*

2 First Steps

Please run the program (the main class is called CVFrame within the view package). After you started your MySQL-Server.

Your first steps will be:

  1. specify the connection to the database in the **DB-dialogue**

  2. choose an existing database or create a new one in the **DB-dialogue**

  3. load a HuDiNe-dataset in your database and select it within the **data import dialogue**.

After you are in pocession of a database and loaded one or more datasets you will only need to choose them on startups.

3 Overview

The program consits of three main dialogues: the already named db dialogue for database connectifity, the data import dialogue and the main window.

The Main window contains panes and tables to control the program. The two other dialogues are reachable from here by using the buttons in the data-toolbar.
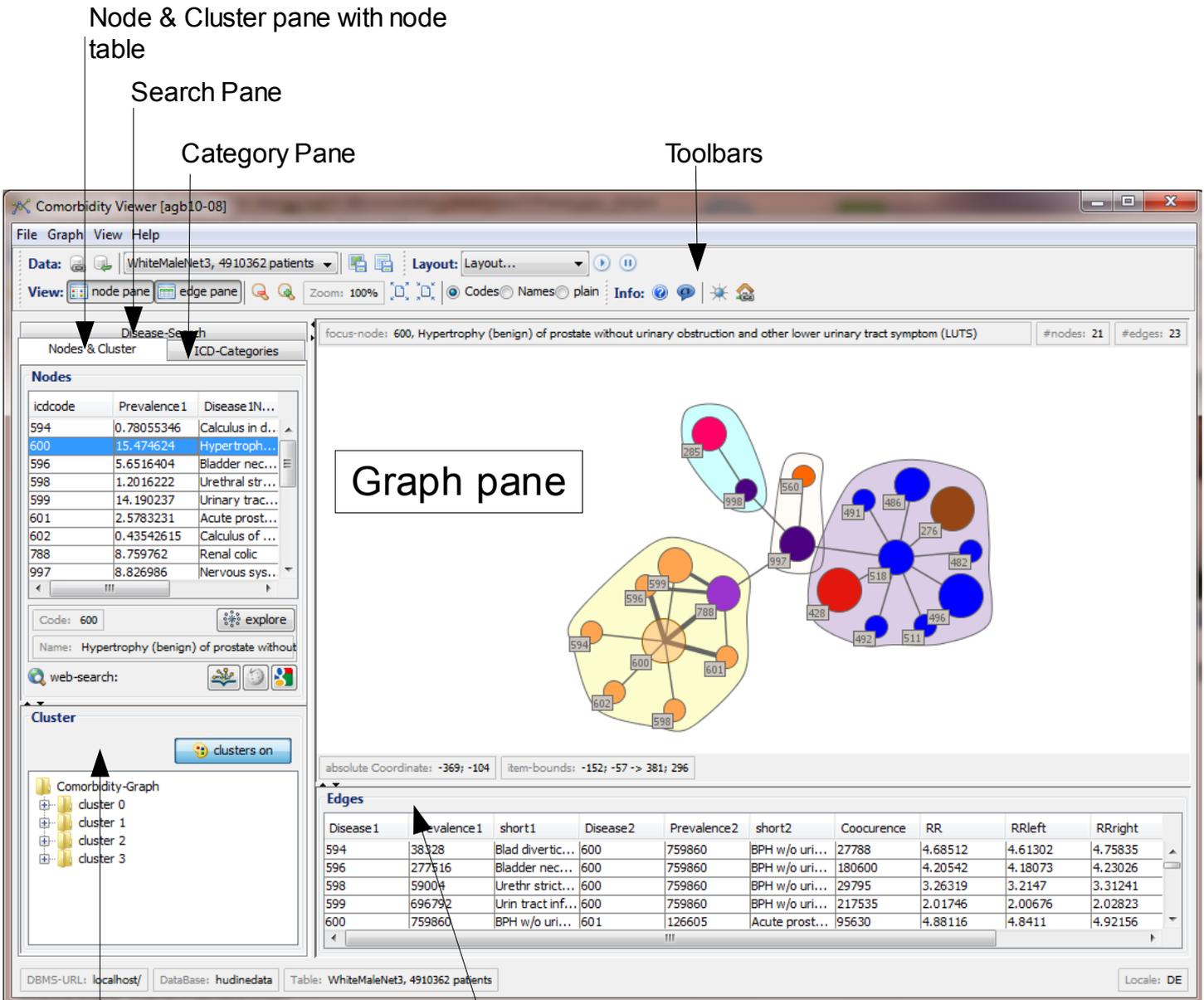
Node & Cluster pane with node table

Search Pane

Category Pane

Toolbars

Graph pane

Cluster Tree

Edge table

Overview

From the 3 panels on the left there is always on active. You can choose which by clicking on the title. In the picture above the Node and Cluser pane is active.

The Category pane is just an explanation of the coulors used to visialize the category of a disease(node) in the graph pane.

Searching a disease is possible in the search pane.

The Node pane provides additional infos to the graph and selected diseases in it.

The 4 toolbars at the top can be moved out in a separate window.

4 DB dialogue

This is the first you see when starting the Comorbidity-Viewer. Its main purpose is to provide a interface to set the database connection poperties.

After you finished all settings and closed this dialogue, it is startable with the 🗄 Button in the data-toolbar. But at this part you're only allowed to load and change the datasets. So make sure that you set connection parameters correct the first time.
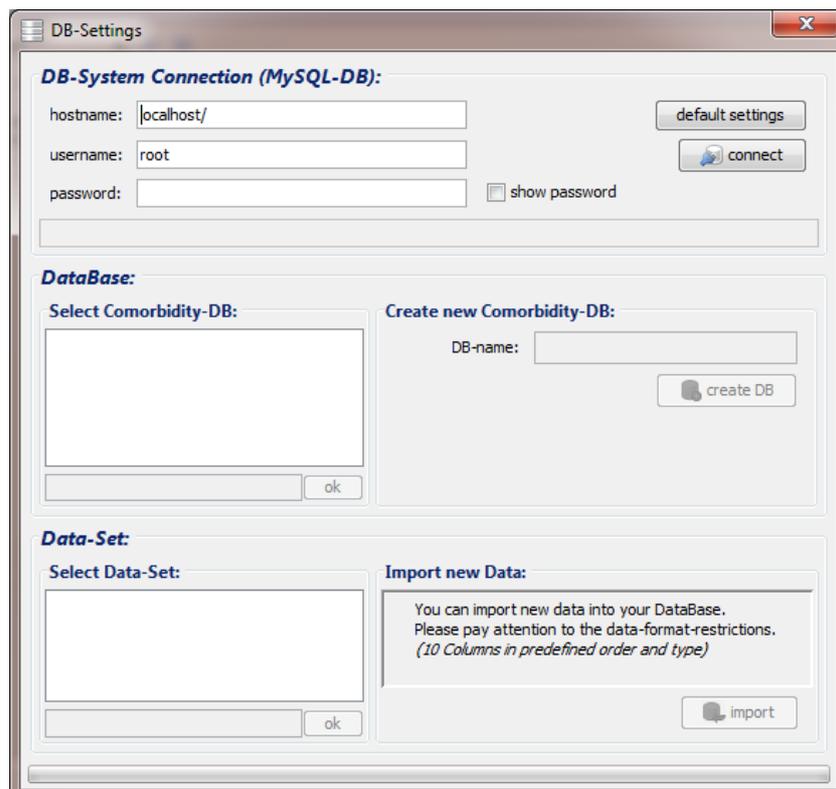

Abbildung 1: db dialogue

4.1 Connection

The fist thing to do is to check all connection parameters to allow the Comorbidity-Viewer a communication with the database. On default the fields contain standard values. These values can be set editing the file *DB.con.xml* in the resources folder.

4.2 Choosing or creating Database

If there is already a comorbidity like schema in your database you can select it from the list and approve it by clicking *ok*. Otherwise please enter a name for a new one in the left part of the dialogue. After clicking on *ok* the program will automatically install a database and create the

neccesary tables. Especially a table containing all names of diseases for ICD-9-CM codes is loaded.
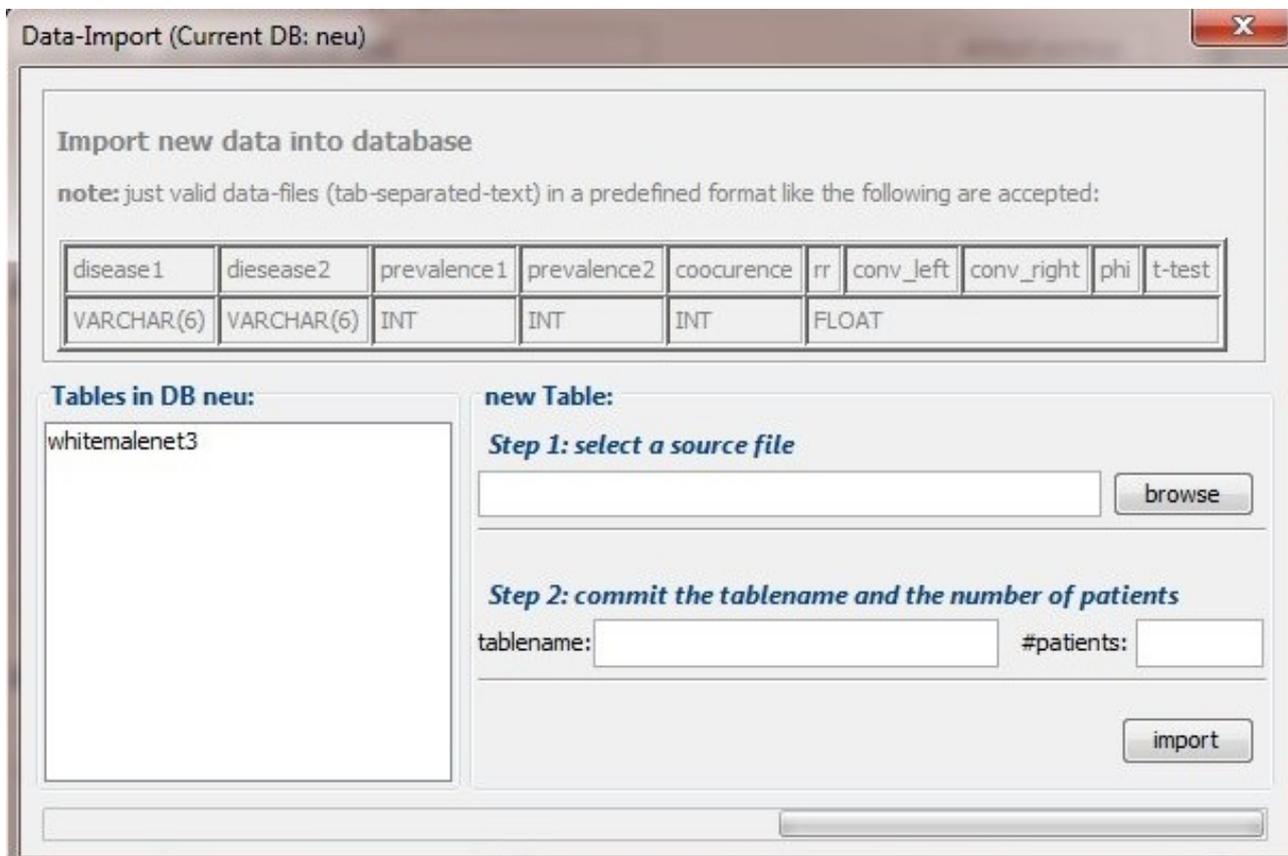So it will take a few secounds to be ready.

4.3 Selecting datasets.

If you already have loaded succesfully HuDiNe-datasets in your database you can select one and
close the dialogue.

Otherwise you can import new ones by clicking on the 🗄️*import* button. This will start the data-
import dialogue.

5 Loading new data: the data-import dialogue

The dataimport dialogue is started using the button in the db dialogue or the 🗄️button int data-
toolbar on the main window.

data import dialogue

With this dialogue you can see all datasets already loaded to the database or select a file in the
HuDiNE-format to load it into the database:

 – select a file by starting a fileselect dialogue with the *browse-Button*

 – give the dataset a name to identify it (should be alphanumeric)

 – enter the number of patients. This number you will find on the HuDiNe-website where you

can download datasets. Please make sure to enter the correct number otherwise the prevalences will be calculated wrong.

– Click on *import* and approve the opening warning message.

Loading big datasets to the database can take several minutes, so please be patient. Loading 200 MB takes 2 to 4 minutes.

6 Explore your data

After establishing a database connection and selecting a dataset you can explore your current dataset.

To begin you will need a root disease. With the disease search you can find disesases in your dataset. After this you can adjust the phi or rr values to find other diseases with a connection to your root disease according aour selecting.

search pane

6.1 Search and find a root disease: the searchpane

With the searchpane diseases can be searched in datasets. Wether by name or ICD-9-CM code. Just enter a search term in the textfield and press

You can search by ICD-9-CM codes. If you are using a 5 digit dataset you will have to enter the digits with you code (e.g „250.0").

If you enter characters your search will be done over the names. You can search for more than one word. You can also put your wors within quotation marks to perform an exact search (e.g. „ „diabetes mellitus" ").

If there are results for your search they will be displayed below in a table. There you can select a disease and perform a seach for neighbors with the *explore graph* Button.

To adjust the phi or rr values use the box on the right hand. To switch between phi and rr press the button.

If the current setting was too big and no neighbors are found a warn-dialogue will appear and inform.

Sometimes values are too short and more then 200 neighbors are found. This will result in a lower performance so we recommend to adjust your phi and rr values.

After the root disease is explored the view will autamatically jump to the nodepane. If you like to perfom a new search just choose the „Disease-Search"-pane.

6.2 Exploring and basic navigation

Your Graph will be displayed in the graphpane. All nodes are also diaplayed in the nodepane.

Graphpane with the node pane on the left hand and active edge table below

6.2.1   Navigation in the Graphpane

In the picture above you see a part of the main window.

On the Graphpane you see a visual representation of the explorerd dataset. You can **move** the image by drag-and-drop over a whitepart in the Grpahpane. Just click and hold the mouse there and move the graph somewhere else.

It is also possible to **move parts of the graph**: click and hold a node and move it somewhere else.

To **zoom** hold the right mouse button pressed and move the mouse upward to zoom out and vice versa.

To **select a** certain **disease** just click once on it and it will be painted transparent. In the nodepane on the left hand the active node is marked in the node table. The web-search buttons are active if a node is selected. By clicking at the buttons you can perform a webseach at Wikipedia, DBMedia or ICD9data.com.

6.2.2   Exploring in the Graphpane

To explore another disease just **double click** on the node and a search in the database will be performed and the results added to the current graph.

Another possibility is to select a disease in the node-table or in the graph and press the *explore* button.

6.2.3   All information in one table: the edge table

All informations provided in the source files loaded in the database is presented here. This table provides the exact representation of the data forming the basis of the graph.

You can sort the table by its columns: just click on a cloumn label.

6.2.4   Clustering

If a graph is shown you can calculat the clusters using the integrated Borderflow algoritthm. Just click on the cluste button to change it to *„clusters on":*

If clusters are enabled the will only be shown in the *Spring*-Layout. So make sure it is selected in the Layout toolbar.
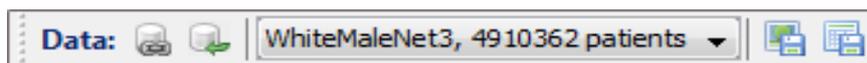
But if you enabled clusters they are always shown in the cluster tree beneath the nodepane.

7 Toolbars

The upper part of the main window conatins the toolbars. There are 4 toolbars available:

the Layout-, Data-, View and Info-Toolbar.

Each button has a

7.1 Load, switch datasets and make image: The Data-Toolbar


data toolbar

The first two buttons open the DB-dialogue and data-import-dialogue.

With help of the dataset switch – ComboBox you can switch between datasets in the current database. But each switch will result in a cleared graph to avoid inconsistencies. The two buttons on the right hand are for date-export.

The first one makes it possible to save a image of the current graph in various formats.

With the second one you can save the edgetable as a .csv-file on your harddrive for further analysis.

7.2 Switch Layouts: the Layout-Toolbar
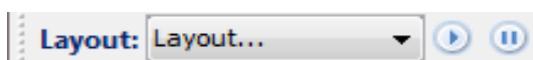
layout toolbar

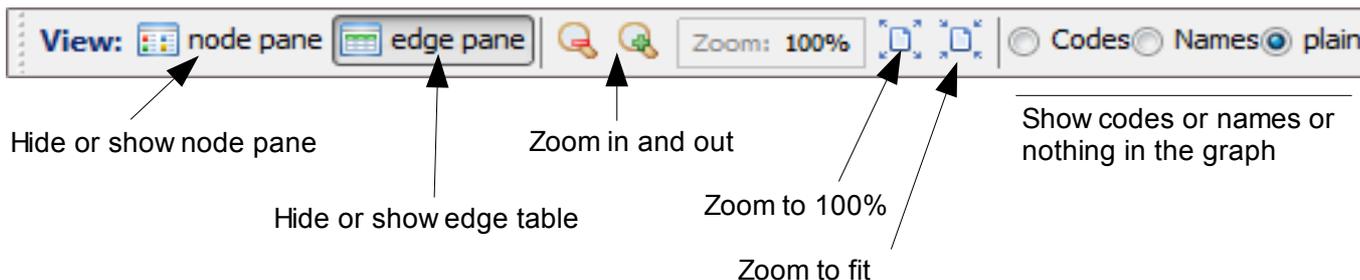You can choos between 5 Layouts: Spring, Circle, Hierachical and Radial-Hierachical.

Just click on the ComboBox and select one.

The with buttons on the right you can run or stop the animations in the Spring-Layout.

Keep in mind that **clusters** are only visible in the **Spring-Layout**.

7.3 Zoom and hide: the View-Toolbar

With help of this toolbar you can zoom-to-fit, zoom 100% , and choose whether if you want to see certain components, like egde and node table or names and ICD9-CM codes.

Hide or show node pane

Hide or show edge table

Zoom in and out

Zoom to 100%

Zoom to fit

Show codes or names or nothing in the graph

7.4 Help and other resources

 In the info toolbar you find Buttons to diplay the manual whithin the software and a button with short references. On the right hand there are two Hyperlinks: the first to the HuDiNe-website, the second wo our project website.