

TSRI Lecture: Applied Bioinformatics

Introduction to Biological Network Analysis and Visualization

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Lecture 1: 5/10/2016 (Tu)

Lecture 2: 5/12/2016 (Th)

GitHub Repository for the Course

<https://github.com/idekerlab/tsri-lecture>

All course materials and data will be available here.

Course Objective

Understanding basic techniques of biological network analysis and visualization, in a reproducible way.

Note: There will be some hands-on exercises in the class. Please bring your laptop to the class.

Core Topics

- Basic concepts of biological network analysis and visualization
- Cytoscape basics
- Reproducible analysis and visualization with cyREST

Course Structure

Prerequisites:

- Basic programming skills (conditional statements, loops, functions, etc.)
- Knowledge of Python (optional)
- Familiarity with Jupyter Notebook

Tools to be covered in the course:

- Cytoscape
- CyREST
- Py2cytoscape
- NetworkX (optional) - for some statistical analysis

System Requirements

- Windows/Mac/Linux laptop
 - Preferably, the latest versions
- [Java 8](#)
- Cytoscape v3.4 (Pre-release version)
- Python 3.5 - [Anaconda](#) distribution
- The following should be installed from **conda** command
 - scipy/numpy
 - Jupyter Notebook
 - Pandas
 - NetworkX
 - py2cytoscape (available via pip command)

Outline

Day 1: Introduction to Network Analysis and Visualization

- What is biological network / pathway?
 - Benefits of network visualization
- Introduction to Cytoscape
 - Network data formats
 - Table data
 - Visual Styles
 - Overview of Cytoscape App universe
- Public data sources and services
 - PSICQUIC compatible services
 - From gene list to known interactions
- Basic visualization techniques
 - Choose proper layout algorithms
 - Manual tweaking with layout tools
 - Understanding Visual Mapping Functions
 - Discrete
 - Continuous
 - Passthrough
- Preview of Day 2: Introduction to cyREST
 - Why cyREST?
 - Reproducibility for data visualization

Homework

- Create a complete network visualization for given set of data files
 - Table 1: Network data
 - Table 2: Annotations, expression profile
 - From the tables above, create visualization by following instruction
 - The instruction will be something like:
 - “Map expression value to node color gradient”
 - “Convert node degree to node size”
 - “Change edge line type based on interaction detection method”
- Install and setup Jupyter Notebook and test basic cyREST API
 - Load network from Notebook
 - Apply layout programmatically

Day 2: Reproducible Visualization with cyREST

(Before class: ~15min. Clinic time. Q/A session for installation. etc.)

- Review: Introduction to cyREST
 - Basic design of API
 - Overview of important API
 - Networks and Styles
- Introduction to **py2cytoscape**
 - (3 min. Introduction to Python)
- Automate data integration, analysis, and visualization
 - Data integration with pandas
 - Loading tables from file
 - Importing data from remote services
 - Filter and merge the dataset
 - Simple network analysis with NetworkX
- Visualizing data in Cytoscape from Jupyter Notebook
 - Embed network visualization using Cytoscape.js widget
 - This is a built-in feature in py2cytoscape
- Advanced topics (Optional)
 - Reproducible environment
 - VM / Docker
 - Other network analysis tools
 - Using analysis result from R/Bioconductor

Suggested Readings

- What is Cytoscape? http://www.cytoscape.org/what_is_cytoscape.html
- CyREST: Turbocharging Cytoscape Access for External Tools via a RESTful

- API <http://f1000research.com/articles/4-478/v1>
Jupyter Notebook Web Site <https://jupyter.org/>