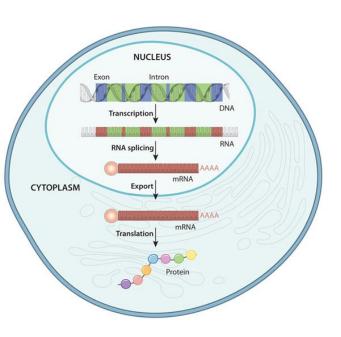
Computing Basics for Bioinformatics

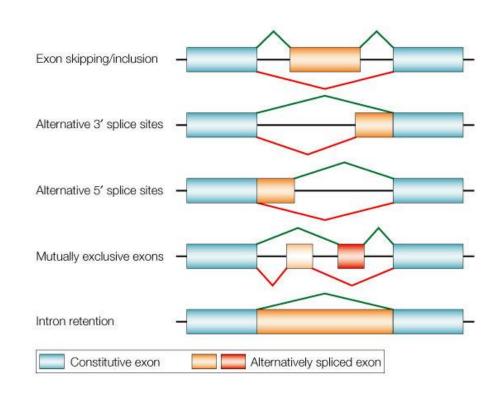
Session 1 Yaoyu Wang





Central Dogma of Molecular Biology









What initial questions do we want to answer using genomic data?

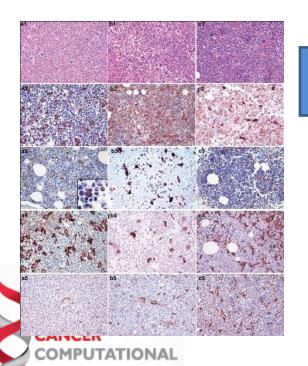
- Which genes are expressed?
- Which genes are differentially expressed among the groups?
- Do my favorite genes/pathways become up/downregulated?
- Can we detect RNA isoforms? Novel ones?
- What are the genomic regions with copy number variations?
- Can we detect structural variants? SNPs, insertions, deletions, RNA-editing?
- What are the TF binding sites?





Genomics Research



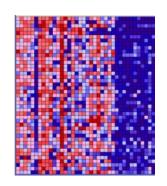


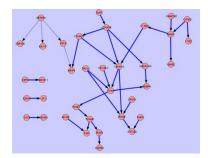


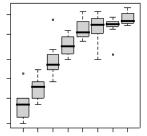






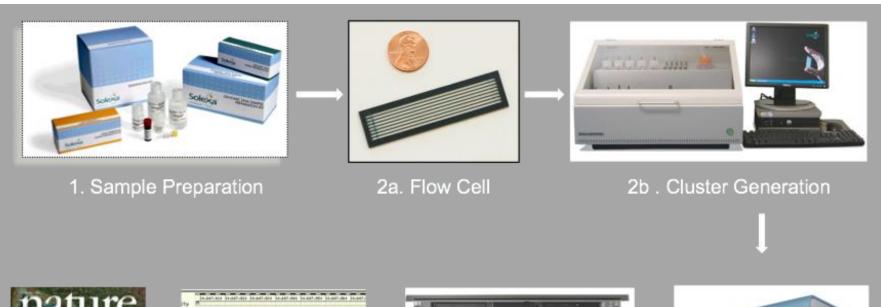








Next-Generation Sequencing Workflow





6. Publication

5 . Data Analysis

4 . Initial Image Analyses

3 . Sequencing & Imaging





Applications of Next-Generation Sequencing

Whole-genome sequencing

- Genome re-sequencing
- de novo genome sequencing
- Metagenomics applications

Targeted re-sequencing

- PCR-amplified regions
- Capture-enriched DNA

Transcriptome mining

- novel RNA classes
- novel splice variants



Sequencing DNA library

100 - 500 bp

Sequencing of



cDNA libraies

Epigenetic profiling

- Methylation sequencing
- Nucleosome footprinting

Genomic footprinting

- ChIP sequencing
- DNase I libraries

RNA footprinting

- ribosome footprinting
- RNA-IP sequencing

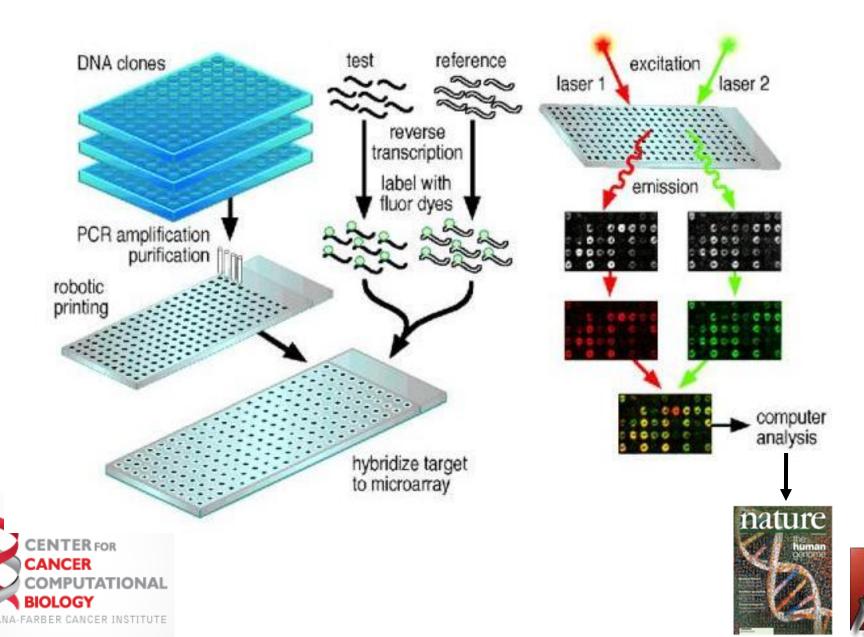
Transcriptome expression profiling

- mRNA
- small RNA (miRNA etc.)

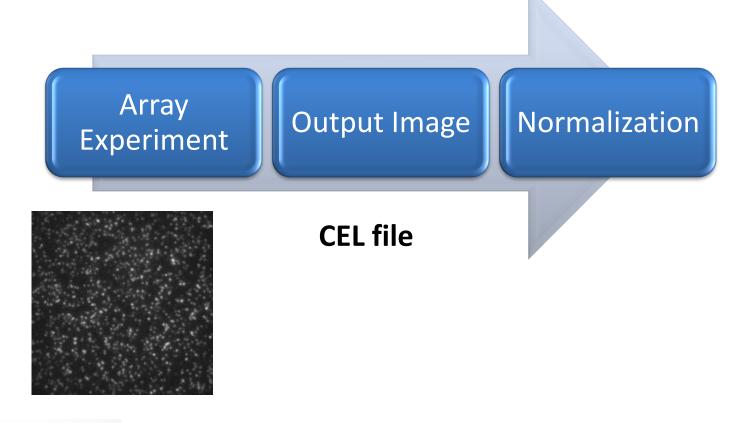




Microarray Experiment Flow



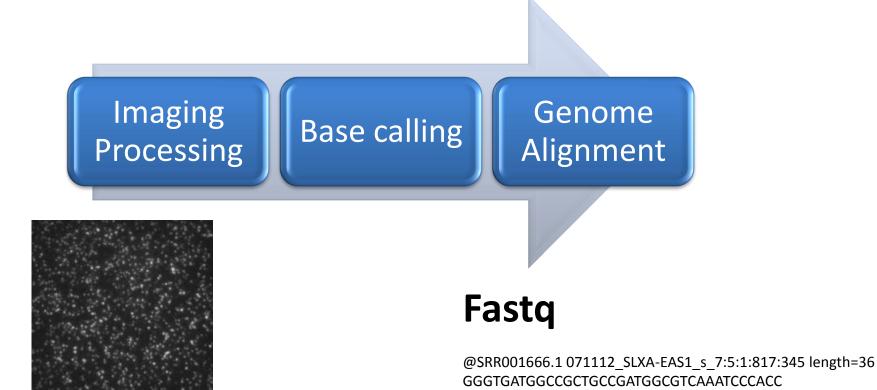
Data Generation Pipeline-NGS







Data Generation Pipeline-Microarray







Data Analysis- Individual Sample Data is huge

Per human sample

Platform	Exome/aCGH	Transcriptome	ChIP
Micoarray	~115 MB	~13-40 MB	~60 MB
HiSeq Run	~67.5-135 GB	~33.75-67.5 GB	~13.5-20 GB

For 20 human sample

Platform	Exome/aCGH	Transcriptome	ChIP
Micoarray	~2 Gb	~260 MB	~1.2 MB
HiSeq Run	~1350 GB	~680 GB	~270 Gb



MacBook Pro

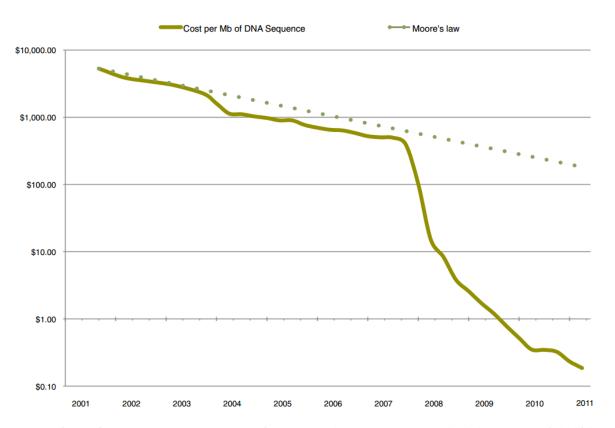
MPUTATIONAL

RBER CANCER INSTITUTE

Price Processor Memory Storage \$2,799 2.6GHz, quad-core 16 GB 768 GB



Data Analysis-DNA Sequencing Cost is Rapidly Dropping



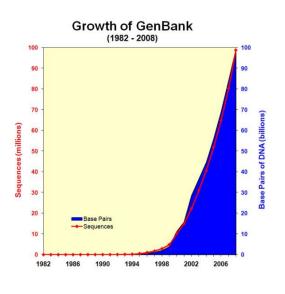


Figure 2. Cost of 1 MB of DNA sequencing. Decreasing cost of sequencing in the past 10 years compared with the expectation if it had followed Moore's law. Adapted from [11]. Cost was calculated in January of each year. MB, megabyte.

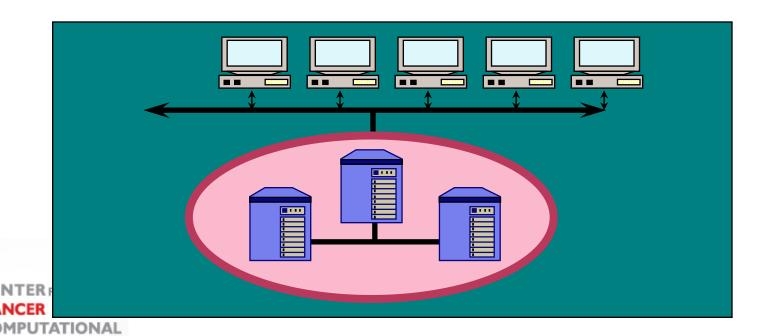


The first genome took 10 yrs and \$3 billion Today, 1 week for \$5000

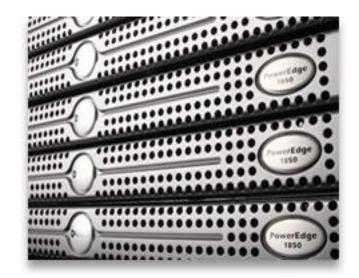


Genomics Data analysis is a job for computer Cluster

- Group of independent systems that
 - Function as a single system
 - Appear to users as a single system
 - And are managed as a single system'
- Clusters are "virtual servers"







The cluster is a stack of "rack mount" servers a bit like pizza boxes





Cluster Resources on Longwood Campus

- Partners Research Computing
 - http://rc.partners.org
- Research IT Group of HMS
 - http://ritg.med.harvard.edu/
- Research Computing at DFCI
 - http://research4.dfci.harvard.edu/
- Amazon Cloud Computing



