CS 466 Introduction to Bioinformatics Lecture 21

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Course Announcements

HW4 due Dec 3rd by 11:59pm

Calendar:

- Nov 26 (Monday) Genome assembly I
- Nov 28 (Wednesday) Genome assembly II
- Dec 3 (Monday) Genome assembly III
 - HW5 on Phylogeny/Genome Assembly
- Dec 5 (Wednesday) No class
- Dec 10 (Monday) HW5 due + Review session
- Dec 12 (Wednesday) Project presentations
- Dec 14 (Friday) Final exam
- Dec 16 (Sunday) Project report

Single Cell Sequencing

<u>https://www.youtube.com/watch?v=Dpq9gAg-5uA</u>

DNA Sequencing Technologies



Next-Gen Sequencing!

illumina











Next-Gen Sequencing



Two Different Protocols



DNA Fragment

A Few Examples

	HiSeq 2500	NextSeq 500	MiSeq	HiSeq X Five	MiniSeq
Read Length	2 x 250 bp	2 x 150bp	2 x 250bp	2 x150bp	2 x 150bp
# Reads: 1 Flow Cell	~ 300 Million	~ 400 Million	24-30 Million	3 Billion	44-50 Million
Run Time:	60 hrs	~29 hrs	~39 hrs	< 3 days	~24 hrs
Output:	125 – 150 Gb	100 – 120 Gb	7.5-8.5 Gb	800-900 Gb	6.6 – 7.5 Gb



~ 1% error rate

** Numbers updated from: http://www.illumina.com/content/illuminamarketing/amr/en_US/systems.html on 2/4/2016 **

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Single Molecule Real Time (SMRT)



<u>Video</u>



~ 15% error rate

http://www.nature.com/nbt/journal/v28/n5/fig_tab/nbt0510-426_F1.html

Longest Read Lengths

Read lengths > 20 kb Data per SMRT Cell: 500 Mb - 1 Gb



Nanopore Technologies





Min**ION**

Portable, real-time biological analyses

Single Cell Sequencing

NATURE | TOOLBOX

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Single-cell sequencing made simple

Data from thousands of single cells can be tricky to analyse, but software advances are making it easier.

Jeffrey M. Perkel



Single Cell Sequencing

<u>https://www.youtube.com/watch?v=Dpq9gAg-5uA</u>

DNA Sequencing Technologies



Challenges in DNA Sequencing



Read: 30-1000 letters

Algorithms for DNA sequencing

1. De novo assembly algorithms



Issues with Reference-based Assembly

https://arstechnica.com/science/2018/11/our-humanreference-genome-is-missing-a-lot-of-material/

De novo Assembly



Let's try this out!