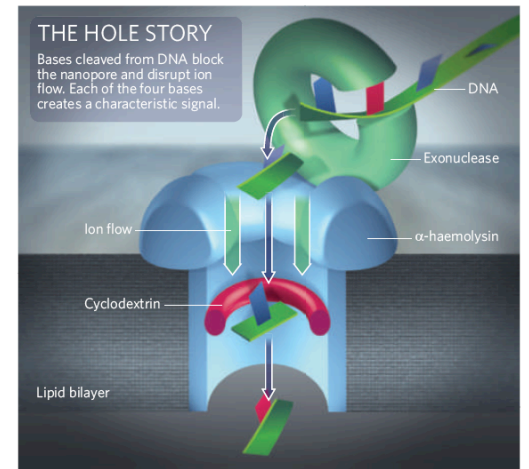
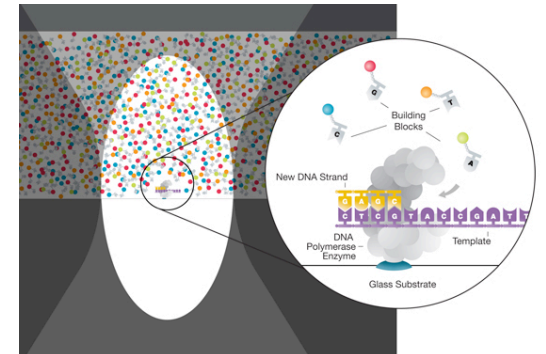
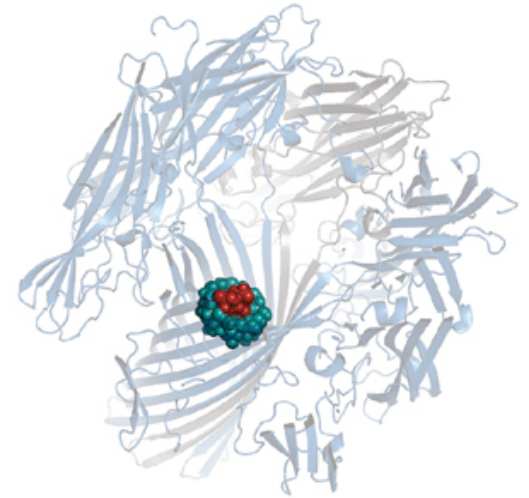
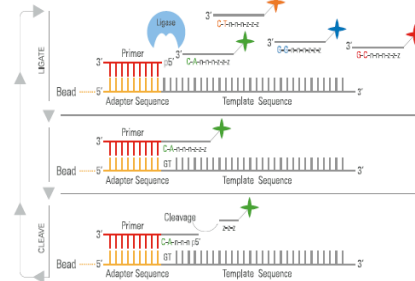
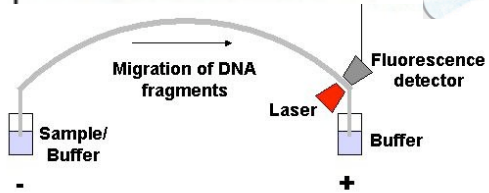
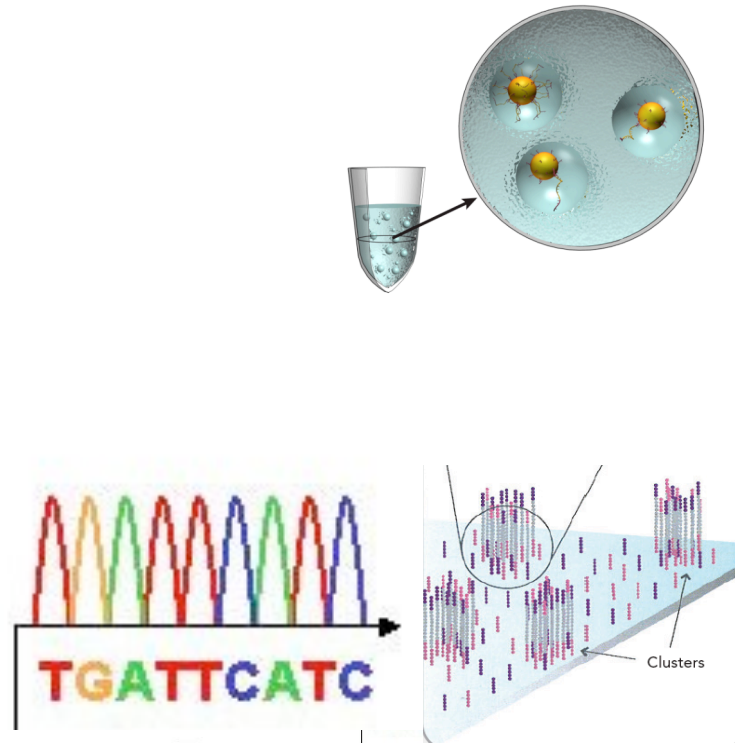
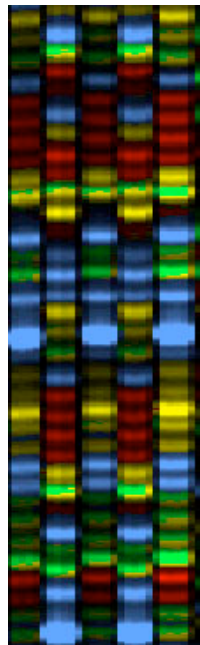
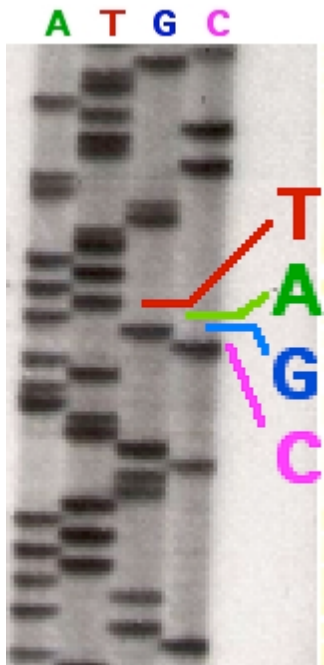


The Evolution of Sequencing

- Sanger sequencing
 - Gels
 - Cycle sequencing
 - Fluorescence
 - Capillary electrophoresis
- Sequencing, the “Next Generation”
 - “Sequencing by synthesis”
 - Pyrosequencing (Roche/454)
 - Cluster sequencing (Illumina/Solexa)
 - Sequencing by ligation (ABI/SOLiD)
- Next “Next Generation”
 - 4th Generation?
 - Single molecule sequencing



Macro versus Micro Reads

Read Length

35 - 75bp \Leftrightarrow 250 - 450bp



Applied Biosystems
SOLiD

Base Pairs Per Run

3 - 10 Gb \Leftrightarrow 0.1 - 0.5 Gb

Base Pairs Per Day

1 - 1.5 Gb \Leftrightarrow 0.2 - 1.0 Gb

Number of Sequences

100 M \Leftrightarrow 1.2 M

Run Time

3 - 7 days \Leftrightarrow 0.5 days

Reagent Cost per Run

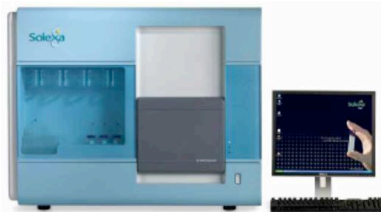
~\$4K - \$12K \Leftrightarrow \$6K

Error Rate

Varies, different characteristics



Roche / 454 FLX



Illumina / Solexa
Genetic Analyzer

Technology and Informatics

PR Space versus Science Space

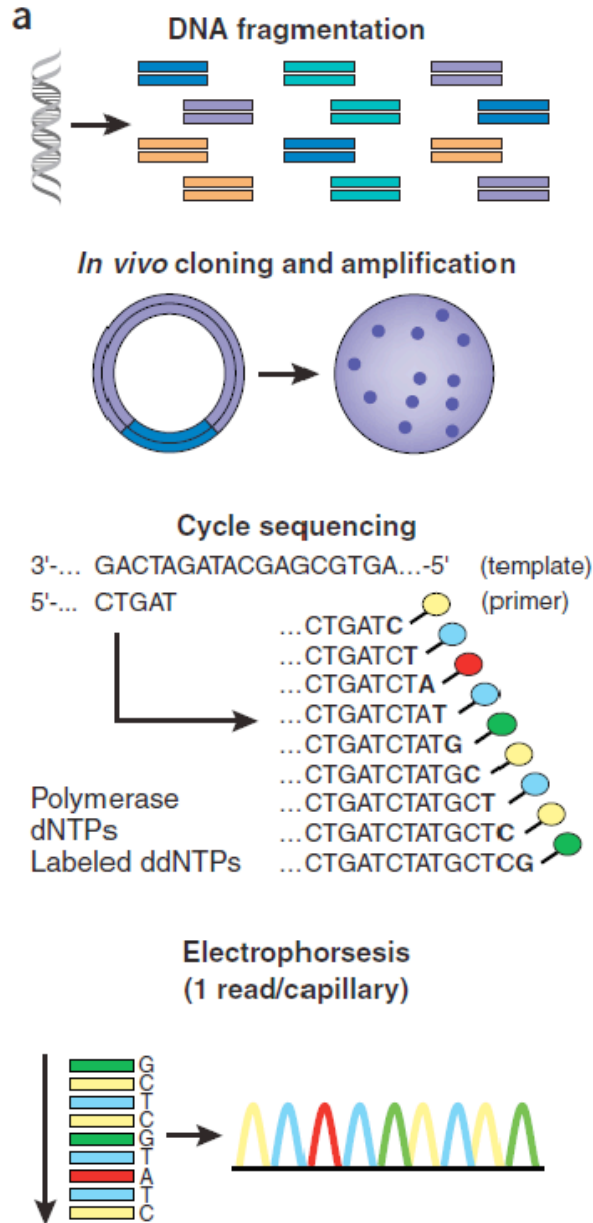
- Flow and phasing
- Data quality and Error rate
 - Variation along sequence
 - Quality scores (Equivalence?)
- Length distribution versus average
- Raw versus recovered sequence
 - How much coverage with different methods?
- Tagging (barcodes) and multiplexing
 - Variation in coverage

Next-Gen Basics

- Library creation
 - Shearing, size selection
 - Size distribution
 - Specific primer sequences (adaptors) flank target sequence
 - Allows amplification
 - Opportunity for extra “mutation”
- Tagging (barcodes)
 - Proportion of sequence wasted
- Ligation or amplification (454)
- Paired ends



Sanger Sequencing



- DNA is fragmented
- **Cloned** to a vector
 - Plasmid, BAC
 - Linkage
- Cyclic sequencing
- Separation by electrophoresis
- Read fluorescent tags