BIOL 351 – Biomedical Informatics – Spring 2014

Instructor: Dr. Eric S. Ho (hoe@lafayette.edu)
Office: Kunkel 13
Office hours: MWF 1-2:30 pm

Course Description:
This course focuses on using genomic information, statistics and computational methods to study the relation between genomic variations and diseases. With the advance of DNA sequencing technologies, the whole genome sequencing at ever-decreasing cost accelerates the mapping of complex diseases on the genome landscape in high precision. Students will learn major biomedical informatics approaches in translating the fount of genomic information into promising actionable treatment options through lectures, journal discussions, and project presentations.

Biomedical informatics encompasses an array of subjects ranging from genetics, genomics, statistics to bioinformatics. Lectures will cover basic principles and methods. Students will learn how researchers apply these principles and methods in studying genomic variations through in-depth review of primary research articles and oral presentations.

Major topics include human genome, genomic variations, genome-wide association study (GWAS), cancer genome, microarray technology, next generation sequencing, pharmacogenomics, and personalized medicine.

Learning Outcomes:
At the completion of this course, students should be able to:
- Recognize the benefits and challenges of biomedical informatics in studying genomic variations
- Explain the molecular basis of genetic variations
- Describe the theoretical basis of major methods in genotype-to-phenotype studies
- Know the source and organization of genomic variations data from international data consortiums
- Interpret methods and results from primary biomedical informatics literatures
- Analyze gene expression data using statistical and computational tools
- Propose plan to harness genomic data and computational methods in studying the genomic basis of complex diseases

Prerequisites:
BIOL 274 or BIOL 255 or permission of instructor

Grading Policy:

- Class participation 10%
- One mid-term exam 20%
- One 45-minute oral presentation 30%
- Participation in your classmate's oral presentation 20%
- One 2-page summary of the presentation 20%

Course Materials:

Books on Skillman library reserve :
THE HUMAN GENOME, Third Edition: A User's Guide, Julia E. Richards, R. Scott Hawley, Third edition, 2010. ISBN 0123334454. QH431 .H353 2011

A Primer of Genome Science, Greg Gibson and Spencer V. Muse, Third edition, 2009. ISBN 0878932364. QH447 .G534 2009

Federal Credit Hour Policy:
The student work in this course is in full compliance with the federal definition of a four [two or one as appropriate for half and quarter unit courses] credit hour course. Please see the Registrar's Office web site (http://registrar.lafayette.edu/additional-resources/cep-course-proposal/) for the full policy and practice statement.

Academic Honesty:
You are expected to abide by the college policy on Intellectual Honesty (see Student Handbook p.7).

Useful Links:

1. Lecture notes, additional reading materials, and announcements are disseminated through Moodle http://moodle.lafayette.edu
2. PLOS Computational Biology: Translational Bioinformatics collection 2012. Open access: http://www.ploscollections.org/downloads/TranslationalBioinformatics.pdf
3. Genetics Home Reference: Your guide to understanding genetics conditions. http://ghr.nlm.nih.gov/handbook.pdf
4. NCBI outreach and education: http://www.ncbi.nlm.nih.gov/About/outreach/courses.html
5. A science primer: http://www.ncbi.nlm.nih.gov/About/primer/index.html
6. The Human Genome Project: http://www.genome.gov/10001772
7. GenomeTV: http://www.youtube.com/user/GenomeTV
8. TEDMED http://www.tedmed.com
9. Biomedical literatures database (PubMed): http://www.ncbi.nlm.nih.gov/pubmed/

Tentative Schedule:

Date	Major Topics	Reading Assignments (read before class)
Jan 29	Introduction of the course	*Charting a course for genomic medicine from base pairs to bedside* (only the introduction on p.204, Box 1-5, Figures 1 and 2) Nature. 2011 Feb 10
Jan 31	Informatics of genetic diseases	
Feb 3	OMIM database	*Initial sequencing and analysis of the human genome.* Nature Feb 15th, 2001.
Feb 5	The human genome project	
Feb 7	Shotgun sequencing	
Feb 10	Hierarchical shotgun sequencing	*Predictive, personalized, preventive, participatory (P4) cancer medicine* Nature Mar 2011
Feb 12	Personalized medicine	
Feb 14	Human genome architecture	
Feb 17	The ENCODE project	*1. Some genes are transmitted to offsprings in groups.* *2. Mapping Genes to Chromosomes: Linkage and Genetic Screens. Adams, J. & Shaw, K. (2008) Nature Education 1(1):11*
Feb 19	Mendelian disease mapping	
Feb 21	Mendelian disease mapping	
Feb 24	Comparative Genomic Hybridization & CGH Array	*Microarray-based Comparative Genomic Hybridization* Nature Education 2008 1(1):45
Feb 26	Single nucleotide polymorphisms	
Feb 28	SNP array	
Mar 3	Mapping of complex diseases	*Mapping the cancer genome* Scientific American Sep 2008
Mar 5	Haplotypes	
Mar 7	Genome wide association study (GWAS)	
Mar 10	Logistic regression – from genotype to disease risk	Read the exam paper *Genetic mapping in human disease* Science, 2008 322:881-887.
Mar 12	Mid-term review	
Mar 14	Mid-term exam	
Mar 17-21	Spring Break	

	Student presentations
Mar 24	Genetic mapping in complex disease. Science. 2008 Nov 7;322(5903):881-8

Mar 26	**Elisabeth Burnor** - Discovery and saturation analysis of cancer genes across 21 tumor types. Nature 2014.
Mar 28	Q&A 1
Mar 31	**Noelle Kosarek** - Ling H, Fabbri M, Calin GA. MicroRNAs and other non-coding RNAs as targets for anticancer drug development. Nat Rev Drug Discov. 2013 Nov;12(11):847-65
Apr 2	Pharmacogenomics
Apr 4	Q&A 2
Apr 7	**Tiffany Phuong -** Fu Y1, Sun Y, Li Y, Li J, Rao X, Chen C, Xu A. Differential genome-wide profiling of tandem 3' UTRs among human breast cancer and normal cells by high-throughput sequencing. Genome Res. 2011 May;21(5):741-7.
Apr 9	Q&A 3
Apr 11	**Erica Gennaro -** Mapping and sequencing of structural variation from eight human genomes. Nature 453, 56-64 (1 May 2008)
Apr 14	Q&A 4
Apr 16	**Anna Peterson -** An integrated map of genetic variation from 1,092 human genomes. Nature Nov 2012
Apr 18	Q&A 5
Apr 21	**Alexandria Battison -** Kimmel SE, et al. A pharmacogenetic versus a clinical algorithm for warfarin dosing. N Engl J Med. 2013 Dec 12;369(24):2283-93.
Apr 23	Q&A 6
Apr 25	**Cassidy Madison -** Tay Y, Rinn J, Pandolfi PP. The multilayered complexity of ceRNA crosstalk and competition. Nature. 2014 Jan 16;505(7483):344-52.
Apr 28	Q&A 7
Apr 30	**Erik Tweten -** Korf BR1, Rehm HL. New approaches to molecular diagnosis. JAMA. 2013 Apr 10;309(14):1511-21. doi: 10.1001/jama.2013.3239
May 2	Q&A 8
May 5	**Maureen Carey -** Geisler S, Coller J. RNA in unexpected places: long non-coding RNA functions in diverse cellular contexts. Nat Rev Mol Cell Biol. 2013 Nov;14(11):699-712
May 7	Q&A 9
May 9	NGS for Cancer biology

Articles for Presentation:

Human genome

1. Geisler S, Coller J. RNA in unexpected places: long non-coding RNA functions in diverse cellular contexts. Nat Rev Mol Cell Biol. 2013 Nov;14(11):699-712. – **by Maureen Carey**
2. Tay Y, Rinn J, Pandolfi PP. The multilayered complexity of ceRNA crosstalk and competition. Nature. 2014 Jan 16;505(7483):344-52. – **by Cassidy Madison**

Genomic variations

3. Mapping and sequencing of structural variation from eight human genomes. Nature 453, 56-64 (1 May 2008) – **by Erica Gennaro**

4. An integrated map of genetic variation from 1,092 human genomes. Nature Nov 2012 – **by Anna Peterson**
5. Global variation in copy number in the human genome. Nature Nov 2007

Biology of Cancer

6. Discovery and saturation analysis of cancer genes across 21 tumor types. Nature 2014. – **by Elisabeth Burnor**
7. Ling H, Fabbri M, Calin GA. MicroRNAs and other non-coding RNAs as targets for anticancer drug development. Nat Rev Drug Discov. 2013 Nov;12(11):847-65. – **by Noel Kosarek**
8. Fu Y1, Sun Y, Li Y, Li J, Rao X, Chen C, Xu A. Differential genome-wide profiling of tandem 3' UTRs among human breast cancer and normal cells by high-throughput sequencing. Genome Res. 2011 May;21(5):741-7. – **by Tiffany Phuong**

Genome wide association studies

9. Pearson TA, Manolio TA. How to interpret a genome-wide association study. JAMA. 2008 Mar 19;299(11):1335-44.

Genetic profiling technologies

10. Carter SL, Cibulskis K, Helman E, McKenna A, Shen H, Zack T, Laird PW, Onofrio RC, Winckler W, Weir BA, Beroukhim R, Pellman D, Levine DA, Lander ES, Meyerson M, Getz G. Absolute quantification of somatic DNA alterations in human cancer. Nature Biotech. 2012 May;30(5):413-21. doi: 10.1038/nbt.2203.
11. Korf BR1, Rehm HL. New approaches to molecular diagnosis. JAMA. 2013 Apr 10;309(14):1511-21. doi: 10.1001/jama.2013.3239. – **by Erik Tweten**

Pharamcogenomics

12. Kimmel SE, et al. A pharmacogenetic versus a clinical algorithm for warfarin dosing. N Engl J Med. 2013 Dec 12;369(24):2283-93. doi: 10.1056/NEJMoa1310669. Epub 2013 Nov 19. – **by Alexandria Battison**
13. Karczewski KJ, Daneshjou R, Altman RB (2012) Chapter 7: Pharmacogenomics. PLoS Comput Biol 8(12): e1002817. doi:10.1371/journal.pcbi.1002817