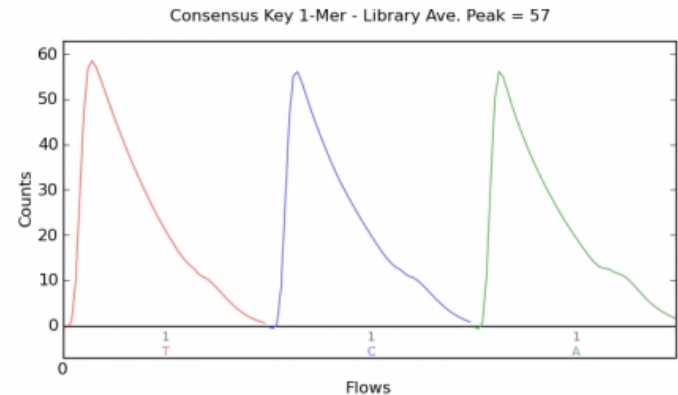
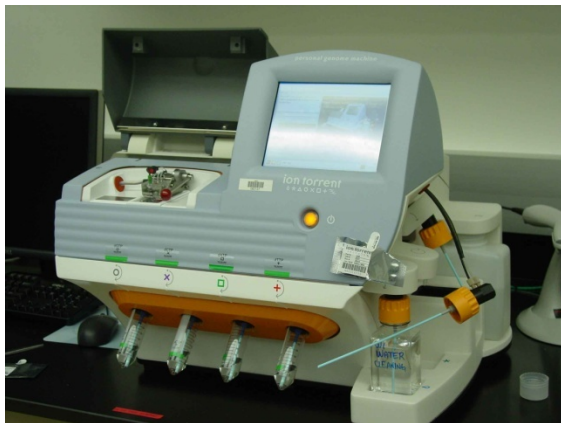


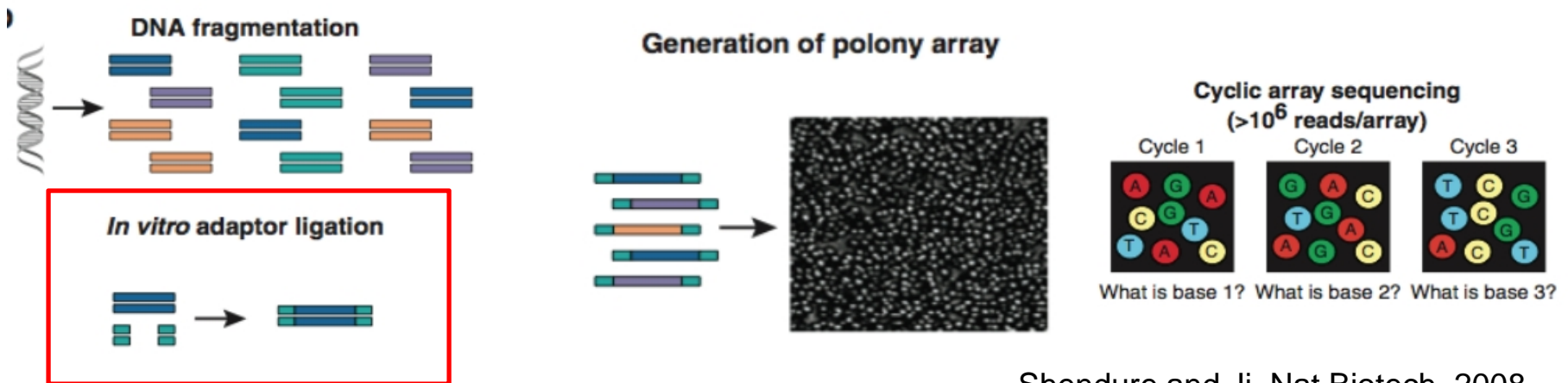
BINF 6350 ITSC 8350
Fall 2011
Biotechnology & Genomics Lab
Creating DNA libraries

<http://webpages.uncc.edu/~jweller2>

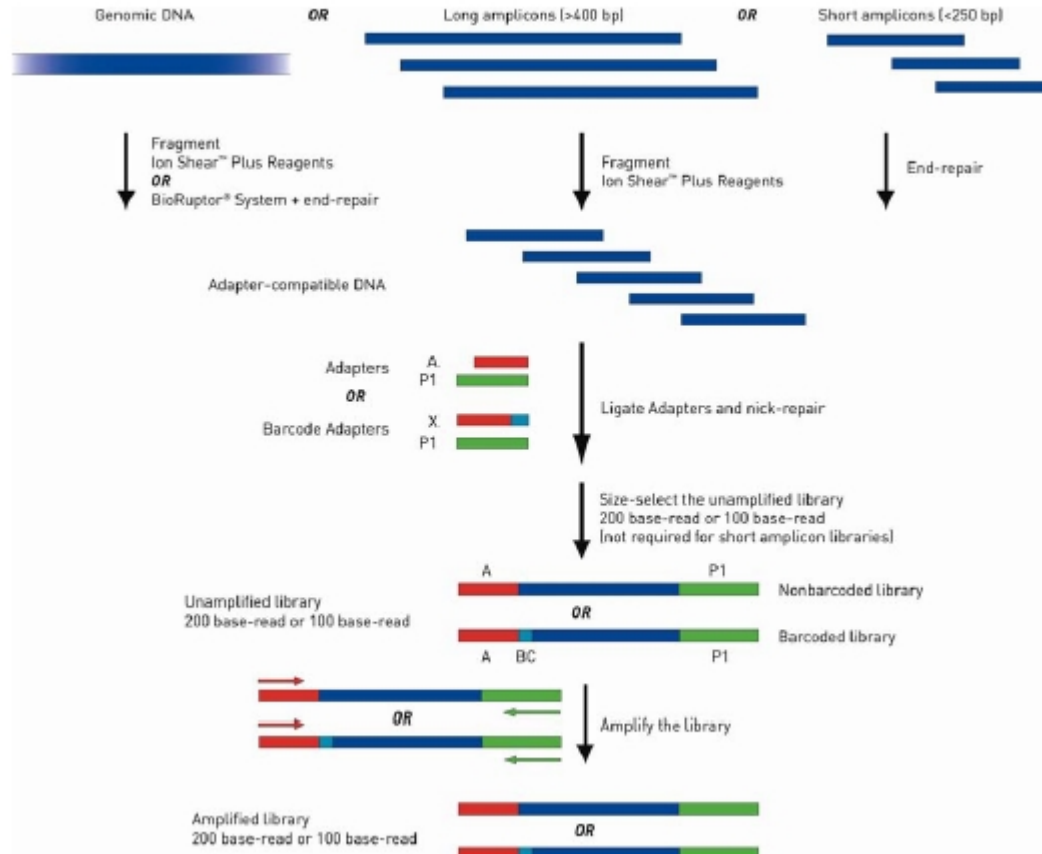


NGS data production steps

- Produce the fragments to be sequenced, clean up
- **Modify fragments for processing, clean up**
- Separate the modified fragments *from each other*
 - so they don't compete in the PCR process: emulsion reactors, dispersed on a surface
- Amplify each fragment to a base mass
- Sequence-by-synthesis (flowgrams, PPI with reversible terminators, etc.)
- Analyze



NGS libraries



QC Of input library

- How do you know if the adaptors have ligated to your product?
- You can perform qPCR - but you need a control fragment.
 - Titrate the fragment with the other reagents
 - Use SYBR Green as the detection standard.
 - Include a DNA polymerase that is SYBR Green tolerant.
- qPCR will only amplify products with adaptors on both ends
- If you want to check the level of pure adaptor dimers you can do a melt phase as well.



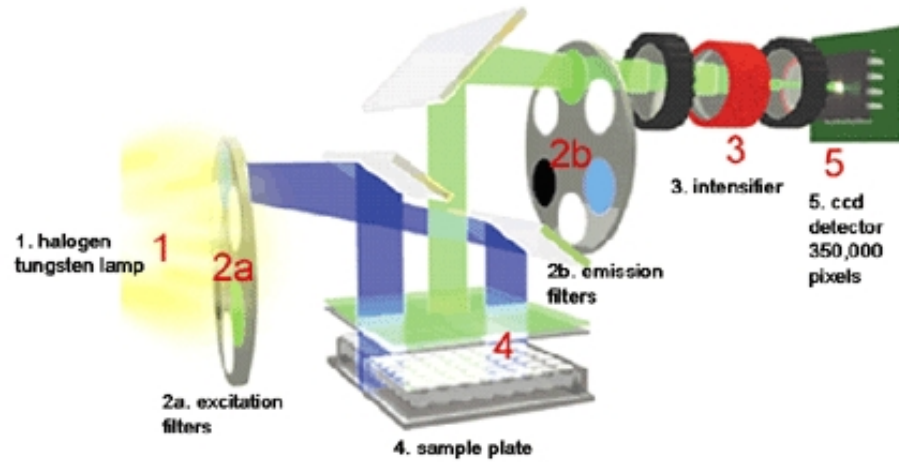
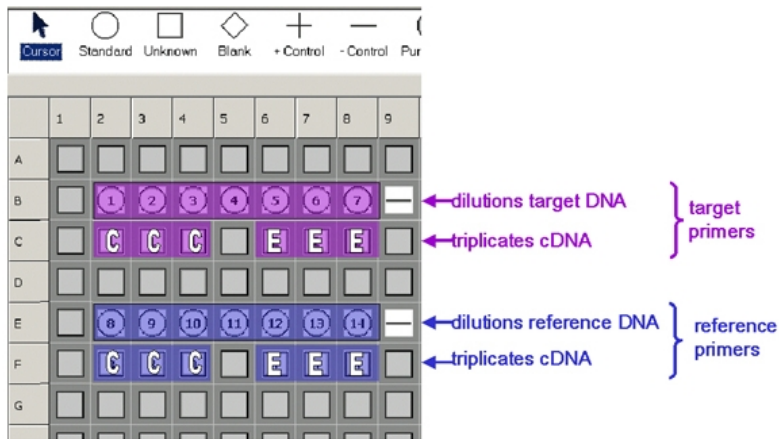
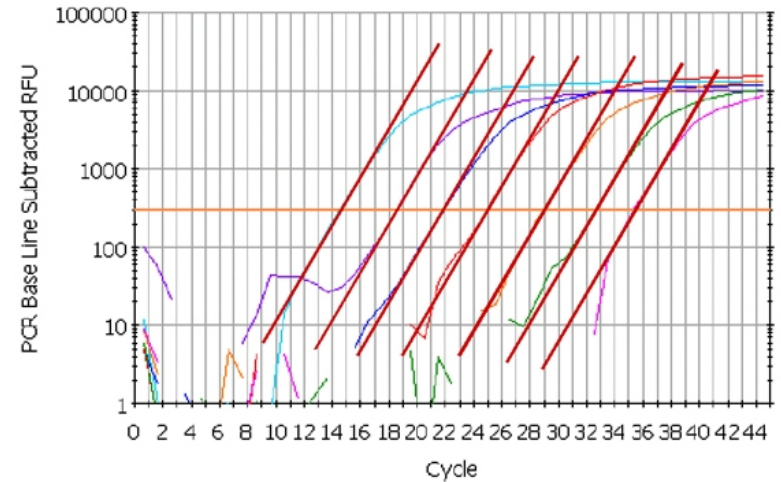


Fig. 1.2. Representation of Optical Detection System layout.

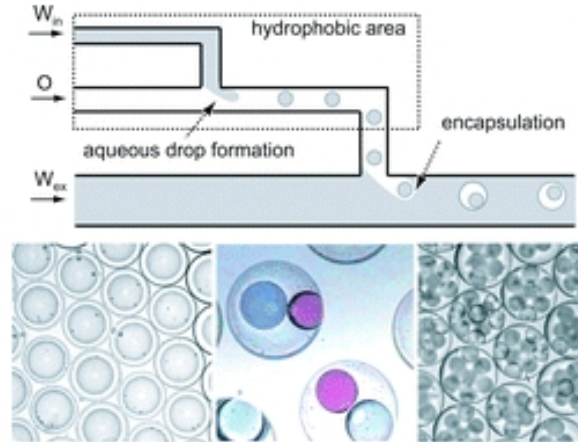
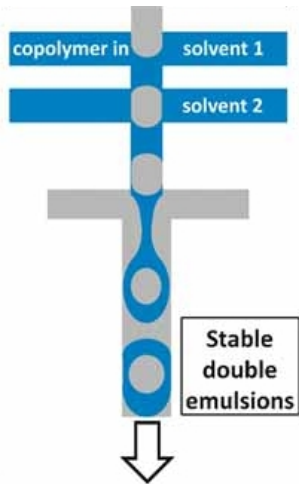


Standard curve method

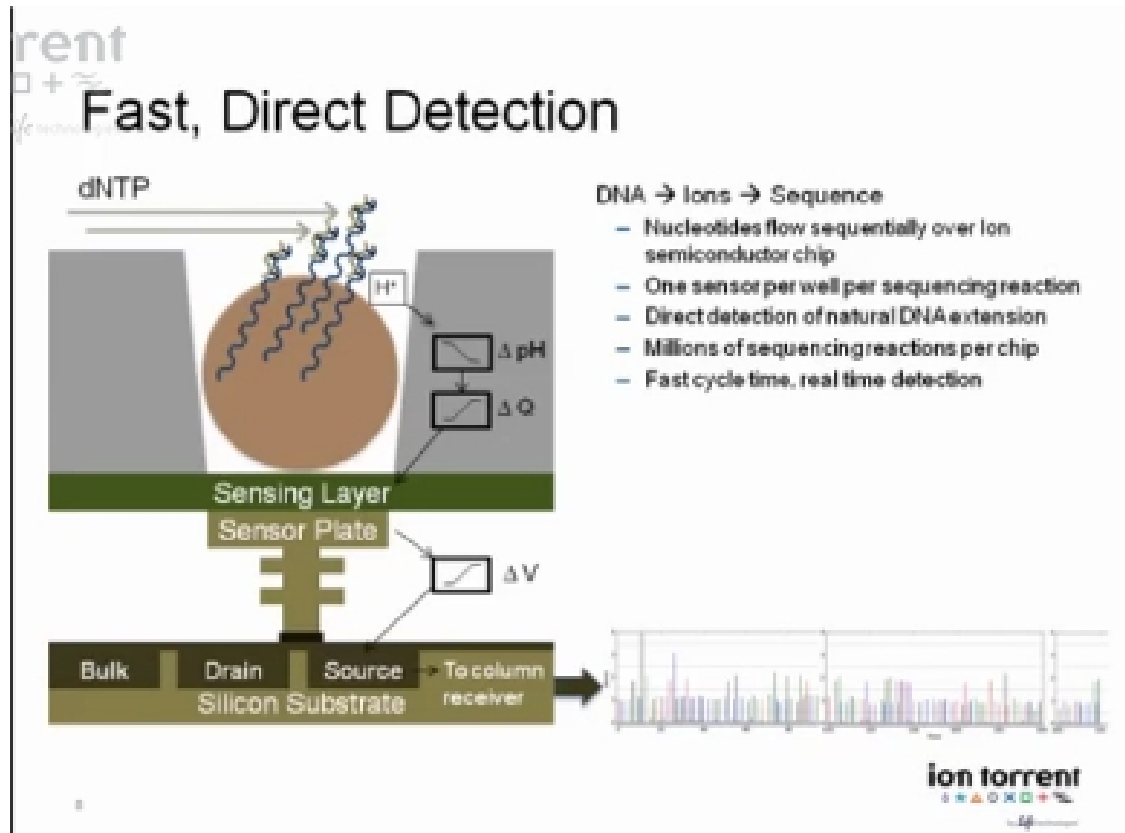


SERIES OF 10-FOLD DILUTIONS

Amplifying the library – Emulsion Reactors

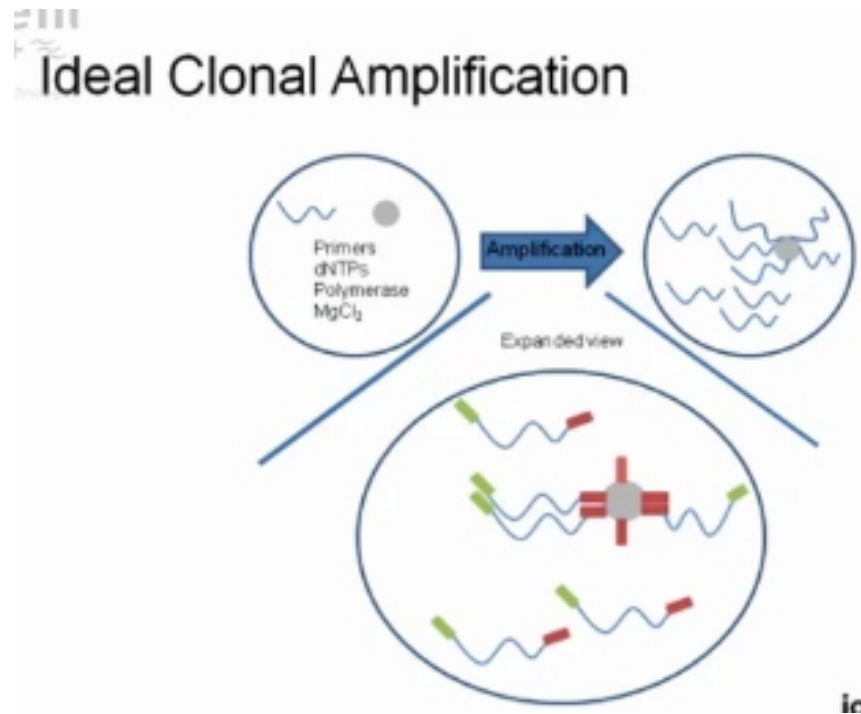


Ion Torrent sequencing chemistry

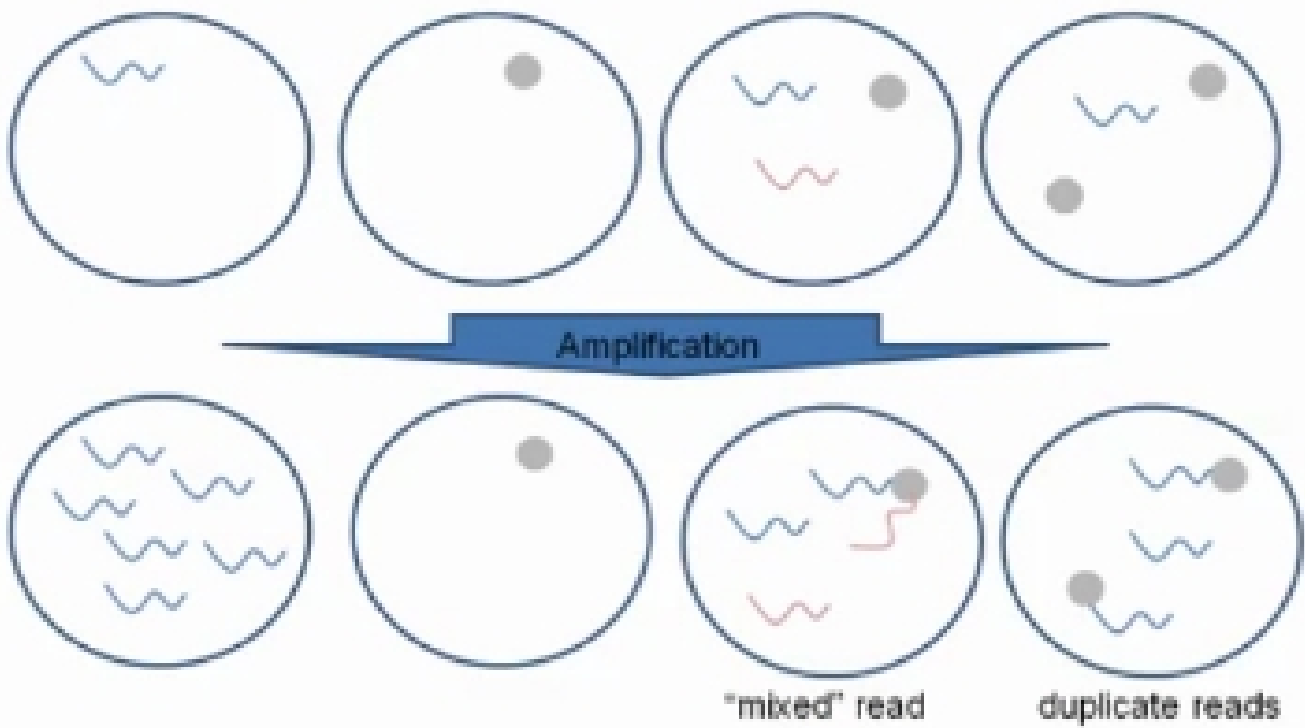


Emulsion and PCR

- emPCR

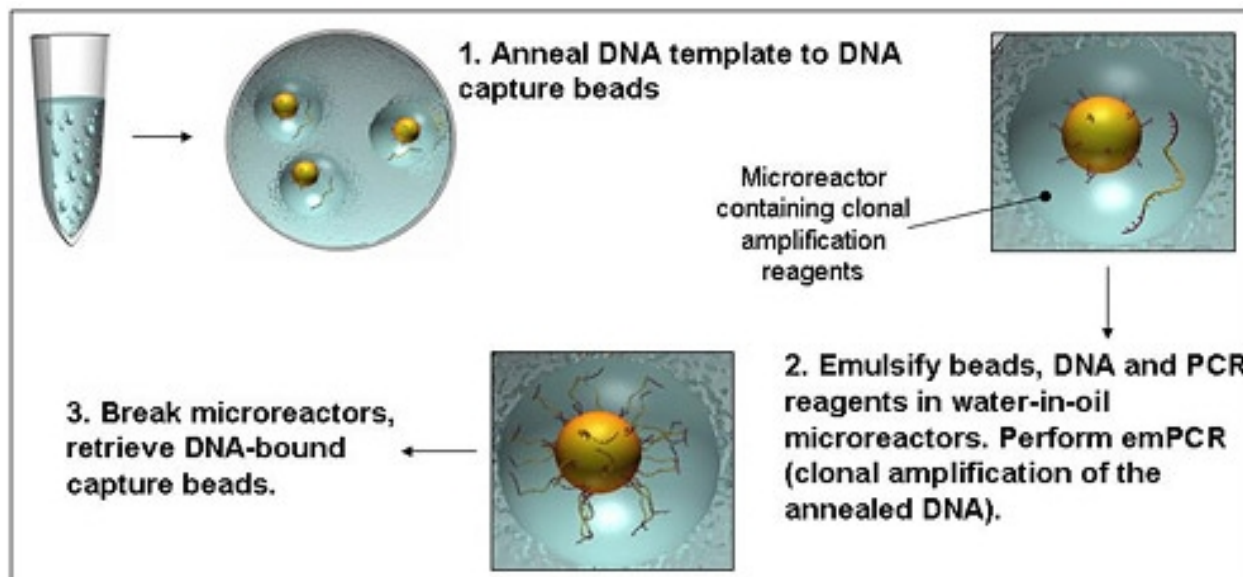


ent
+
Non-Ideal Cases

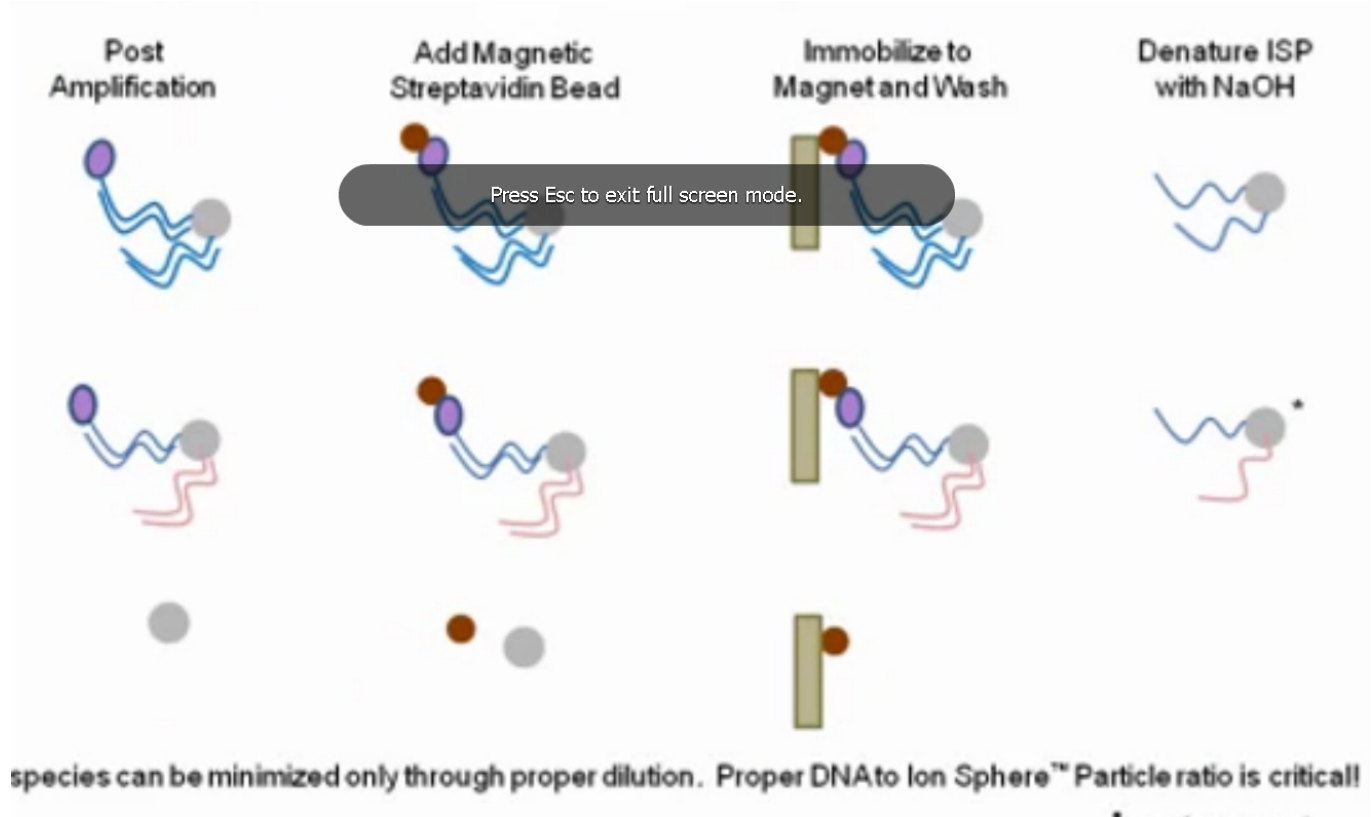




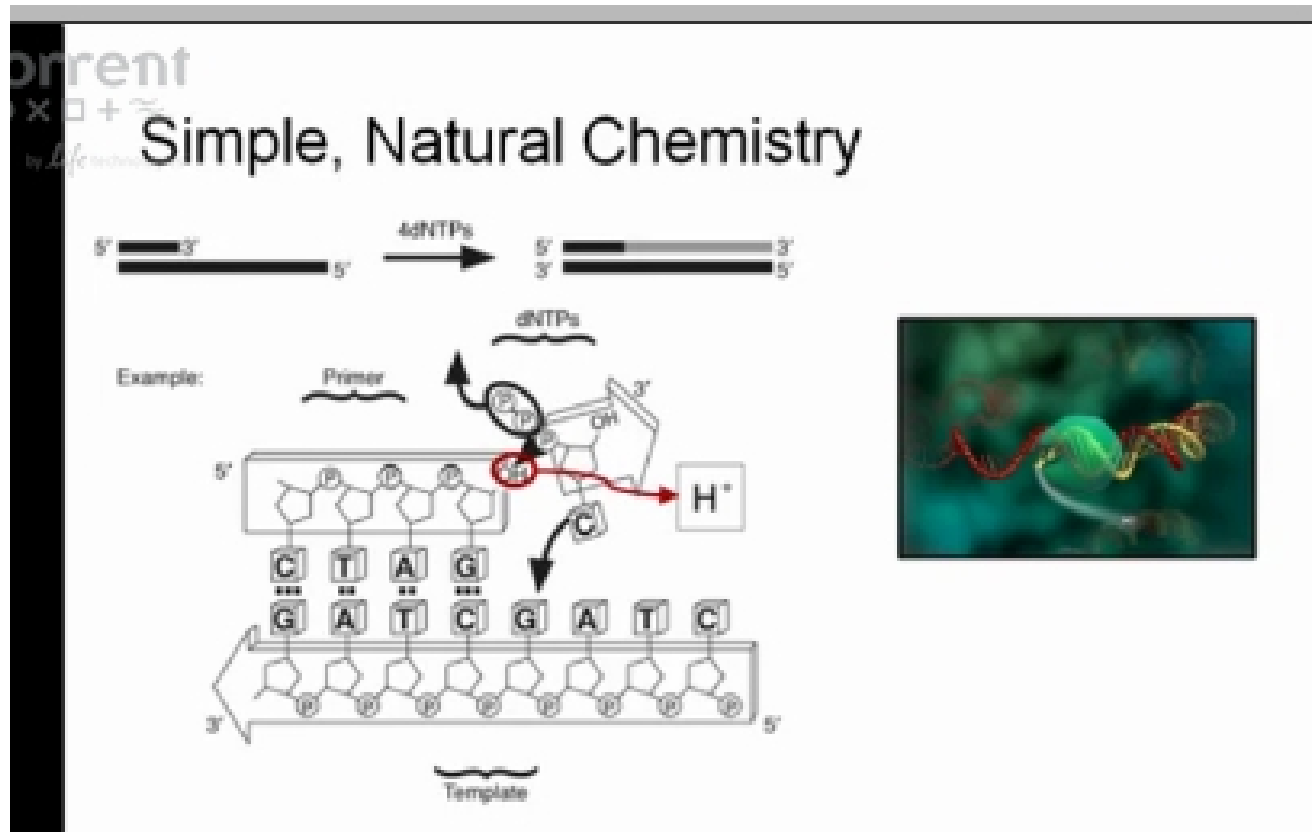
emPCR



Enrichment

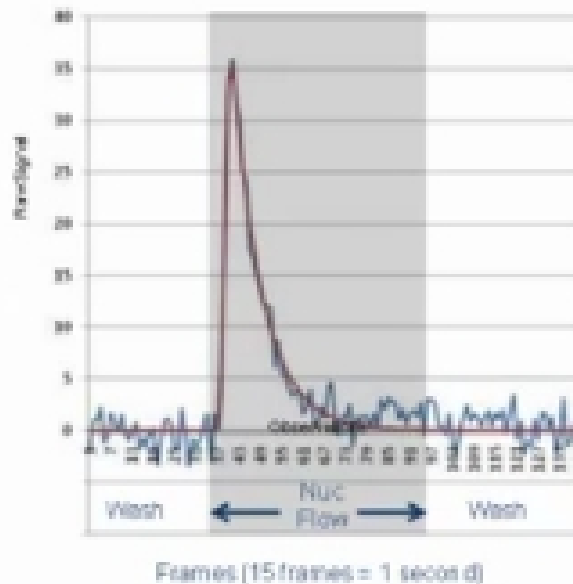


Detection and flowgrams



Signal characteristics

Single Well Incorporation Trace

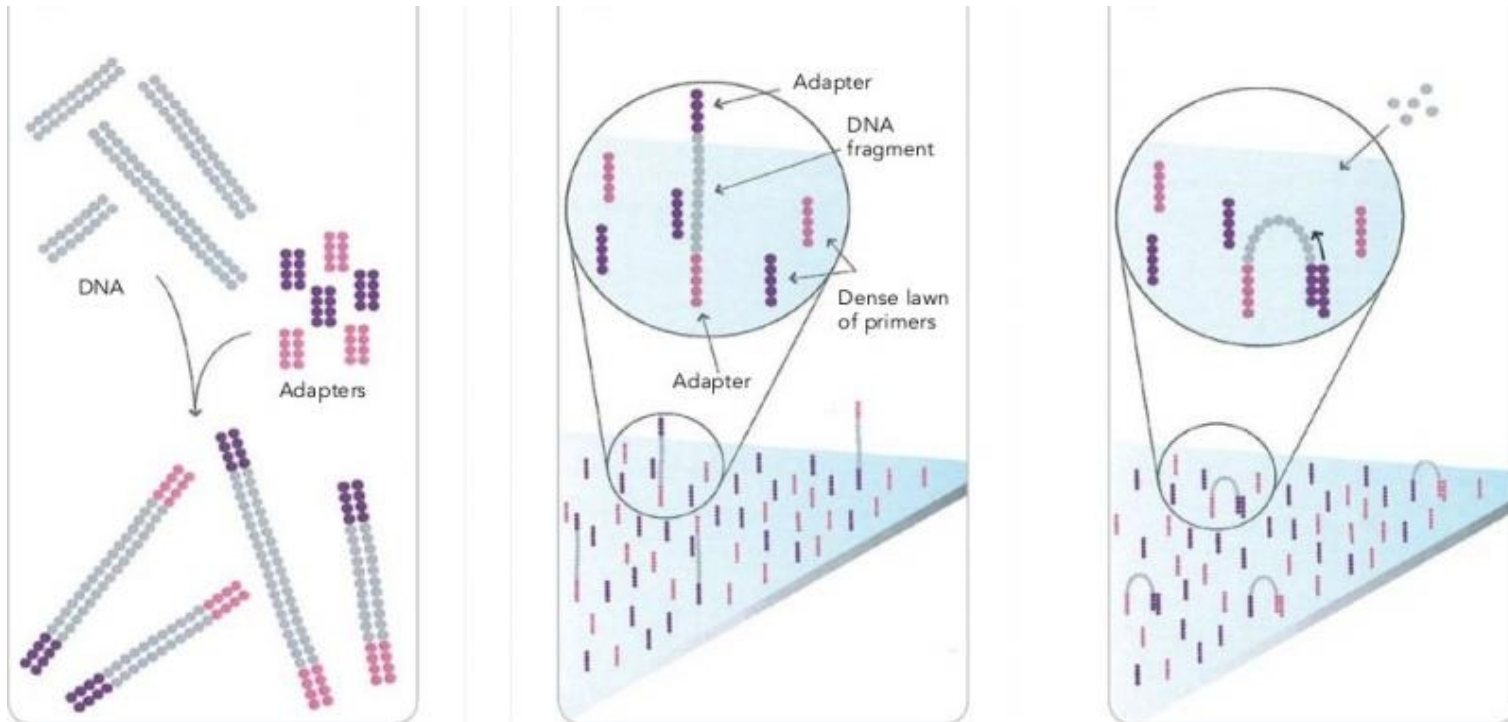


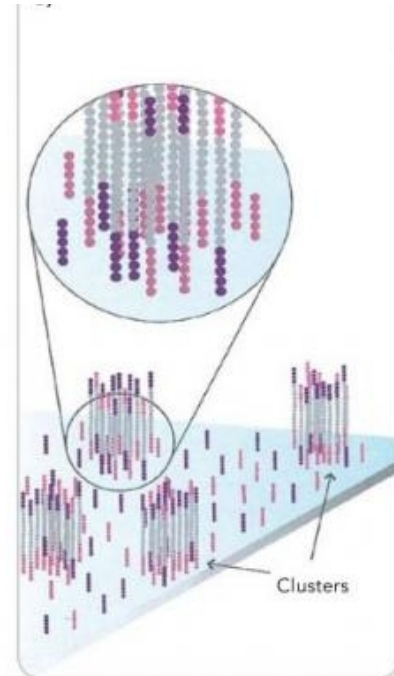
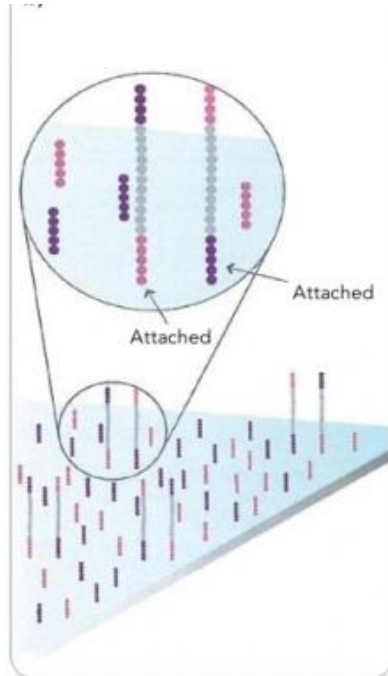
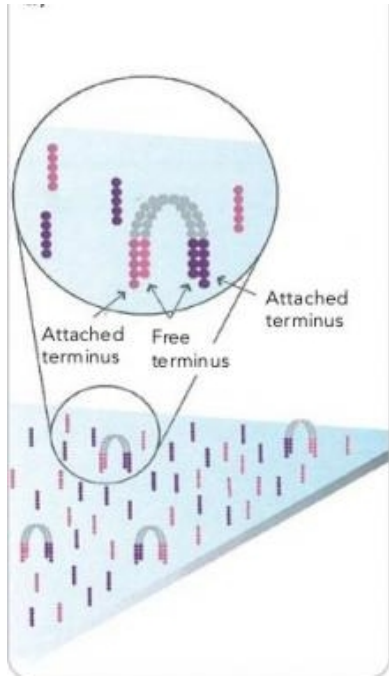
- Fast sequencing
A few seconds per incorporation
- High signal to noise
Many data points per incorporation trace
- Enables high raw accuracy

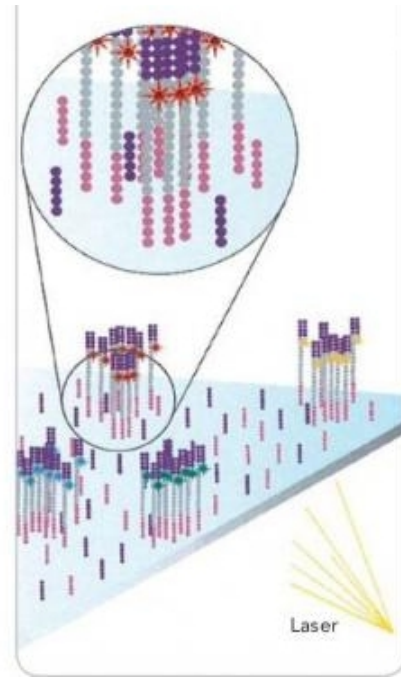
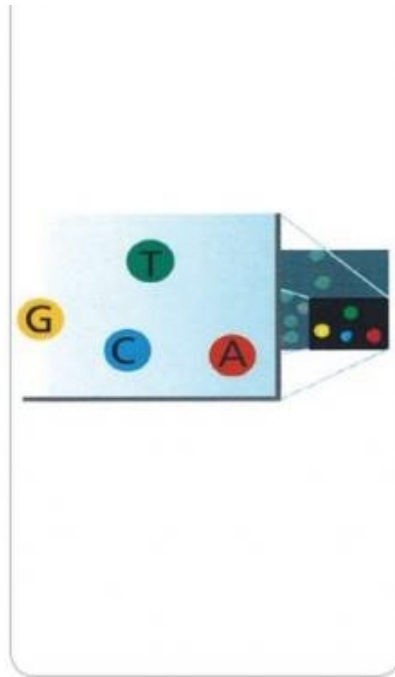
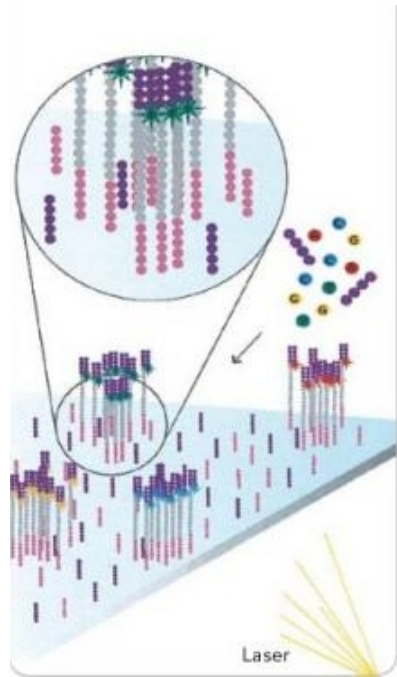
Other surface attachment methods

- Fragments are distributed randomly on a surface that is covered with DNA complementary to the adaptor sequences.
- The fragments are attached to the surface and then multiplied by bridge amplification
 - They form small clusters or ssDNA (because they don't diffuse very far).
 - Once the clusters are formed sequencing can begin
 - In Illumina, the nucleotides have reversible terminators and carry fluorescent dyes. After incorporation the spot is imaged, then the terminator is removed so along with the dye, extension can happen.

Illumina



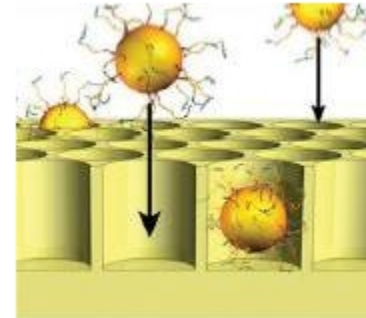
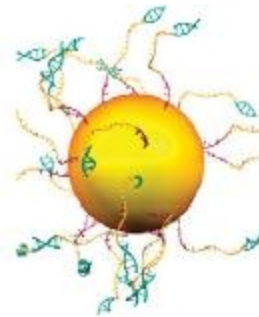
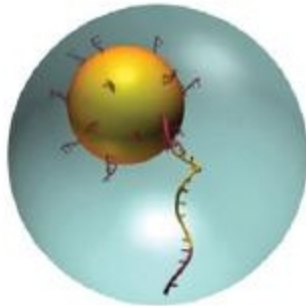
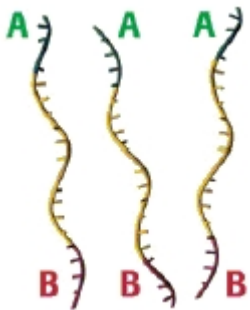




Roche 454 sequencing

- The GS FLX sequencer uses 454 chemistry and technology.
- Adaptors are added. One strand has a biotin group, so it can be removed, leaving ssDNA behind
- The adaptor allows bead capture.
- A water-oil emulsion makes a microreactor so one target has a bead all to itself, which it colonizes.
- After several million-fold amplification the emulsion is broken.
- The beads are deposited in pico-lieter fiber-optic wells for sequencing.
- The complementary strand is synthesized by adding the primer anmer and nucleotides.
- An inorganic phosphate cleavage leads to an enzymatic cascade that releases light.

Figures from Roche Diagnostics.



454 Chemistry (GS FLX)

