# High Throughput sequencing and biological research:

# Paradigm switches from genetics to ecophysiology

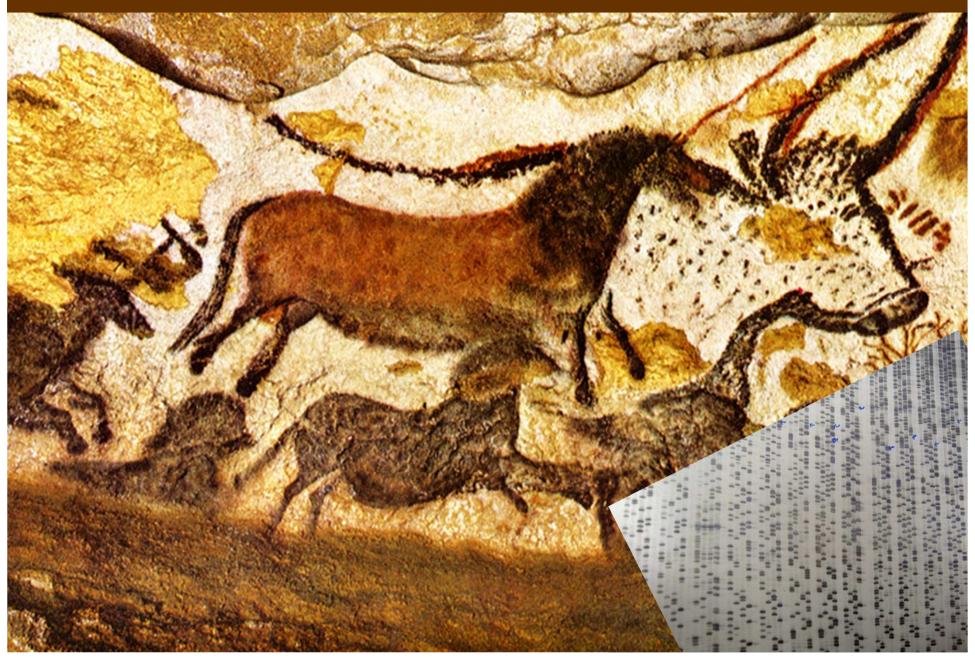
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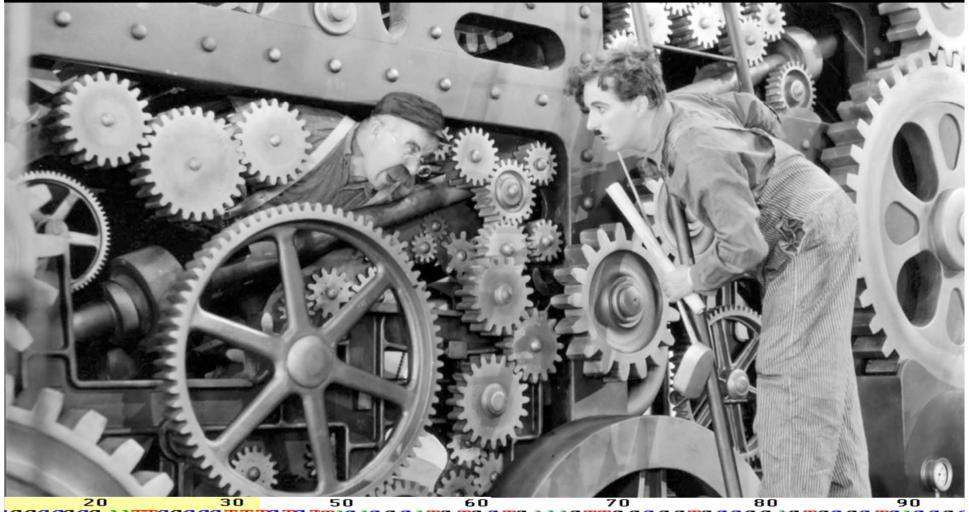


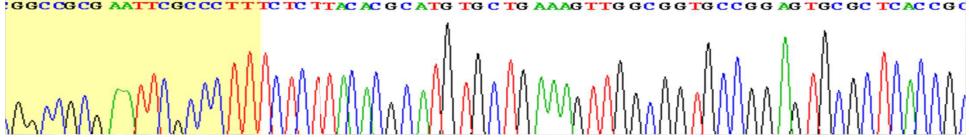
90'ies 1.000



## 2000'ies

## 1.000.000



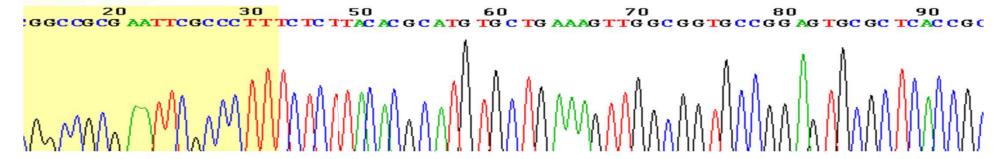










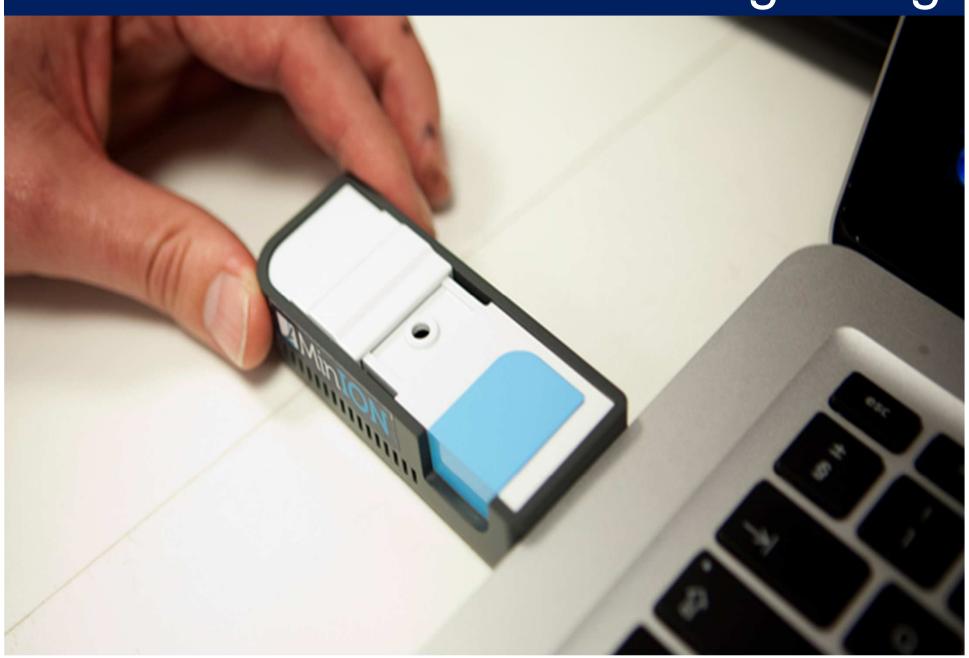


## 4.500.000.000.000

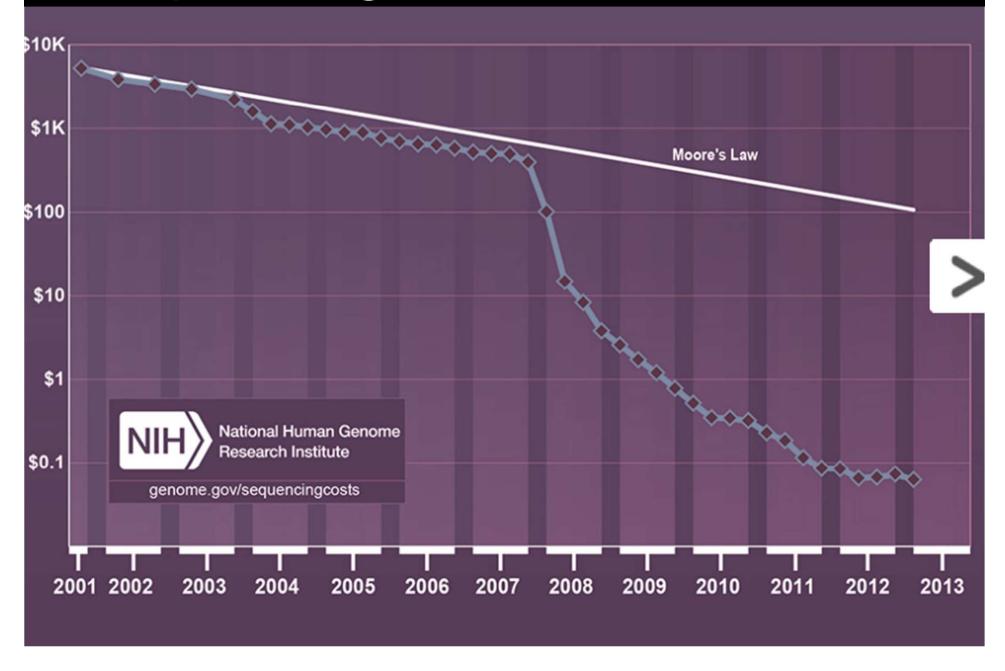


## 2015

## Next Big Thing



## Cost per megabase



## Sequencing as « Big Science »



Encyclopedy of life is available



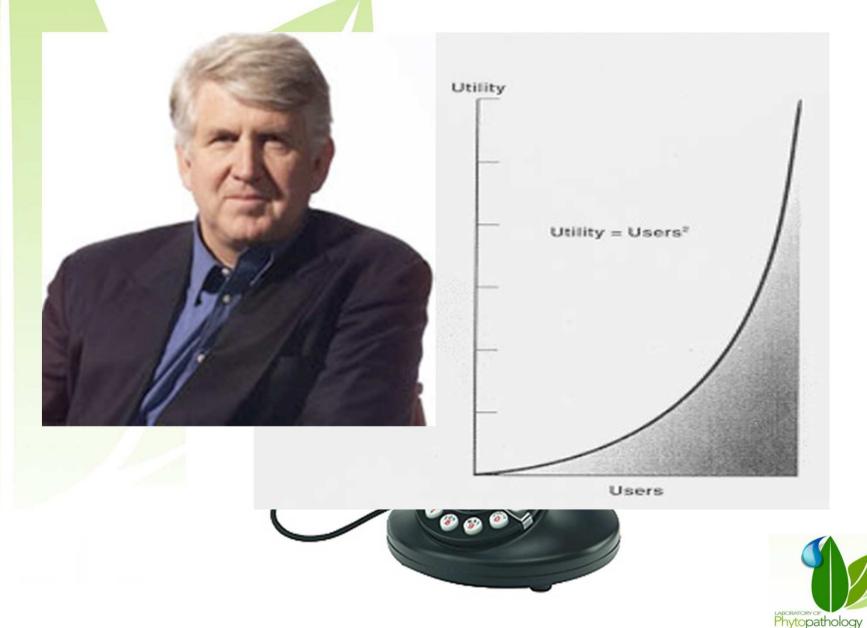
Smart harvest is revolutionizing R&D



Genome-based R&D?



## Genome knowledge & phone



AACGTCTGCGTCCTGCTGTCCCAGAGCCGGC CCATCGACGCACAGGCCGAGATGGCCCTGCG SATCAAGGCCCTCAACACCAGGAGGCGGTGG AGAGGCAGGGGCTGCCAGTCACCCCACAAAA



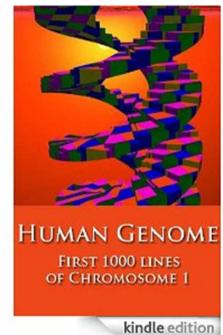
CCCCACCTGACCCACAACGTCTGGTCCTGCT TCTGTGAGATGGACCTCATCGACGCCACAGGCC GTCCTGAACTGGGCCCATCAAGGCCCTCAACA TTTTGGGGCCAGCCCAGAGGCAGGGGCTGCCA



GGCTGTTTGAGGAGCCCGACCTGACCCAG GCGGTCCGAAGGCTTCTGTGAGATGGACC TGGTCTTCAAGGCCGTCCTGAACTGGGCC AAACAAGAGGCATGTTTTGGGGCCAGCCC

AATTCCAACCATCACCCTACACCACTTT IGGAGGAGACC CAAGAGGAAGG CAGTACCGCGG **IGTGTGGGTCC** GCTCAGAATC STCCAGGTTGA GCAGGAGGGG CAACGGGACTG **IGCAGCAGGTC** CACTTAACCTT CACAGCCAGAG AAGATTTAGGG GCATGTTCCTG( AAATCGGCAAA CAGAGCCGCTC CCCGACGCCCC CCCACAGCAAC CGCGCCCGCGC GCGAGAGGAAC GGCGACCAGGA TACTGGGACCT TATTAAAGTAC TAAGAAGTACA AACGTCTGCGT TCATCGACGCA

GATCAAGGCCC



#### Human Genome: First 1000 lines of Chromosome 1 [Kindle Edition]

Eliana Brown (Author)

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Kindle Price: \$33.34 includes VAT & free international wireless delivery via *Amazon Whispernet* 

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COCA A COCCOCTOCCCAGTCAGACATCCA ACAAGCCCCGCCTGG GTCTTCTGCCTACCG AGAAGGGTATTTATT TTGAGCTCAAGAGGC CACCTTCCCGGTCTG CTGGATGGCAGCAAC TCCAGTTCCAGTGCT CTTCTATGCCTGAGG AACTGCTTCTTGACA TGATTCTGTGAAGTA ACACTGGGGTGCATG GCACCCATGCCACCT TTAACTGTAGACCTT AAGGTTGCCTACAAT GCGGGGGTCCACAGG :CCCGCCAGCGCCGCG :AGCGCAGCCTGCACC CCCCAAATGGCGCGG ACGTGCACTTTGTCG :CTGCAGCTCCGTCTT GACTTGGAGCCCGCA ATACGGTGCTGGCCA CTTTCTGGGGACAAG CCCGACCTGACCCAG TCTGTGAGATGGACC :GTCCTGAACTGGGCC

### Bio-IT in 2010







## **Bio-IT in 2014**







### **BioIT:** how does it works?

#### de novo assembly:

CTGGGTGTTTAACAAAACTATGCTCACAAACAAC

CAAAACTATGCTCACAAACAACAAGTCCTCCTAT

Aligned seq.

GTTTAACAAAACTATGCTCACAAACAACAAGTCC

GGTGTTTAACAAAACTATGCTCACAAACAACAAG

TAACAAAACTATGCTCACAAACAACAAGTCCTCC

Contig assembly

CTGGGTGTTTAACAAAACTATGCTCACAAACAACAAGTCCTCCTAT

#### Mapping on reference genome:

Reference genome

Mapped reads

AAGCCCAACAGTAAACATATGGTGAGCCCAAACCATGAAGCCAAACGTTGCTATTCCTATCATGGCATAAACCATTCCCATATAA

CAACAGTAAACATATGGTG

**ACATATGGTGAGCCC** 

TTGCTATCATGTCATAAA

ATTGCTATCATGTCATA

CTATTCCTATCATGTCAT



## Balance between wet lab and computer





#### **Prenatal detection of Trisomy 21**:

- ✓ Clinical test in Belgium from 2014
- ✓ Easy, quick and cheap pre-screening test from maternal blood
- ✓ More than trisomy

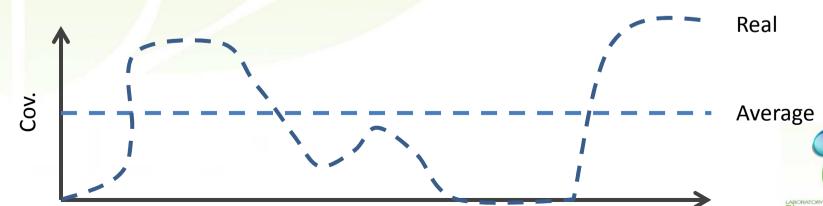


ethical & societal implications ....

.... which will be by-passed

#### Oncology:

- ✓ Millions of tumor genomes scheduled: map of mutation
- ✓ Boom of gene panels for personalized medicine
- ✓ False positives / false negatives / misinterpretations
  - ✓ Genome coverage: behind the 50X average



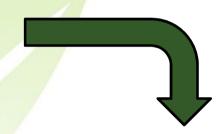
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  - ✓ Probability heterozygosy low coverage



#### **Heterozygosity – low coverage - probability**

Real	Seq 1	Seq 2	Seq 3
A/T	A	AA	AAA
		-	AAT
		AT	ATA
			ATT
	Т	TA	TAA
			TAT
		TT	TTA
			TTT



25% probability of missing heterozygosity!!



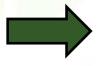
#### Oncology:

- ✓ Millions of tumor genomes scheduled: map of mutation
- ✓ Boom of gene panels for personalized medicine
- ✓ False positives / false negatives / misinterpretations
  - ✓ Genome coverage: behind the 50X average
  - ✓ Probability heterozygosy low coverage
  - ✓ Sequencing errors
  - ✓ Activable mutations for other cancer



#### Oncology:

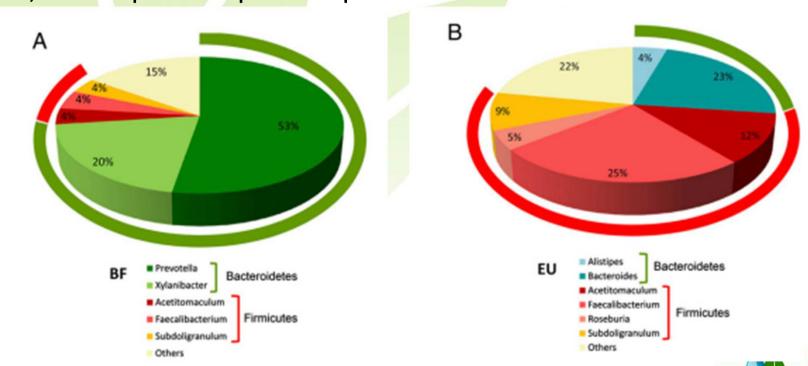
- ✓ Millions of tumor genomes scheduled: map of mutation
- ✓ Boom of gene panels for personalized medicine
- ✓ False positives / false negatives / misinterpretations
- ✓ No yet a medical utility but opens the way to « charlatanism » and « cobaye patients »



Still a long way for tumors but interest for early detection based on blood signature

#### Stone age microbiome:

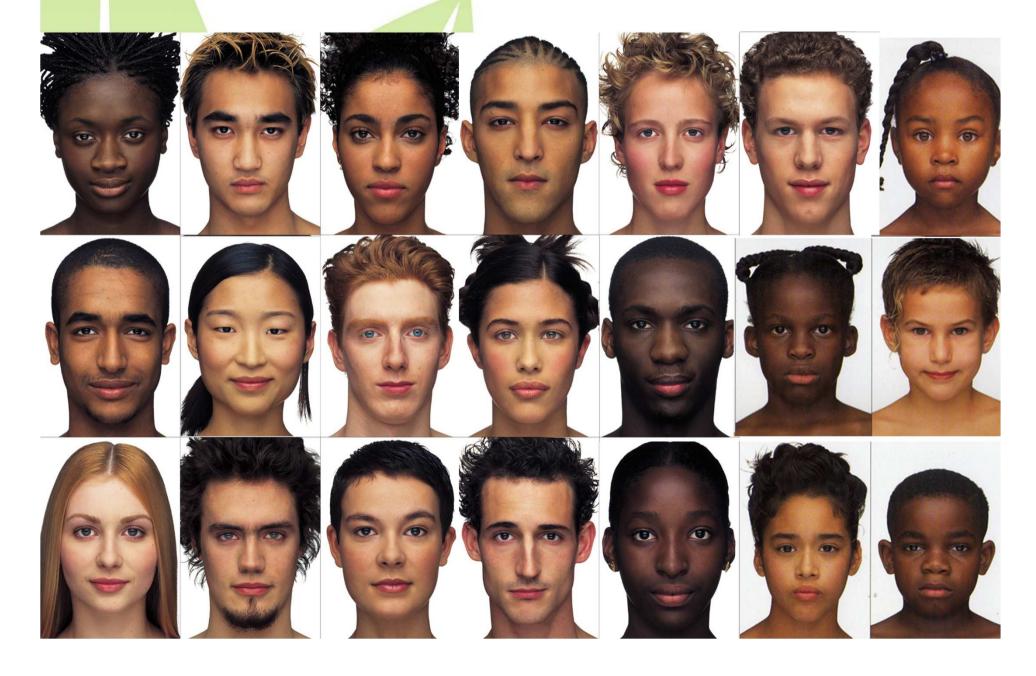
- ✓ Healthy children: urban Italy vs. rural Burkina Faso
- ✓ Analysis of 16S rDNA gene
- ✓ 15,000 sequences per sample



✓ Very interesting but .... frustrating as only Genders...



## Homo sapiens



#### **Future:**

- ✓ Simple tests by 16s sequencing :
- ✓ Deep analysis of the genes and genomes of the microflora
- ✓ Same process as genome sequencing but incomplete genomes (prevalence, size and complexity)
- ✓ Reconstruction of metabolic pathway, understanding of the functionality



#### **Future:** functional analysis

- ✓ Aphids symbionts: Buchnera sp. and Wolbachia sp.
- ✓ Sampling and sequencing (30 M sequences per sample)
- ✓ Genome reconstruction and comparison with other strains or close species



#### **Ecophysiology:**

- ✓ Project from Laura Llorens and Dolors Verdaguer
- ✓ Climate change and natural ecosystems
- ✓ Plant physiology, botanic composition, soil analysis

+ microbial population (with Lluis Banyeras)



- Environmental DNA
- Application of genetic to study ecosystem from a decade but...





& now:



Scientific knowledge :



- 78.620 arthropods
- 11.407 insects
- 3.883 aves
- 1.850 mammalians



- **➢ Biodiversity**:
  - √ Ecosystems

√ Species



✓ Genes and genomes

NGS opportunities !!!



- >Answered questions:
  - ✓ Monitor invasion of alien species through water sampling (bullfrog in France: better sensitivity)
  - ✓ Study the species diversity in water (filtering, 50 ml ...) for nearly any branch of the tree of life
  - ✓ What is the plant taxonomic diversity of any environment?
    - ✓ Soil (from toundra to rainforest)
    - ✓ Pollen sampling (*Graminaceae*)



- >Answered questions:
  - ✓ Determine the diet of any animal from fecal samples (lemur, herbivore,...)
  - ✓ History of ecosystem by scanning lake sediments
  - ✓ Study animal diversity through coprophagous insects
  - ✓ Confirming presence of endangered species by coprophagous insects



VS.



New promising research area with complementarities which cannot be ignored



## **Key concepts**

- Garbage in / garbage out (design & quality)
- Minimal a priori... but hypotheses
- Complexity reduction & prioritization
- > Iterative, trials & errors
- « Loteria de Navidad » for heterozygous
- No clearcut: Black & White -> grey
- Confirmation of results



#### Conclusion

- > Technological revolution with decreasing costs
- Open new research areas in traditional and new disciplines
- Many research needed to exploit full potential of the technologies

