

Translational Bioinformatics

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It is the responsibility of those of us involved in today's biomedical research enterprise to translate the remarkable scientific innovations we are witnessing into health gains for the nation... At no other time has the need for a robust, bidirectional information flow between basic and translational scientists been so necessary.

- Elias A. Zerhouni, M.D.,
- Former Director, National Institutes of Health
New England Journal of Medicine, 353:1621, 2005

Translational Bioinformatics is the development of analytic, storage, and interpretive methods to optimize the transformation of increasingly voluminous genetic, genomic, and biological data into diagnostics and therapeutics for medicine.

Topics covered in this course:

- Access and utility of publicly available data sources.
- Types of genome-scale measurements in molecular biology and genomic medicine.
- Analysis of microarray data.
- Analysis of polymorphisms, proteomics, and protein interactions.
- Linking genome-scale data to clinical data and phenotypes.
- How phenotypes and diseases may relate.
- New questions in biomedicine using bioinformatics, including case studies.

This course is designed for:

- Graduate students in biomedical informatics, genetics, computer science, or other related disciplines
- Medical students
- Medical, pediatric, surgical or other fellows with an interest in learning and using bioinformatics in research
- Interested undergraduates
- Auditors welcome including medical staff, medical/pediatric/surgical fellows, post-doctoral fellows, and undergraduates.

Teaching Assistants & Office Hours

Tiffany Chen: Ph.D. candidate in Biomedical Informatics, working in the lab of Serafim Batzoglou. Recent research involves cell-cycle inhibitors, phospho-flow (fluorescent-activated cell sorting), machine learning, miRNA target prediction, and systems biology. **Office hours: Friday, 2:00-3:00 PM in Clark S260 (time and location may change depending on attendance)**

Erik Corona: Ph.D. candidate in Biomedical Informatics, working in the lab of Atul Butte. Research involves positive selection, genetic variation, and finding attributes of disease associated SNPs. **Office hours: Thursday, 2:00-3:00 PM in MSOB 2nd floor. First carrel to the right of X-215, right in front of Joel Dudley's office (time and location may change depending on attendance)**

Atul Butte: Office hours: Monday 12:00 – 1:00 pm in MSOB 2nd floor, room X-265, with some exceptions.

Wiki (web-site)

- Course information on wiki: bmi217.stanford.edu. Check the wiki daily for updates.
- We have a **newsgroup-style Q&A on the wiki**, where students can answer each other, and TAs step in if necessary. Most questions should be posted to the wiki.
- Other queries should be directed at biomedin217-win0809-staff@lists.stanford.edu.

Work involved

- Two-three readings per class as preparation. All available on the course wiki.
- 4 problem sets (10% each): hands-on analysis of data, which start with reproducing the findings in one or two publications given their raw data, then adding a twist.
 - One week to do each problem set. Problem sets due 5 pm Pacific time on Mondays.
 - Problem sets must be handed in to TAs online. Instructions will be in the problem sets.
 - Four free late days available this quarter, so use them wisely for your four problem sets. After that, 20% off grade per day late. Not using all your late days may influence your final grade if borderline.
 - Please do not start problem sets on the night before they are due.
- 1 midterm exam and 1 final exam (15% each): specifically testing you on the readings.
 - Open-book, open-notes, but timed.
 - Questions will query your knowledge of the readings, and in class presentations. Questions may give case examples of experiments, and you may be asked to match a problem with a reading.
- 1 final project (30%): similar in spirit and scope to the problem sets.
 - Final project title, aims and abstract are due on February 25, 2008.
 - Final presentations to the class on March 19 from 12:15 to 3:15 pm.
 - Final write-up absolutely due March 20.
 - **Individual** final projects: work on these by yourself.

Books

- No required text book.
- Four **recommended** text books
 - *Genomic and Personalized Medicine, Vol 1-2*. Ed. Huntington Willard and Geoffrey Ginsburg. 2008. These two books cover a comprehensive look at “advances in the diagnosis, prevention and treatment of human disease.”
 - Peter Dalgaard. *Introductory Statistics with R*. 2002. This short book serves as a handbook and tutorial for learning the free statistical system R, used in this course. This book is not specific for biological data analysis.
 - Robert Gentleman, Vince Carey, Wolfgang Huber, Rafael Irizarry, Sandrine Dudoit. *Bioinformatics and Computational Biology Solutions Using R and Bioconductor*. 2005. This large book serves as a comprehensive book on using the Bioconductor libraries in R for biomedical data analysis.
 - Terry Brown. *Genomes 3*. 2006. A great non-overwhelming reference on molecular biology, with specific focus on novel genome-era measurement tools, such as microarrays. The second edition of this text is available free on the NCBI Bookshelf. HIGHLY RECOMMEND for those with not enough biology background.

Signup

- If you are auditing, sign up with teaching assistants.
- Auditing means attending the lectures, not doing the problem sets, not doing the mid-term, not doing the final project.
- Signing up for BMI218 = attending the lectures or viewing online, doing the reading, and getting credit. It means not doing the mid-term or problem sets. But it does mean writing up a title, aims, and abstract for the final project, and presenting it to the class. The BMI218 designation is meant only for medical students.
- You must have a SUnet id and password to access the wiki. See the teaching assistants immediately if you don't have one.

Other

- All lectures will be videotaped and available through Stanford Center for Professional Development (SCPD)
- No class January 19, February 16.