**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](http://www.oracle.com/technetwork/java/javase/downloads/jdk8-downloads-2133151.html)
* Cytoscape v3.4 (Pre-release version)
* Python 3.5 - [Anaconda](https://www.continuum.io/why-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/>