Computational Systems Biology

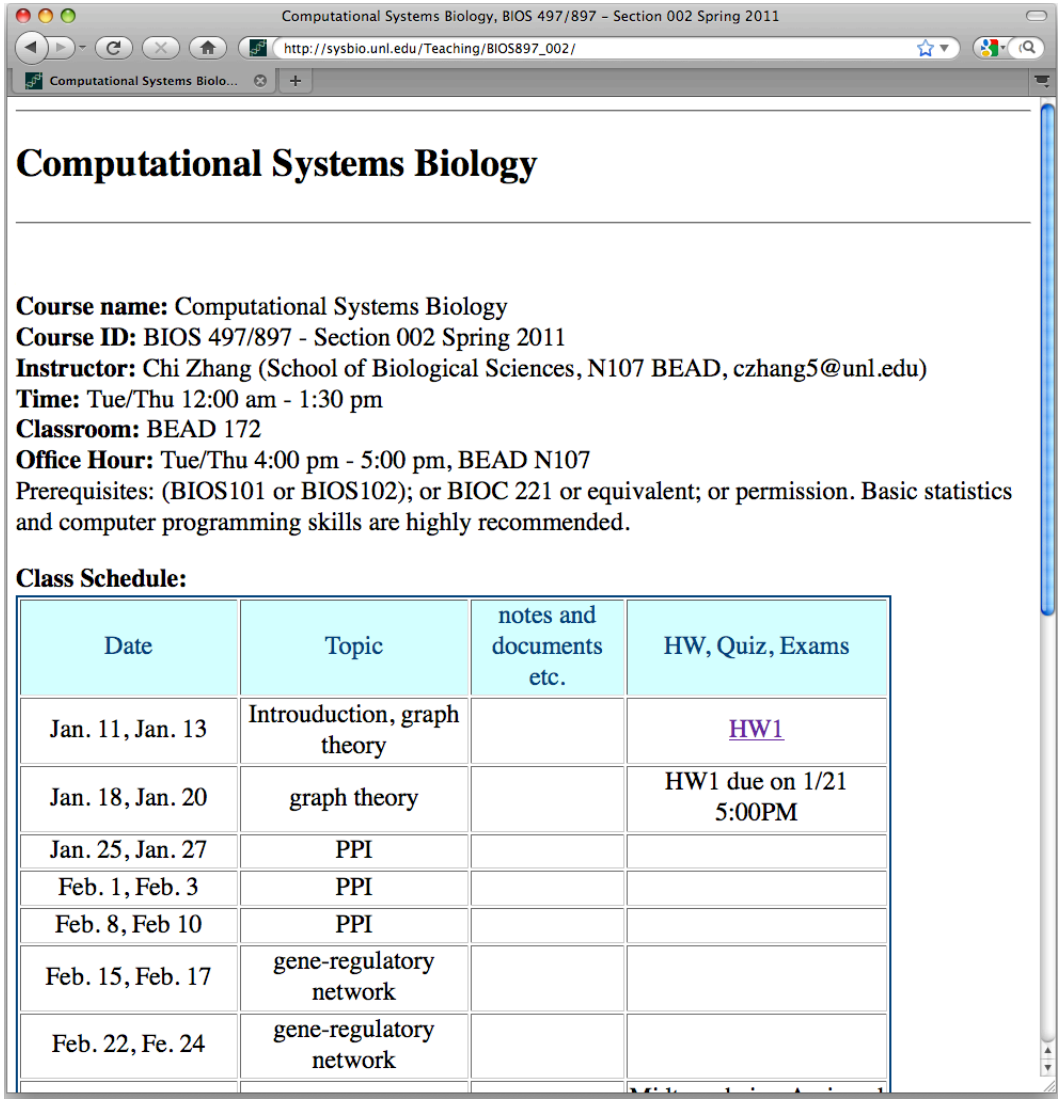
BIOS 497/897 - Section 001 Spring 2014

Chi Zhang

- **Time:** Tue/Thu 12:30 am – 1:45 pm
- **Classroom:** BEAD N176
- **Office Hours:** Tue/Thu 1:45 pm – 2:30 pm, BEAD N107 or email me for other time.
- My email is czhang5@unl.edu

Course website

- http://sysbio.unl.edu/Teaching/BIOS497897_2014/



Computational Systems Biology

Course name: Computational Systems Biology
Course ID: BIOS 497/897 - Section 002 Spring 2011
Instructor: Chi Zhang (School of Biological Sciences, N107 BEAD, czhang5@unl.edu)
Time: Tue/Thu 12:00 am - 1:30 pm
Classroom: BEAD 172
Office Hour: Tue/Thu 4:00 pm - 5:00 pm, BEAD N107
Prerequisites: (BIOS101 or BIOS102); or BIOC 221 or equivalent; or permission. Basic statistics and computer programming skills are highly recommended.

Class Schedule:

Date	Topic	notes and documents etc.	HW, Quiz, Exams
Jan. 11, Jan. 13	Introuduction, graph theory		HW1
Jan. 18, Jan. 20	graph theory		HW1 due on 1/21 5:00PM
Jan. 25, Jan. 27	PPI		
Feb. 1, Feb. 3	PPI		
Feb. 8, Feb 10	PPI		
Feb. 15, Feb. 17	gene-regulatory network		
Feb. 22, Fe. 24	gene-regulatory network		

Teaching materials

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

Recommended text: Computational Systems Biology, Edited by Jason McDermott et al. ISSN 1064-3745, ISBN 978-1-58829-905-5

Course Objectives

- To introduce the field of Computational Systems Biology.
- To sharpen students' skills on independent learning.
- To help students conduct research in their field.

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 on 11:59PM, Jan 20, 2014)

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 March 15th.
- 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 (10-15 minutes).

What to do?

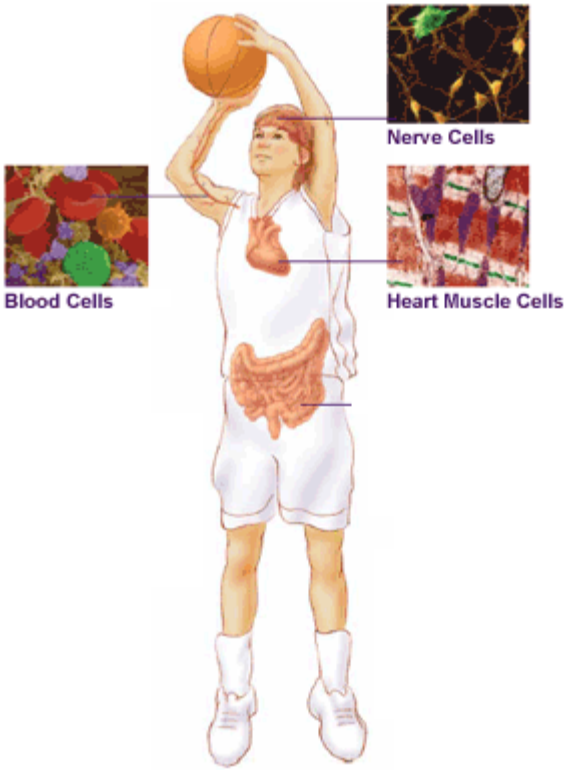
- To search for a paper.
- To decide when you want to give a talk.
- To check course website periodically to see if I upload any information for you.

Tentative Schedule

Week	Content	
1st	(1/14, 1/16)	Syllabus and Introduction
2nd	(1/21, 1/23)	Next-generation seq data analysis
3rd	(1/28, 1/30)	Next-generation seq data analysis
4th	(2/4, 2/6)	Transcriptome and epigenetics (RNA-seq)
5th	(2/11, 2/13)	microarray data analysis
6th	(2/18, 2/20)	microarray data analysis
7th	(2/25, 2/27)	Transcriptome
8th	(3/4, 3/6)	Transcriptome
9th	(3/11, 3/13)	Go database and gene function annotation
10th	(3/18, 3/20)	Midterm Exam
11th	(3/25, 3/27)	Spring break (no class)
12th	(4/1, 4/3)	Graph theory
13th	(4/8, 4/10)	PPI network
14th	(4/15, 4/17)	PPI network and Gene network
15th	(4/22, 4/24)	Network dynamics and Data Integration
16th	(4/29, 5/1)	Final Exam presentation

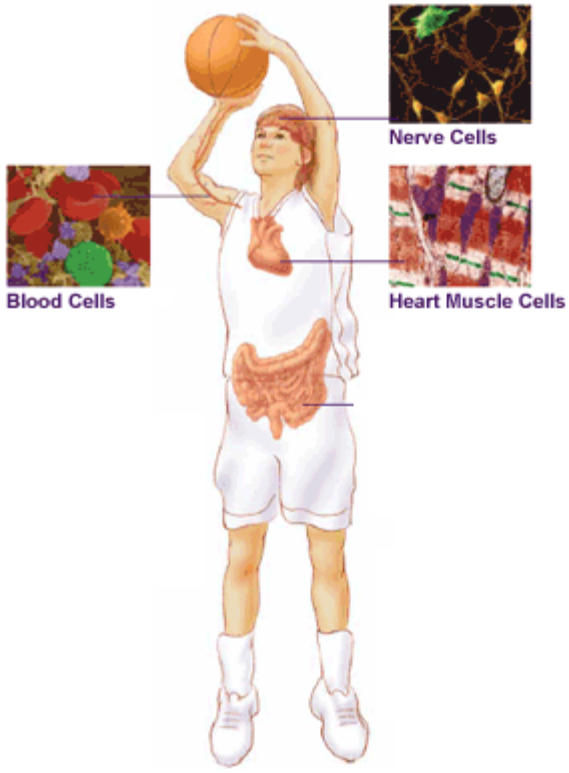
Why are cells different?

- 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.

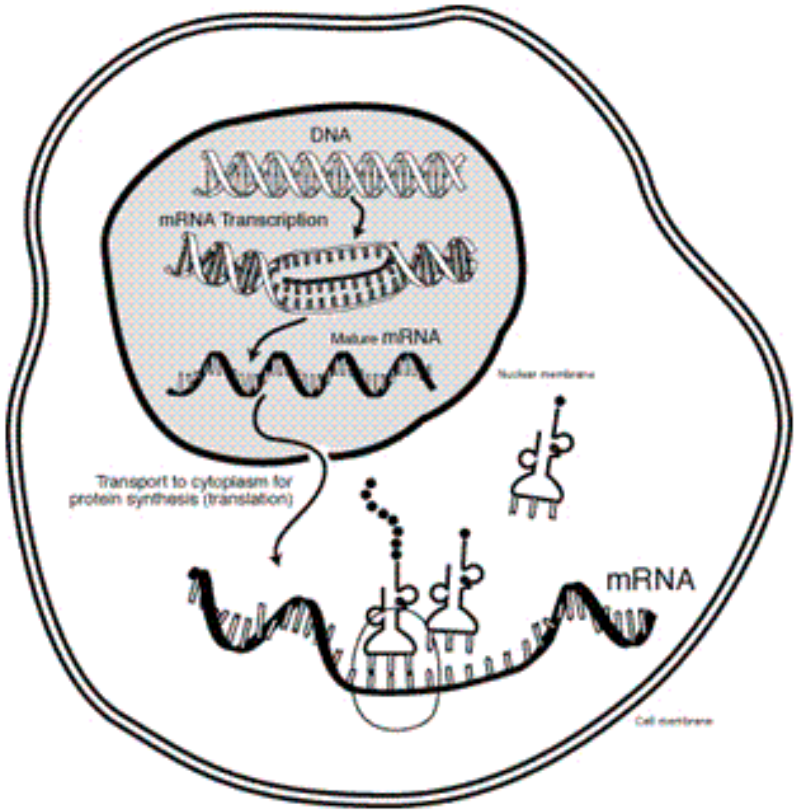


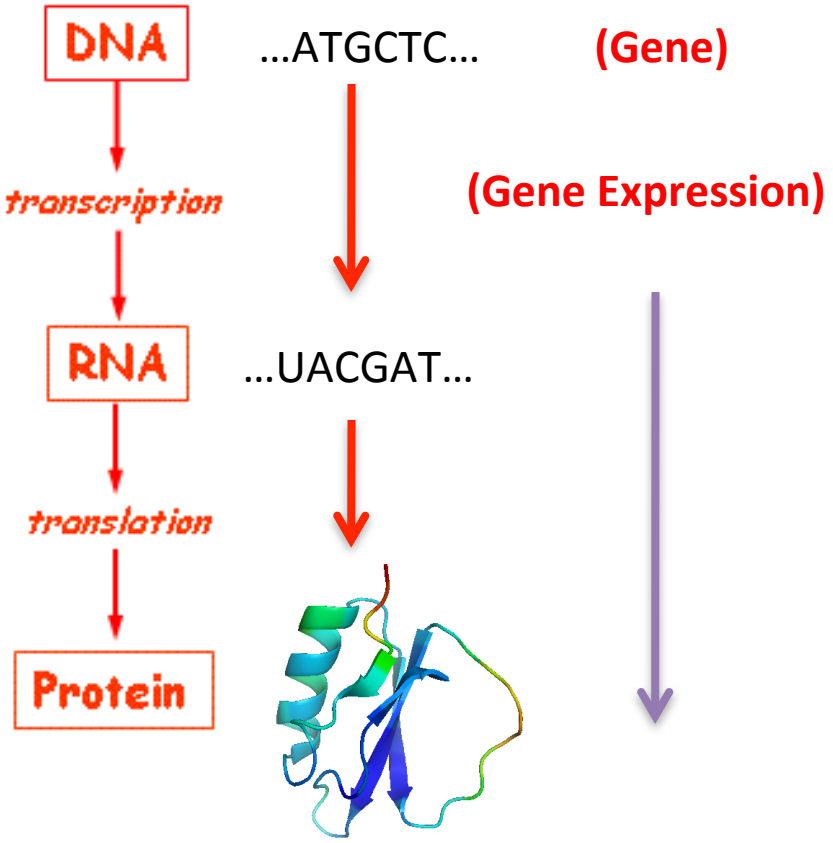
Why are cells different?

- 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.



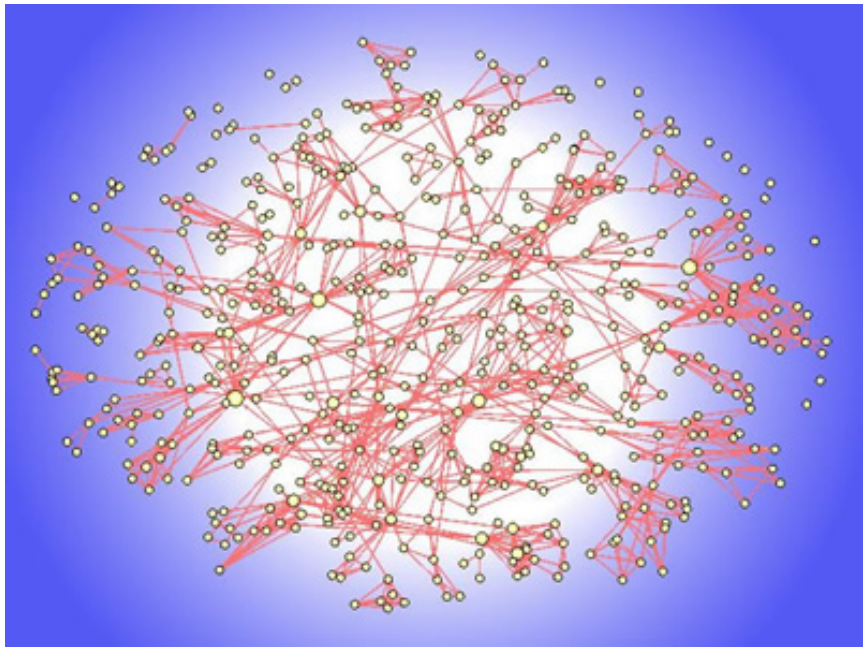
Flow of Genetic Information





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.

Transcriptome

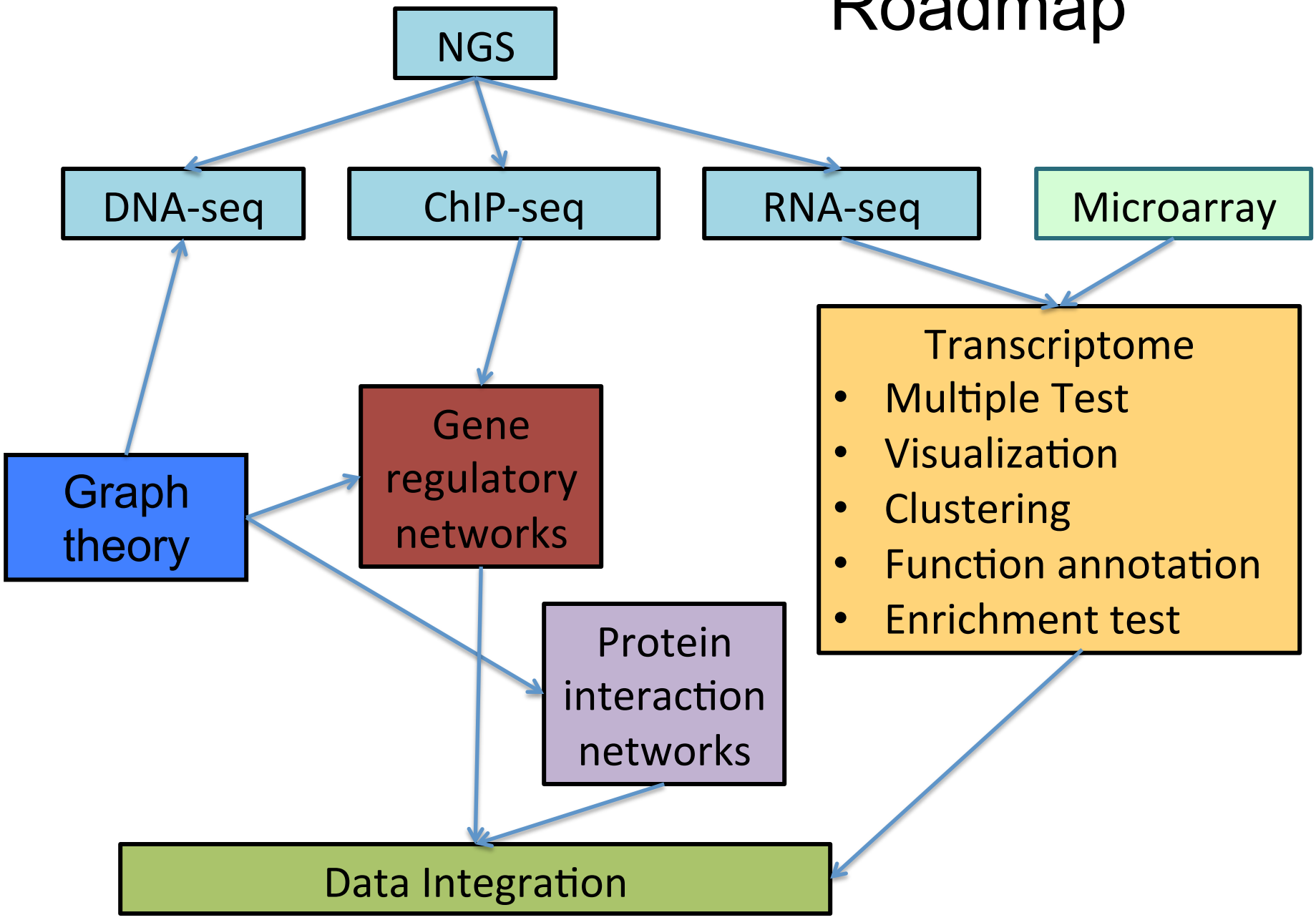
- Transcriptome: How to genome-wide measure the expression of those genes? How to get the gene expression profiles.
- **gene expression profiling** is the measurement of the expression of thousands of genes at once, to create a global picture of cellular function.
- These profiles can distinguish between cells that actively dividing, or show how the cells react to a particular treatment.

How to measure gene expression?

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

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

Roadmap


NGS
DNA-seq
ChIP-seq
RNA-seq
Microarray
Transcriptome
• Multiple Test
• Visualization
• Clustering
• Function annotation
• Enrichment test
Graph theory
Gene regulatory networks
Protein interaction networks
Data Integration