Content

Powerpoint lectures, Required Readings and Resources

Section 1 — Introduction

An introduction the course and my objectives (hopefully not to ambitious!) for everyone. Because this is my first time through the course, undoubtedly things are going to change. In lieu, I'll provide as much guidance as I can: studying to exams and completing assignments. My Powerpoint slides are in Office 2007/2008 format (.pptx). Microsoft provides a converter tools for older version of MS Office. I've provided the link below.

- MS Office tools for converting files (for windows)
- MS Powerpoint 2007 viewer (for windows)
- powerpoint file for this section (in pptx format)
- powerpoint file for this section (in ppt format)

Section 2 — Genome Projects

This sections provides a history of the human genome project and how the whole sequencing of an organism's genome can provide new insights into its biology. In this section and those to follow, I will be providing various media links. You are responsible for knowing the main points of

- powerpoint file for this section (in ppt format)
- interview with the Nobel Laureate, Paul Berg
- Exploring Genome Space minireview
- a manuscript describing the sequencing of a Korean individual
- the first of two manuscripts describing the sequencing of a parasite
- the second of two manuscripts describing the sequencing of a parasite

Section 3 — Single Nucleotide Polymorphisms

There are millions of SNPs throughout the human genome. Alone, or clusters called haplogroups, they are extremely powerful diagnostic tools. This is a big section covering my own lecture material, three presentations by leaders in the field and a self-study project.

- powerpoint file for this section (in ppt format)
- a manuscript on chromosome 21 haplotypes
- a manuscript on using SNPs to predict drug efficacy
- a presentation by Eric Lander (24 MB, iPod friendly)
- a presentation by Gil McVean (51 MB)
- a presentation by Karen Edwards (282 MB, iPod friendly)
- a manuscript describing Y chromosomal mutation rates
- a manuscript on using SNPs to predict HCV therapy outcomes
- a short comparison of 23andme.com and Navigenics genotyping

Section 4 — Bacterial Genomics

Primarily due to their relevance in human health, bacterial genomics have taken the forefront. With the current technology, a bacterial

http://farq047c.biol.yorku.ca/biol4020/?page_id=137
genome can be fully sequenced in only one day thereby setting the stage for tracking pathogenicity over time. This section will concentrate on one innocuous bacterium, *Staphylococcus aureus*, which has become a large problem in hospitals due to its acquisition of multiple modes of antibiotic resistance.

- the powerpoint file for this section (in .ppt format)
- a manuscript on two *S. aureus* sequences
- a Canadian report on *S. aureus* infections in Canada
- a manuscript on the evolution of resistance of *S. aureus* in a patient
- a manuscript on a resistance to linezolid, a last resort antibiotic
- a presentation on methicillin *S. aureus* by Christina Burch (a good place to start)

Section 5 — Sequencing Methods

A brief discussion some of the new technologies being used to rapidly sequence genomes. At the end of this section, you should be able to identify the main features of each method, their similarities and their differences.

- the powerpoint file for this section (in .ppt format) *new Oct 7*
- single molecule sequencing overview from Pacific Biosciences
- manuscript on next generation methods (great review)
- manuscript describing 454 sequencing (original paper)
- manuscript describing 454 sequencing (in review format)
- YouTube link for the Helicos single molecule sequencer (video)
- technology report on the Illumina sequencing method
- manuscript on the issues of sequencing bacteria and short reads
- manuscript on single molecule sequencing of a human genome
- two page review on faster sequencing methods
- short discussion of combinatorics
- manuscript describing human exon-based sequencing
- a two page review on sequencing tumors

Section 6 — Sequence Analysis

Bioinformatics really came to the forefront of research with the advent of large genomics datasets. In this section, I will present the basics of a BLAST search which will aid you in Project 2 and Project 3.

- the powerpoint file for this section (in .ppt format)
- NCBI BLAST web site

Section 7 — Gene Expression

This short one- to two-class section covers aspects of gene expression and codon bias.

- the powerpoint file for this section
- Manuscript on the effect of nonsynonymous mutations on bacterial gene expression

Section 8 — Exome Sequencing

This section is short, too. As it stands right now, I'll be chalk-talk lecturing this one, beginning with a discussion of the first exome analysis done on Craig Venter and then proceeding to later strategies and technologies.

- "Genetic Variation in an Individual Human Exome” manuscript
- blog post from Genetic-Future
- Genetic diagnosis by whole exome sequencing
- Massively parallel sequencing of 12 human exomes

http://farq047c.biol.yorku.ca/biol4020/?page_id=137
Section 9 -- Non-coding RNAs in the genome

A significant proportion of the genome is comprised of transcripts that do not encode protein. These transcripts have been implicated in a number of major processes. I will cover a few recent developments in this area plus a discussion of human endogenous retroviral elements.

- PowerPoint slides on long intergenic non-coding RNA
- A manuscript describing the identification of lincRNAs
- A short review on the ChiP-Seq methodology

Section 10 -- Yet another DNA sequencing technology

In this class, I covered sequencing technology that was just published recently. The authors claim a 10x reduction in cost.

- PowerPoint slides
- Complete Genomics website
- Manuscript describing the sequencing