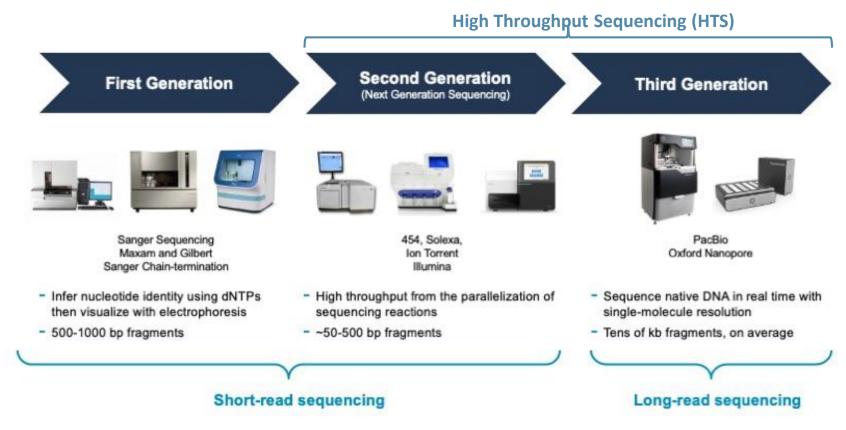
Introduction to NGS data analysis

Dr Gustavo A. Silva-Arias

Technische Universität München

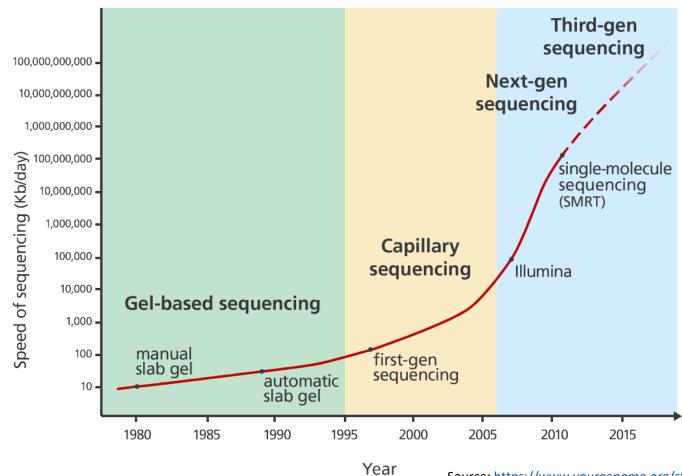
Bogotá, 23 de Agosto 2021

The evolution of sequencing technology



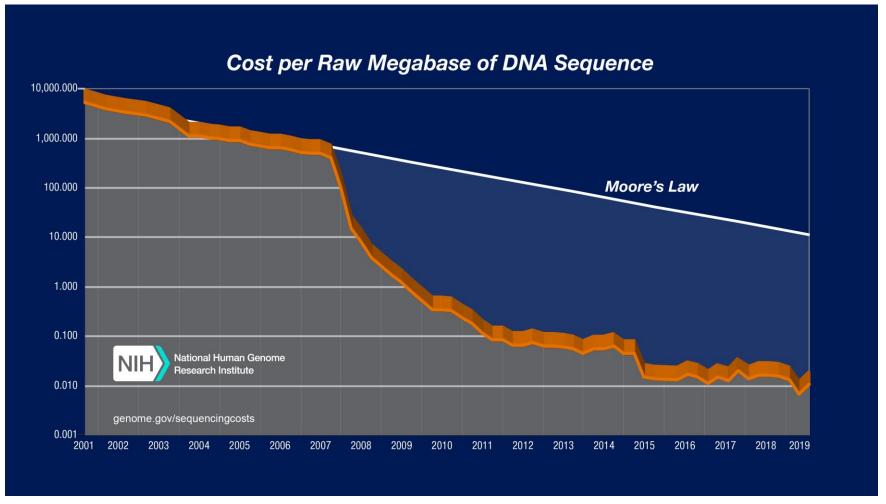
Source: https://www.pacb.com/blog/the-evolution-of-dna-sequencing-tools/

The evolution of sequencing technology - efficiency

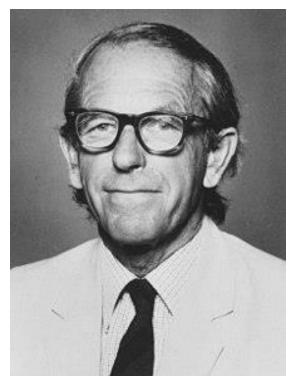


Source: https://www.yourgenome.org/stories/third-generation-sequencing

The evolution of sequencing technology - cost



First Generation: Sanger sequencing



- Frederick Sanger (1918-2013)
- British biochemist

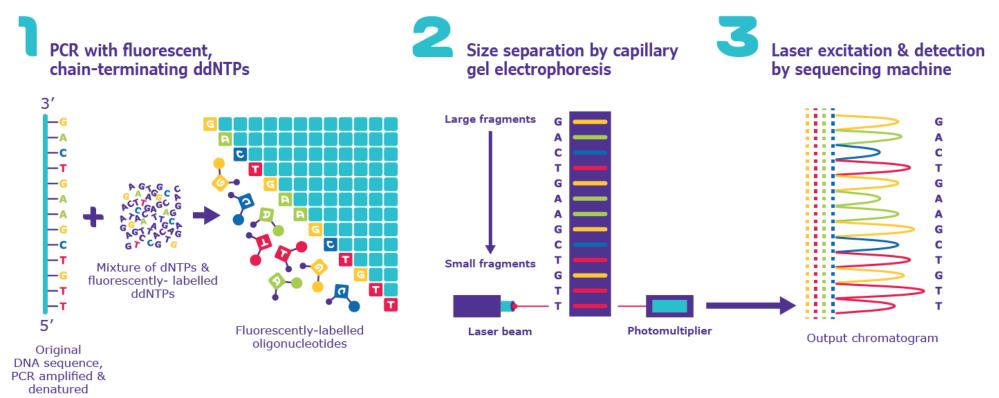
Nobel Prize in Chemistry 1958:

- "for his work on the structure of proteins, especially that of insulin."
- He determined the complete aminoacid sequence of bovine insuline using electrophoresis and chromatography

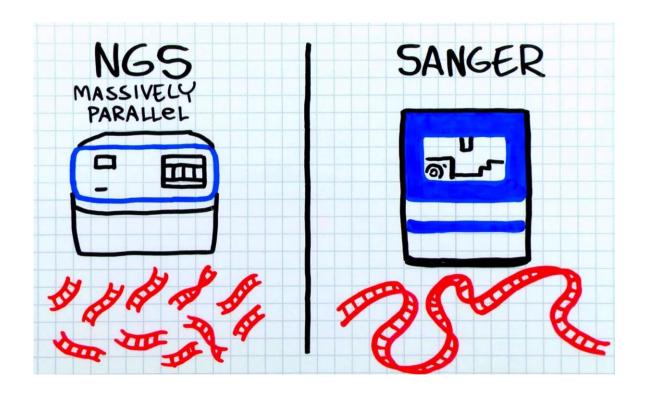
Nobel Prize in Chemistry 1980:

- "for their contributions concerning the determination of base sequences in nucleic acids."
- Developed the "dideoxy" chain-termination method for sequencing DNA molecules, now known as the "Sanger method".

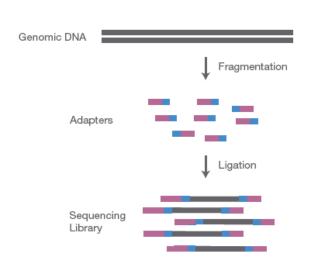
First Generation: Sanger sequencing



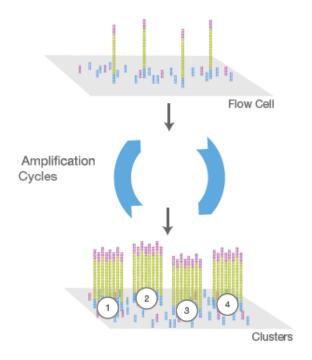
- Old gel "slab" method: https://www.youtube.com/watch?v=3M0PyxFPwkQ
- Capillary gel method: https://www.youtube.com/watch?v=x7PUqNA0eOA



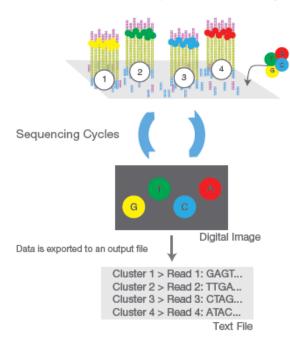
• 1. Library preparation



2. Template Amplification



• 3. Sequencing



Source: https://emea.illumina.com/content/dam/illumina-marketing/documents/products/other/ivf-reproductive-genetic-health-ngs-primer-1570-2015-012.pdf

<u>Template amplification methods</u>

Emulsion PCR

454 (Roche)

SOLiD (Thermo Fisher)

GeneReader (Quiagen)

Ion Torrent (Thermo Fisher)

- Solid-phase bridge amplification
 - Illumina
- Solid-phase template walking

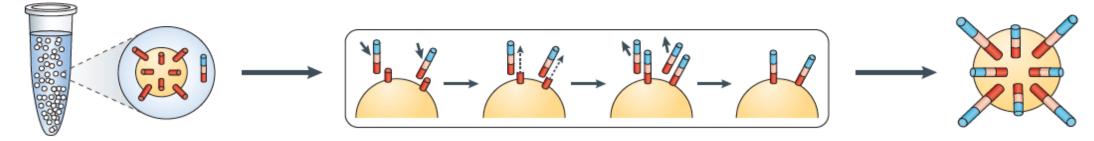
SOLiD Wilfire – Thermo Fischer

In-solution DNA nanoball generation

Complete Genomics - BGI

Template amplification methods

a Emulsion PCR (454 (Roche), SOLiD (Thermo Fisher), GeneReader (Qiagen), Ion Torrent (Thermo Fisher))



EmulsionMicelle droplets are loaded with primer, template, dNTPs and polymerase

On-bead amplification Templates hybridize to bead-bound primers and are amplified; after amplification, the complement strand disassociates, leaving bead-bound ssDNA templates

Final product 100–200 million beads with thousands of bound template

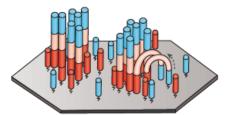
Template amplification methods

Solid-phase bridge amplification (Illumina)

Template binding Free templates hybridize with slide-bound adapters

Bridge amplification

Distal ends of hybridized templates interact with nearby primers where amplification can take place

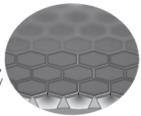


Cluster generation

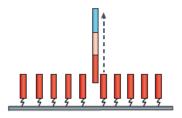
After several rounds of amplification, 100–200 million clonal clusters are formed



Microwells on flow cell direct cluster generation, increasing cluster density

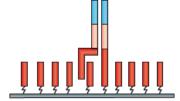


Solid-phase template walking (SOLiD Wildfire (Thermo Fisher))



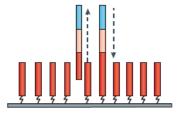
Template binding

Free DNA templates hybridize to bound primers and the second strand is amplified



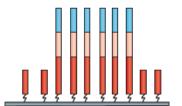
Primer walking

dsDNA is partially denatured, allowing the free end to hybridize to a nearby primer



Template regeneration

Bound template is amplified to regenerate free DNA templates



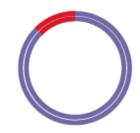
Cluster generation

After several cycles of amplification, clusters on a patterned flow cell are generated

Template amplification methods

DNBSEQ (BGI)

d In-solution DNA nanoball generation (Complete Genomics (BGI))



Adapter ligation One set of adapters is ligated to either end of a DNA template, followed by template circularization

Cleavage

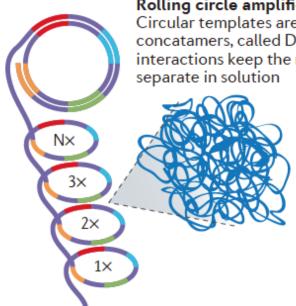
Circular DNA templates are cleaved downstream of the adapter sequence





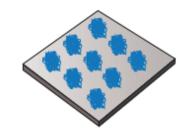
Iterative ligation

Three additional rounds of ligation, circularization and cleavage generate a circular template with four different adapters



Rolling circle amplification

Circular templates are amplified to generated long concatamers, called DNA nanoballs; intermolecular interactions keep the nanoballs cohesive and



Hybridization DNA nanoballs are immobilized on a patterned flow cell

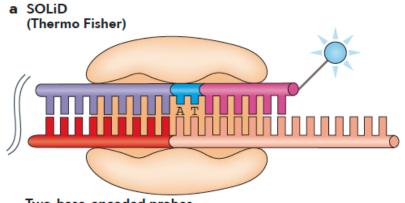
Sequencing Methods

- By Ligation (SBL)
 SOLID (Thermo Fisher)
- By Synthesis (SBS)
 - Cyclic Reversible Termination (CRT)

Illumina GeneReader (QiaGen) DNBSEQ (BGI)

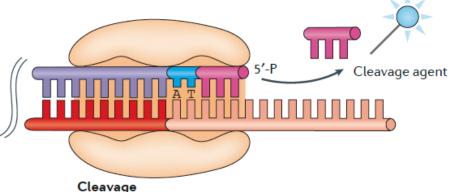
 SNA: Single Nucleotide Addition 454 (Roche) IonTorrent (ThermoFisher)

Sequencing Methods - By Ligation (SBL)



Two-base-encoded probes

Probes with two known bases followed by degenerate or universal bases hybridize to a template; ligase immobilizes the complex and the slide is imaged

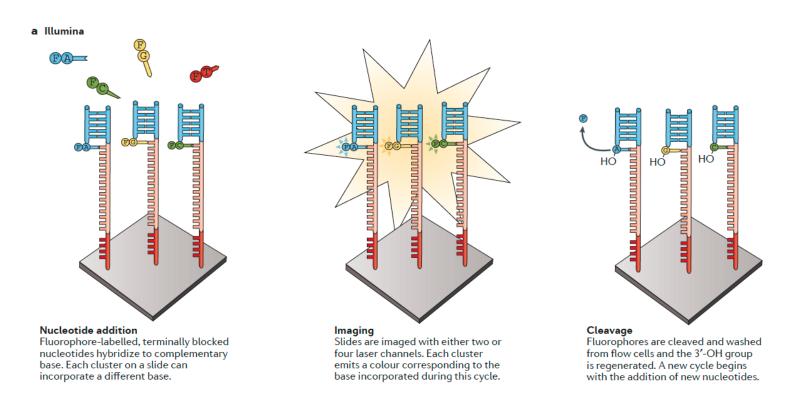


The fluorophore is cleaved from the probe along with several bases, revealing a 5' phosphate

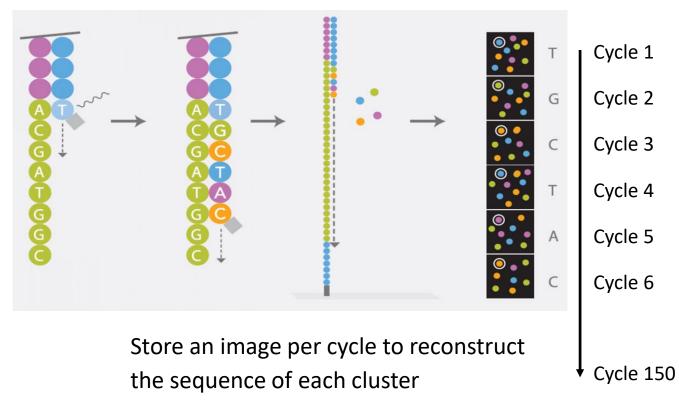
Full explanation: https://www.youtube.com/watch?v=PPEKybWYOBA

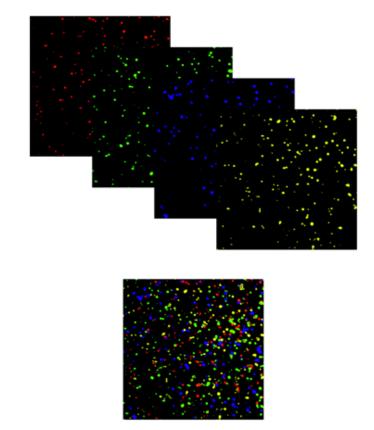
*Note: DNBSEQ (BGI) also used a ligation technique but has switched to SBS to obtain longer reads

CRT: Cyclic Reversible Termination, used by Illumina, GeneReader (QiaGen), DNBSEQ (BGI)



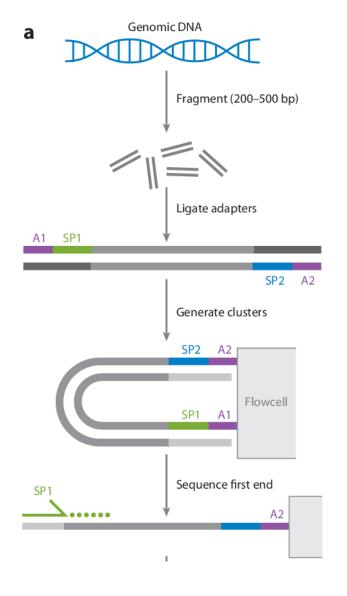
CRT: Cyclic Reversible Termination, used by Illumina, GeneReader (QiaGen), DNBSEQ (BGI)





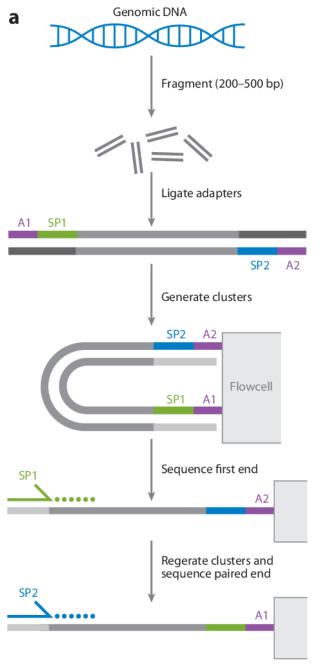
Source: Sara Goodwin et al. 2016 - Nature Reviews Genetics - https://doi.org/10.1038/nrg.2016.49

Source: https://doi.org/10.1373/clinchem.2008.112789



Single-End vs. Paired-End (Illumina, DNBSEQ)

Single-End



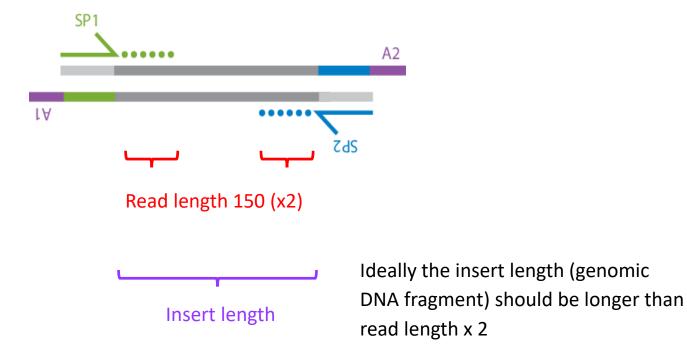
Single-End vs. Paired-End (Illumina, DNBSEQ)

Paired-End

Source: Elaine R. Mardis 2013 - Annual Review of Analytical Chemistry - https://doi.org/10.1146/annurev-anchem-062012-092628

Genomic DNA a Fragment (200-500 bp) Ligate adapters A1 SP1 Generate clusters Flowcell Sequence first end Regerate clusters and sequence paired end

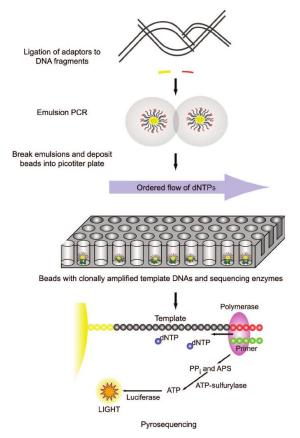
Single-End vs. Paired-End (Illumina, DNBSEQ)



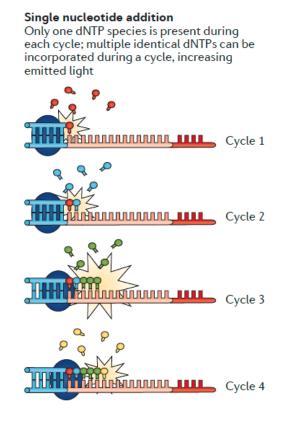
Paired-End

Source: Elaine R. Mardis 2013 - Annual Review of Analytical Chemistry - https://doi.org/10.1146/annurev-anchem-062012-092628

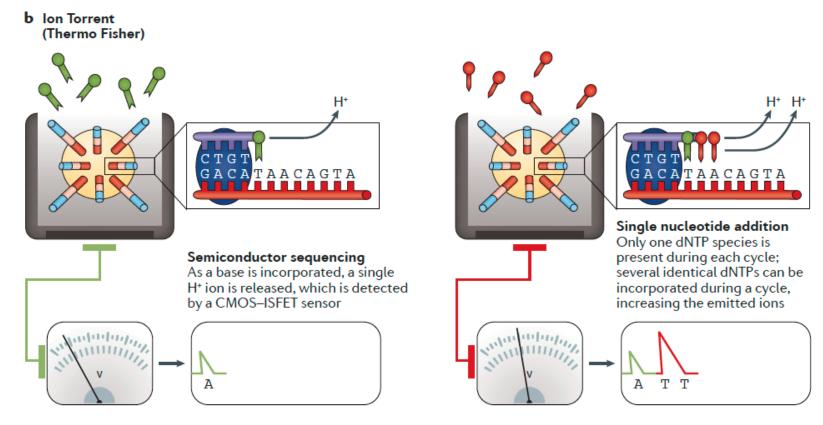
SNA: Single Nucleotide Addition. 454 (Roche), IonTorrent (ThermoFisher)



Source: https://doi.org/10.1373/clinchem.2008.112789



• SNA: Single Nucleotide Addition, used by 454 (Roche), IonTorrent (ThermoFisher)



Full explanation videos:

• Illumina [CRT]:

https://www.youtube.com/watch?v=fCd6B5HRaZ8

• DNBSEQ (BGI) [CRT]:

https://www.youtube.com/watch?v=RGcpftDHpng&t

• 454 pyrosequencing [SNA]:

https://www.youtube.com/watch?v=bNKEhOGvcal

IonTorrent [SNA]:

https://www.youtube.com/watch?v=ZL7DXFPz8rU

Third Generation:

Parallel Sequencing of Long Reads in Real Time

A Real-time long-read sequencing **Ab** Oxford Nanopore Technologies Aa Pacific Biosciences SMRTbell template Two hairpin adapters allow continuous circular sequencing ZMW wells Motor Sites where proteinsequencing takes place Labelled nucleotides All four dNTPs are labelled and available for incorporation

Modified polymerase As a nucleotide is incorporated by the polymerase, a camera records the emitted light

PacBio output

A camera records the changing colours from all ZMWs; each colour change corresponds to one base



MADOOOOO Alpha-hemolysin A large biological pore capable of sensing DNA Current Passes through the pore and is modulated as DNA passes through ONT output (squiggles) Each current shift as DNA translocates through the pore corresponds to a particular k-mer Time (seconds)

Source: Sara Goodwin et al. 2016 - Nature Reviews Genetics - https://doi.org/10.1038/nrg.2016.49

Leader-Hairpin template The leader sequence interacts

with the pore and a motor

protein to direct DNA,

bidirectional sequencing

a hairpin allows for

Third Generation:

Parallel Sequencing of Long Reads in Real Time

Full explanation videos:

• PacBio:

https://www.youtube.com/watch?v=v8p4ph2MAvI

https://www.youtube.com/watch?v=NHCJ8PtYCFc

https://www.youtube.com/watch?v= ID8JyAbwEo

Nanopore:

https://www.youtube.com/watch?v=E9-Rm5AoZGw

https://www.youtube.com/watch?v=CGWZvHIi3i0