

# Analysing Biological Networks with Cytoscape

Alberto Calderone

Bioinformatics and Computational Biology Unit  
Molecular Genetics Laboratory - University of Rome Tor Vergata - prof. Gianni Cesareni

## What is Cytoscape



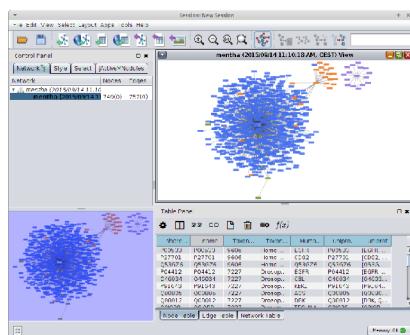
Cytoscape is an open source software platform for visualizing molecular interaction networks and biological pathways and integrating these networks with annotations, gene expression profiles and other state data.

Cytoscape core distribution provides a basic set of features for data integration, analysis, and visualization. Additional features are available as Apps (formerly called Plugins).

Apps are available for network and molecular profiling analyses, new layouts, additional file format support, scripting, and connection with databases.

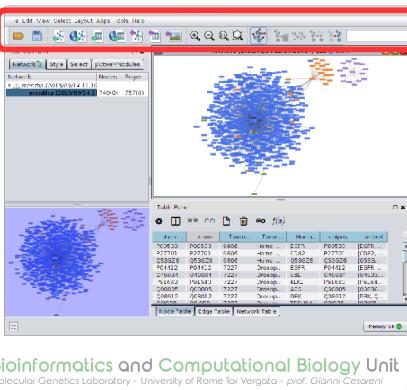
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## Cytoscape Interface



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## Cytoscape Interface

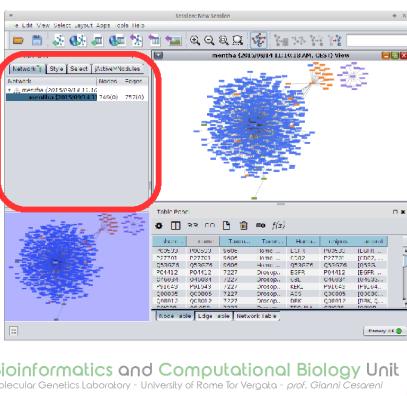


**Top Menu and Buttons**

- Open
- Save
- Import
- Export
- Layout
- Search
- ...

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## Cytoscape Interface

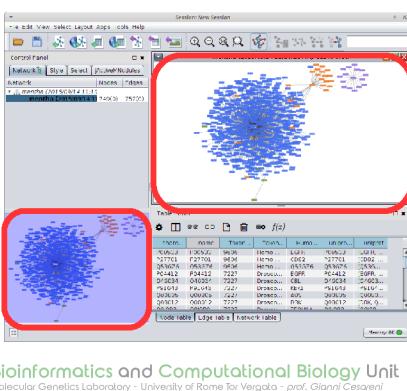


**Attributes, Appearance and Some Plugins**

- Handle multiple networks
- Number of nodes and edges
- Change colors
- Filter nodes and edges
- Plugins
- ...

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## Cytoscape Interface



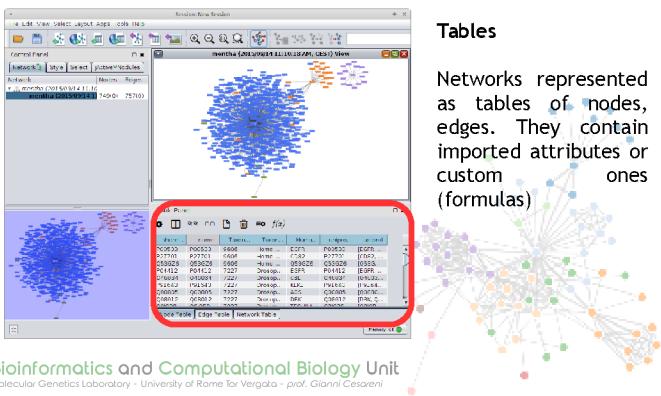
**Window-Based Working place**

Multiple networks can be shown at the same time as separated windows. Nodes and edges are dragable and clickable.

**Network overview**

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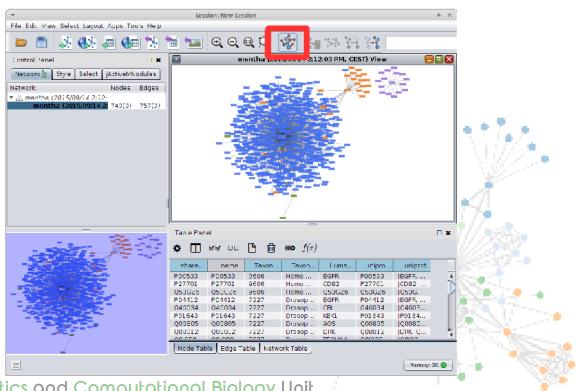
## Cytoscape Interface



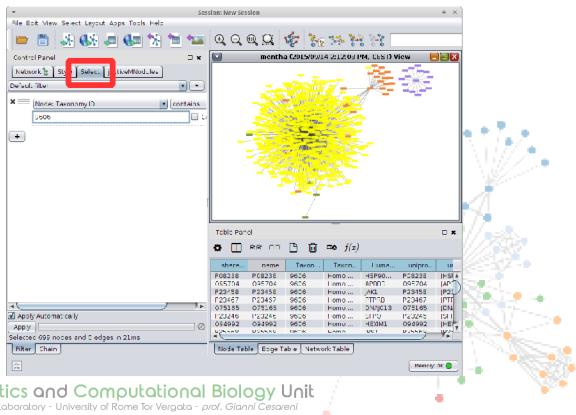
## Tables

Networks represented as tables of nodes, edges. They contain imported attributes or custom ones (formulas)

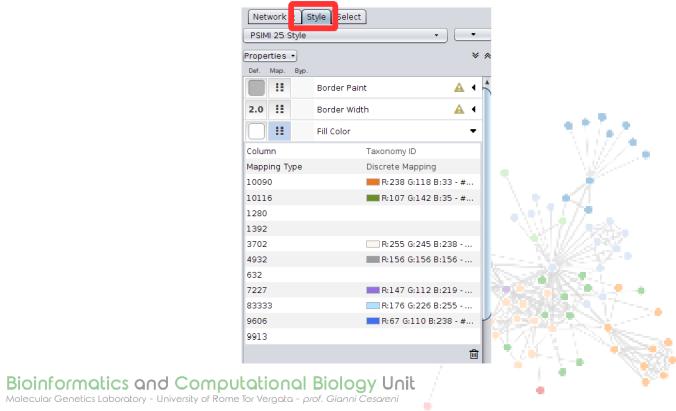
## Layout



## Selecting Objects

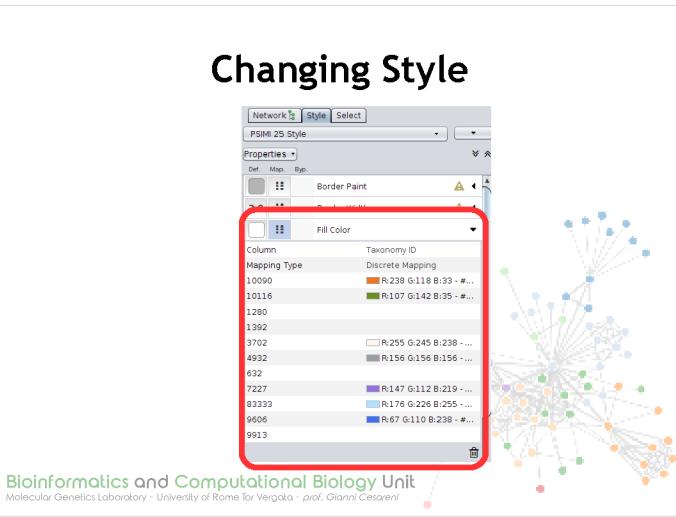


## Changing Style



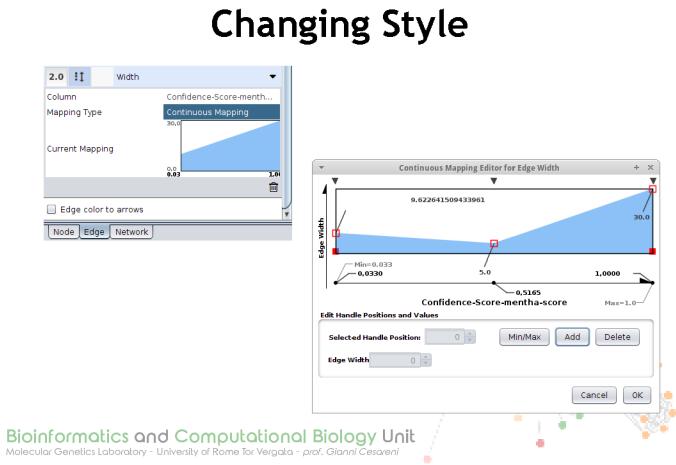
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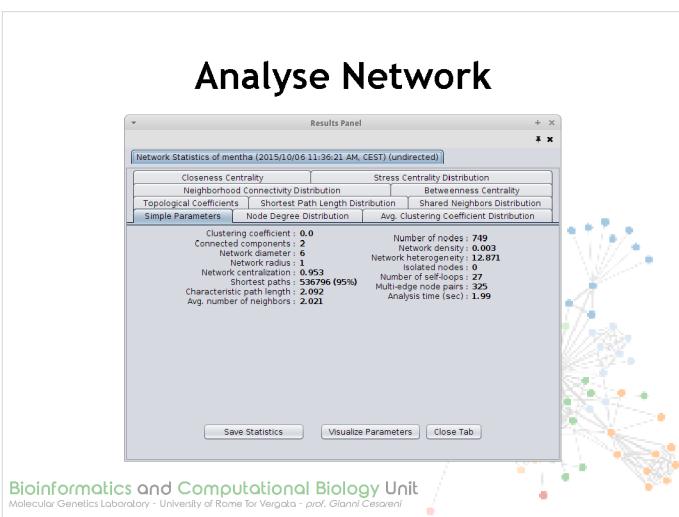
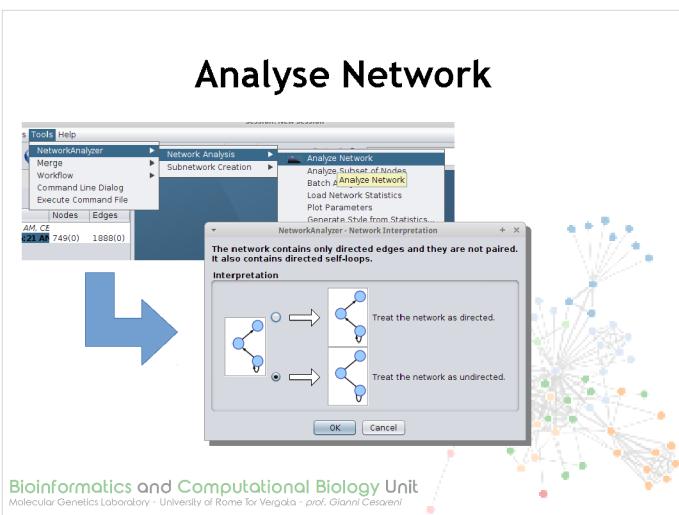
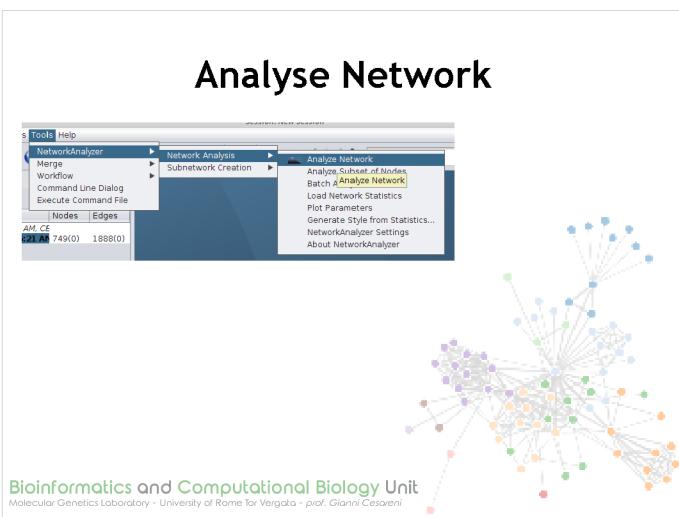


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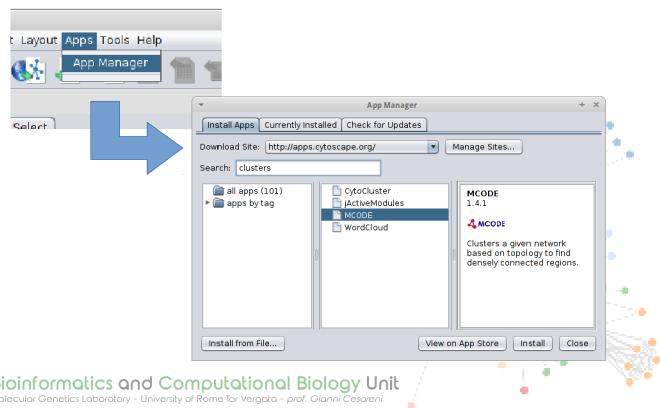
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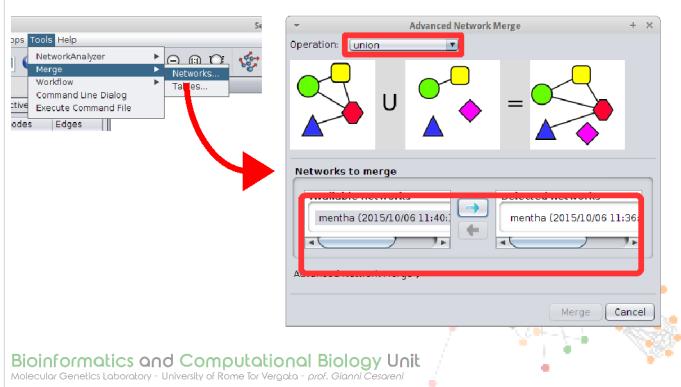
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## Doing More: Plug-ins (Apps)

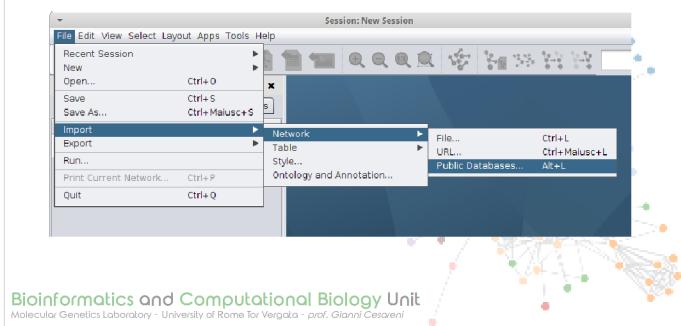


## Merging Networks

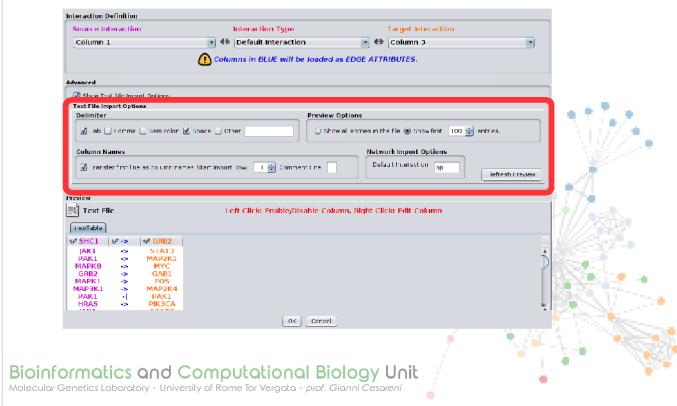


## Importing a Network

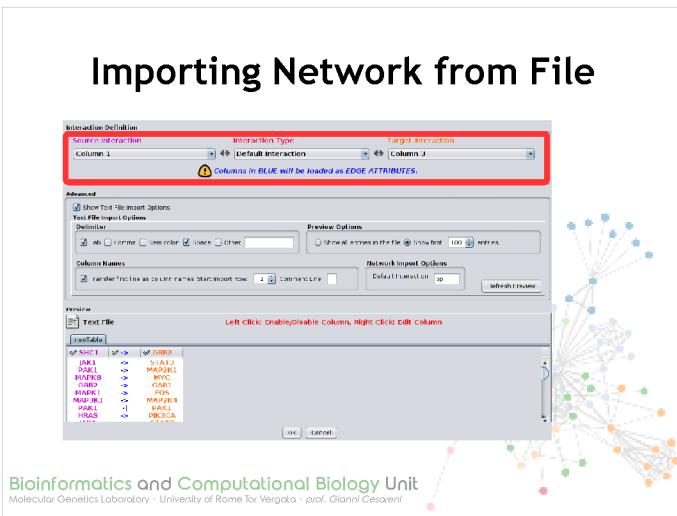
It is possible to import networks from text files, Excel files and other formats, including external PSICQUIC resources



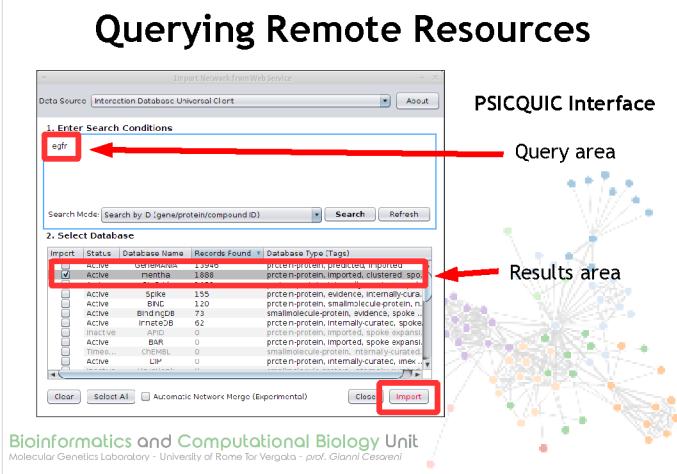
## Importing Network from File



## Importing Network from File



# Querying Remote Resources





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## An Example

What can we learn from the analysis of the network formed starting from all proteins annotated to be part of the apoptotic process?

The network graph shows a complex web of interactions between various proteins. Nodes are represented by colored circles (purple, blue, green, orange) and edges by gray lines. A prominent cluster of purple nodes is on the left, connected to a more dispersed cluster of orange and green nodes on the right.

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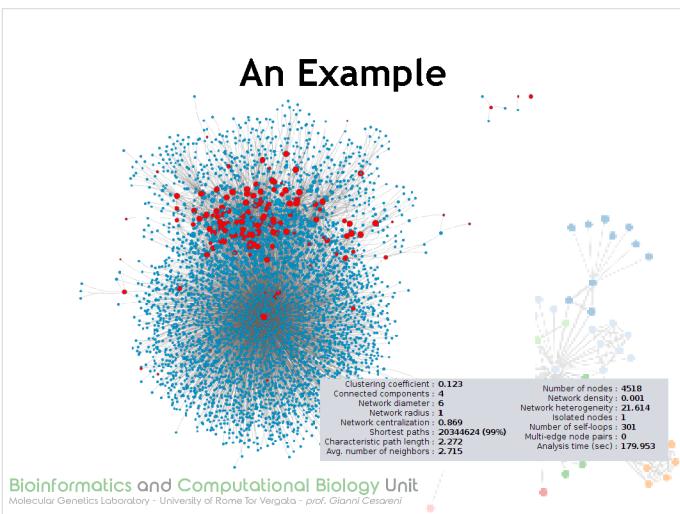
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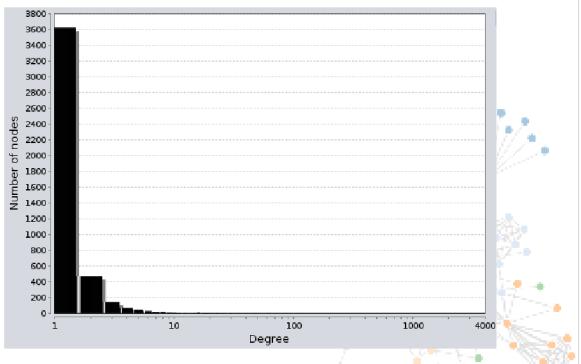
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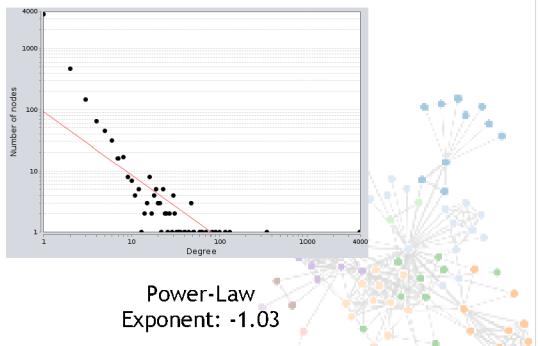
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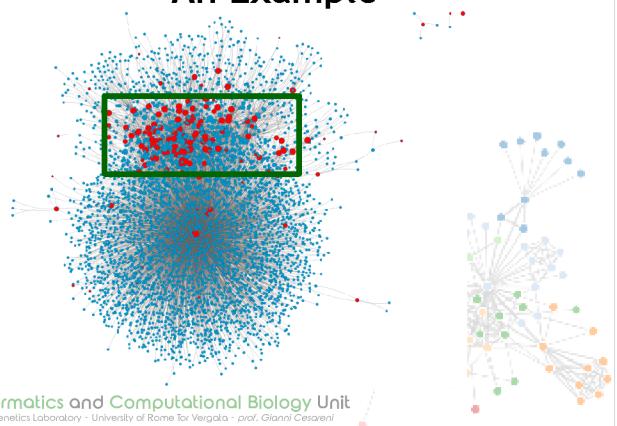
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## An Example



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## An Example

POMP  
ABL1  
MDM2  
LRRK2  
RAF1  
UCHL5

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## An Example

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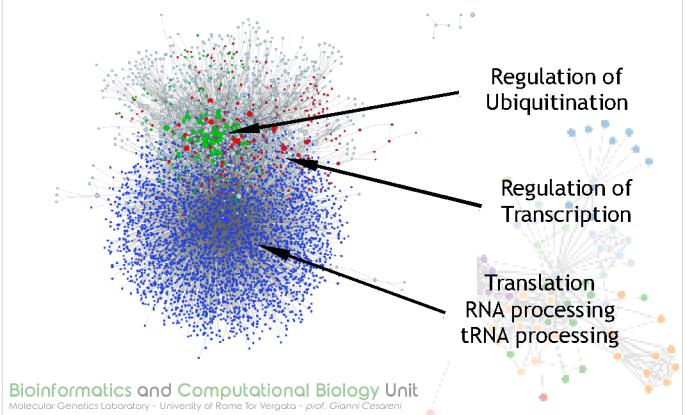
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## An Example



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