Cytoscape

Texte

A powerful bioinformatic tool
Plan

- What is cytoscape?
- Cytoscape’s core features
- Cytoscape 3.0
What is Cytoscape?

- An open source Java-based bioinformatics software platform developed by a team of developers.
What is Cytoscape?

- Used to visualize molecular interaction networks and biological pathways
What is Cytoscape?

- **Integration** of annotations, biological data (gene expression profiles)

Example network information, where a connection means two genes are co-regulated.

Example condition from gene expression profile.

Genes and their expression values are mapped together by Cytoscape.
What is Cytoscape?

- Create a visual style based on data integrated with network information.

Here, the color of the gene depends on the numerical value of the gene expression level (see previous panel). Many other aspects of the visual style, like node color or edge width, can be controlled by the data mapped to the network.
What is Cytoscape?

- **History:**
  - July, 2002: 1st release of 0.8
  - November, 2002: 2nd release of 0.9
  - March 2003: 1.0
  - Since then, multiple versions
  - Actual release: 2.7
  - 3.0 is coming
What is Cytoscape?

- Website:
  http://www.cytoscape.org/
What is Cytoscape?

- A powerful tool that supports large networks of more than 100,000 nodes and edges

GalFiltered network
331 nodes
362 edges
What is Cytoscape?

- Or:

Human network
19905 nodes
31704 edges
(from Biomolecular Interaction Network Database)
What is Cytoscape?

- **nodes** can represent proteins, genes, molecules, metabolites, or enzymes

- **edges** are the interactions
What is Cytoscape?

- **The core**: provides basic set of functions to visualize networks and integrate data
  - network layouts
  - expression profile integration
  - linking network to databases
What is Cytoscape?

- Additional features (Plugins) can be integrated in Cytoscape:
  - add new layouts
  - more file format support
  - connection with databases
- Plugins are developed using the Cytoscape API and are most freely available.
What is Cytoscape?

- Huge community of developers (about 100 plugins are available in the plugin manager)
- Download from the Cytoscape website!

- **Analysis** -- Used for analyzing existing networks (39)
- **Network and Attribute I/O** -- Used for importing networks and attributes in different file formats (24)
- **Network Inference** -- Used for inferring new networks (6)
- **Functional Enrichment** -- Used for functional enrichment of networks (7)
- **Communication/Scripting** -- Used for communicating with or scripting Cytoscape (7)
- **Other** -- None of the above (18)
Plan

- What is cytoscape?
- Cytoscape’s core features
- Cytoscape 3.0
Cytoscape’s core features

Data integration:
- networks, attributes, sessions, data files

Visual style:
- Node/edges representation, layouts, browsing
- attribute browser, vizmapper, image export

Analysis:
- Filter, find Clusters/modules, ...

Others
Cytoscape’s core features:

Data integration

- **SIF**: Simple Interaction Format
- **GML**: Graph Modelling Language
- **BioPax**: Biological Pathway eXchange
- **PSI-MI**: Proteomics Standards Initiative - Molecular Interactions
- ...

![Image of file formats]
Cytoscape’s core features:

Data integration

- Data integration of files:
  - Expression profiles
  - Gene Ontology annotations

- Interoperability:
  - insert cytoscape into a workflow to load data generated from another
Cytoscape’s core features:

Data integration

- Session files:
  - .cys (Cytoscape Session)
  - save loaded networks
  - attributes of networks (for nodes, edges, networks)
  - desktop settings, data, plugins state...
Cytoscape’s core features:

Data integration

- Web service client:
  - Cytoscape can connect to the external public databases and imports network and annotation data
Cytoscape's core features:
Visualization

* Vizmapper:
Cytoscape’s core features:

Visualization

- **Vizmapper:**
Cytoscape’s core features:
Visualization

- **Vizmapper:**
  - Map graph attributes to visual attributes
  - Customize visual styles for later use
  - Graph has node and edge attributes (expression data, interaction type, GO function)
Cytoscape’s core features:

Visualization

- Mapped to visual attributes (node/edge size, shape, color, font,...)
- Take continuous gene expression data and visualize it as continuous node colors
Cytoscape’s core features:

Visualization
Cytoscape’s core features: Visualization

- **Layouts**:
  - Layout networks in 2 dimensions.
  - Multiple available layouts: cyclic, tree, force-directed, edge-weight, and yFiles organic.
Cytoscape’s core features:

Visualization

Circular

Hierarchical
Cytoscape’s core features:

Visualization

Orthogonal

Grid
Visual Styles

Load "Your Favorite Network"
Visual Styles

Load “Your Favorite Expression” Dataset
Visual Styles

Expression data mapped to node colors
Cytoscape’s core features:

Visualization

- **Browsing:**
  - zoom in/out, pan for browsing network
  - With network manager: easiest way to organize multiple networks
  - Bird’s view to navigate large networks
- Export your networks as image files:
  - PDF, EPS, SVG, PNG, JPEG, BMP files
Cytoscape’s core features:

Analysis

- **Filter**: to select some nodes/interactions based on some loaded data.
Cytoscape’s core features :
Analysis

- **Filter** :
  - exemple : select nodes involved in certain metabolic pathway, that share a particular GO annotation, or genes whose expression level changes due to p-values loaded from gene expression data...
  - Used to create subnetwork from filtered elements
Cytoscape’s core features:

Analysis

**Filter:**
Cytoscape’s core features:

Analysis

Filter:
Cytoscape’s core features:

Analysis

- Find active subnetworks, pathway modules:
  - they can be highlighted by integrating gene expression data --> interaction subnetworks (genes with high level of different expression)
Cytoscape’s core features: Analysis
Cytoscape’s core features:

Analysis

- Find active subnetworks, pathway modules:
- Provide hypotheses for the regulatory and signaling interactions in control of the observed expression changes
Find clusters (highly interconnected regions) from loaded networks

- clusters may have different mean depending on the type of network:
  - in ppi: they have been shown to be protein complexes and part of pathways
  - in protein similarity network: they represent protein families
Cytoscape’s core features: Analysis
Cytoscape’s core features:

Other features

- Multilingual, and Plugins!
  - jActiveModules
  - MCode
  - GOlorize
  - BinGO
  - Dynamic expression,...
Comparison of network analysis platforms with Cytoscape

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Cline et al. (2007) Nature Protocols
Cytoscape 3.0

- Developed in a modular architecture.
Cytoscape 3.0

- Developed in a modular architecture.
- Use of new technologies:
  - OSGi: Cytoscape made of independant modules (kind of plugins)
  - osgi website: www.osgi.org
  - Spring: web technology to link the modules through “services”.
  - Maven: builder of application that loads the
Cytoscape 3.0

- Plugins are more easily integrated in the core using the OSGi technology

- OSGi module --> Spring configuration file
  --> plugin integrated
Spring configuration file:
- defines **Services** (objects) through their Interface
- Implements these **Services** in other **Beans**
- Consequence: no java class is communicating directly with another one
Cytoscape 3.0