Computational Systems Biology

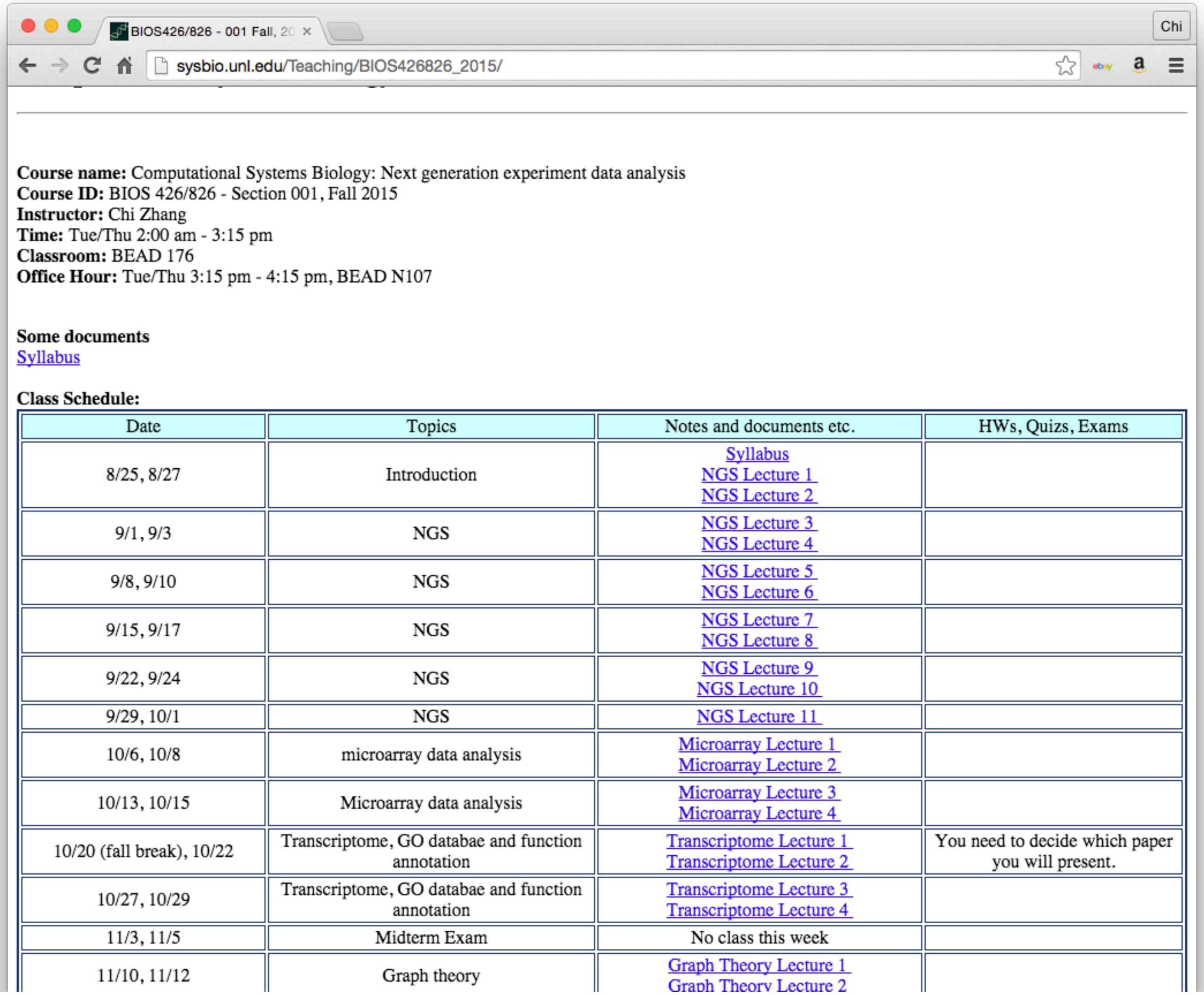
BIOS 426/826 – Section 1 Fall 2015

Chi Zhang

- **Time:** Tue/Thu 2:00 am – 3:15 pm
- **Classroom:** BEAD N176
- **Office Hours:** Tue/Thu 3:15 pm – 4:15 pm, BEAD N107 or email me for other time.
- My email is czhang5@unl.edu
- My office is N107 in BEAD

Course website

- http://sysbio.unl.edu/Teaching/BIOS426826_2015/



Course name: Computational Systems Biology: Next generation experiment data analysis
Course ID: BIOS 426/826 - Section 001, Fall 2015
Instructor: Chi Zhang
Time: Tue/Thu 2:00 am - 3:15 pm
Classroom: BEAD 176
Office Hour: Tue/Thu 3:15 pm - 4:15 pm, BEAD N107

Some documents
Syllabus

Class Schedule:

Date	Topics	Notes and documents etc.	HWs, Quizs, Exams
8/25, 8/27	Introduction	Syllabus NGS Lecture 1 NGS Lecture 2	
9/1, 9/3	NGS	NGS Lecture 3 NGS Lecture 4	
9/8, 9/10	NGS	NGS Lecture 5 NGS Lecture 6	
9/15, 9/17	NGS	NGS Lecture 7 NGS Lecture 8	
9/22, 9/24	NGS	NGS Lecture 9 NGS Lecture 10	
9/29, 10/1	NGS	NGS Lecture 11	
10/6, 10/8	microarray data analysis	Microarray Lecture 1 Microarray Lecture 2	
10/13, 10/15	Microarray data analysis	Microarray Lecture 3 Microarray Lecture 4	
10/20 (fall break), 10/22	Transcriptome, GO databae and function annotation	Transcriptome Lecture 1 Transcriptome Lecture 2	You need to decide which paper you will present.
10/27, 10/29	Transcriptome, GO databae and function annotation	Transcriptome Lecture 3 Transcriptome Lecture 4	
11/3, 11/5	Midterm Exam	No class this week	
11/10, 11/12	Graph theory	Graph Theory Lecture 1 Graph Theory Lecture 2	

Teaching materials

- No text book
- Most materials are from various articles.
- Slides will be posted online for downloading.

Course Objectives

- To introduce the field of Computational Systems Biology.
  - next-generation sequencing data analyzing
  - Transcriptome data analyzing
  - Network modeling
  - Data mining technology
- To sharpen students’ skills on independent learning.
- To help students conduct research in their field.

Tentative Schedule

Week	Content
1st	Introduction
2nd	Next-generation seq data analysis
3rd	Next-generation seq data analysis
4th	Transcriptome and epigenetics (RNA-seq)
5th	microarray data analysis
6th	microarray data analysis
7th	Transcriptome
8th	Transcriptome
9th	Transcriptome
10th	Go database and gene function annotation
11th	Midterm Exam (no class)
12th	Graph theory
13th	PPI network
14th	PPI network and Gene network
15th	Network dynamics and Data Integration
16th	Final Exam presentation

Home works and Exams

Home work assignments (~10)	40%
Mid-term exam (1)	20%
Final exam (1)	20%
Oral Presentation (1)	10%
In-class activities	10%

Homework Assignments

- Simple questions or using a software.
- Save your answer in the MS Word format or PDF, and turn in them via email.
- Handwritten answers will not be accepted.
- To use a software tool, please describe: where you downloaded the software, how you installed the software, what operating system you used, how you used this software, and what results you obtained. Use screen captures to get snap shots of your results, and submit them in your answer.
- If you make a program to answer the questions, please submit your source code files with your answers.

Homework Assignment (1)

- Your Name
- Do you have a computer? Or do you have chances to use a computer?
- If yes, what operating system does this computer have? (MS Windows, Mac OS, UNIX/Linux)
- Do you have permission to install a software on this computer?
- Do you have experience in programming? If yes, what programming language did you use? (C/C++, Fortran, Perl, Python, Ruby, VB etc.)
- Do you know how to use R? If no, how difficult is it for you to master this software? (easy; need time and help; very difficult; impossible for me to master it)

(due by 11:59PM, August 31, 2015)

Midterm

- A take-home open-book exam
- Questions to answer.
  1. Around ten questions to you.
  2. Those questions are relevant to our class but there are no direct answers from our slides.
  3. You can try any method to finger out the answer except to ask any other people.
  4. For some questions, if you can make a program to solve them, you will get extra points for your source codes.

Oral Presentation

- Find an research article for yourself.
- Make slides and present this article in class.
- You need to decide which article you want to talk before Oct. 22nd.
- This article must be a research article, which uses some computational methods for systems biology.
- This article will be used for the oral presentation and final exam.

Final Exam

- Based on the paper you selected for oral presentation, you will write a proposal.
- Present your proposal in class (10 minutes).

What to do?

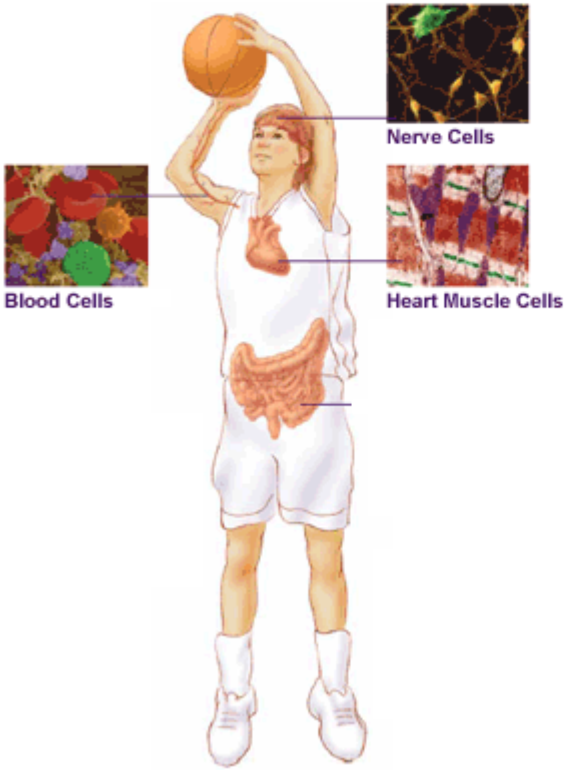
- To search for a paper.
- To decide when you want to give a talk.
- To check course website periodically to see if I upload any information for you.

Overview and Rationale

- Why do we study systems biology?
- How?

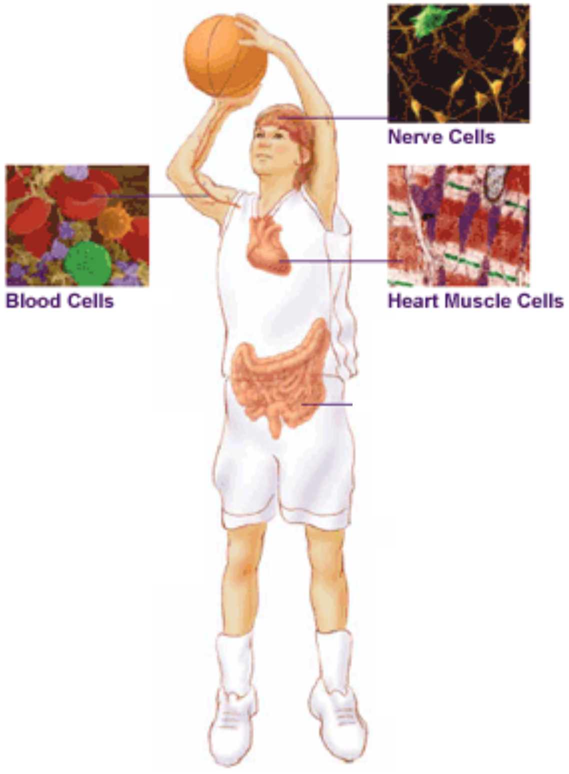
Why are cells different?

- The trillions of cells in human body are organized into >200 major tissue types, each customized for a particular role, for example
  - Red blood cells carry life-giving oxygen to every corner of your body.
  - Nerve cells sling chemical and electrical messages that allow you to think and move.
  - Heart cells constantly pump blood, enabling life itself.

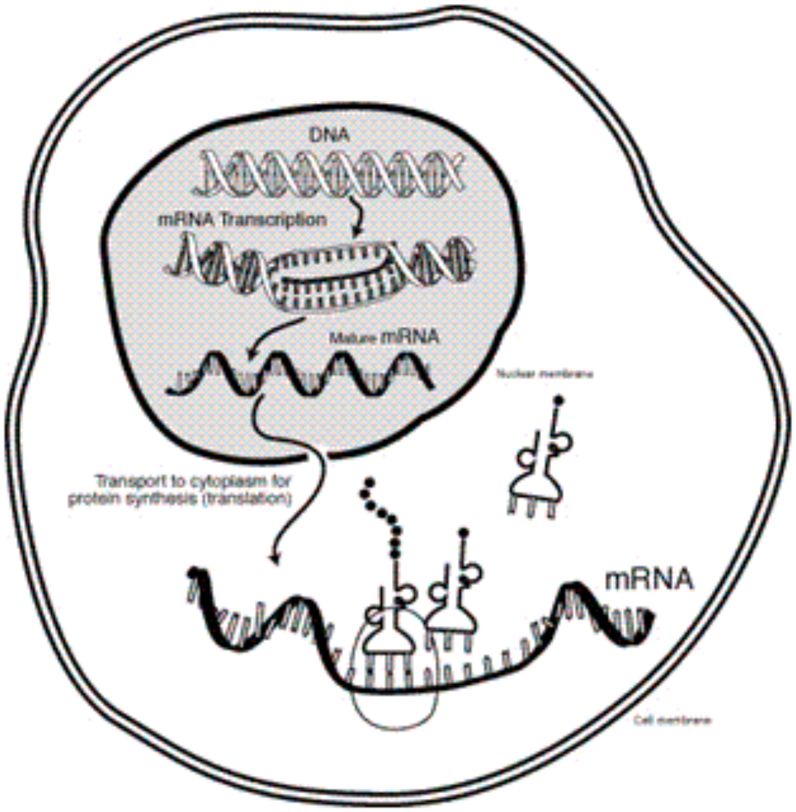


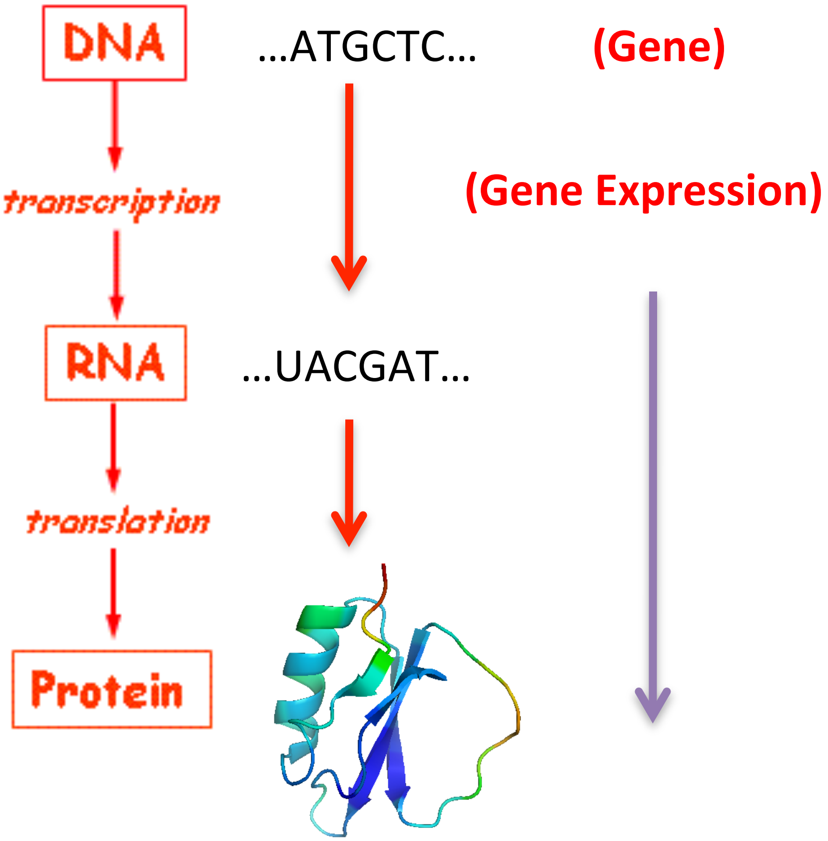
Why are cells different?

- Q: Since the cells contain the same genetic information (3 billion DNA based pairs), what make them different?
- A: The ~25,000 genes in our DNA are like a tool kit, are used (i.e., expressed) by different cells in different ways at different time.
- Gene expression is regulated by different cells.



Flow of Genetic Information





DNA ...ATGCTC... **(Gene)**

transcription

(Gene Expression)

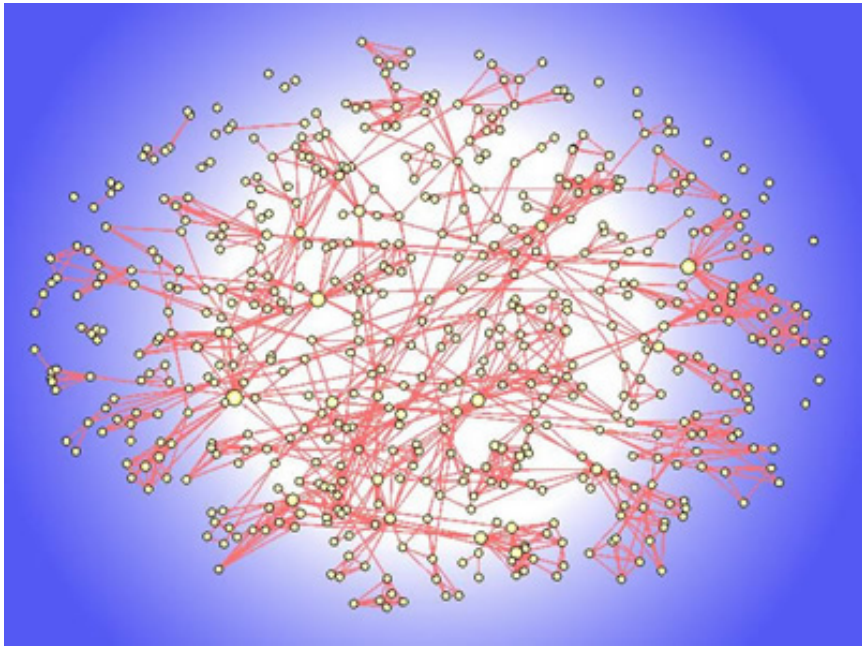
RNA ...UACGAT...

translation

Protein

Gene expression is the process by which information from a gene is used in the synthesis of a functional gene product.

System as a Whole



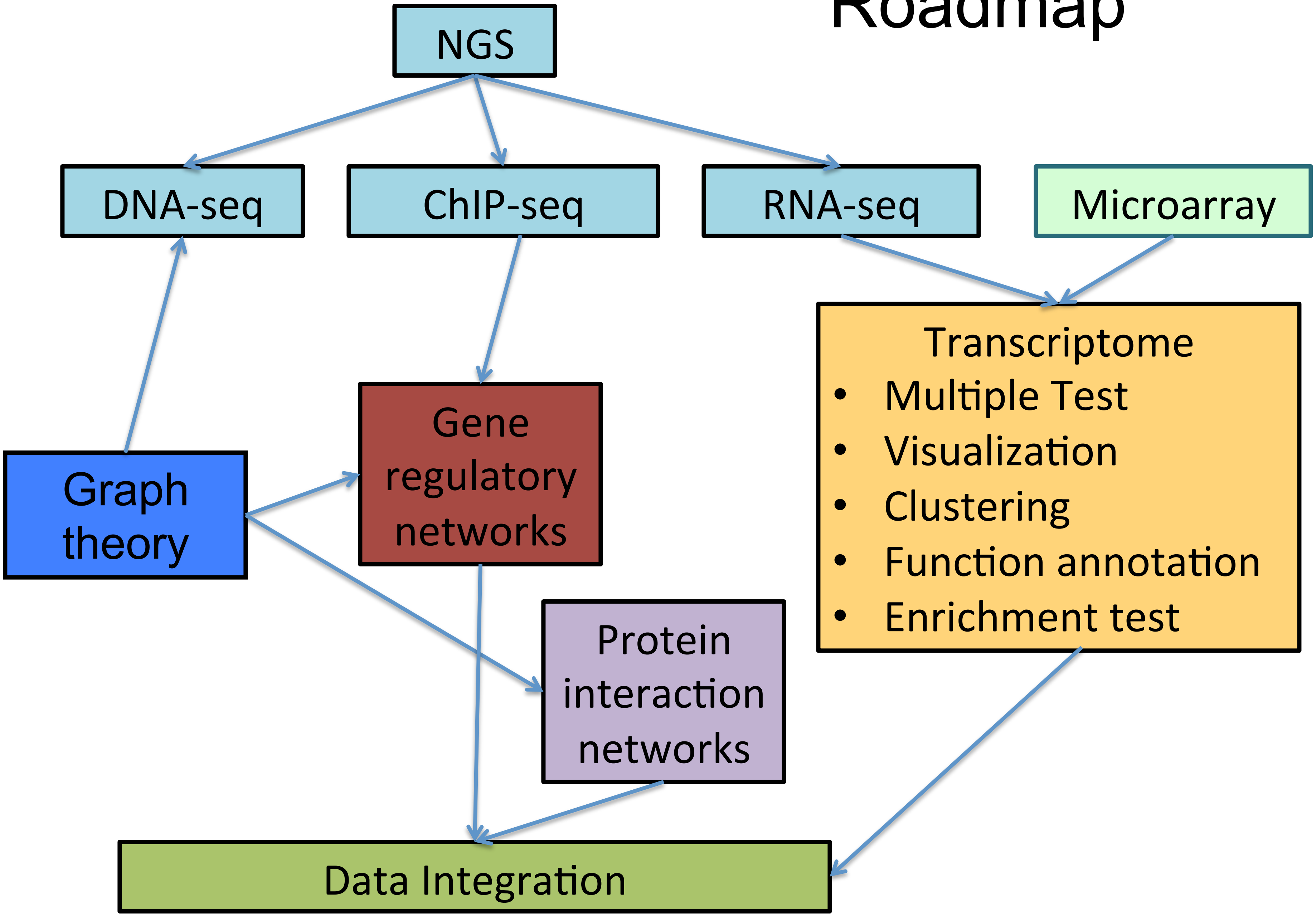
Gene regulation network: who regulates those genes expression.

How to measure?

- Good news: High throughput experiments
  - Microarray
  - Next generation sequencing

- Bad news: Challenging to extract useful information from the massive data (omic data)

Roadmap



NGS

DNA-seq

ChIP-seq

RNA-seq

Microarray

Graph theory

Gene regulatory networks

Protein interaction networks

Transcriptome

- Multiple Test
- Visualization
- Clustering
- Function annotation
- Enrichment test

Data Integration