

# *Cytoscape and microarray annotations*

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# Training course web page

<http://www.sigenae.org/index.php?id=171>

The screenshot shows the SIGEN@E website interface. The main content area is titled 'Cytoscape' and includes a description of the software, a 'Documentation' section with links to a video tutorial, user guide, and official tutorials, and an 'EADGENE Documentation' section with links to course slides and exercises. A red circle highlights the 'EADGENE Documentation' section.

**You are here**

- Public
- Cytoscape

**Navigation**

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## Cytoscape

Cytoscape is a software that enable the users to visualize molecular interaction networks and metabolite pathways, with their annotations, expression profiles or any associated attributes.

The Cytoscape core distribution provides basic tools for data integration and visualisation. Advanced fonctionnalités are available as plugins. Plugins are, for example, network analysis tools, layouts, additional file format import /export features, scripting modules, data source connectors. Many plugins are [freely available](#).

For any information about Cytoscape, see the <http://www.cytoscape.org>

### Documentation

- >> [video tutorial in french](#)
- >> [user guide](#)
- >> [official Cytoscape tutorials](#)

### EADGENE Documentation

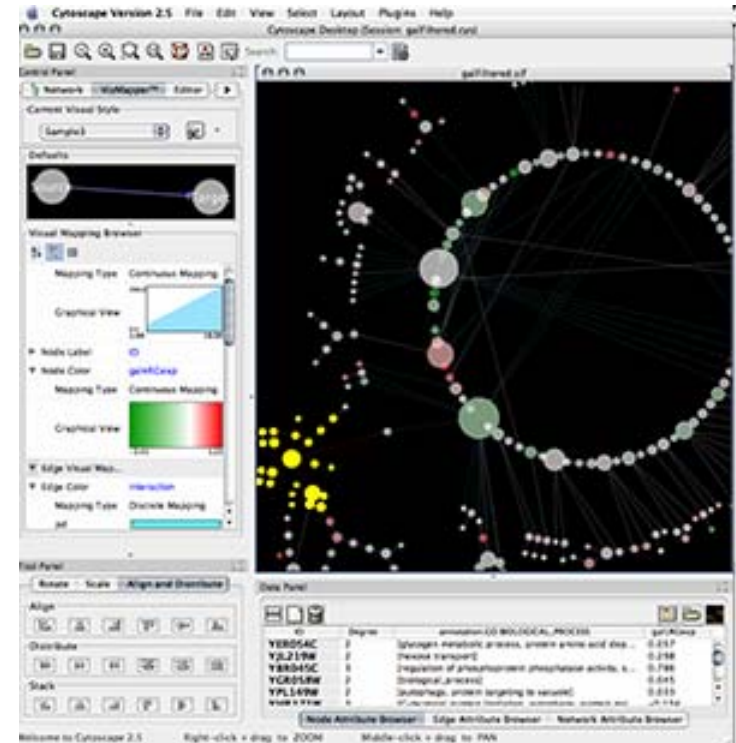
- >> [eadgene course slides:pdf,ppt](#)
- >> [eadgene course exercises:pdf,doc,data](#)

### Download

- >> to install cytoscape, you need first to [install java](#)
- >> then you can [download cytoscape](#)
- >> to a quick overview of Cytoscape, you can try this [custom Cytoscape 2.5.1 Install with plugins](#) (useful for video tutorial)
- >> or use this [Java Web Start link](#)

# Cytoscape : presentation

- Context
- Software presentation
- History
- Functionalities
- User Interface
- User cases for biologists
- **Exercises**

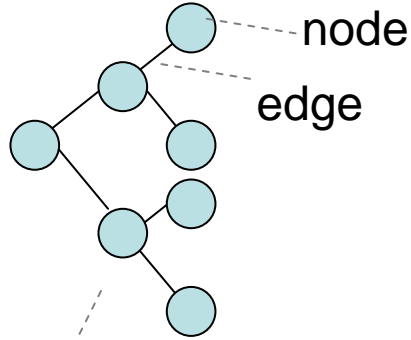


# Why to choose Cytoscape ?

- Biologists store their annotation **data** in table formats (Excel...)
- These formats are suited to store simple annotations like blast best hit, IDS...
- But are inappropriate with lists (hit lists...). Many tables are needed.
- Pathways and biological networks can't be represented in Excel because they are based on **graph structures**

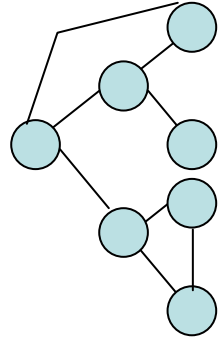
# Graph structures in biology

**tree**

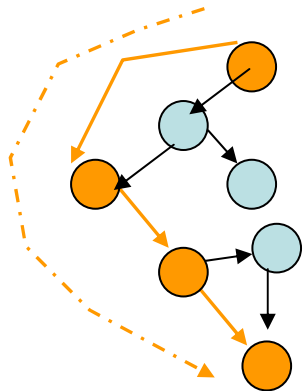
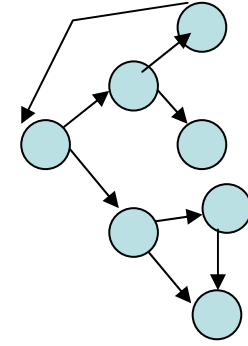


ontologies

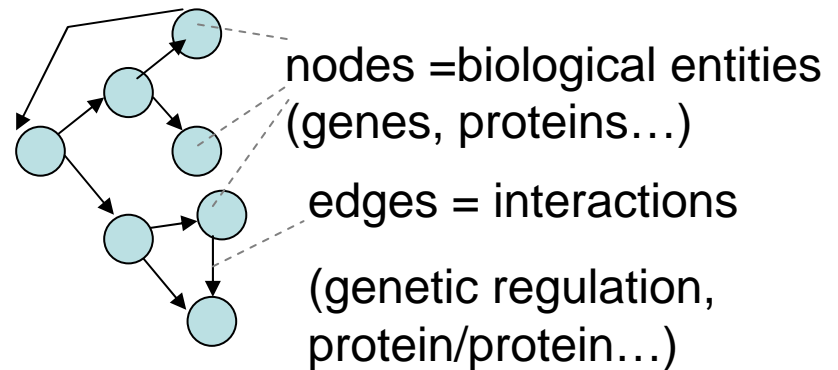
**undirected graph**



**directed graph**

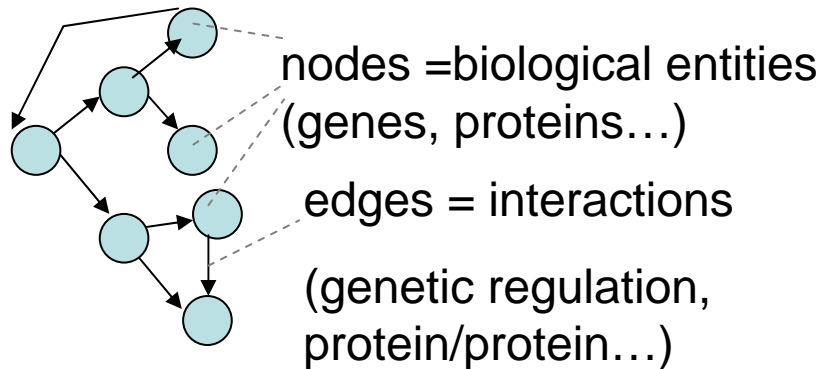


a graph pathway



biological interaction networks

# Cytoscape : a tool to work with graph structures



IDs, expression values, cluster name, GO, xref,, sequence...

biological interaction networks

+

nodes and edges attributes

**CYTOSCAPE**

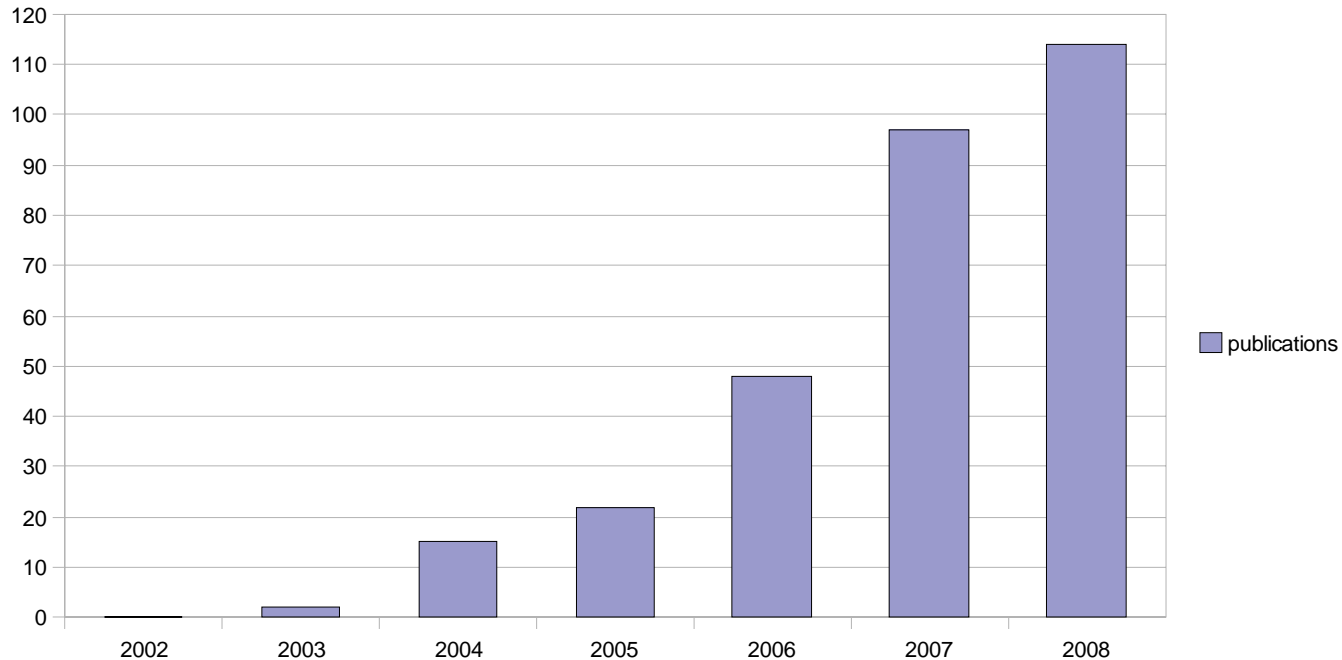
# What is Cytoscape?

*Cytoscape* is a software that allows to

- **visualize molecular interaction network and metabolic pathways,**
- with there **annotations**, expression profiles or other associated attributes.

- *Cytoscape* was initially made public in July, 2002
- *Cytoscape* is open source and community driven
- Plugins may be developed by anyone using the Cytoscape open API based on [Java™](#) technology

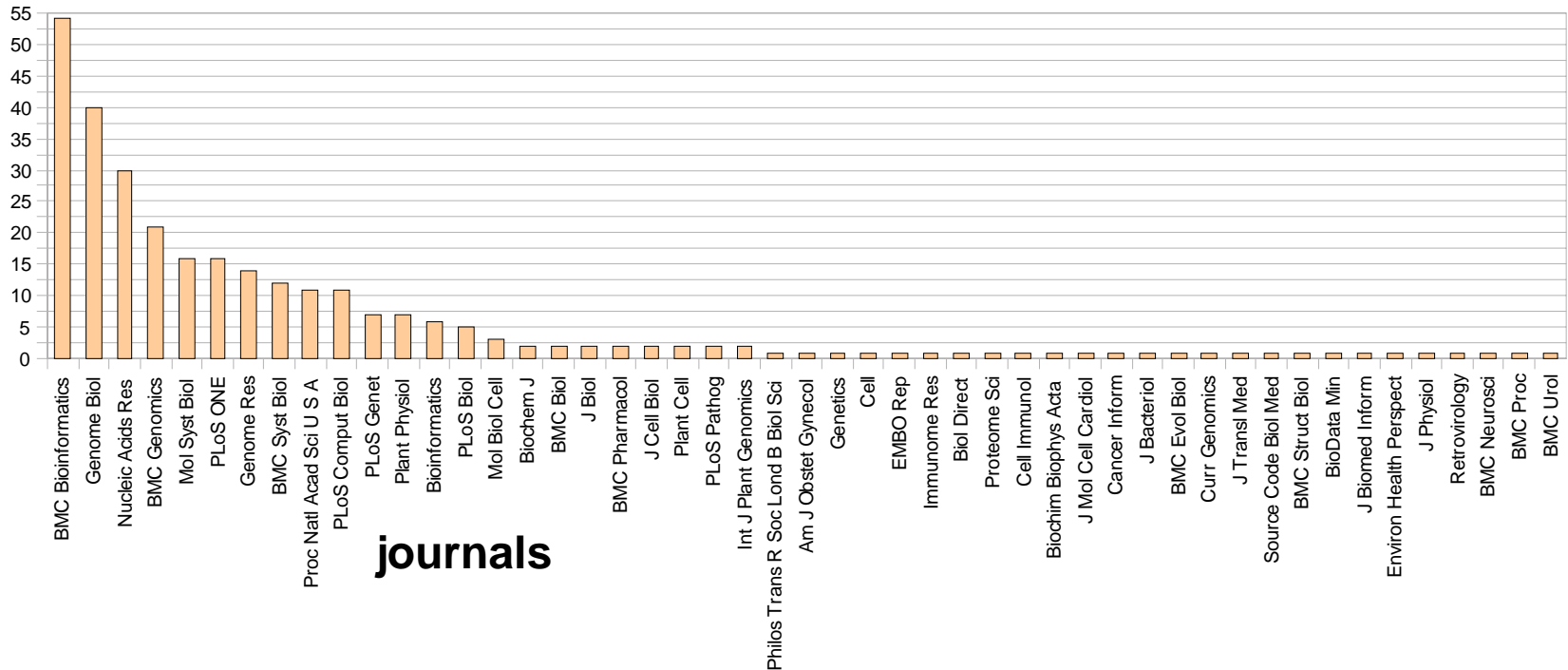
# Is Cytoscape used by biologists ?



PubMed Central publications related to *Cytoscape*

295 citations (evaluated on november 2008)

# Is Cytoscape used by biologists ?

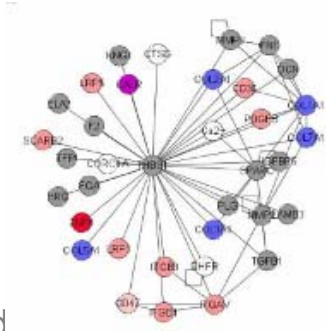
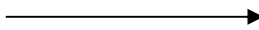


journals

BMC Genomics, Genome Res, Genome Biol, Nat Protoc, Plant Physiol...

**Example:**

[Stefano Campanaro et al, BMC genomics 2007](#)



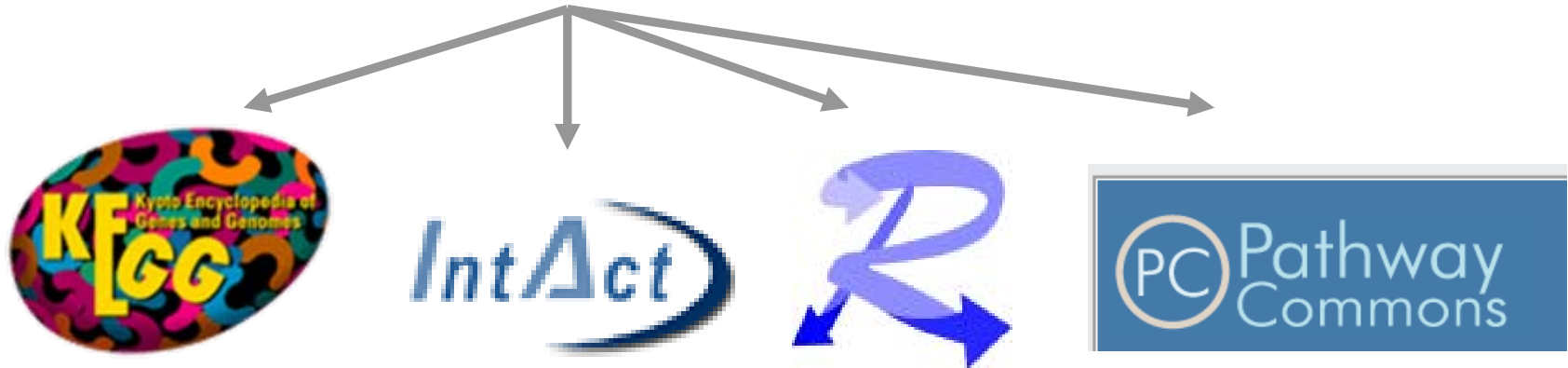
# Advanced functionalities: plugins

- the *Cytoscape core* distribution contains the basic tools for data integration and visualization.
- The Advanced functionalities are available as ***plugins*** developed by the community:
  - **Analysis** -- analyzing existing networks
  - **Network and Attribute I/O** -- importing networks and attributes
  - **Network Inference** -- inferring new networks
  - **Functional Enrichment** -- functional enrichment of networks
  - **Communication/Scripting** and **Other**

More than 65 plugins available

# Data source connectors

Embedded connectors to online data ( *Pathway Commons, Biomart...* ) give  
a quick **access to interactions data sources.**



# Visualize and explore graphs

Zoom

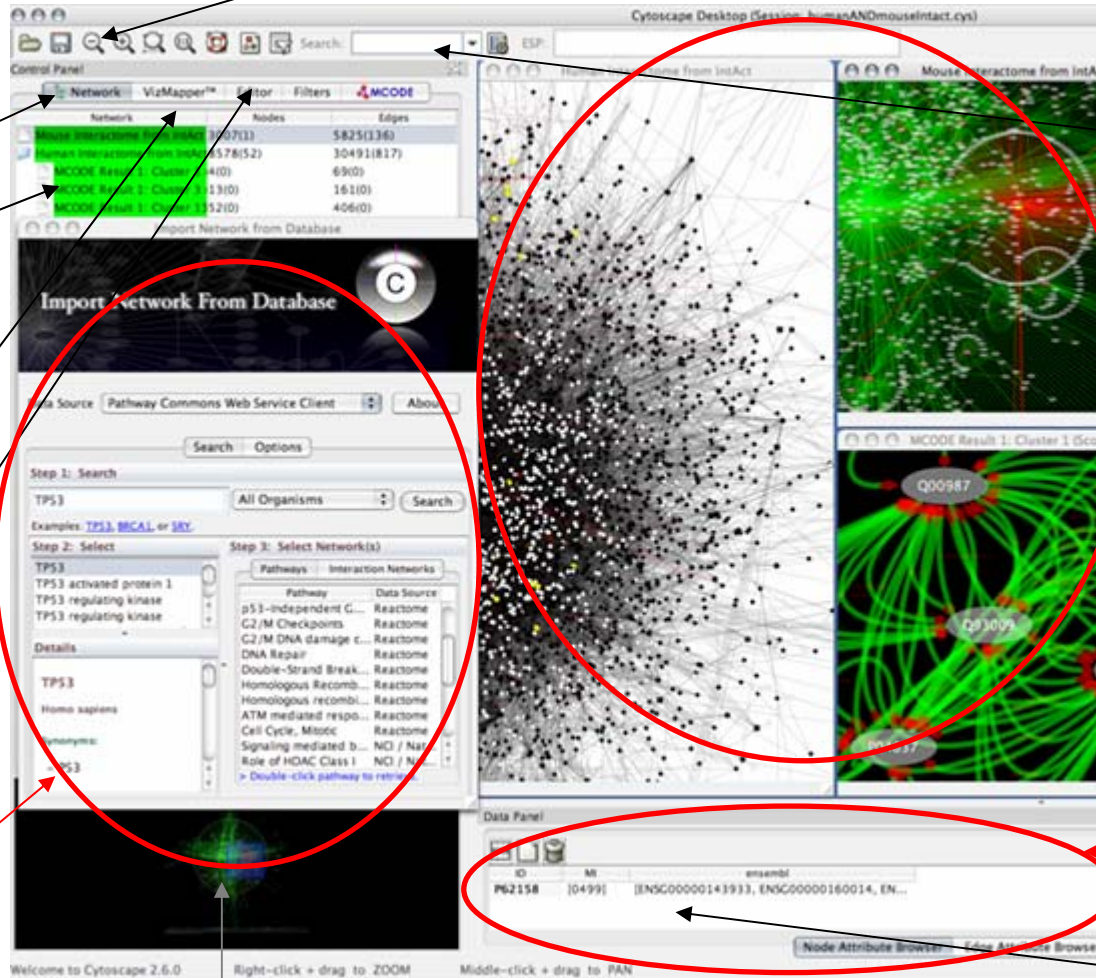
file management

Networks management

Graphic style editor and manager  
 « VizMapper »

Graph editor

**data import**



search and indexation

**Explore and visualize**

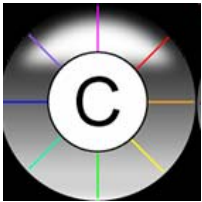
**annotations**

Navigator view

Data panel

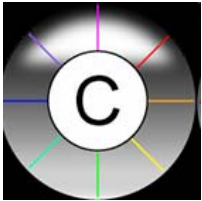
# What can I do with Cytoscape ?

- **Illustrate a publication** (GO summary, interactions graph, metabolic schema)



- **Explore the literature** from the neighbourhood of a target gene list.
- **Capture from experiments and literature my own interaction model**, used to summarize the available knowledge on a subject

# What can I do with Cytoscape ?



- **Give meaning to a group of co-expressed genes by finding common regulations**
- **Check the coherence of a network and experimental data**
- **Model genetic and metabolic regulations**
- ...

# Cytoscape exercises

- Cytoscape User Interface presentation
- Using networks with microarray probes annotations
  - Co expression Clusters
  - Hugo gene name annotation and expression values
  - KEGG annotations
- Advanced features with plugins

# How to run Cytoscape

- **Java Web Start** (from <http://www.pathwaycommons.org>)
- or [download](#)
- **test your Java Installation now**  
(for MS windows : start, execute, cmd, JAVA –version)