CS 681 Advanced Topics in Computational Biology

Spring 2013
Instructor: Can Alkan

- Week 1: A brief introduction to genomes and concepts in genomics. Genome structure. Genomic variation.
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- Week 2: Introduction to high throughput sequencing (HTS). Different sequencing platforms, pyrosequencing, sequencing by synthesis, sequencing by ligation, single molecule sequencing. Upcoming platforms based on nanotechnology. Advantages and disadvantages. Computational challanges in analyzing HTS data.
- Week 3: Read mapping. Burrows-Wheeler Transform and Ferragina-Manzini index. Hash based and BWT-FM based aligners. Project proposals due.
- Week 4: SNP and small indel discovery using HTS. Haplotype resolution using pooled clone sequencing.
- Week 5: Structural variation, copy number variation, copy number polymorphism and segmental duplications.
- Week 6: Sequence assembly algorithms. De Bruijn graphs for genome assembly. String graphs. Techniques and shortcomings of assembly.
- Week 7: Transcriptome analysis. Transcriptome assembly, alternative splicing and fusion gene discovery.
- Week 8: Epigenetics. Methylation, histone modification. Finding “active” genes using DNAseI hypersensitivity assays.
- Week 9: Non-coding RNA identification and search, RNA-RNA interaction prediction and search.
- Week 10: Paper presentations.
- Week 11: Paper presentations.
- Week 12: Paper presentations.
- Week 13: Project presentations.