Draft Syllabus

MCB3895-004: Practical methods in microbial genomics

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Modern biology has been revolutionized by the advent of inexpensive genomic sequencing. However, biology students generally lack familiarity with the computational techniques required to analyze these data. This course will address this need by introducing students to basic concepts in genomics, and guiding them through a series of practical exercises where the students themselves analyze publically-available genomic data. These exercises will focus on converting raw sequencing data to an assembled and annotated product that can be used for further functional and evolutionary analyses. Basic computational biology skills such as using UNIX-based operating systems and basic scripting will also be covered, targeting biologists with minimal experience with computational biology. Students will leave this course with a series of scripts and protocols that they can apply in their future independent research.

Draft outline:

Week 1: Introduction to UNIX and the terminal; the NCBI database
Week 2: Genomes on NCBI; Perl strings and basic operations
Week 3: Manipulating sequences #1; Perl loops and arrays
Week 4: Manipulating sequences #2; Perl hashes
Week 5: Principles of genome sequencing; preparing genomic data for assembly
Week 6: De novo genome assembly; assembly quality
Week 7: Midterm exam
Week 8: Genome assembly competition
Week 9: Genome alignment
Week 10: Genome annotation #1; a brief introduction to BLAST
Week 11: Genome annotation #2
Week 12: Reference mapping; SNP finding
Week 13: RNAseq and differential expression
Week 14: Metabolic pathway maps