Computational microbial genomics

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Chapter 1

Escherichia Coli general informations

1.1 *E. coli* genomics

Escherichia Coli is a Gram-negative, facultative anaerobic, rodshaped, coliform bacterium, it pertains to the phylum of proteobacteria and to the family of Enterobacteriaceae. It can be grown easily and inexpensively. It has got genome with a length between 4.5 - 4.7 M bases, including about 4000-5000 genes, and about seven ribosomal RNA operons. Only the 38% of the genes of K-12 (one of the most studied bacterial strains of *E. coli*) were experimentally identified, overall 40-50% of the genes are to date without a known function. The original *E. coli* strain K-12 was obtained from a stool sample of a diphtheria patient in Palo Alto, CA in 1922.

1.1.1 *E. coli* long-term evolution experiment

The *E. coli* long-term evolution experiment led by Richard Lenski is one of the longest evolutionary experiments ever made (search "*The Longest-Running Evolution Experiment*"). The experiment started on 24th February 1988, and since that moment 12 populations of *E. coli* have been cultivated in the same environment. After each day (corresponding to the time of development of approximately 7 generations), a portion of bacteria from each flask was introduced in a new one, and let proliferating in it. Every 500 generation, it has been saved a sample of the bacteria of each flask, in order to track the evolutionary changes made. Today the experiment is on-going, and researchers reached approximately the 66000th generation. The study suggests a series of conclusions, to cyte "long-term adaptation to a fixed environment can be characterized by a rich and dynamic set of population genetic processes, in stark contrast to the evolutionary desert expected near a fitness optimum" (Good et al 2017). In fact, despite of the fixed environment, some bacteria developed the capacity to aerobically grow on citrate, which is unusual in *E. coli* (around generation 31,000) and developed complex mutation patterns.

1.1.2 *E. coli* strains

E. coli could be found as commensal strains, pathogenic strains, or environmental strains. The pathogenic strains could pertein to these categories (which are not exclusive): enteropathogenic

(EPEC), enteroinvasive (EIEC), enterotoxigenic (ETEC), diffusely adherent (DAEC), adherent invasive (AIEC), shiga-toxin producing (STEC), enteroaggregative(EAEC), extraintestinal pathogenic (ExPEC). Resistances to antibiotics make even more difficult the process of categorization of *E. coli*. In 2011 in Germany, an outbreak of Stx-EAEC was responsible of the death of some people. An efficient counter-measure was found by sequencing the genome of those bacteria.

Shigella is *E. coli* with shiga toxin. It had been an issue for toxonomists.

Most of the genes are on plasmids, circular, additional to chromosome, and can be moved easily horizontally. Plasmids between different strains can be moved in enterobacteriacae, this doesn't happen normally in other families. Some *E. coli* strains are even capable of causing tumors in humans: for example, colibactin-positive E. coli can cause colon and rectal cancer, by creating mutations which are responsable of the of the cancer onset.

several antigens can be used by taxonomists to cathegorize *E. coli* strains. In particular there are the O, H, K antigens, respectively related to the somatic, the flagella and the capsule. O antigens are 171, Ks are 80 and Hs are 56.

1.1.3 PanPhlAn - strain detection and characterization

Pangenome-based Phylogenomic Analysis (PanPhlAn) is a strain-level metagenomic profiling tool for identifying the gene composition and in-vivo transcriptional activity of individual strains in metagenomic samples. PanPhlAn's ability for strain-tracking and functional analysis of unknown pathogens makes it an efficient tool for culture-free infectious outbreak epidemiology and microbial population studies (PanPhlAn reference). This tool was for example used to study the strain responsible of an outbreak in Germany in 2011. This strain was a shiga-toxigenic Escherichia coli (STEC), and the study was conducted by Loman and collegues in 2013. This method outlasted the traditional one.

sequencing means generally to sequence everything, it's normally difficult where to find it, although in E. coli is quite easy to understand the provenience. from all the world, populating diversity of E. coli, every time we sample we find points which are different from the reference genomes. points overlapping are people living together and share bacterias

1.1.4 Genomes of *E. coli*

In the genome of *E. coli* strains, it is possible to distinguish:

- **Core genome**: the set of all genes shared by all membrers of a bacterial species, it includes 1000 up to 3000 genes.
- **Accessory or dispensable genome**: the set of genes present in some but not all genomes within the same bacterial species. found on a single strain or in a subset of strains.
- **Pangenome**: core genome + accessory genome. set of all the genes foundable in the species strains. It is said to be ***"closed"*** when pangenome size tends to a maximum as number of genomes increases, instead it is ***"open"*** when pangenome keeps increasing as you add new genomes

Sequencing more organism of the same species means to lower the amount of genes in the core genome and augment the numer of those in the pan-genome (figure **??**). Because of technical problems the probability of getting a gene and not forget it is different from 0, so why probably the sequencing of other genomes would lead technically to a plummet to 0 of the pangenome. With some mathematical formulations we can predict a more probable plateau (Rasko David 2008).

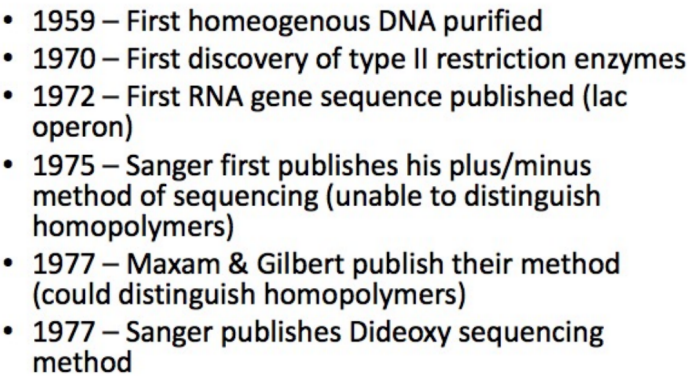
each *E. Coli* genome contains in a balanced way genes of the core genome and of the pan genome, for a total amount of genes correspondant to about 4700 genes (figure **??**). Core genomes' genes are responsible of some basic cellular functionalities and utilities to survive environent, while instead elements of the pangenome are quite usually specific to the single strains, they are not always functionally well known.

ratios of the pan-genome and the core-genome are not equal in other organisms behave differently.

Chapter 2

NGS principles (second gen. sequencing) - From Sanger to third gen sequencing

Figure 2.1



NGS stands for ***Next Generation Sequencing***, and it represents the method of sequencing most used nowadays. Before that, a series of other discoveries were done, elencated in the figure 2.1.

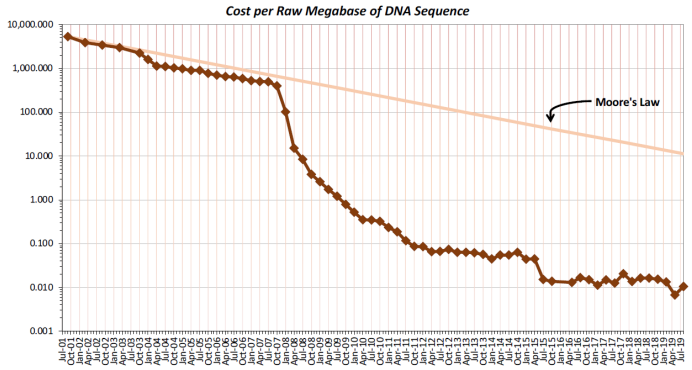
2.1 History of Sequencing

2.1.1 Progresses of sequencing

As the time passes, the cost of sequencing the DNA is diminishing. The rate of decrease actually is higher than the one predicted by the **Moore's Law**, *"Democratization of sequencing"* is seen nowadays, because of the costs lowering. After the Human genome project, several other animals and plants' genomes were sequenced.

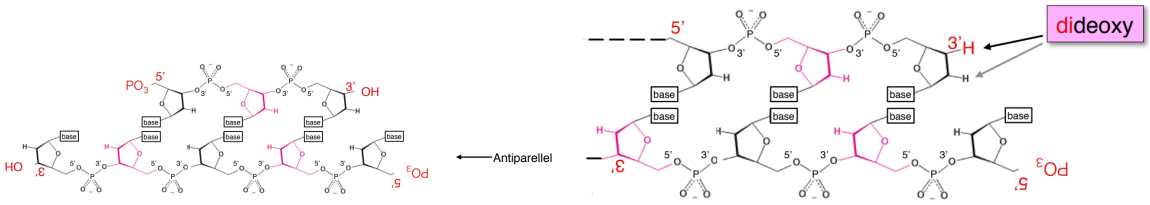
The methods of sequencing actually can be grouped in three **groups**, that are:

Figure 2.2



- **Chemical degradation** of DNA: it includes the method of Maxam-Gilbert
- **Sequencing by synthesis ("SBS")** which is the most common approach and the first to be developed. It uses DNA polymerases in primer extension reactions Illumina, Pacific Bioscences, Ion Torren and 454
- **Ligation-based**: sequencing using short probes that hybridize to the template, the technologies perteining to this class are SOLiD, Complete Genomics
- **Other:** Nanopores

2.1.2 The Chain Terminators



(a) Normal DNA molecule, with oxydrilic group ligated to 3′-ends

(b) Figure representing the difference between a normal DNA chain and one with chain terminators

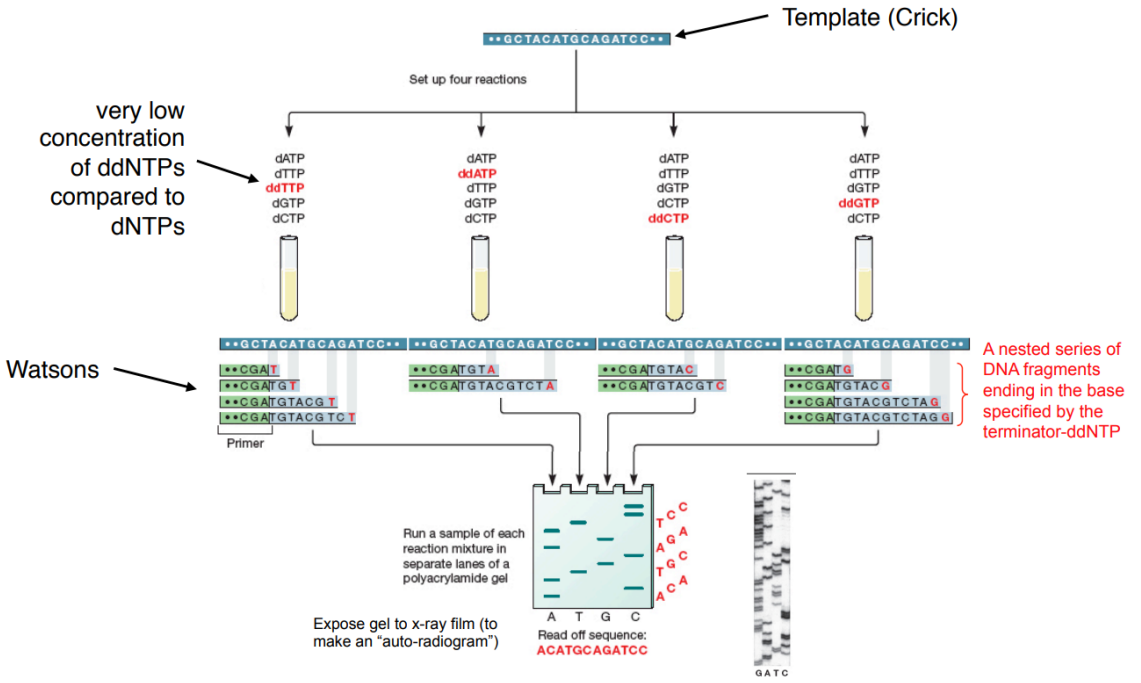
Figure 2.3: Normal DNA synthesys *vs* Chain terminators

Normally, the addition of new nucleotides to a generated molecule of DNA happens with the 3′-end of the nucleotide chain (figure 2.3a). Chain terminators are dideoxy nucleotides, ddNTPs, that cannot be further extended. These nucleotides aren't able to add a new nucleotide on the 3′-end, as they have not the needed oxydrilic group (figure 2.3b).

2.1.3 Sanger method: the first one

The first method ever used to sequence DNA was designed by Frederick Sanger. The Sanger manual sequencing system consists in an *in vitro* process, which is described in figure 2.4, also named as

Figure 2.4: The *Sanger*'s method process



"primer extension" method. It is performed over a single-filament DNA sample, and it uses the chain terminators nucleotides, a type for each nucleobase: ddATP, ddGTP, ddTTP, ddCTP.

The reaction is done inside four different reactions tubes, each containing the sample DNA to be reproduced, a DNA polymerase, the normal nucleotides and one of the four possible chain terminator. The chain terminators are marked with sulfur-35, a radioactive atom. In each tube, the corresponding dideoxy-nucleotide was used with a concentration 10 times lower than the other "normal" nucleotides.

From the polymerization reactions, several molecules of DNA were produced, with different length: each replicative cycle is in fact terminated after the addition of a chain terminator nucleotide.

To reconstruct the initial DNA sequence, a long PAGE gel was prepeared, with high concentration of urea $(6-7M)$ to avoid the coiling of the DNA single-filaments. To run the gel, high voltages were required and it had to be higly resolutive, as DNA's fragments are different only for a nucleotide. It was needed to do an auto-radiography of the gel in order to see the bands, in order to evidentiate the fosphorescent signals.

To read the sequence you have to start from the shortest fragments, at the end of the gel, and carefully go up along the gel, looking for the first presence of a band in one of the four runs.

Past procedures: In the past, the Klenow's fragment (part of the 1^{st} DNA polymerase) was used to perform the Sanger method, and the DNA to be sequenced was inserted inside the genome of an M13 phage.

2.1.3.1 Automatic sequencing

It does not use the radioactive signals, instead it uses fluorescent proteins. Several versions were developed after modifications of the Sanger method, in this order:

1. fluorescent primers marked with a single fluorochrome.
2. four aliquotes of the same primer were used marked with four different fluorochromes, able to emit different fluorescences.
3. four different fluorochromes were used to mark the single ddNTPs

Thanks to the use of 4 different fluorochromes, it was possible to use a single electrophoretic lane to carry the sequencing reaction. For this type of sequencing also, a cyclic replicative reaction was performed, with this procedure, made possible by using a thermal cycler:

1. **Denaturation at** $95°\mathbf{C}$ of the DNA to be sequences
2. **Annealing at** $50 - 70°\mathbf{C}$ of the primer specific to one of the two filaments
3. **Extension at** $72°\mathbf{C}$ by using a *Taq*-polymerase. The use of the Taq-polymerase makes it possible to avoid the formation of coiled structures in the DNA molecule to be sequenced.

Traditionally, also in this type of sequencing it is used a long PAGE gel, as the Sanger's one, but with a great difference: all the ddNTPs are inserted in the same electrophoretic run, and after it, it is not needed an auto-radiography. Fluorescence, instead, can be triggered simply by irradiating the DNA molecules synthesyzed, which produce different fluorescences with different wavelengths.

More usefully, this sequencing method is performed by using a capillar, filled with a synthetic polymer, with the same function of polyacrillamide.

At the end of the analysis, it is produced an electropherogram, with a color depicting the probability of each nytrogen base in each position. The production of the electropherogram is made better thanks to algorithms to boost signal/noise ratio, to correct the dye-effects, and other effects that generate systemic errors.

Regarding the Sanger machines in use, the upgrades viewable in figure **??**. Based on the same technology, new machines were developed and it was obtained a $\tilde{1}000$ fold improvement.
When talking about the **human projec**t, it is important to specify that most of the job was done by using the Sanger automatic sequencing method.

2.2 Development of Sequencing Machines

The way you can get to the point could be different based on technology and the wanted output, comprised quality.

SOLID gave only 35-75 sequenced bases, and it is not used anymore; Sanger sequencing, the capillary, can give up to 1000 read length, with a low output; on MINION it was possible to sequence an entire genome of *E. coli* A pletora of sequence machines are available today. None of the machines are able to sequence DNA from a sample of blood, some things have to be done. Nowadays machines producing bigger outputs of short reads are prefeared.

Figure 2.5

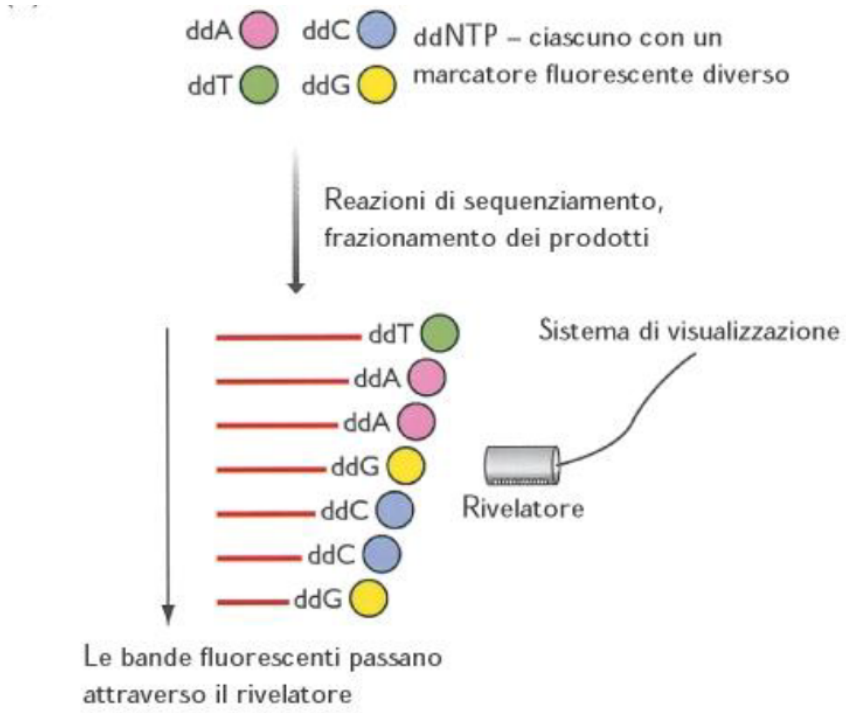


Figure 2.8: It can be noticed how recent developments had the scope of increasing the output data

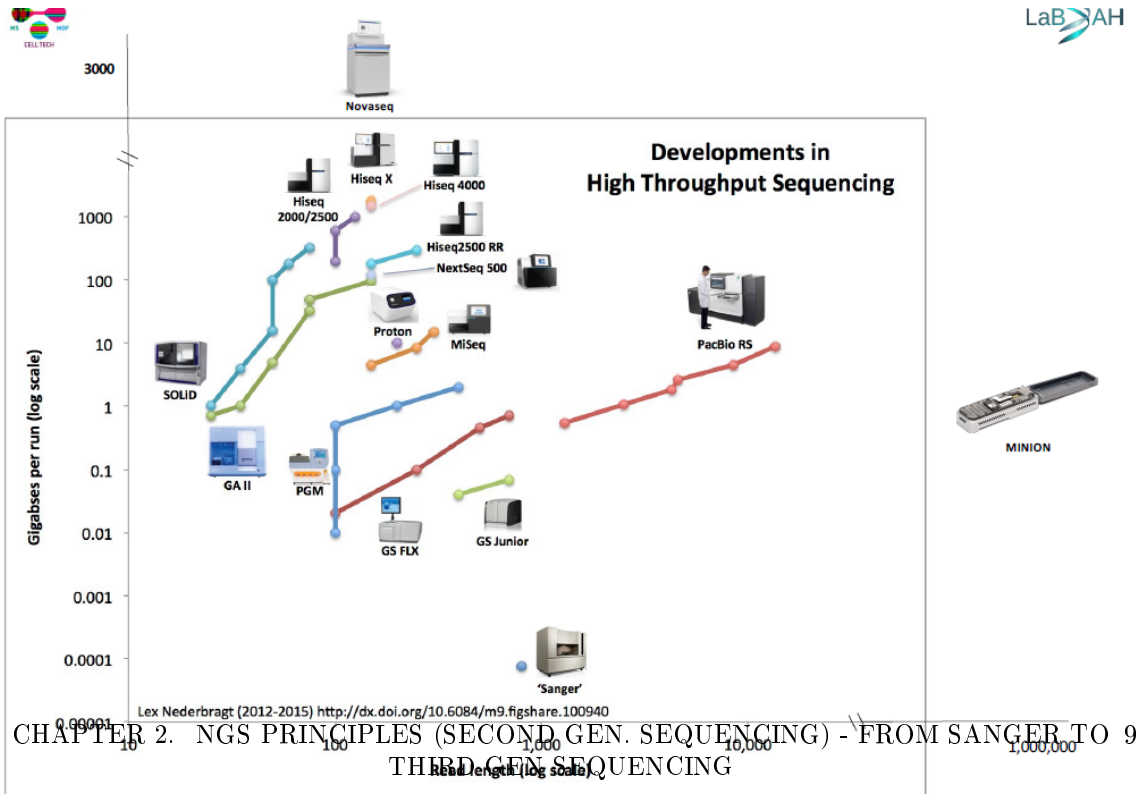
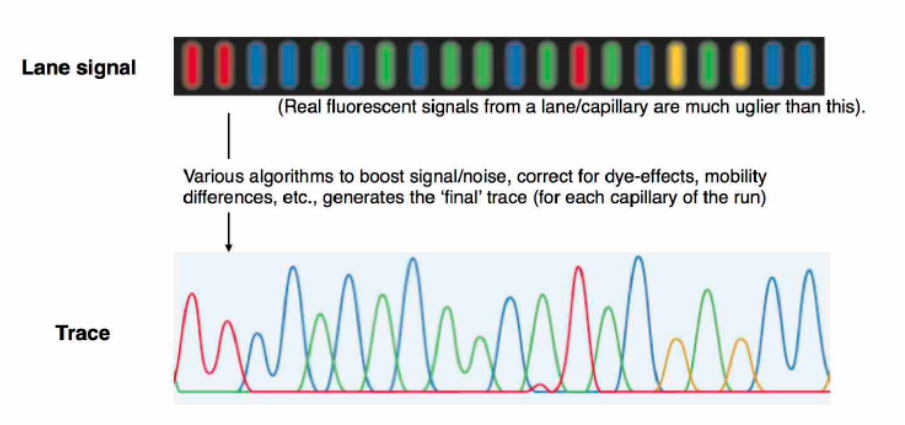
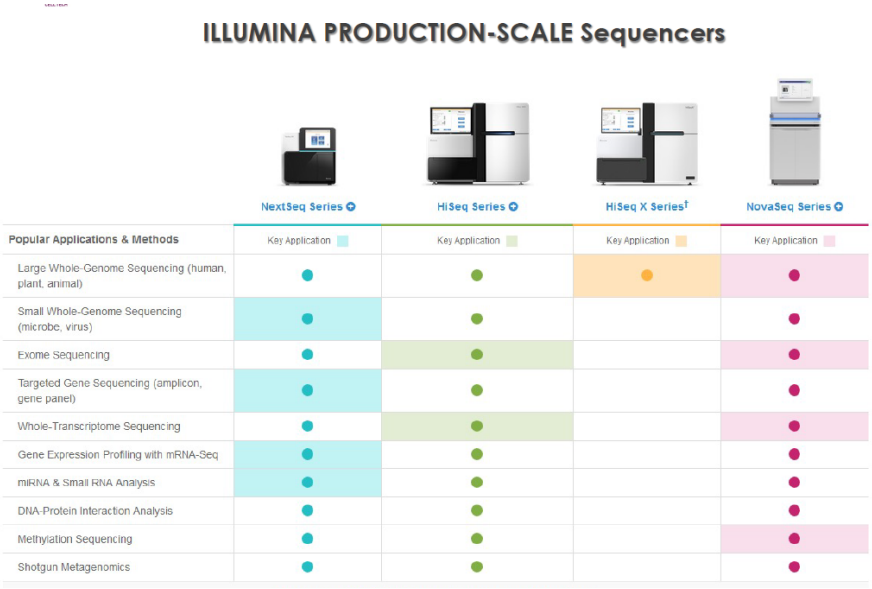


Figure 2.6



At the top of the market nowadays there are ILLUMINA machines, that use sequencing by synthesis method, NovaSeq is the biggest one. They need to amplify the signal through clusters formation.

Figure 2.9



2.3 Next Generation Sequencing NGS

The NGS protocol requires 3 steps, that are:

1. **Sample preparation**: series of fragments added

Figure 2.7: The implementation of capillary sequencing machines gave the possiblity to make more runs than with the others. A $\tilde{1}000$ fold productivity increase was allowed

Radioactive
polyacrylamide
slab gel
Low throughput,
labor intensive

AB slab gel sequencers
(370, 373, 377)
Fluorescent sequencing
1990-1999
6 runs/day
96 reads/run
500 bp/read
288,000 bp/day

AB capillary sequencers
(3700, 3730)
1998-now
24 runs/day
96 reads/run
550 – 1,000 bp/read
1-2 million bp/day

2. **Clonal amplification**: which is is needed to replicate fragments attached to the solid surfaces, since machines are not sensible to single molecules

3. **Sequencing**: ILLUMINA sequencing is one of the techniques used to obtain sequence data nowadays

Tools pertaining to the 3^{rd} generation are those that permit to read a molecule without replicating it.

2.3.1 Fragments/Library preparation

Most of the sequences sequenced are fragmented in short read sequences, since most of the machines today used aren't able to sequence reads longer than some hundreds of nucleotides.

The fragments obtained have to be prepeared for the sequencing process, through a process called **tagmentation**. The obtained fragments are shown in the figure. Those fragments are provided with one or two indexes, called also barcodes, two sequencing primer binding sites and regions complementary to the oligonucleotides present in the chamber (see in Clonal amplification chapter). The fragments' length has to be checked, depending on the scope of the process. Indexes are needed to run sequencing process on multiple samples, they are needed to distinguish those; when they are two, they permit to distinguisch also the 2 types of sequencing that are performed, forward and reverse.

P5 and P7 are the oligos needed to attach fragments to ILLUMINA sequencing machines.

2.3.2 Clonal amplification and ILLUMINA sequencing procedure

Clonal amplification are necessary to amplify the signal from each single fragment. ILLUMINA machines make use of clusters to sequence DNA. Clusters are a group of DNA strands positioned closely together and generated from a single DNA filament. Generally, Each cluster represents thousands of copies of the same DNA strand in a 1–2 micron spot (figure 2.11).

Figure 2.10: Figure representing the a good prepeared fragment, it has two indexes, two sequencing primer binding sites and regions complementary to the oligonucleotides present in the chamber

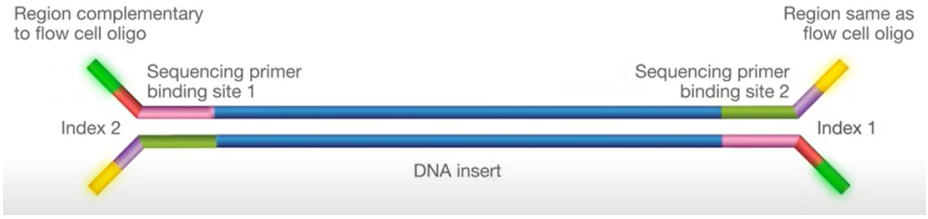


Figure 2.11

On patterned flow cells, the clusters' formation location could be known or not, in the first case it is said that there is a "Rigid registration" (figure 2.12).

ILLUMINA sequencers normally use slides of glass, named flow cells, and the fragments to be sequenced are able to flow over the channels. The temperature inside the cells can be changed to produce ligations or separations. The surface of the cells is functionalized with a series of oligos complementary to library adapters.

Two kids of flow cells, the *patterned* flow cell permits to create clusters in specific positions, inside nanowalls, contrarily to *Random Flow Cell* which instead have randomly positioned clusters.

Once the fragments are made flow over the chambers, they can bind only to p5 or p7 (ILLUMINA oligos), the two oligos functionalizing the plate. Once the fragments are attached to the surface, using temperature and solvents flows you can control the sequencing process. To see the entire procedure: (procedure on Youtube: video about ILLUMINA sequencing). In the video, it is shown the two index sequencing process.

Figure 2.12

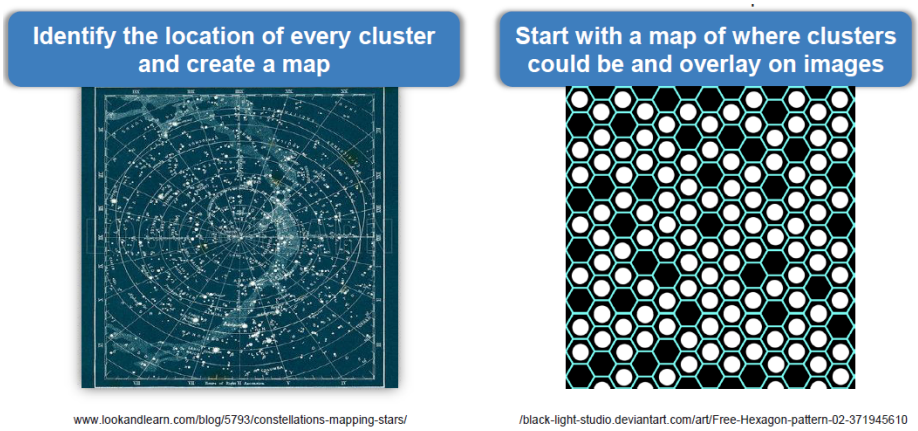
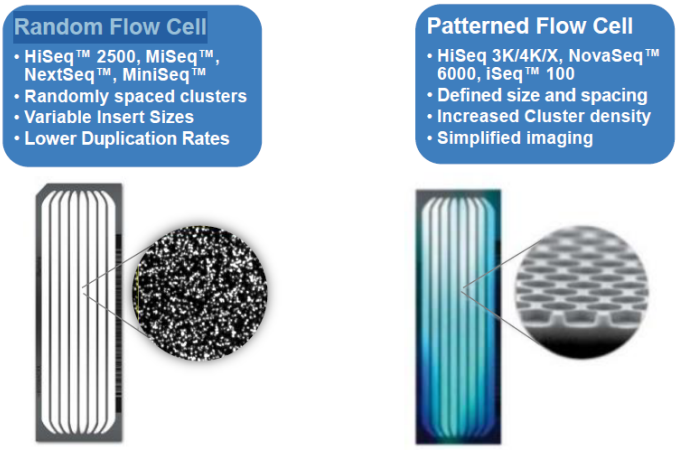
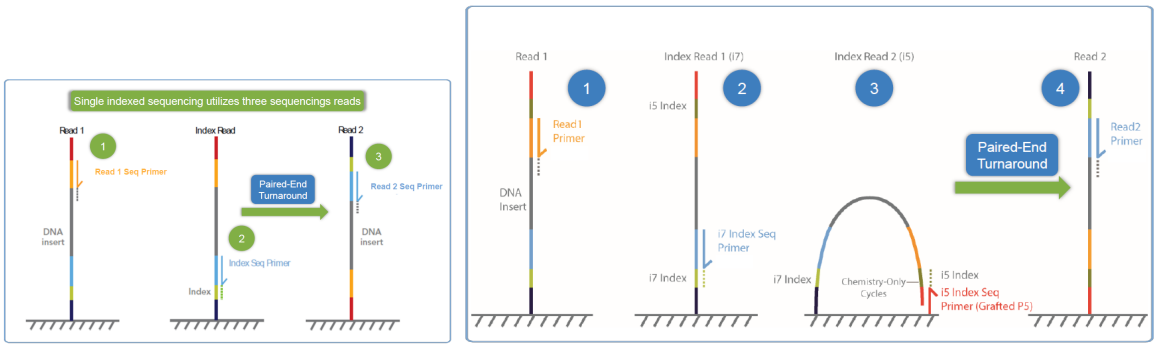


Figure 2.13



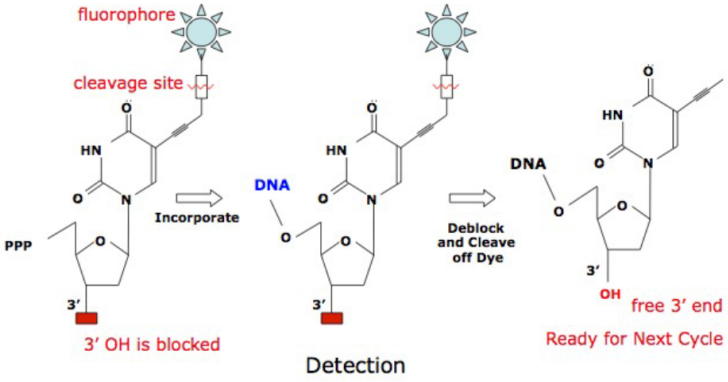


(a) single index **(b)** double index

Figure 2.14: Single/double index for ILLUMINA sequencing

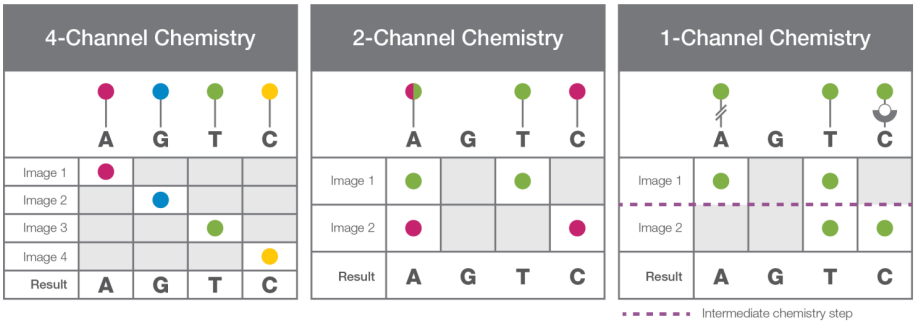
With 1 and 2 indexes the sequencing process actually differs, as shown in figure 2.14

Figure 2.15



To perform the sequencing process, ILLUMINA machines utilize *reversible terminators* (figure 2.15). They permit a real time analysis of the sequencing by synthesys reaction, and because of this they are different from the Sanger method. Fluorophores are reversible, they can be cleaved to eliminate the light signal.

Figure 2.16



To perform their activity, ILLUMINA sequencers could be of 3 different types: 4-Channel, 2-Channel or 1-Channel, depending on the number of fluorescent molecules used. In the case of the 4-Channel technology, 4 images are taken in each cycle, and each cluster appears in only one of four images 2.16. 2-Channel technique is used by some sequencing machines, like NextSeq 550, MiniSeq, NovaSeq 6000

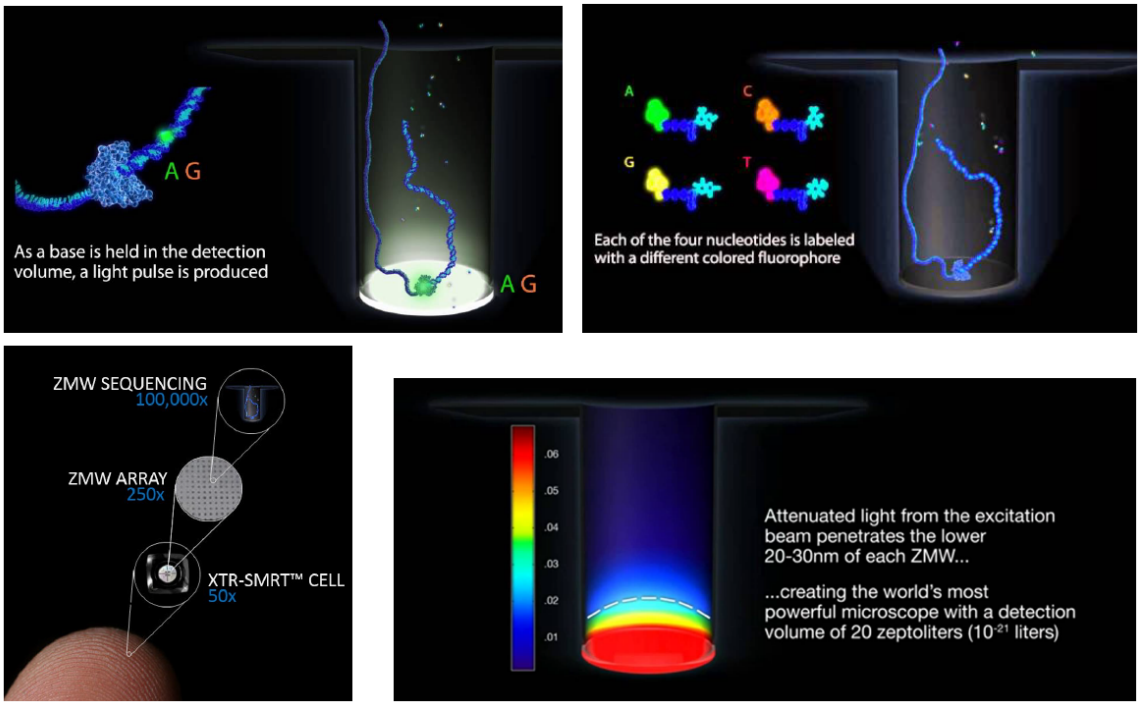
4-Colors base calling is needed to to make the true signal the purest, and after, The base with the highest intensity becomes the called base for that cluster. In the case no base is clearly related to a position, N is the result.

The reading process could be done in two ways: through single reads, on a single extreme of the fragments, of paired-end, on both the extremes. The second one in particular gives structural and 2 sequence informations.

2.3.3 Pacific Bioscience (PacBio)

the long DNA filement to be sequenced is attached to a polymerase, over the surface of a SMRT (Single Molecule Real Time) cell. This cell is really small, and at each nucleation process a light signal is emitted. The produced light is not able to get out of the walls, and its duration is extremely restricted. Sequencing, also in this case, is made by sequencing, and the main advantage consists in the possiblity of sequencing really big DNA molecules.
In the video PacBio procedure it is briefly shown how the process works and what are the strategies used to reduce errors.

Figure 2.17



2.3.4 Nanopore sequencing

Intramembrane proteins are used, sequence detected through the passage of DNA nucleotides, which produce different voltage changes. During the first periods, this type of instruments gave great amount of errors, nowadays the technique is improving. Nanopore Sequencing

input fragments. the order of the contigs cannot be established unless we have a connection. De novo assembly without prior information about the sequence of the organism. Sometimes it could be useful to use abailable reference sequences. Artifacts have to be discriminated. It is possible to genearte a consensus sequence.

Sequence mapping aligning: find dna sequences dsimilarities betwen query sequences and reference sequences.

2.4 Sequence mapping

Query short sequence and reference is much longer. Could be deletions, insertions, substitutions. THe first rwo can be longer than 1. You would search for the best match or the best matches, or all matches, the latter is very computationally demanding.

2.4.1 Coverage

Average numberof reads representing a given nucleotide in the reconstructed sequence. Some positions could have 0 coverage.

$$Cov = \frac{NxL}{G}$$

where G: length of hte genome, N: number of reads, L: average read length.

The coverage is an essential parameter, more coverage means more reads to do.

Exercise: I want to sequence a genome which I knw is 3M bases. I can use Illumina single.end sequencing with read length of 100 nt.

From sequence comparison it is possible to obtain new informations.

Simplest aligning algorithm: start from 0 position and slide along the sequence. It doesn't consider indels.

Global alignments focuses on total sequence, while local alignment only in fractions of the total sequence.

Evolutionary distance doesn't reflect precisely evolutionary distances when the observed percent identities are low.

2.4.2 Smit-Waterman algorithm

"Identification of Common Molecular Subsequences", how many changes to make two sequences identical. they wanted a solution such that gives the best matches.

We have to find best substrings. It has to be built a big matrix, consider a score, used when nucleotides match or not. Populate the matrix, in each cell a number described by the formula. Select values of match and mismatch and a penalty value for gaps.

more than one best solutions.

This is not used anymore, as it would result in too much computational expense.

2.4.3 Needleman-Wunsch algorithm

Optimal align algorithm. initialized with 0, 0 is not possible anymore for iteration. Termination in the bottom right corner.

If we want an accurate alignment, these algorithms could in some cases used. People developed different strategies algorithms, FastA, Blast, BLAT, BWA, BowTie2. THe last two are optimized for short reads. heuristic means that you are considering a threshold, if a certain level of identity is not respected, than the program doesn't retrieve any output.

2.5 Blast

very used nowadays, still working. Allowed sequence matching to everyone through affordable computers. It can be run online, they set very high seeds, to avoid computing too much

Find k-mer matches. Once you find some good seeds, it is possible to extend the matches to seee if there are some more extended regions. The evaluations are made with algorithms inspired on...

k is generally between 5 and much larger numbers.

several BLAST programmes are available depending on the type of need.

E-value: the number of distinct alignments with a score equivalent to or higher than S, that are expected to occut in a dataase search by chance

$$E = Kmne^{-\lambda} \tag{2.1}$$

There is a relation between P.value and the E- value. P-value: the provavil to obtain by chance another score with an equal or better score.

$$\frac{E}{mn} \tag{2.2}$$

where

1. Parameter K and λ depend on the substit matrix and on the gap...

2.5.1 Scoring matrices

A protein which changes an AA with another not always changes it with a completely different AA. Points are established through biochemical evaluations.

2.6 Spaced seed alignment

They are not used anymore. Reads are cut down in small seeds. The seeds are stored in an index, and then seeds are searched inside the sequence.

It is possible to have SNPs. The look up table is actually enormous in human genome

Maq, SOAP, MOSAIK, Novoalign are based on this approach.

2.7 Burrows-Wheeler transform

Reversible permutation of the characters in a text. Compress a file, it takes a lot of time to compress a file.

Fast reconstruction using the LF property: the ith occurrence of character X...

Several ways to decompress com

Chapter 3

Sequencing data

After all, genetics/genomics studies a code of a digital information (4bases/2bits). We should try to be as hypothesis driven as possible and use the already available and processed data to guide new data analysis. Be aware that, in genomics, data generation is the starting point of the study (the ratio of wet experiments vs computational effort is 1:10)!
Given the biological problem at hand, we need to choose the optimal sequencing machine. To achieve this, we need to consider:

- Throughput;
- Cost;
- Read lenghts,
- Data output (reads per run);
- Coverage;
- Seuencing errors (indel, substitution, CG delation, AT bias). Altough the error rate is decreasing wit new technologies;
- Library preparation compatibility;
- Speed (run time)

Suppose that we want to sequence a genome of a bacterium: which is the best machine that we can use?

Illumina NovaSeq : if one wants to sequence a lot of DNA molecules at the same time, genomes, metagenomes. It can't go over the 300 bp readlines runned, but it has the highest throughput so far (3TB of output). It is capable of multiplexing, so we have a unique barcode for any input sample.

Illumina iSeq : If you need to sequence shorter genomes. From iSeq to NextSeq (increasing the reads lengths).

NanoPore (minion) : pocket-sized wet-lab free sequencer for DNA, RNA and (possibly) proteins, but the read lengths is smaller than Illumina's. The machine is cheap; the running flow is more expensive (going down by time). It's a real-time sequencer.

Chapter 4

Staphylococcus aureus