



Bridging the gaps in bioinformatics/Raw data QC

# Introduction to sequencing

February 2024, Søren Hallstrøm, Statens Serum Institut, Denmark

# Outline

This session consists of the following elements

1. Introduction to Sequencing
2. Brief summary of the evolution of sequencing technology
3. Basics of sequencing in clinical microbiology

# Objectives

Specific objectives of this session:

1. What is sequencing
2. The technological advancements
3. When is sequencing an advantage

# The Lecturer – Background

Søren Hallstrøm

Ph.D. in molecular microbiology

Extensive experience with development of custom workflows

- Amplicon sequencing (16S, functional gene targets)
- Whole Genome Sequencing (WGS)

# The Lecturer - Presently

Academic staff at the Sequencing Core Facility -  
NGS laboratory at Statens Serum Institute, Denmark  
Department for infectious disease surveillance

- Method development, mainly bacterial WGS
- Quality assurance and maintenance NGS workflows
- Illumina and Oxford Nanopore Technology (ONT or nanopore)

# The Definition

DNA sequencing is the determination of a precise order of the nucleotides – adenine, guanine, cytosine and thymine in a given DNA fragment.



# The Basics

Genetic information is stored in DNA sequences

This information can be extracted by determining the correct order of the nucleotides in a given DNA sequence.

Finding the precise order of the nucleotides in a DNA fragment is very important to know about the structure and function of the genes.





# A brief history of sequencing technologies

## 1st generation

### Sanger Sequencing

Chain termination  
Single gene fragments

First sequence of a DNA genome: bacteriophage  $\phi$ X174, in 1977

Q20 - Q30 data

## 2nd generation

### Illumina

Sequencing by Synthesis  
Parallel sequencing  
Complex DNA Libraries

Illumina (Solexa)  
On board amplification of sequencing library (Bridge amplification)

Q30 – Q40 data

## 3rd generation

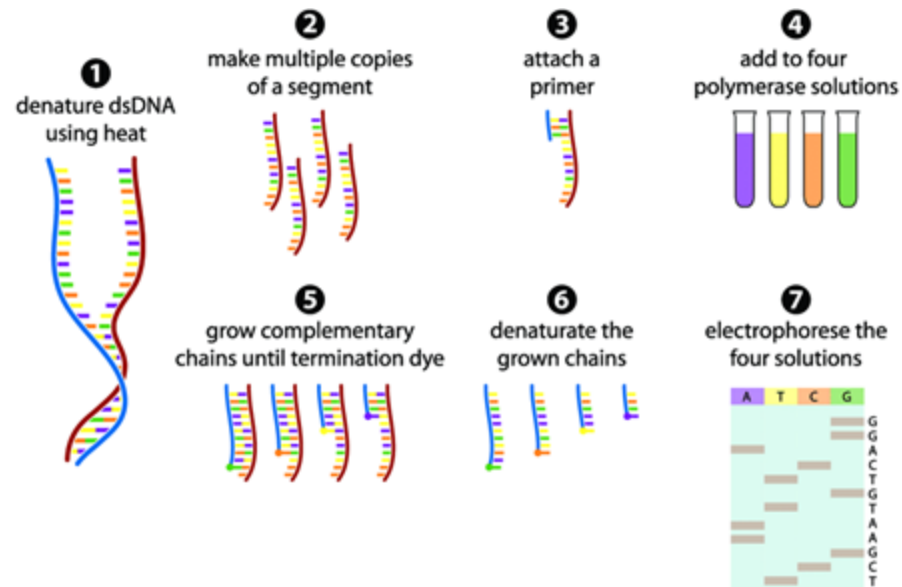
### Nanopore

Long read sequencing  
Real time basecalling

Oxford Nanopore Technologies  
Low price -Low quality  
Q10-20 data

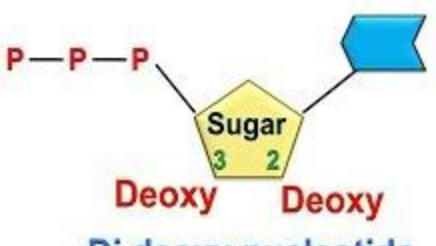
Pacific Biosciences  
PacBIO  
High price -> High quality  
Q30-40 data

# 1st generation Sanger sequencing



## Quickly understand


## Sanger's sequencing




**Deoxy Deoxy**  
**Di deoxy nucleotide**

	A	T	G	C
Tube 1	—	—	—	—
Tube 2	—	—	—	—
Tube 3	—	—	—	—
Tube 4	—	—	—	—

fluorescence



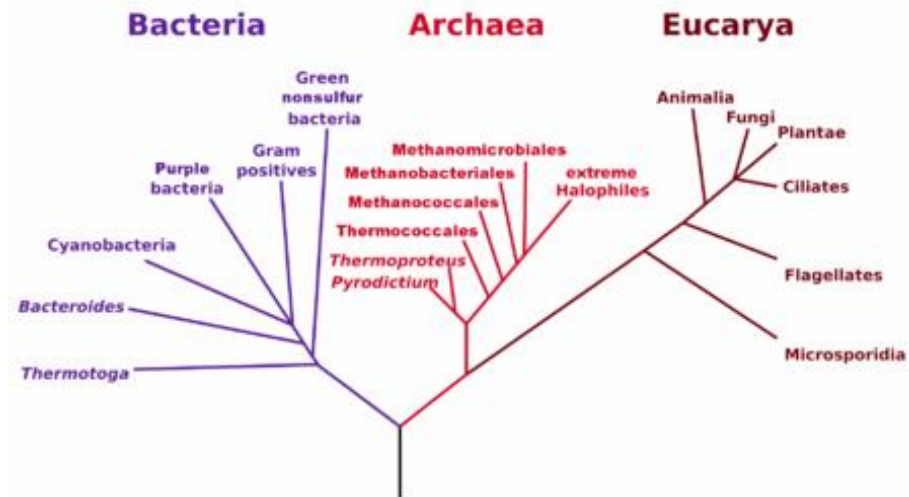


AAGCTTAGCC

# Sanger sequencing – The tree of life and the third domain



## Phylogenetic Tree of Life

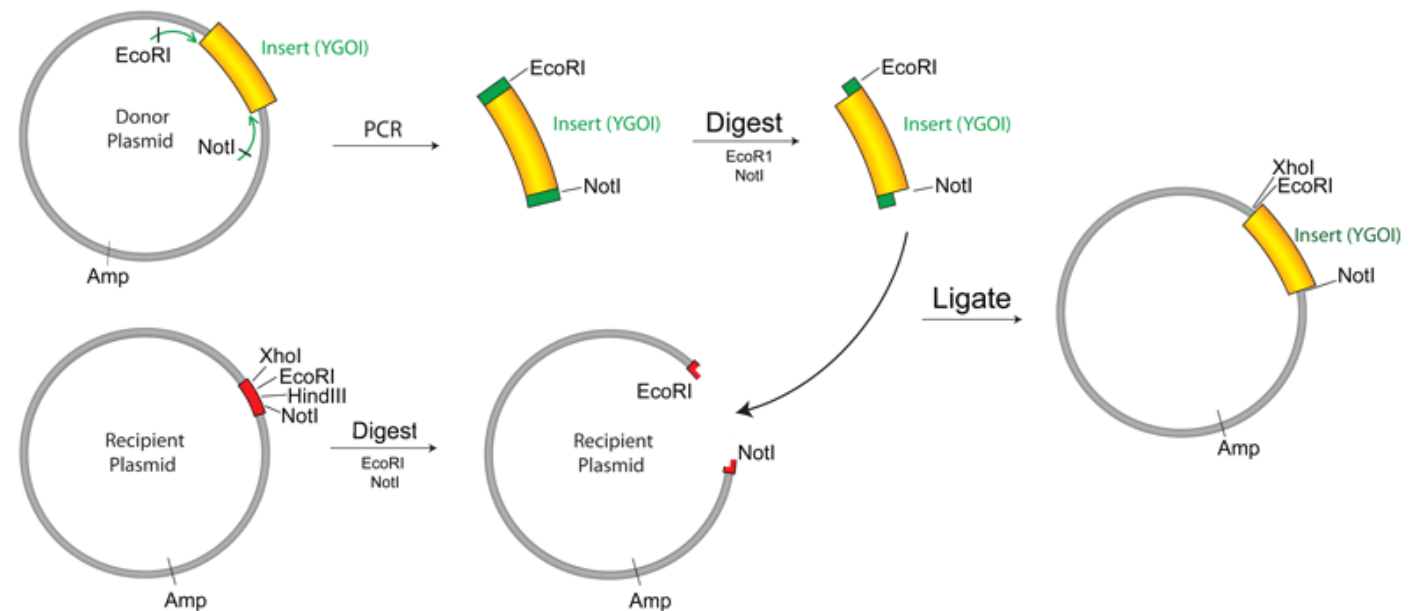


Carl Woese, 1928 - 2012

# Sanger Sequencing in use today

Still the method of choice for confirming correct insertion of gene fragments into plasmids for cloning

- Requires a primer site upstream of the insert site to act as starting point for the PCR reaction
- Read length  $\sim 1$  kb



# The rapid evolution of the Technology

## Sequencing the human Genome

2000  
1st generation  
(Sanger Sequencing)

Scientist: Hundreds  
Machines: Hundreds

Cost: \$3 billion  
Time: 10 years

2010  
2nd generation  
(Next-generation)

Illumina<sup>®</sup> - Sequencing  
by synthesis

Scientist: 1 - 2  
Machines: 1

Cost: \$5 – 10.000  
Time: 2 weeks

2015 - Now  
3rd generation  
(Next-Next-generation)

Nanopore<sup>®</sup> and  
PacBIO<sup>®</sup>

Scientist: 1-2  
Machines: 1

Cost: \$1000?  
Time: Hours

# The rapid evolution of the Technology

## Sequencing the human Genome

2000  
1st generation  
(Sanger Sequencing)

2010  
2nd generation  
(Next-generation)

2015  
3rd generation  
(Next-Next-generation)

Closed Bacterial genome <\$50

Scientist: Hundreds  
Machines: Hundreds

Cost: \$3 billion  
Time: 10 years

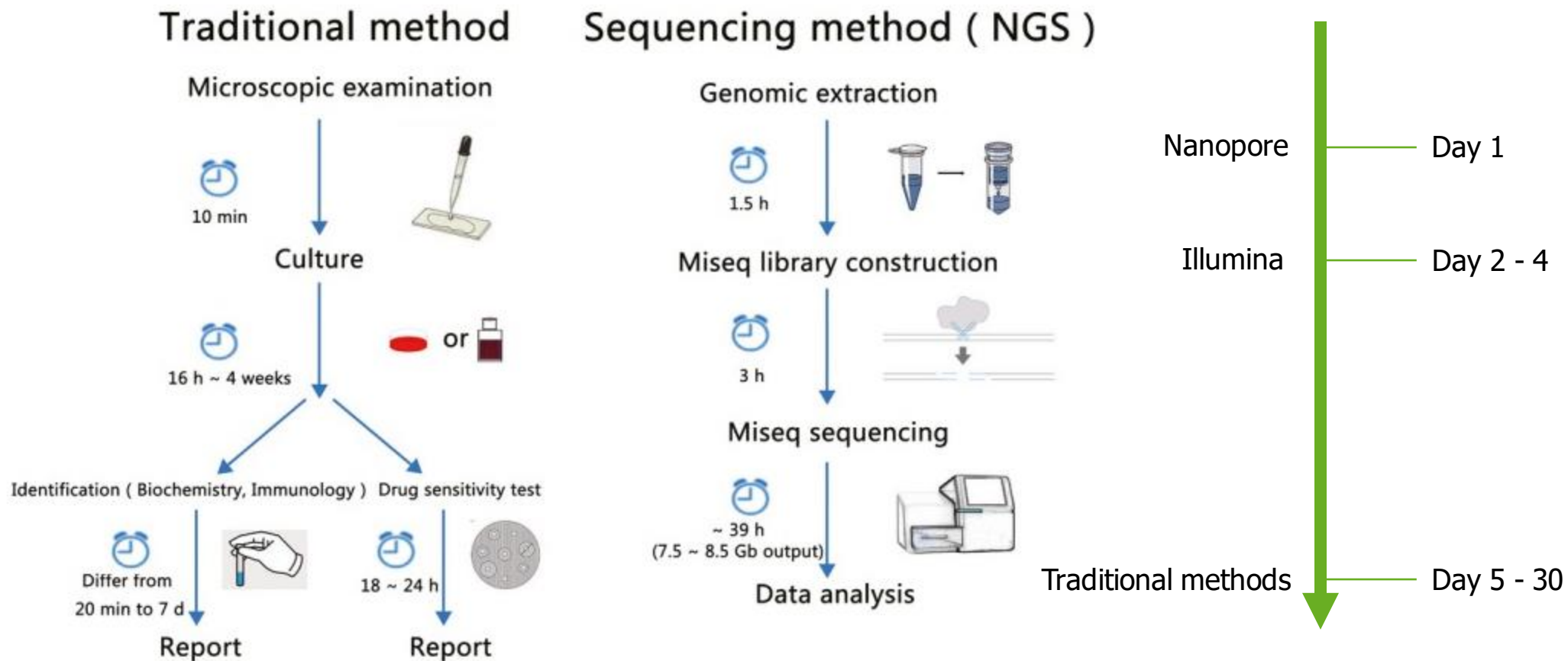
Scientist: 1 - 2  
Machines: 1

Cost: \$5 – 10.000  
Time: 2 weeks

Scientist: 1-2  
Machines: 1

Cost: \$1000?  
Time: Hours

# Why is sequencing an advantage - example from a clinical setting



# When is sequencing an advantage

## High resolution sequence typing (cgMLST)

- core genome multi locus sequence typing cgMLST

## Outbreak detection

- SNP = Single Nucleotide Polymorphism

## Resistance specific genotype

- Plasmid mediated resistance tracking

## Genomic epidemiology

- Evolution and spread of clones



# When is sequencing an advantage

## The genomic evolution SARS-CoV-2

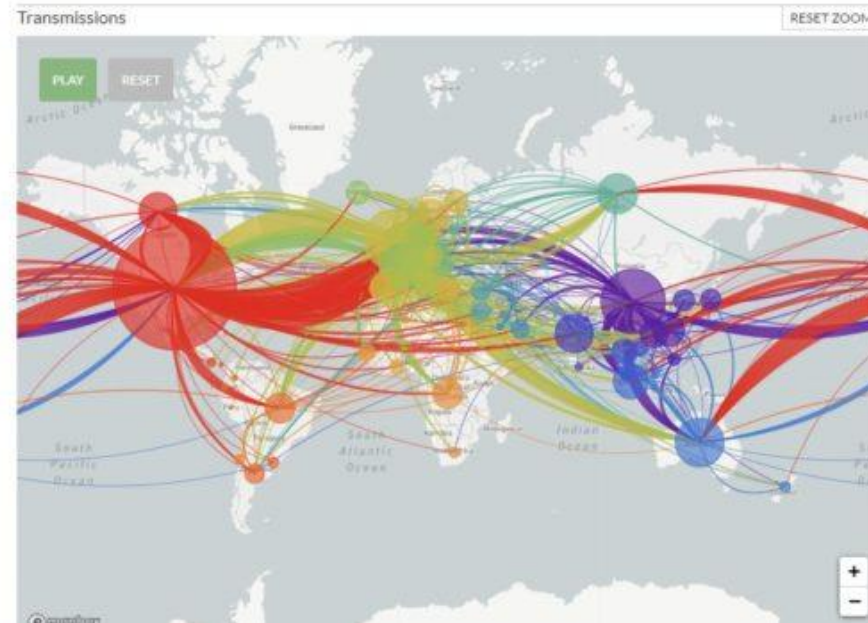
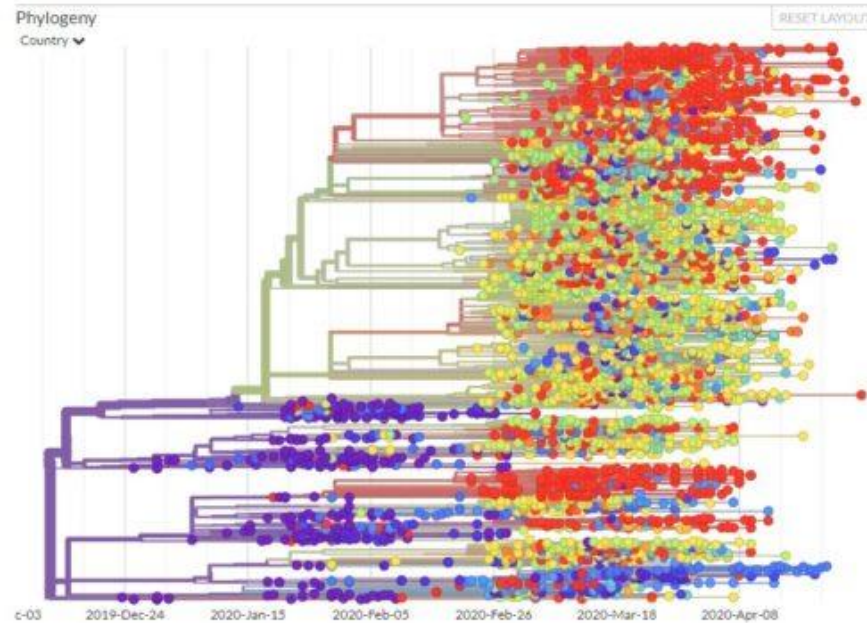
### Genomic epidemiology

- Evolution and spread of clones

Genomic epidemiology of novel coronavirus - Global subsampling

Maintained by the Nextstrain team. Enabled by data from **GISAI**

Showing 4645 of 4645 genomes sampled between Dec. 2019 and Apr. 2020.



# Selection of the most suited sequencing assay

## Sanger Sequencing

- Short single gene fragments
- Genetic constructs (e.g. gene insertions into cloning vectors)
- Research

## Massive parallel sequencing (Illumina)

- Short reads – High quality
- Genetic epidemiology
- SNP variant detection
- Research and Clinic

## Long Read sequencing

- Closed genomes and plasmids
- Research... but moving towards clinical applications(?)

**Which sequencing platforms do you have available?**

# Key take home

DNA sequencing is fundamental to modern surveillance of infectious disease including outbreak detection and genomic epidemiology

To select the right technology for the right task one need to think about

- The technology
- The sample
- The aim

# Acknowledgements

The creation of this training material was commissioned by ECDC to Statens Serum Institute (SSI) with the direct involvement of Søren Hallstrøm