Network Biology and Biomedicine (BNFO286/MED283)

1. Overview:

Most biological systems are structured as networks – from molecular signaling and metabolic networks to immune cell and neural networks to vast networks of social and environmental interactions. Elucidating these networks is key not only to our biological understanding, but also to the next generation of patient data analysis, diagnosis and therapy. For these reasons, much recent technology development has focused on mapping biological networks at multiple scales, resulting in an expansive collection of network data and ways in which networks are becoming instrumental in biological and clinical studies.

This course teaches an understanding of the types, roles, and uses of networks in the biomedical sciences. It covers theory and practice of network analysis through classroom discussions, reading assignments, and project-oriented problem sets using tools such as Python and Cytoscape.

Students who have successfully completed the course will understand how to generate molecular network information for cells and tissues, how these networks are used in human genetic analysis and for mapping disease pathways, and applications of molecular networks as biomarkers in the clinic. Students will also gain an appreciation for how network knowledge is increasingly combined in concert with techniques from machine learning.

The course will meet twice per week for 1.5 hours each and will involve advance preparation for class in critical reading and exercises. Course grading will follow the ability of the student in class discussions, problem sets, practical statistical analysis laboratory projects, and written examinations. The course is appropriate for beginning graduate students or advanced undergraduates in the biomedical and computational analysis fields; it may also be of interest to medical students as an elective.

2. General information
- **Course name:** Network Biology and Biomedicine
- **Subject & Number:** MED 283 / BNFO 286
- **Course catalog description:** Networks are pervasive in molecular biology and medicine. This course introduces biomolecular networks and their major analysis techniques and roles in biomedical research, including pathway-based genetic analysis. Recommended familiarity with bioinformatics programming; course examples are taught in Python.
- **Prerequisites:** Graduate Level Statistics (MED268, MATH 283, MATH 281A, MATH 281B, MATH 281C, FMPH 221, FMPH 222, or equivalent). Prior exposure to basic genetics is strongly recommended. These prerequisites may be waived with consent of instructor.
- **Credits:** 4.0 units
- **Course director:**
  - Prof. Trey Ideker, Dept of Medicine (MC-0688 / 858-822-4558 / tideker@ucsd.edu)
- **Teaching assistant:**
  - Gibraan Rahman (grahman@eng.ucsd.edu)
- **Course administrator:**
  - Charlotte Marquez (MC-0688 / (858) 534-7726 / idekeradmin@ucsd.edu)
- **Participating instructors:**
  - Drs. Chris Benner, Dan Carlin, Mark Kelly, Abe Palmer, Rudolf Pillich, Dexter Pratt
- **Teaching methods:**
  - One-on-one observation and teaching
  - Demonstrations
  - Self-directed learning by student
  - Symposiums

o   Multimedia and computer support
o   Independent reading

3. Schedule of required student activities:

The course will meet twice per week for 1.5 hours each and will involve advance preparation for class in critical reading and exercises.

- Days: Tue / Thu
- Time: 1:30pm – 3:00pm
- **Location: LFFB 107**

An optional hour-long tutorial, led by the TA, will also be scheduled during the first week of class.

Optional office hours will be held by Prof. Trey Ideker every Wed at 1:30pm – 3:00pm. Location: BRF2 3A13

4. Course materials/resources:

- **Textbooks:**
  o   <u>Required</u>: "Networks: An Introduction" by Mark Newman
      Available online at https://search-library.ucsd.edu/permalink/01UCS_SDI/ld412s/alma991004237319704876
  o   <u>Optional</u>: "Introduction to Genomics" by Arthur Lesk
      Reserves, Front Desk, Geisel Floor2 QH447 .L47 2017
- **Biomedical journals:** A compendium of peer-reviewed journal articles drawn from the network biomedicine literature will be assigned for reading and discussion in class.
- **Software:** Python, Cytoscape Network Analysis Environment: http://www.cytoscape.org/
- **Websites:** TritonEd

5. Course learning objectives:

This course teaches an understanding of the types, roles, and uses of networks in the biomedical sciences. It covers theory and practice of network analysis through classroom discussions, reading assignments, and project-oriented problem sets using tools such as Python and Cytoscape. Students who have successfully completed the course will understand how to generate molecular network information for cells and tissues, how these networks are used in human genetic analysis and for mapping disease pathways, and the emerging applications of molecular networks as biomarkers in the clinic. Students will also gain an appreciation for how network knowledge is increasingly combined in concert with techniques from machine learning.

6. Grading/Assessment and evaluation of student performance:

Course grading will follow the ability of the student in class discussions, short problem sets, practical statistical analysis laboratory projects, and written examinations. Although assignments will be letter-graded, students will also have the option of taking the course pass/fail.

- **Graded problem sets and projects (40%)**: Approximately six problem sets will be assigned, incorporating a selection of short-answer theory questions and longer practical "hand-on" exercises involving statistical analysis of large biomedical datasets. Students may elect to drop one problem set from the final grade. Late policy: After the due date for problem sets, students may still receive up to 80% credit by handing in the assignment before solutions are posted (approximately one week later).
- **Midterm written examination (25%)**
- **Class final project (25%)**
- **Class participation (5%)**: While each class will involve a lecture, the first 15 minutes will be devoted to student-led discussions. At the beginning of each class, a group of students should summarize the reading assignment (2-3 slides max) and discuss what they see as a major opportunity and what the see as a major challenge.
- **Class attendance (5%)**