BIOL 356 – Biomedical Informatics – Spring 2015

Instructor: Dr. Eric S. Ho (hoe@lafayette.edu)
Office: Kunkel 13
Class hours: MWF 11:00-11:50 am
Office hours: TR 2-4 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 cost of whole genome sequencing decreases dramatically in recent years which accelerates the mapping of complex diseases on the genome landscape with high precision. Students in this course 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:

- Reading assignments 10%
- One mid-term exam 20%
- One 45-minute oral presentation followed by a 45-minute Q&A session 30%
- Participation in your classmates' oral presentations 20%
- One 2-page summary of the presentation 20%

Course Materials:

There is no required textbook for this course. But the following three books provide excellent and comprehensive background information in genomics, human genetics, gene mapping, recombinant DNA, and DNA sequencing. Some lecture materials are based on selected topics from these books. I highly recommend you to reference these books if you encounter unfamiliar concepts or topics in reading assigned research articles.

eBook from the Library:

Human genes and genomes: science, health, society / Leon E. Rosenberg and Diane Drobnis Rosenberg. 1st edition. Amsterdam : Elsevier/Academic Press, 2012.

Books reserved in Skillman Library:

THE HUMAN GENOME: 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, reading materials, reading assignments 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
Week 1	Introduction	TED video
	OMIM database	
	OMIM database	OMIM NAR 2015
Week 2 Feb 2-6	Human genetic disorders	
	Human genetic disorders	The price of silent mutations
	The human genome project	
Week 3 Feb 9-13	Whole genome shotgun sequencing	
	Hierarchical seqeuencing	*Initial sequencing and analysis of the human genome.* Nature Feb 15th, 2001.
	Mendelian disease mapping	
Week 4 Feb 16-20	Informativeness of Genetic Markers	
	Positional Cloning	
	ENCODE project	*The Human Encyclopedia* Nature vol 489. 6 Sep 2012
Week 5 Feb 23-27	Single Nucleotide Polymorphism	
	Haplotypes	
	Genome wide association study (GWAS)	
Week 6 Mar 2-6	SNP Array	Assignment of midterm exam article
	SNP array & Genetic Association Tests	
	NGS for clinical diagnosis	
Week 7 Mar 9-13	NGS & GWAS	
	Mid-term review	
Mar 12	Mid-term exam	5-7pm
Mar 16-20	Spring Break	

	Student presentations	
Mar 23	Post mid-term exam review	
Mar 25	**Group 1: Priscilla & Lindsey Cherry** [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.	
Mar 27	Q&A 1	
Mar 30	**Group 2: Maria Cano Garcia & Alex Van Hoof** [15] Dorn GW et al. Mechanisms of Pharmacogenomic effects of genetic variation within the Cardiac adrenergic Network in heart failure. Mol Pharmacol. 2009 Sep;76(3):466-80.	
Apr 1	Q&A 2	
Apr 3	**Group 3: Tim Blackwell & Marc Teitelbaum** [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.	
Apr 6	Q&A 3	
Apr 8	**Group 4: Stephanie Benko & Alex Farina** [6] Discovery and saturation analysis of cancer genes across 21 tumor types. Nature 2014.	
Apr 10	Q&A 4	
Apr 13	**Group 5: Jason Hill** [14] 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.	
Apr 15	Q&A 5	
Apr 17	**Group 6: Ashley Allee & Ariel Yi** [11] Bartlett CW et al. A genome scan for loci shared by autism spectrum disorder and language impairment. Am J Psychiatry. 2014 Jan;171(1):72-81.	
Apr 20	Q&A 6	
Apr 22	**Group 7: Stephanie Schreiber & Tyler Ruch** [10] Jarick et al. Novel common copy number variation for early onset extreme obesity on chromosome 11q11 identified by a genome-wide analysis. Hum Mol Genet. 2011 Feb 15;20(4):840-52.	
Apr 24	Q&A 7	
Apr 27	**Group 8: Ashley Goreshnik & Jaimie Bandur** [3] Mapping and sequencing of structural variation from eight human genomes. Nature 453, 56-64 (1 May 2008)	
Apr 29	Q&A 8	
May 1	**Group 9: Evan Newbold & David Perlow** [9] The Wellcome Trust Case Control Consortium, "Genome-wide association study of CNV in 16,00 cases of eight common diseases and 3,000 shared controls". Nature. 2010 Apr 1;464(7289):713-20.	
May 4	Q&A 9	
May 6	NGS for Cancer biology	*Predictive, personalized, preventive, participatory (P4) cancer medicine*

	Nature Mar 2011
May 8	Personalized Medicine

Articles for Presentation (subject to change):

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.
2. Tay Y, Rinn J, Pandolfi PP. The multilayered complexity of ceRNA crosstalk and competition. Nature. 2014 Jan 16;505(7483):344-52.

Genomic variations

3. Mapping and sequencing of structural variation from eight human genomes. Nature 453, 56-64 (1 May 2008)
4. An integrated map of genetic variation from 1,092 human genomes. Nature Nov 2012
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.
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.
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.

Genome wide association studies

9. The Wellcome Trust Case Control Consortium, "Genome-wide association study of CNV in 16,00 cases of eight common diseases and 3,000 shared controls". Nature. 2010 Apr 1;464(7289):713-20.
10. Jarick et al. Novel common copy number variation for early onset extreme obesity on chromosome 11q11 identified by a genome-wide analysis. Hum Mol Genet. 2011 Feb 15;20(4):840-52.
11. Bartlett CW et al. A genome scan for loci shared by autism spectrum disorder and language impairment. Am J Psychiatry. 2014 Jan;171(1):72-81.

Genetic profiling technologies

12. 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.
13. Wang Y et al. Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature. 2014 Aug 14;512(7513):155-60.

Pharamcogenomics

14. 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.

15. Dorn GW et al. Mechanisms of Pharmacogenomic effects of genetic variation within the Cardiac adrenergic Network in heart failure. Mol Pharmacol. 2009 Sep;76(3):466-80.