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Mining Microbiomes

Computational Biology approaches to uncover the complexity of bacterial communities

February 10, 2015

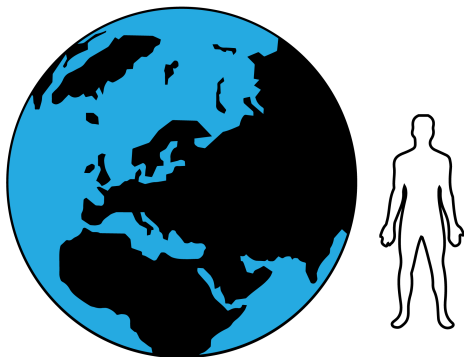
A bacterial World...

Bacteria are often cited as examples of one of the Earth's most primitive living forms



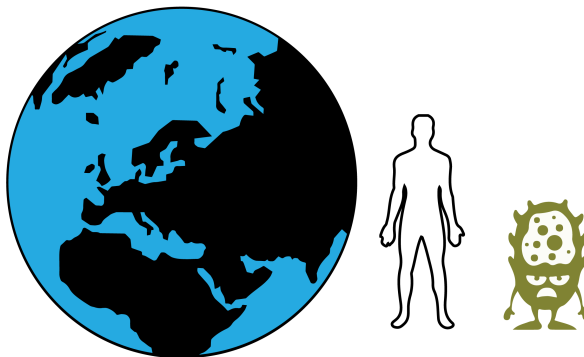
A bacterial World...

They have been always considered from an anthropocentric perspective



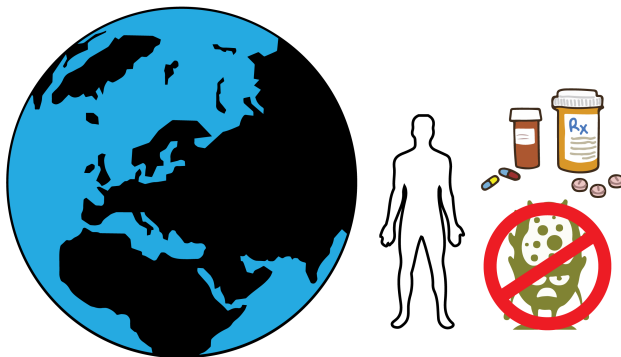
A bacterial World...

They are still associated almost exclusively to infection diseases



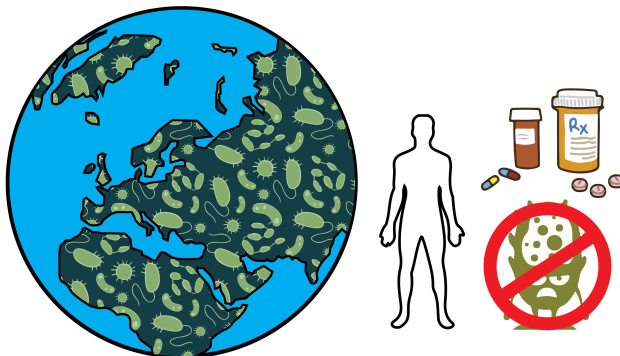
A bacterial World...

They are often studied to develop new antibiotic treatments



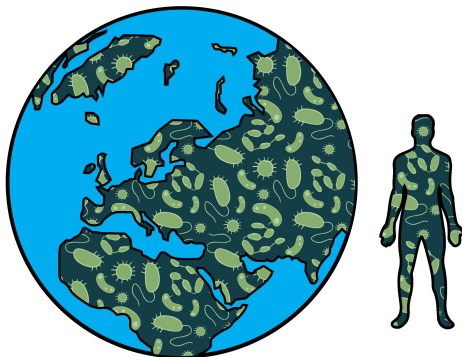
A bacterial World...

But reality is rather different



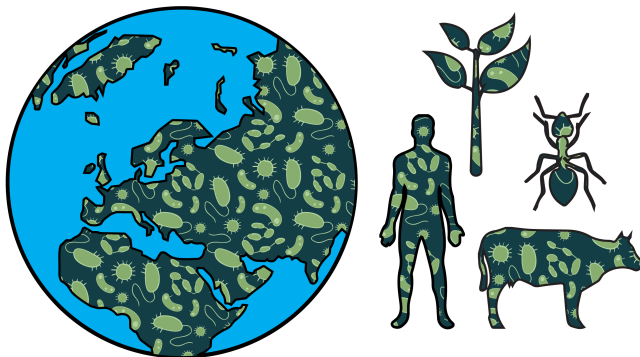
A bacterial World...

Only a very small fraction of bacteria is able to cause infections



A bacterial World...

A highly diversified and beneficial bacterial world exists



Studying bacterial diversity

Biochemical-based

Plate counts

CLPP

FAME

Molecular-based

G/C content

DNA microarrays

DNA reassociation

DGGE and TGGE

T-RFLP

DNA sequence analysis

Studying bacterial diversity

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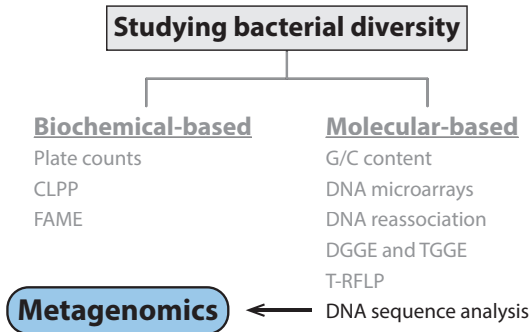
DNA microarrays

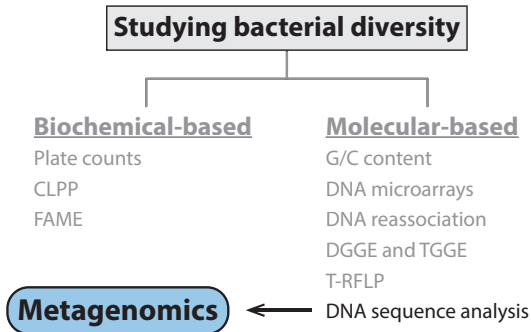
DNA reassociation

DGGE and TGGE

T-RFLP

DNA sequence analysis



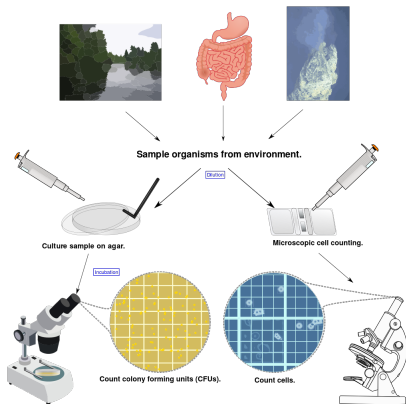


Metagenomics (also referred to as environmental and community genomics) is the genomic analysis of microorganisms by direct extraction and cloning of DNA from an assemblage of microorganisms.

[Handelsman, 2004]

Great plate count anomaly

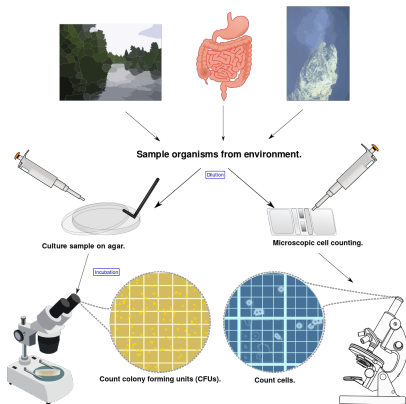
Counts of cells obtained via cultivation are orders of magnitude lower than those directly observed via microscope
[Staley and Konopka, 1985]



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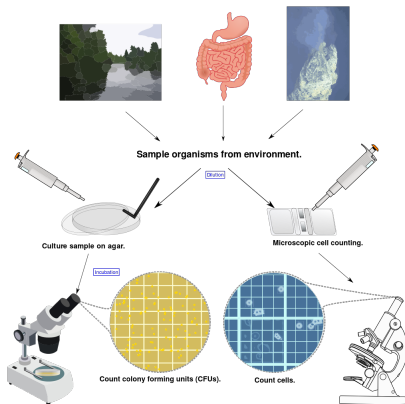
Using standard laboratory techniques, microbiologists are able to cultivate only 1% of existent bacteria [Hugenholtz et al., 2002]

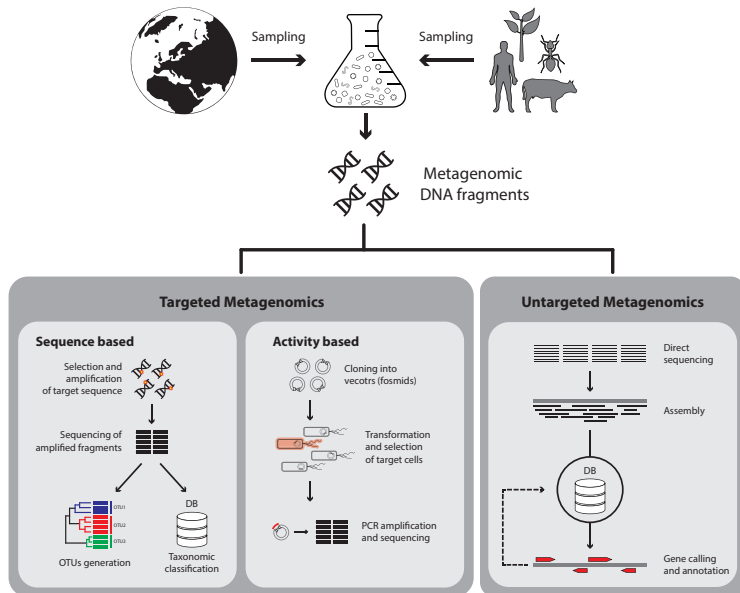


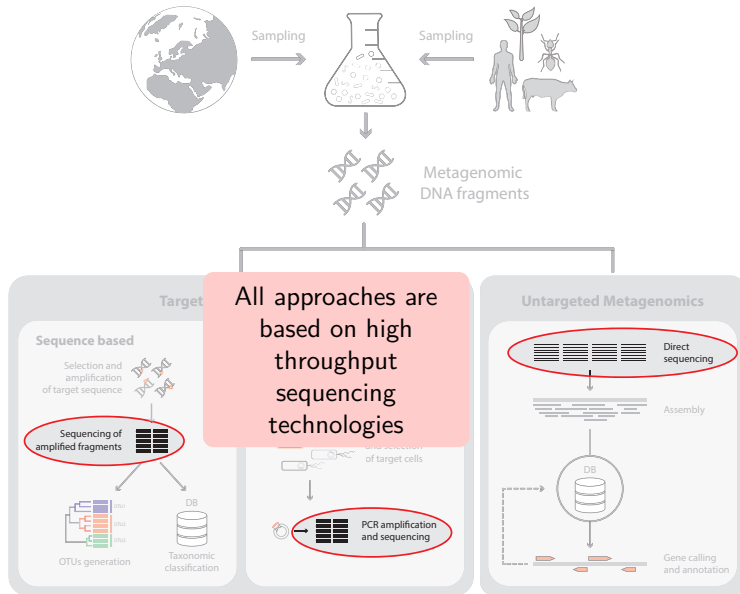
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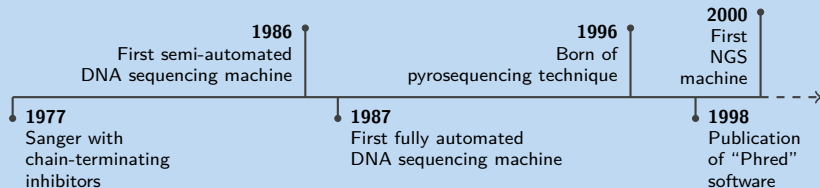
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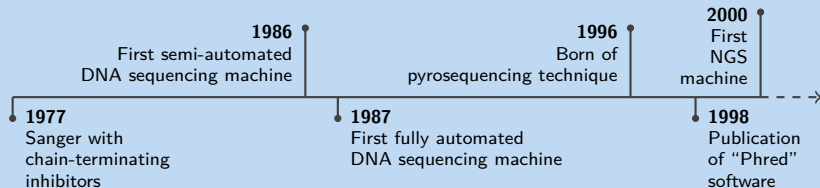


DNA sequencing timeline



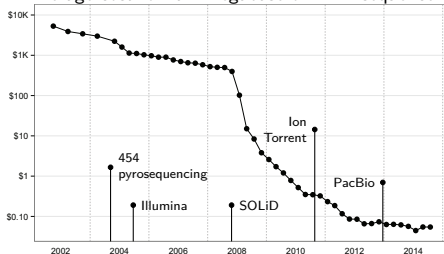
[Sanger et al., 1977, Smith et al., 1986, Prober et al., 1987, Ronaghi et al., 1996, Ewing and Green, 1998, Brenner et al., 2000]

DNA sequencing timeline



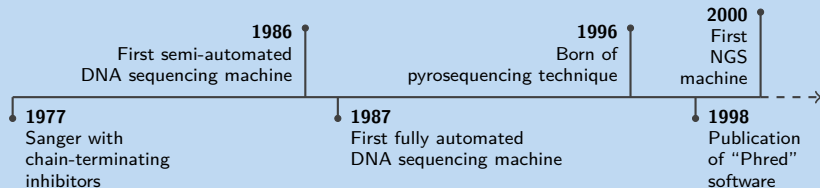
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Average cost for raw megabase of DNA sequence



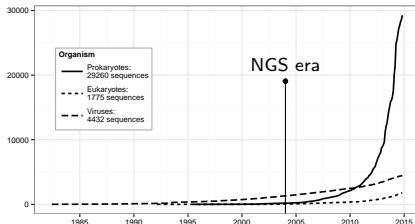
With the development of new technologies the cost for sequencing one megabase of DNA has been reduced by more than 1000 times

DNA sequencing timeline

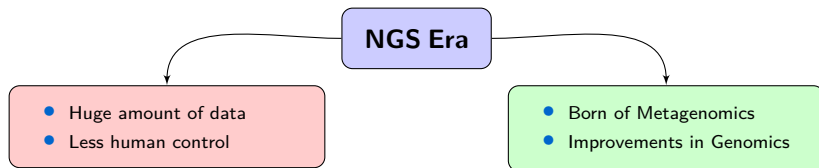


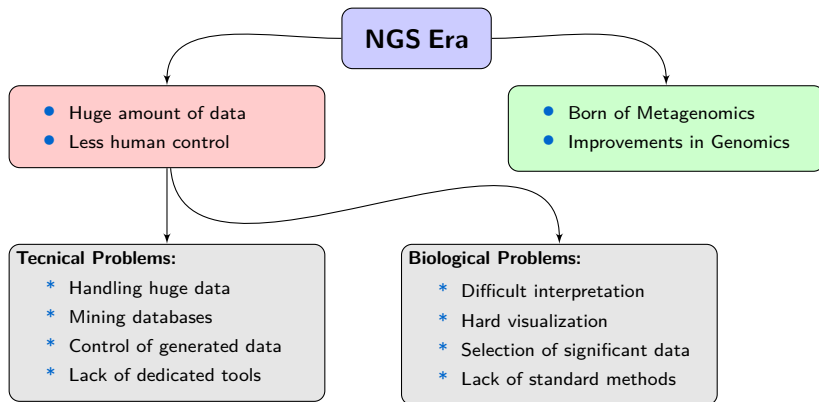
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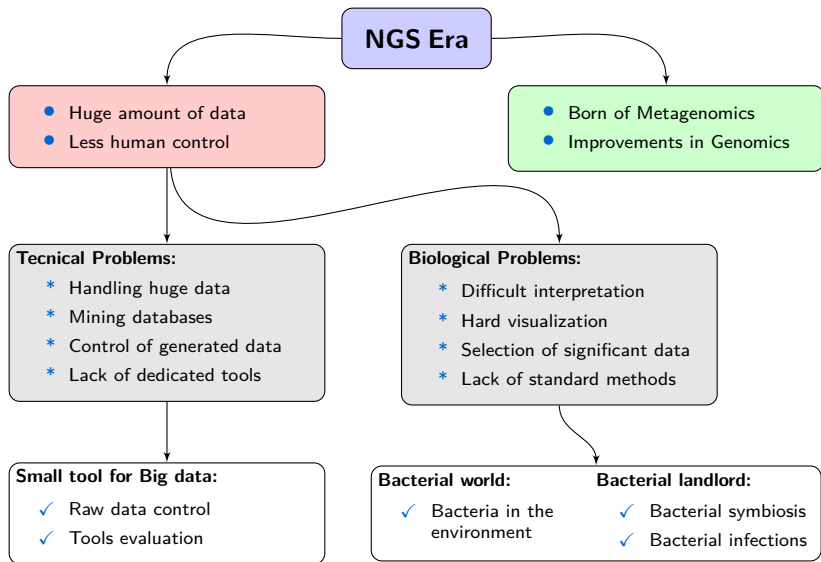
Number of genome sequences submitted to Genbank



The "NGS era" has led to a drastic increment of genome sequences available in public databases







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