



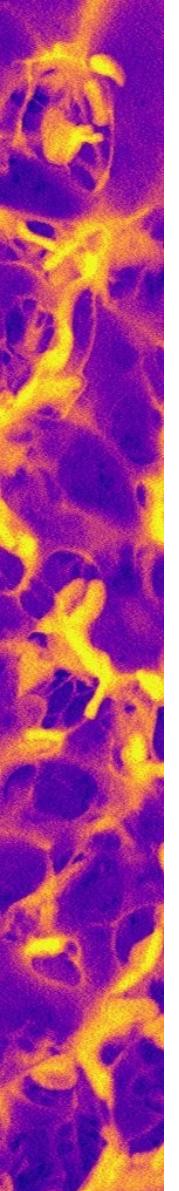
University of Naples "Federico II"

Marine Microbial Diversity

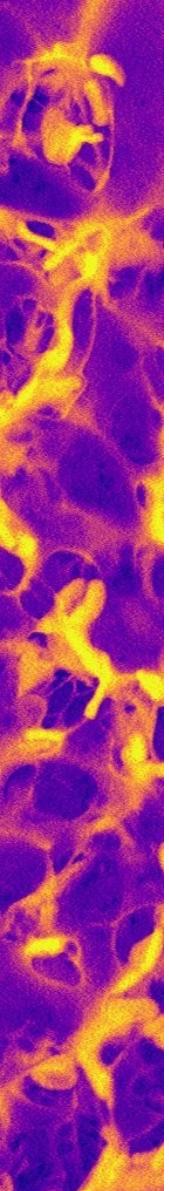
aa 2022-2023

MICROBIAL PHYSIOLOGY, EVOLUTION AND ECOLOGY: A BRIEF RECAP

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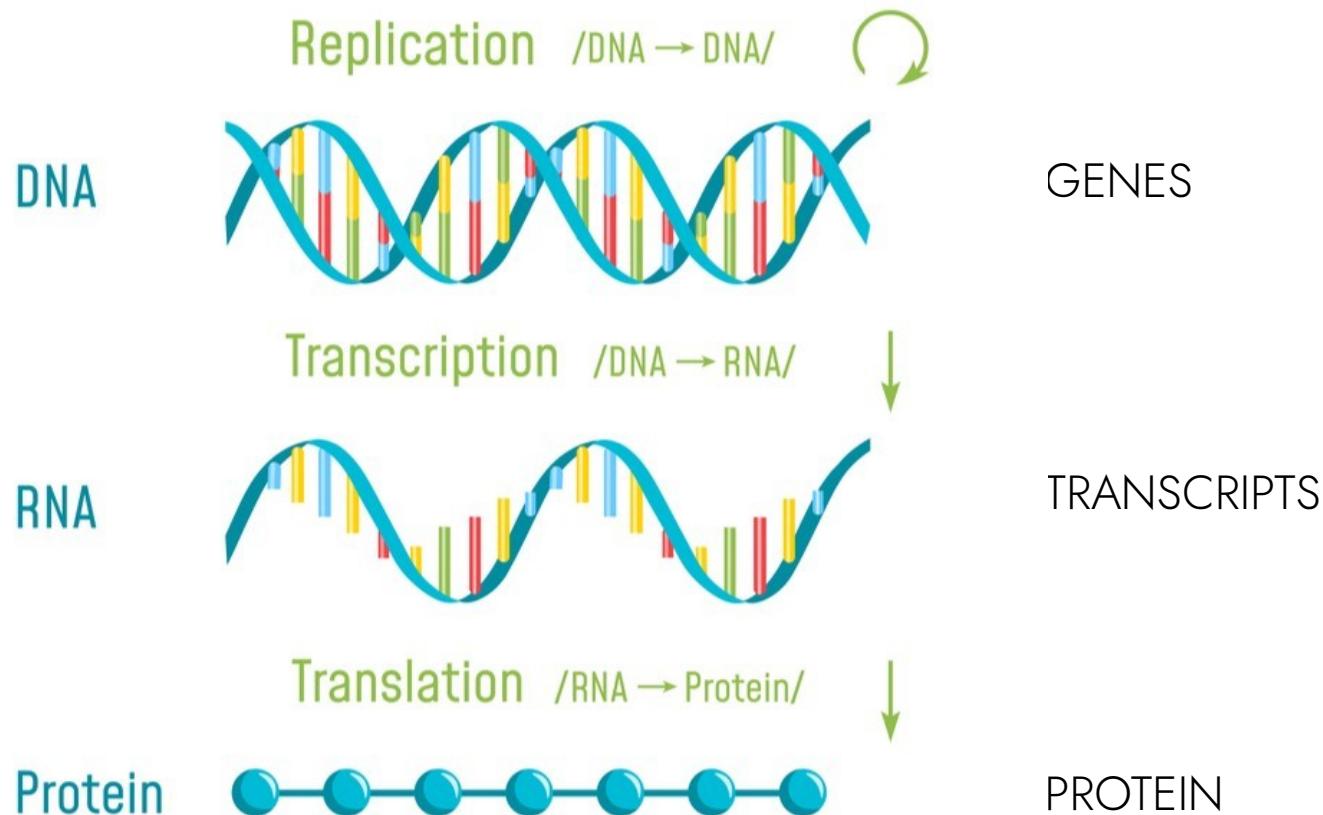
A vertical strip of a microscopic image showing numerous small, rod-shaped and spherical microorganisms against a dark background.

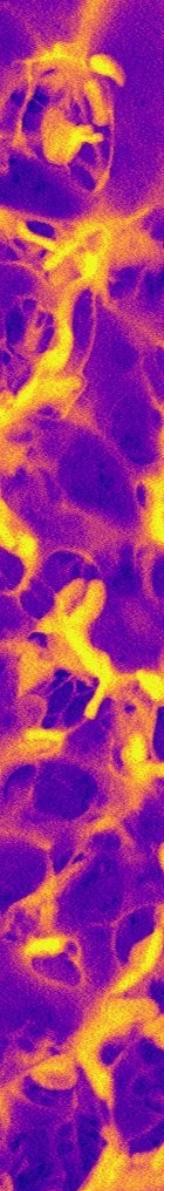
MICROBIAL PHYSIOLOGY: A VERY BRIEF GUIDE



Gene and Genomes

Genes and genomes

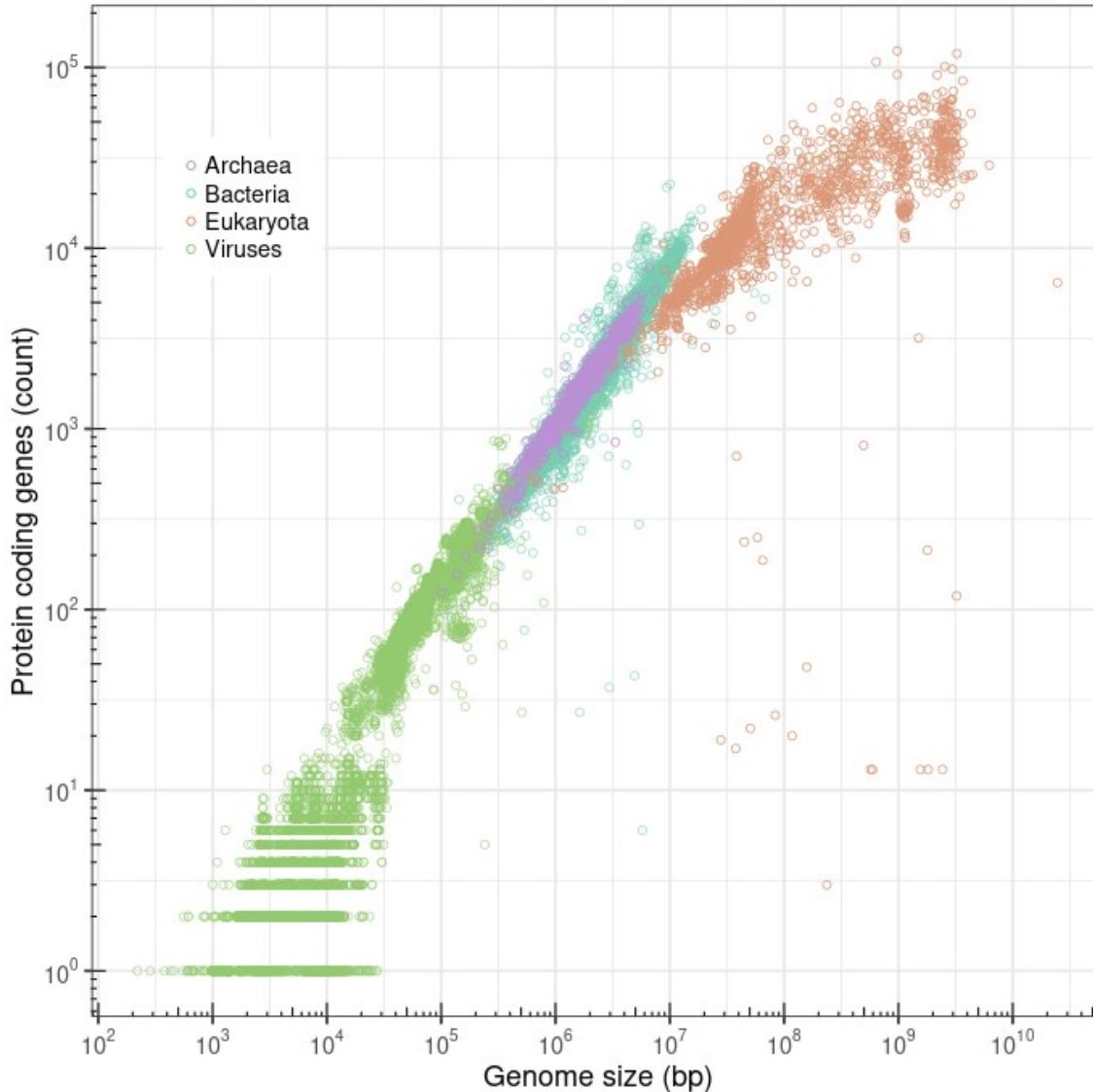


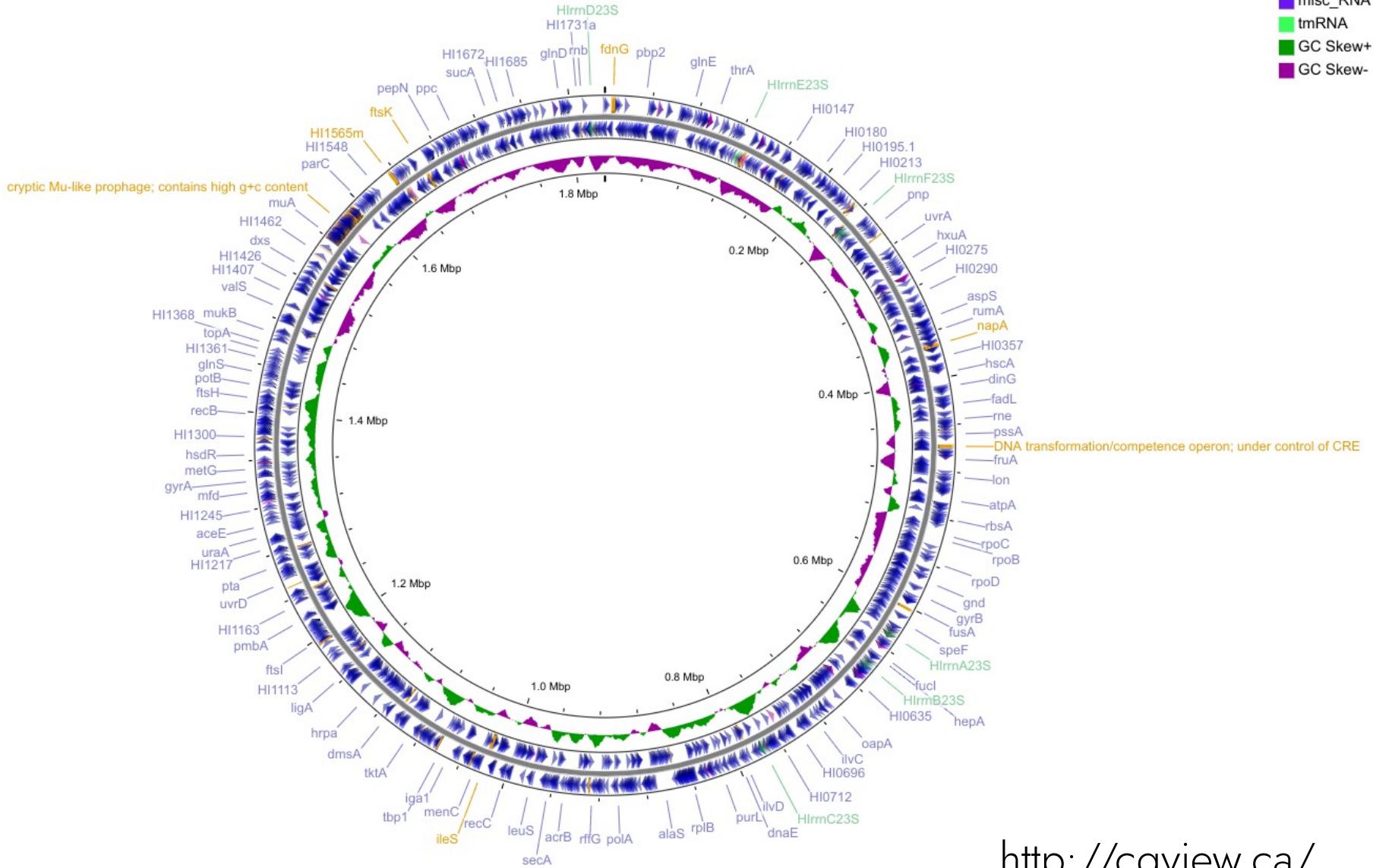
A vertical strip on the left side of the slide showing a microscopic view of various microorganisms, possibly bacteria or yeasts, under a fluorescence microscope. The organisms appear as small, bright yellow and orange spots against a dark background.

Genes and genomes

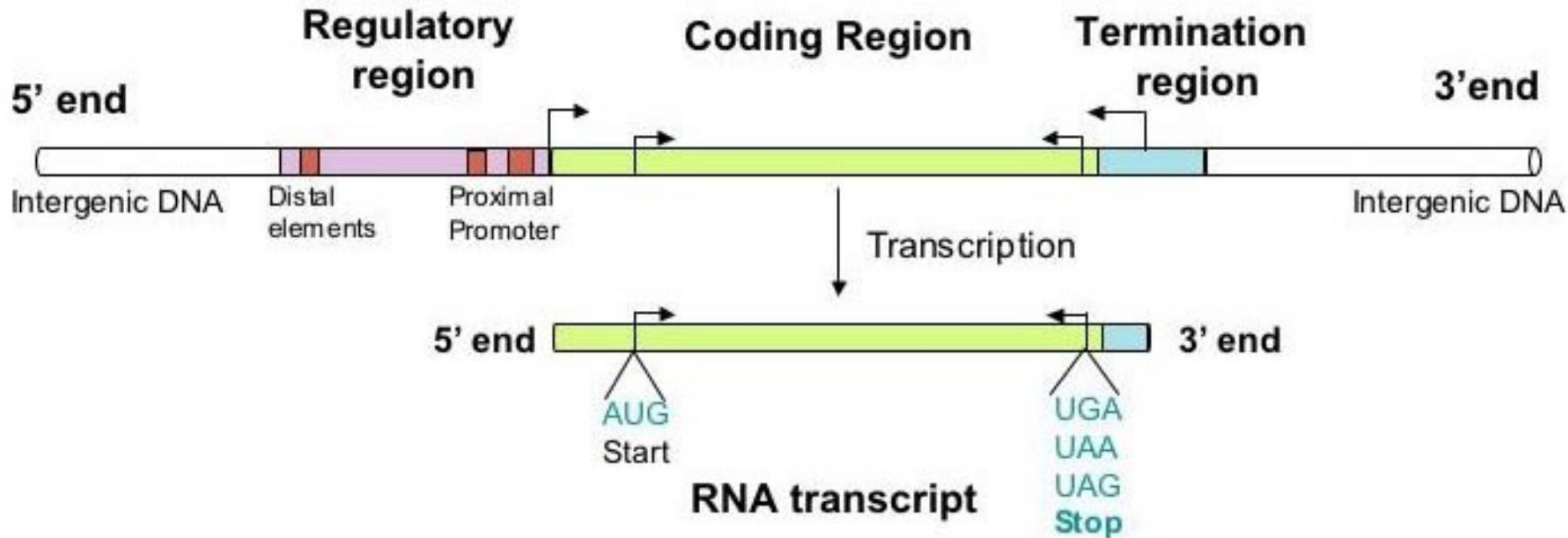
- Prokaryotic **genomes range in size** from those of large viruses to those of eukaryotic microbes
- Prokaryotic genomes are **generally circular**. One or more chromosome may be present
- One or more **plasmid** can be present (**circular or linear**), coding (often) for non essential genes conferring additional characteristics
- The **gene density for 1 kbp is around 1**, and number of genome repeat is small. By comparison simple eukaryotes (*C. elegans*) has a gene density of 0.2, while humans have a gene density of 0.015
- Unlike prokaryotes, eukaryotic genomes contain a large fraction of noncoding DNA

Genome size vs. protein count across NCBI genomes

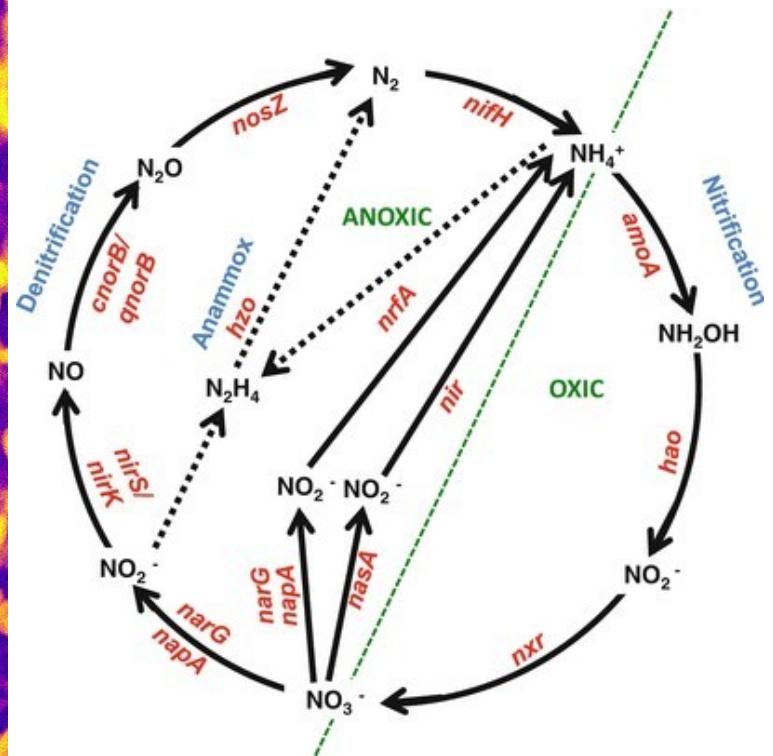




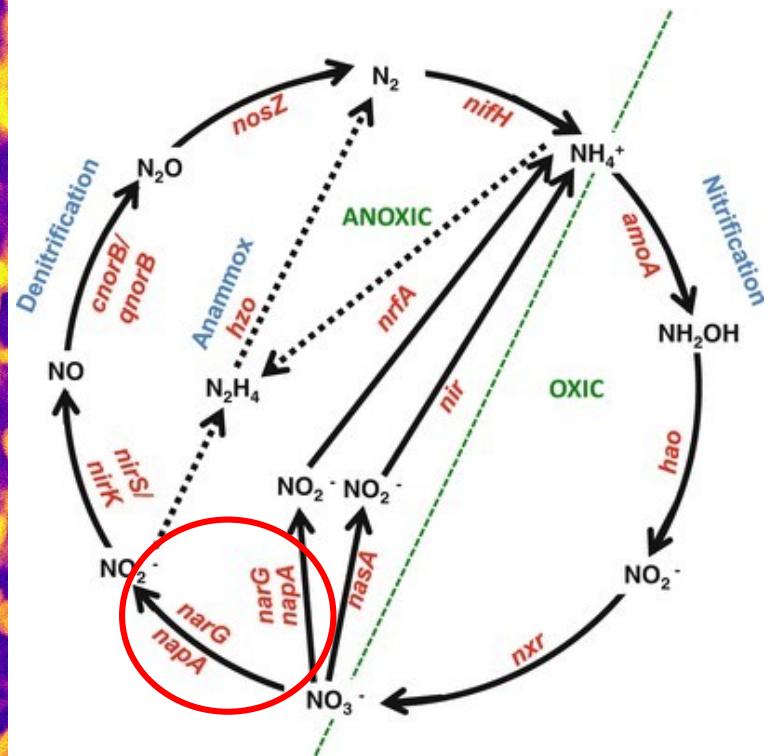
Gene organization in Prokaryotes



Visualizing genes organization



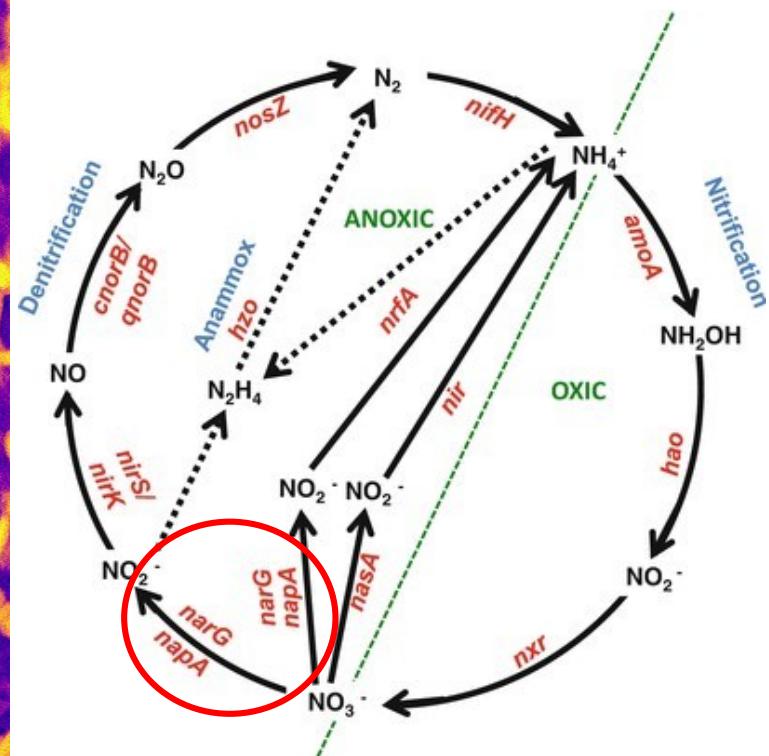
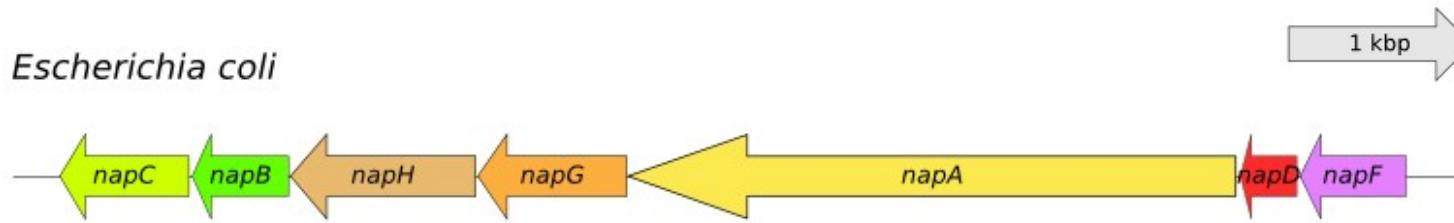
Visualizing genes organization



Visualizing genes organization

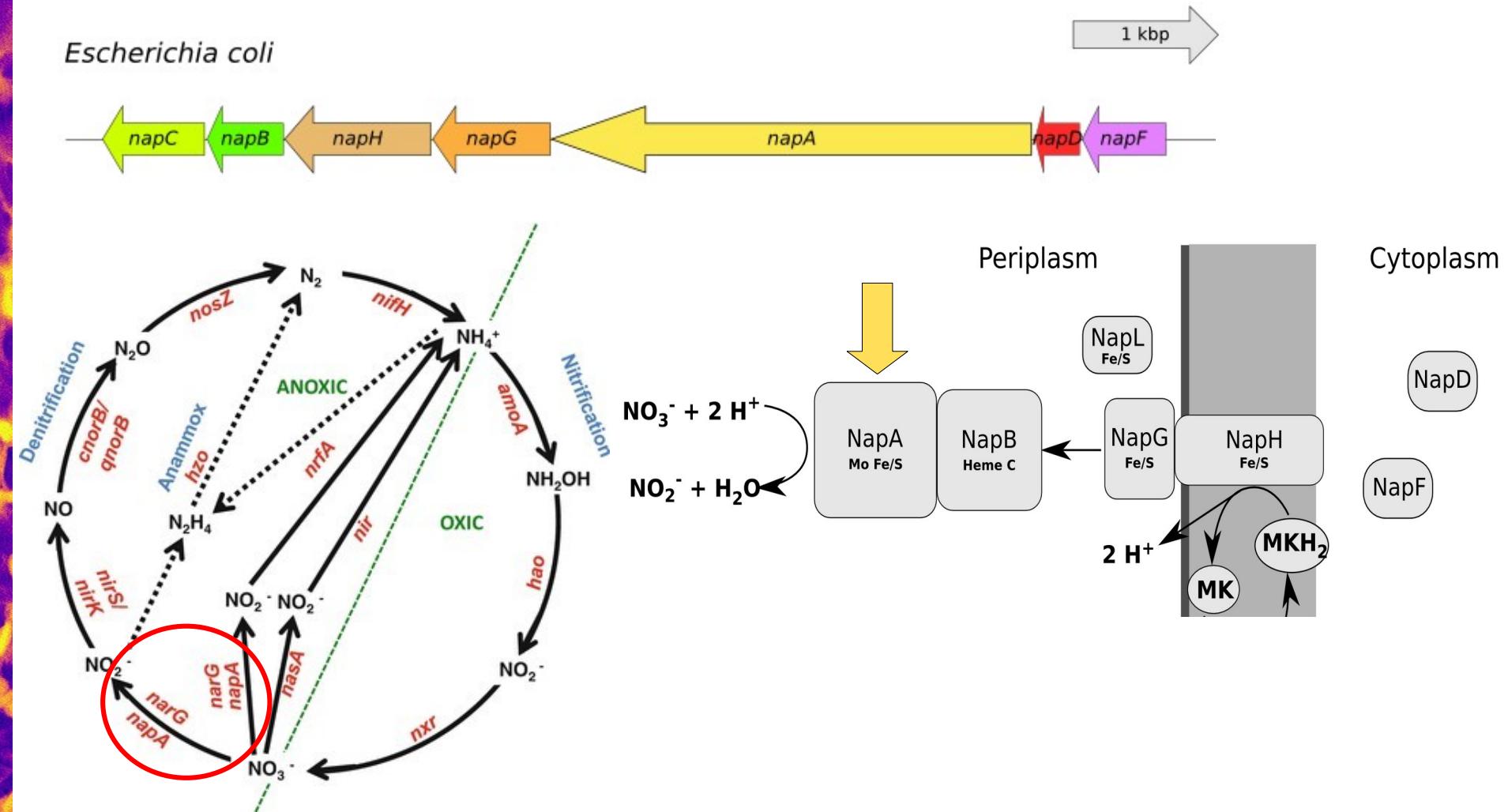
Escherichia coli

1 kbp



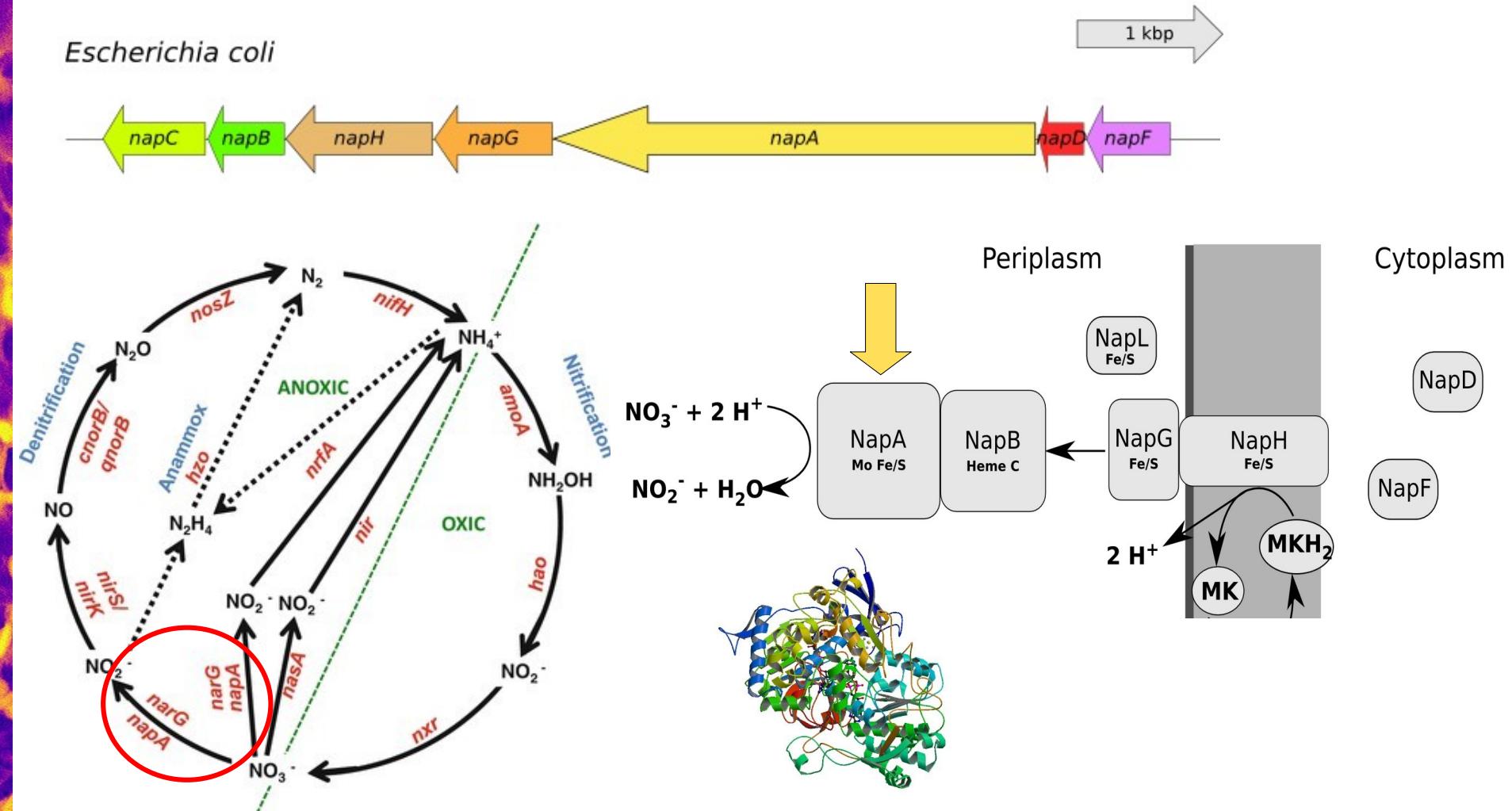
Visualizing genes organization

Escherichia coli



Visualizing genes organization

Escherichia coli



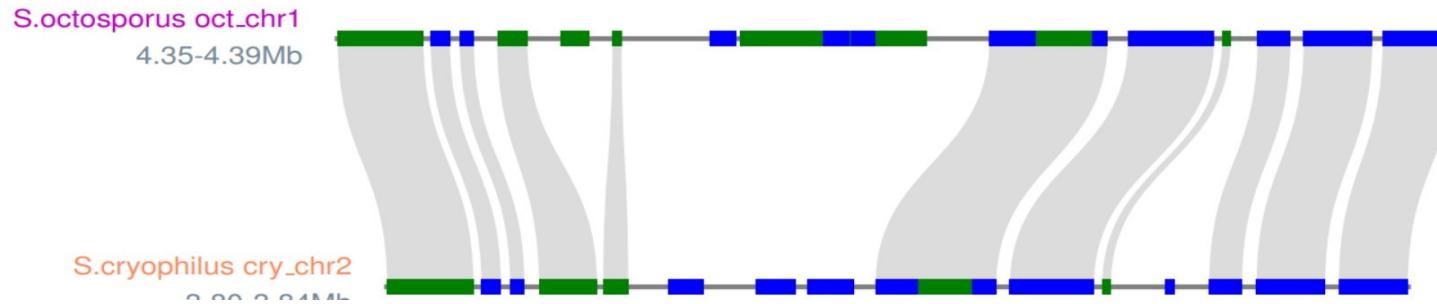
Sequence Homology

Sequence similarity: Defines the degree of similarity between two sequences. Similarity is calculated by different algorithms assigning a different weight to gaps

Sequence homology: assumes that the similarity observed is derived from common ancestry

Conserved regions: portion of a gene that do not change significantly when comparing homologs

Synteny: area of a gene/genome that is conserved in organization across different organisms



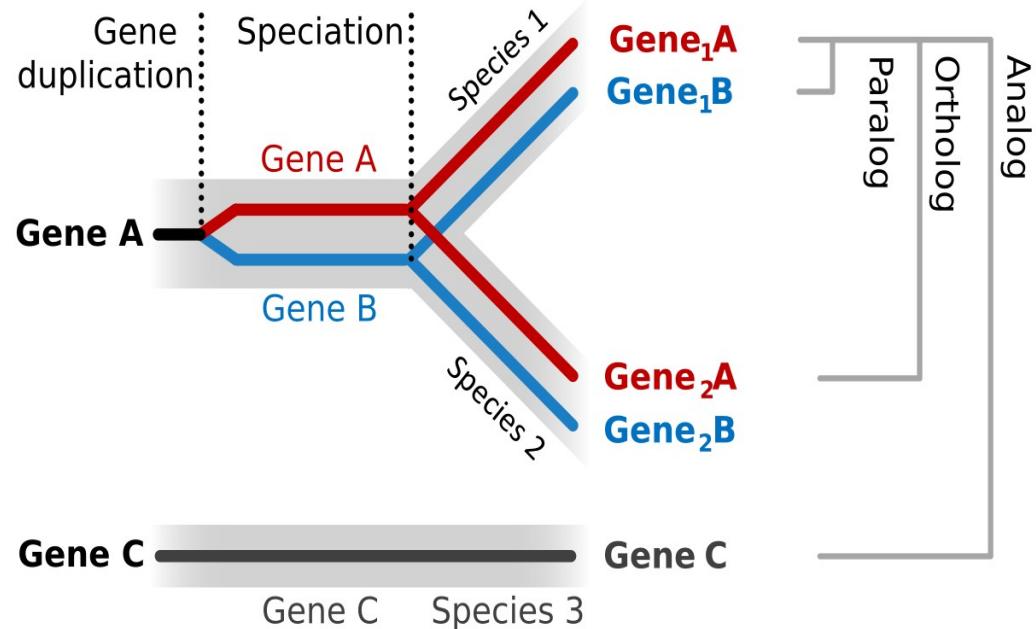
Gene Families, Duplications, and Deletions

Homologs: related sequence that have common genetic ancestry

Paralogs: genes within an organism whose similarity to one or more genes in the same organism is the result of gene duplication

Gene families: groups of homologous genes

Orthologs: genes found in one organism that are similar to those in another organism but differ because of speciation



position 12

↓

helix H0

sheet

oooooooooooo

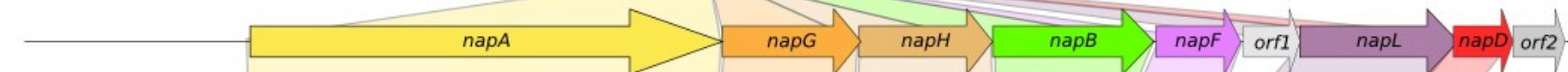
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R	Y	D	S	R	T	T	I	F	S	P	L	R	E	G	R	L	Y	Q	V	E	Y	A	M	E	A	I	S	H	A	.	G	T	C	L	G	I	L	S
R	Y	D	S	R	T	T	I	F	S	P	.	.	E	G	R	L	Y	Q	V	E	Y	A	Q	E	A	I	S	N	A	.	G	T	A	I	G	I	L	S
R	Y	D	S	R	T	T	I	F	S	P	.	.	E	G	R	L	Y	Q	V	E	Y	A	M	E	A	I	S	H	A	.	G	T	C	L	G	I	L	A
R	Y	D	S	R	T	T	I	F	S	P	.	.	E	G	R	L	Y	Q	V	E	Y	A	M	E	A	I	G	H	A	.	G	T	C	L	G	I	L	A
R	Y	D	S	R	T	T	I	F	S	P	.	.	E	G	R	L	Y	Q	V	E	Y	A	M	E	A	I	G	N	A	.	G	S	A	L	G	V	L	A
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S	Y	D	S	R	T	T	I	F	S	P	.	.	E	G	R	L	Y	Q	V	E	Y	A	L	E	A	I	N	H	A	.	G	V	A	L	G	I	V	A

C. mediatlanticus

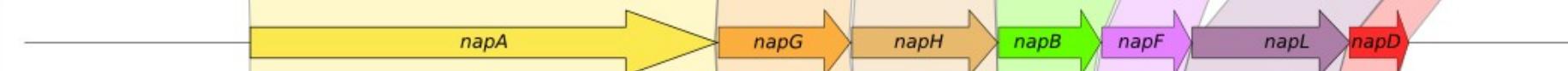
1 kbp



Sulfurovum sp.



Sulfurohydrogenibium sp.



Hydrogenivirga sp.



Desulfovibrio desulfuricans



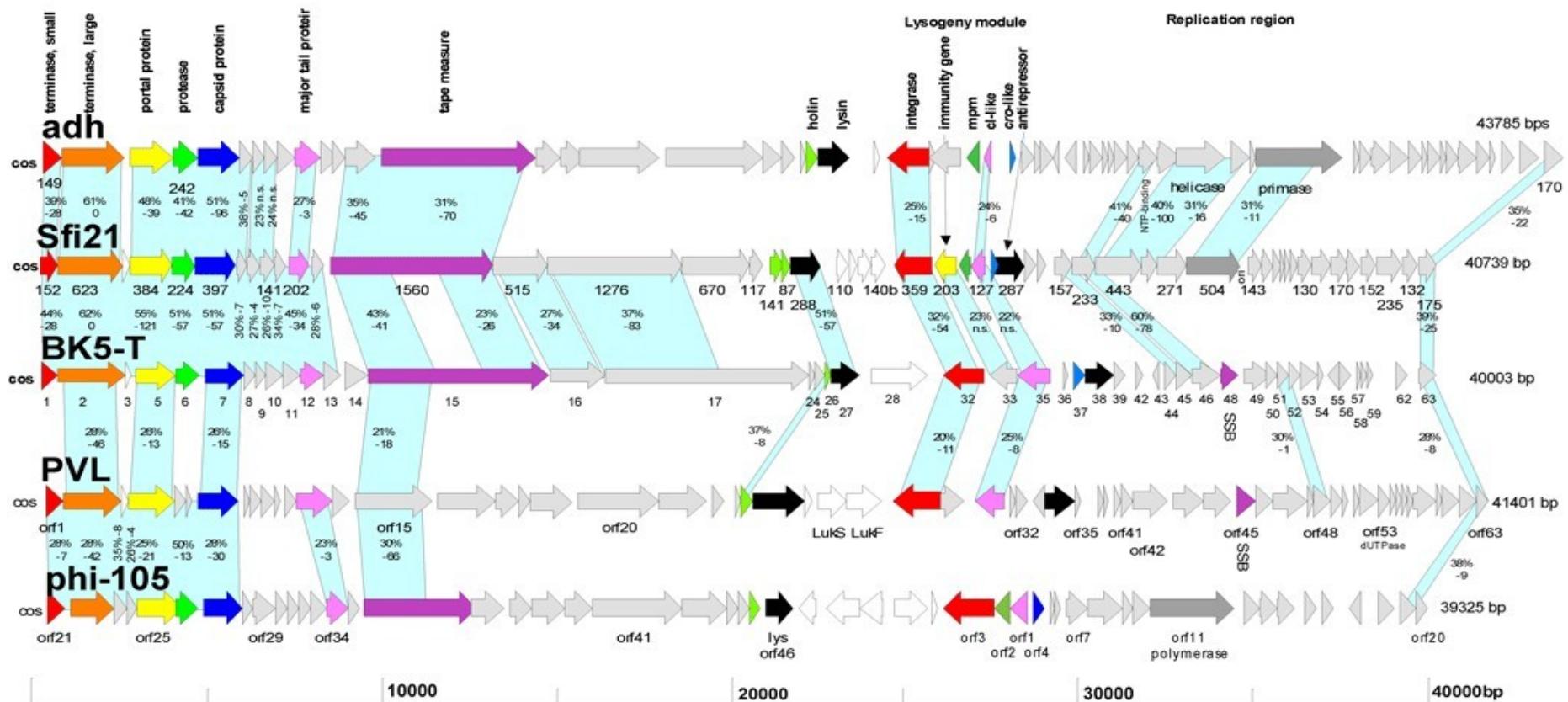
T. ammonificans



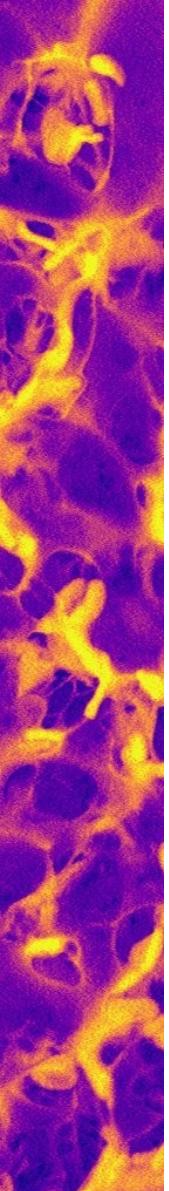
Desulfobulbus propionicus



Viral Genomes

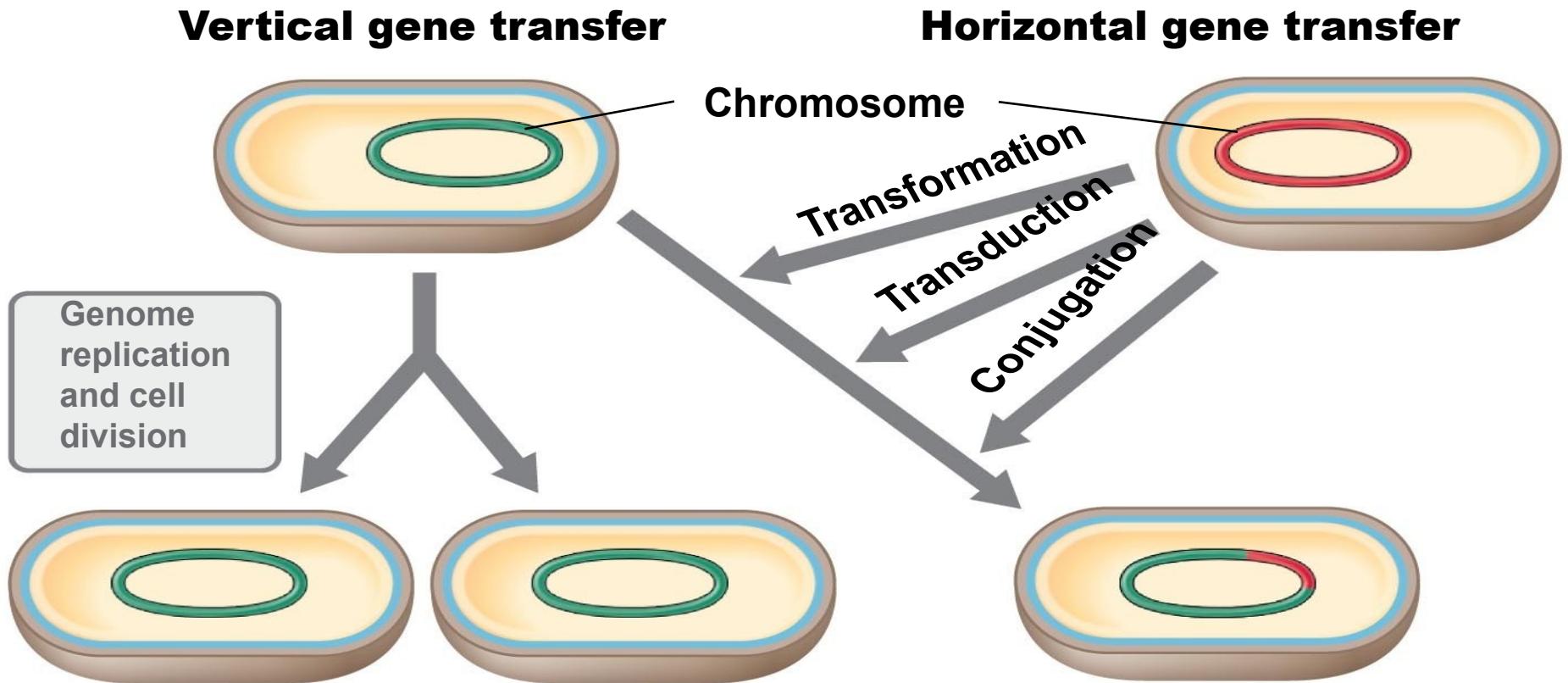


20,000-100,000 bp in size (30-100 genes) on average

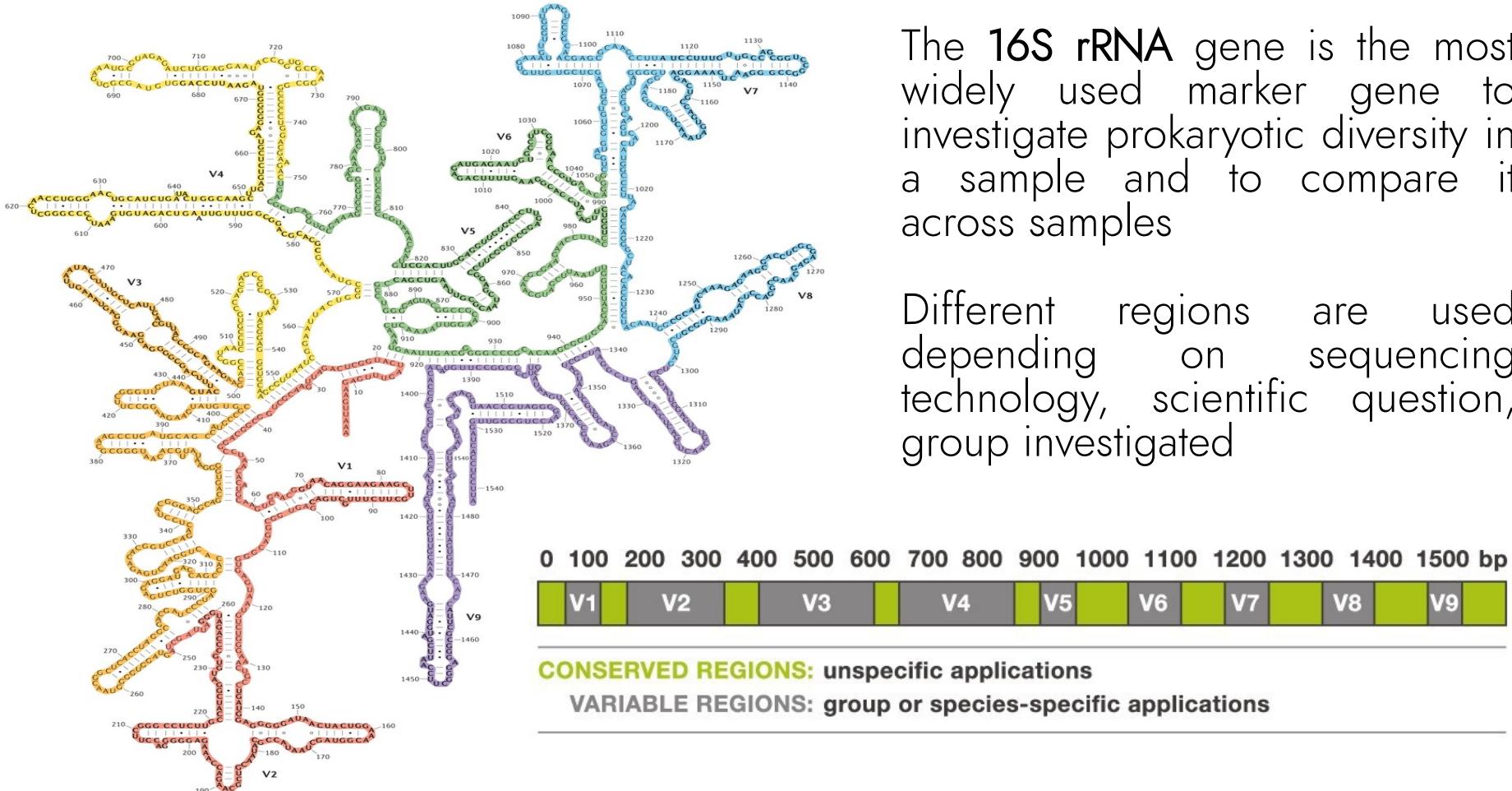


Horizontal Gene Transfer

- Horizontal gene transfer is the transfer of genetic information between organisms, as opposed to vertical inheritance from parental organism(s)
- It is considered one of the **major mode** of prokaryotic evolution
- May be extensive in nature
- It is a major confounding mechanism when studying prokaryotic evolution



Diversity and Marker Genes



Proc Natl Acad Sci U S A. 2002 Dec 24;99(26):17020-4. Epub 2002 Dec 5.

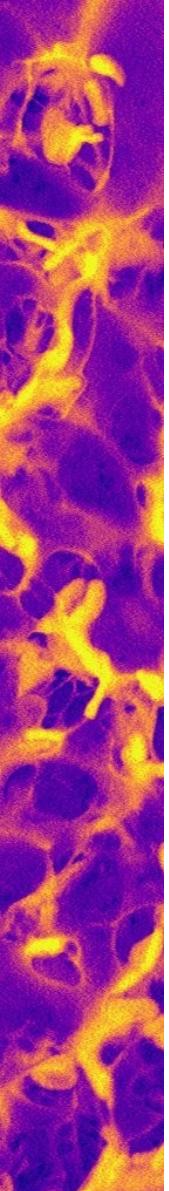
Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*.

Welch RA¹, Burland V, Plunkett G 3rd, Redford P, Roesch P, Rasko D, Buckles EL, Liou SR, Boutin A, Hackett J, Stroud D, Mayhew GF, Rose DJ, Zhou S, Schwartz DC, Perna NT, Mobley HL, Donnenberg MS, Blattner FR.

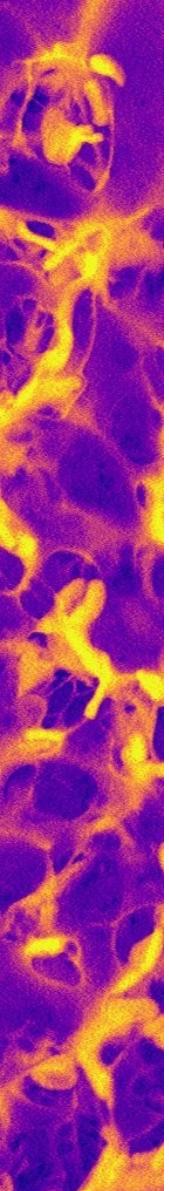
Author information

Abstract

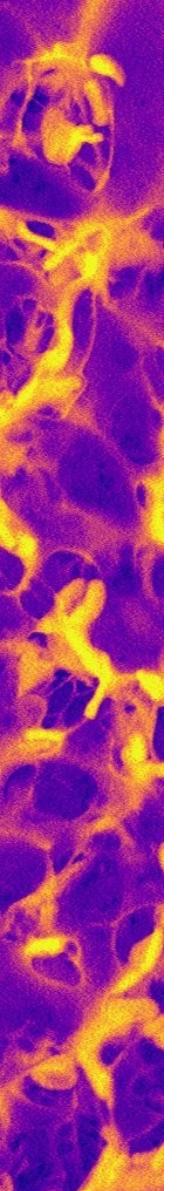
We present the complete genome sequence of uropathogenic *Escherichia coli*, strain CFT073. A three-way genome comparison of the CFT073, enterohemorrhagic *E. coli* EDL933, and laboratory strain MG1655 reveals that, amazingly, only 39.2% of their combined (nonredundant) set of proteins actually are common to all three strains. The pathogen genomes are as different from each other as each pathogen is from the benign strain. The difference in disease potential between O157:H7 and CFT073 is reflected in the absence of genes for type III secretion system or phage- and plasmid-encoded toxins found in some classes of diarrheagenic *E. coli*. The CFT073 genome is particularly rich in genes that encode potential fimbrial adhesins, autotransporters, iron-sequestration systems, and phase-switch recombinases. Striking differences exist between the large pathogenicity islands of CFT073 and two other well-studied uropathogenic *E. coli* strains, J96 and 536. Comparisons indicate that extraintestinal pathogenic *E. coli* arose independently from multiple clonal lineages. The different *E. coli* pathotypes have maintained a remarkable synteny of common, vertically evolved genes, whereas many islands interrupting this common backbone have been acquired by different horizontal transfer events in each strain.



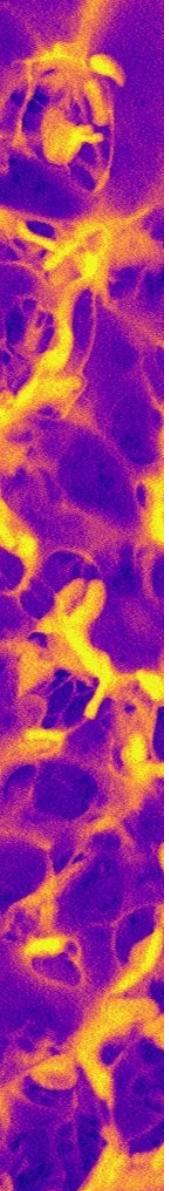
Microbial growth curve



GASP

A vertical strip on the left side of the slide showing a microscopic view of various microorganisms, possibly bacteria or fungi, with a color palette ranging from purple to yellow.

MICROBIAL EVOLUTION: A VERY BRIEF GUIDE



Microbial Species Concept

Microbial species concept. The species concept is complex when applied to microbiology. In biology species are defined primarily based on their sexual segregation, either by genetic, behavioral or geographical barrier (and even this can be sometimes challenging, as all human-imposed categories).

For microbes the **absence of sexual reproduction, horizontal gene transfer** and a **high genome plasticity** make the classic species concept difficult to apply.

The current golden standard for defining a species is called a **polyphasic approach**, combining **phylogenetics, physiology and chemotaxonomy**.

In more simple terms, microbial species are defined based on their genetic properties, specifically the similarity of the **16S rRNA marker gene** (since it is a conserved universal marker not subject to HGT) or the **whole genome similarity** (also called ANI, Average Nucleotide Identity).

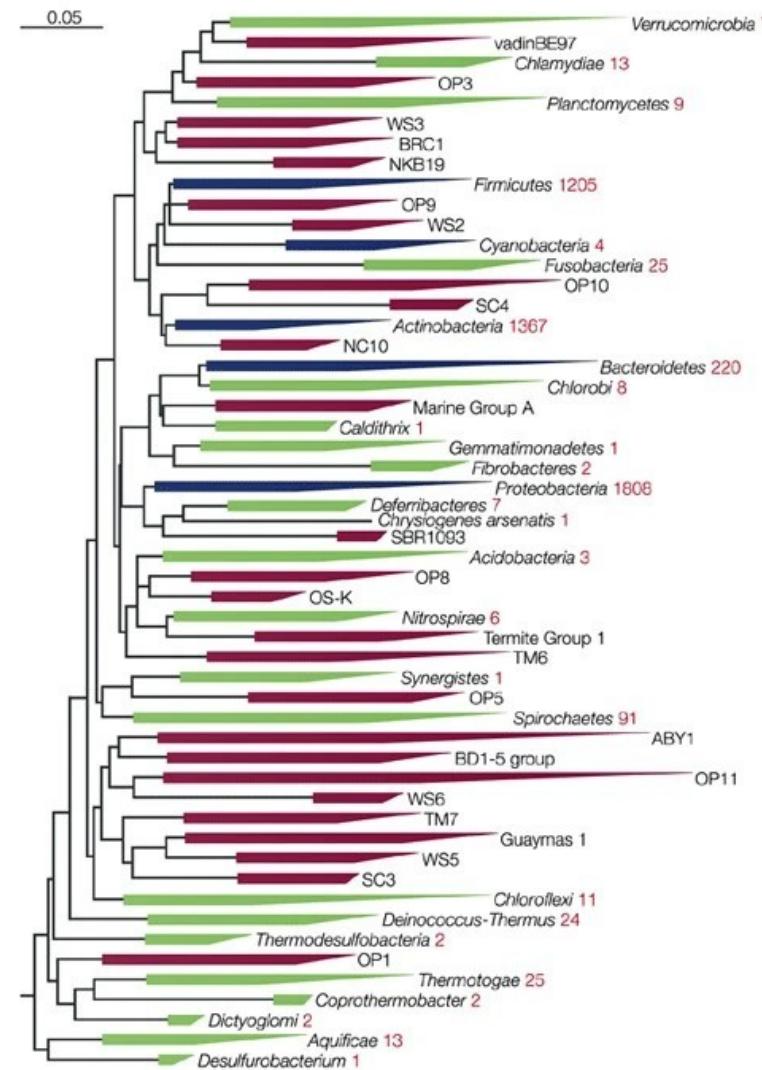
Current standard are **16S rRNA similarity >97%** for the same species and an **whole genome ANI >70%**.

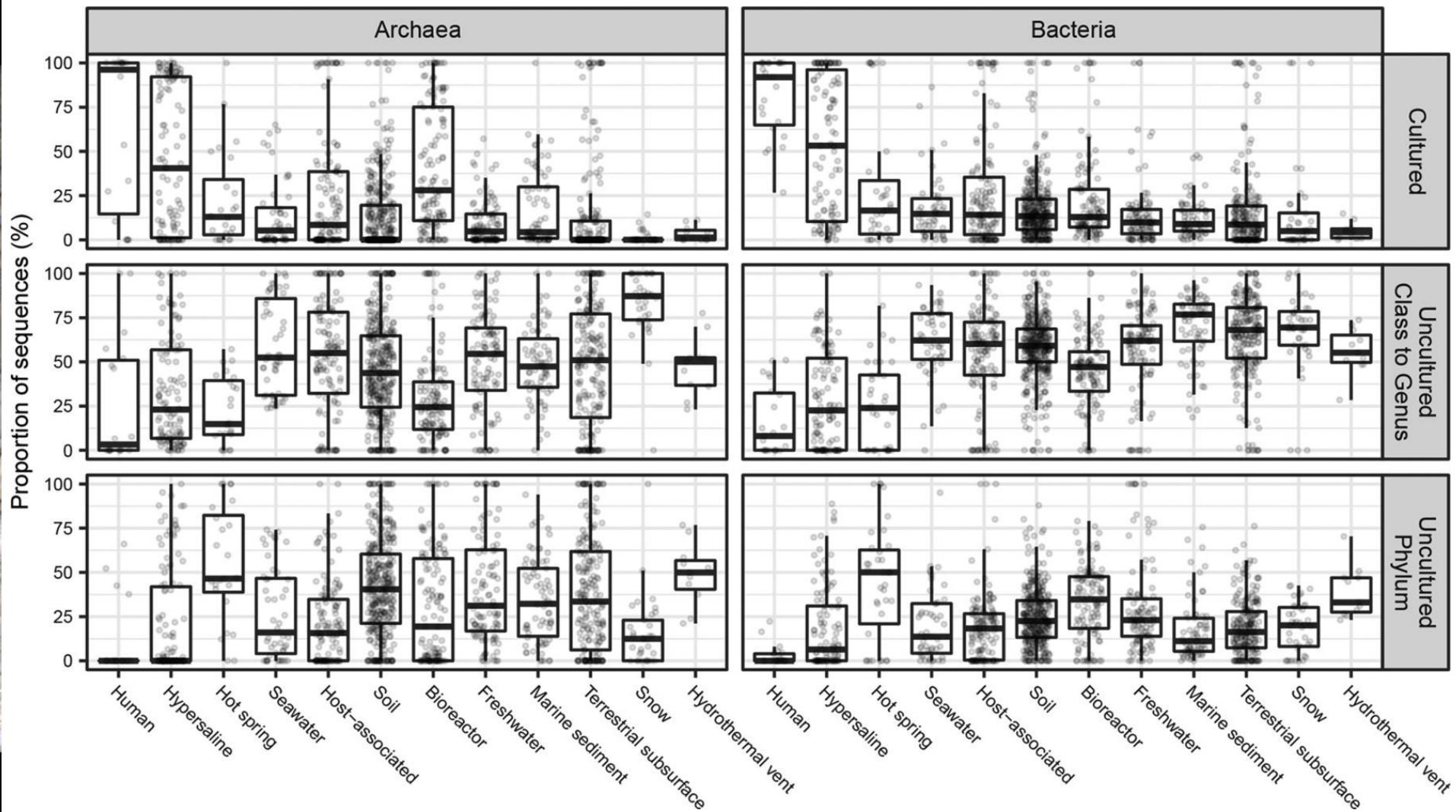
The Uncultured Majority

The uncultured majority refers to our current inability to cultivate the large majority of microorganisms in many environments. The first description is from Staley and Konopka, 1985, and was later dubbed the “Great Plate Count Anomaly”.

The simple observation that counts of growing microbes on plates differed greatly from counts using microscopy suggested that the known diversity was dwarfed by the actual diversity.

Metagenomic has revolutionized the study of microbial diversity in many ways, allowing us to probe into the unknown.

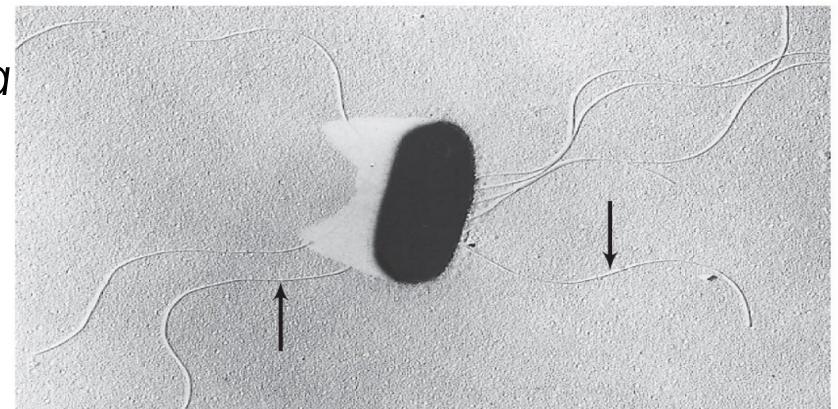




Microbial Species Concept: Taxonomy

Taxonomic nomenclature follows the binomial systems. There are numerous rules and conventions, all established by the International Committee on the Systematics of Prokaryotes.

Domain: Bacteria
Phylum: Proteobacteria
Class: Gammaproteobacteria
Order: Enterobacterales
Family: Enterobacteraceae
Genus: Escherichia
Species: *Escherichia coli*
Strain: K12



Arthur Kelman

Diverse uncultivated ultra-small bacterial cells in groundwater

Birgit Luef, Kyle R. Frischkorn, Kelly C. Wrighton, Hoi-Ying N. Holman, Giovanni Birarda, Brian C. Thomas, Andrea Singh, Kenneth H. Williams, Cristina E. Siegerist, Susannah G. Tringe, Kenneth H. Downing, Luis R. Comolli & Jillian F. Banfield

[Affiliations](#) | [Contributions](#) | [Corresponding authors](#)

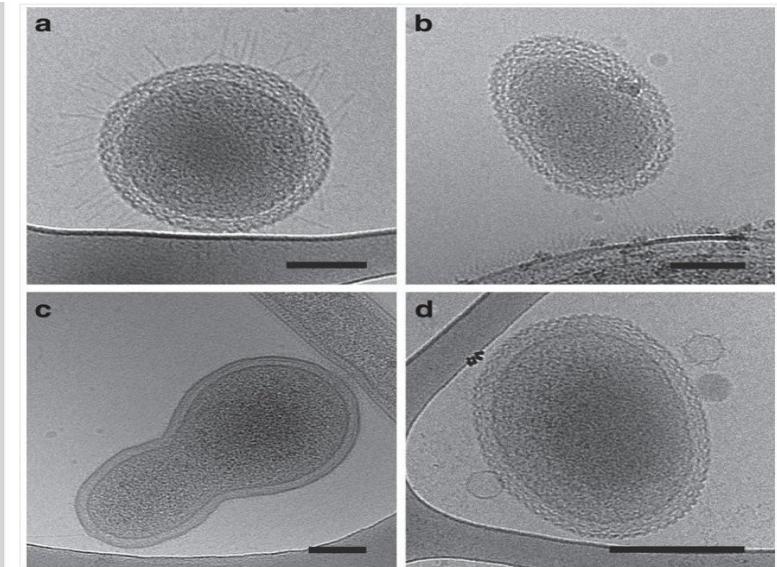
Nature Communications 6, Article number: 6372 | doi:10.1038/ncomms7372

Received 08 August 2014 | Accepted 23 January 2015 | Published 27 February 2015

OP11, DO1 was detected using metagenomic analysis of 0.2 µm filtered water

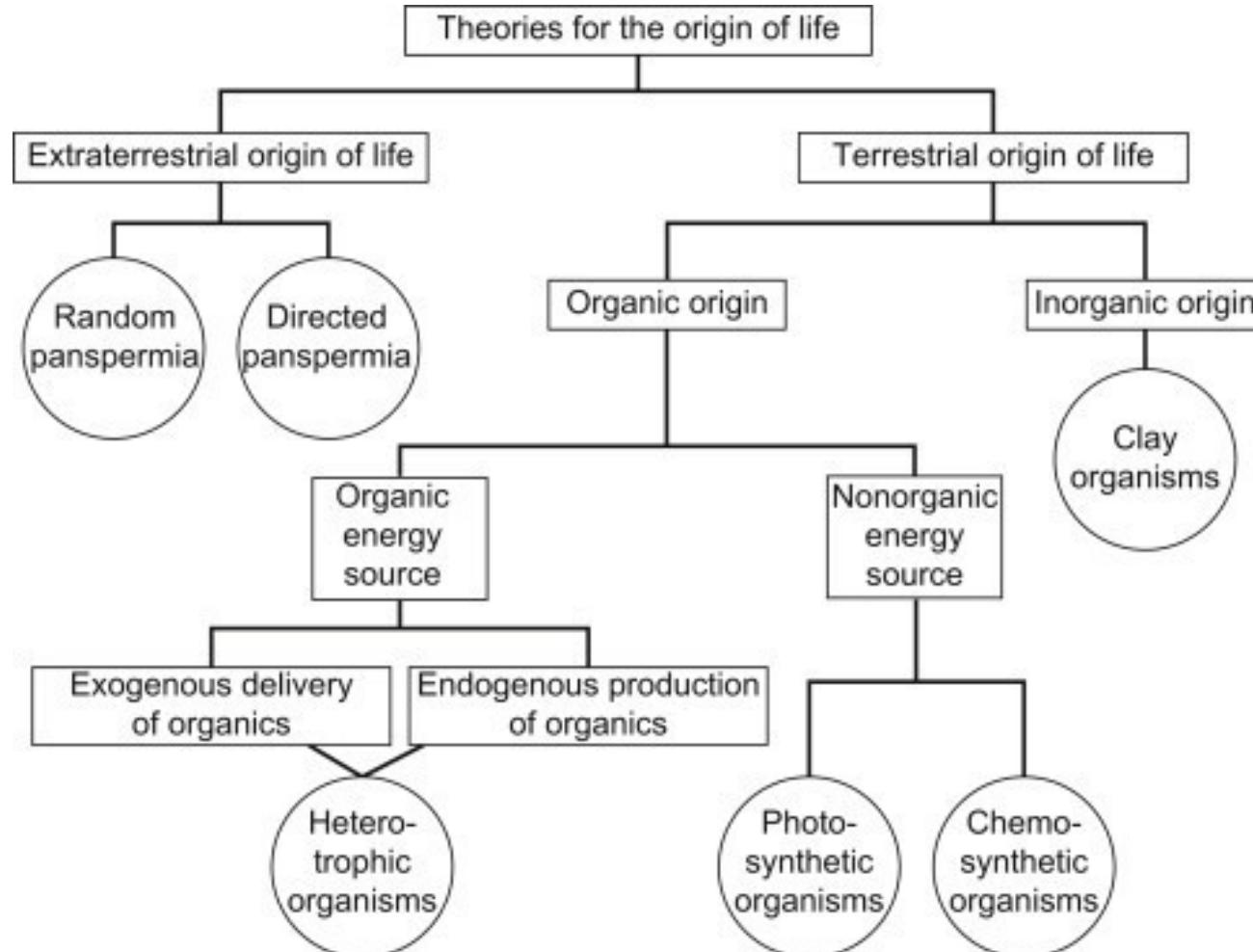
The genome size is < 1 Mbp

These bacteria rely on other community members for basic resources

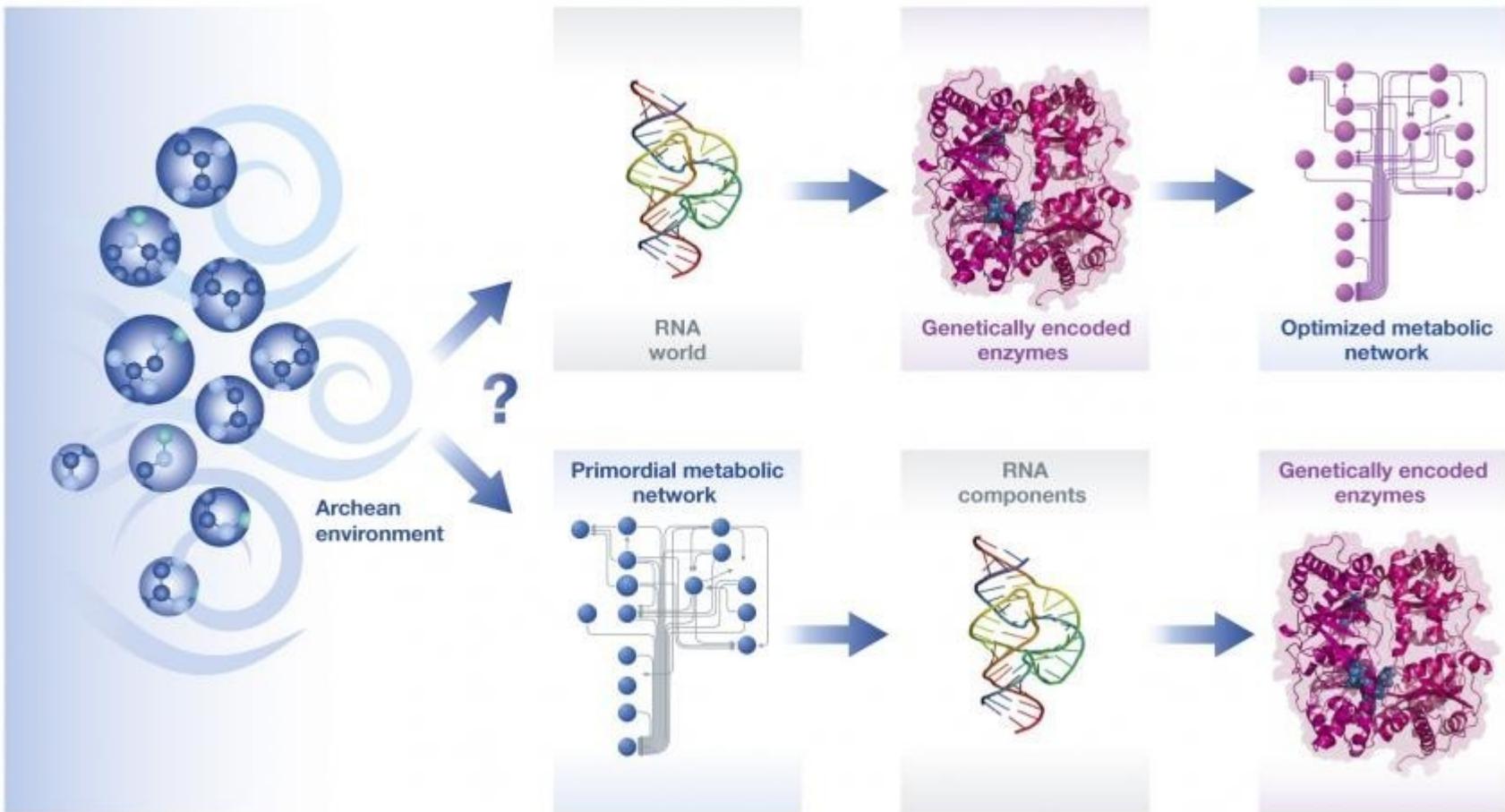


The cell envelope includes a remarkable and distinct S-layer. Pilus-like structures are clearly discernible: numerous radiating pilus-like structures cover the surface of the cell in **a**, whereas polar pilus-like structures occur on the cell in **b**, apparently connecting it to an adjacent bacterium (only part of the bacterium shown). (**c**) A dividing ultra-small bacterium in contact with a Spirochete cell (only small region shown; also see Supplementary Fig. 14). Note the contrast at the interface, suggesting cell-to-cell interaction. Three bacteriophages are associated with the surface of the cell in **d**. Scale bars, 100 nm.

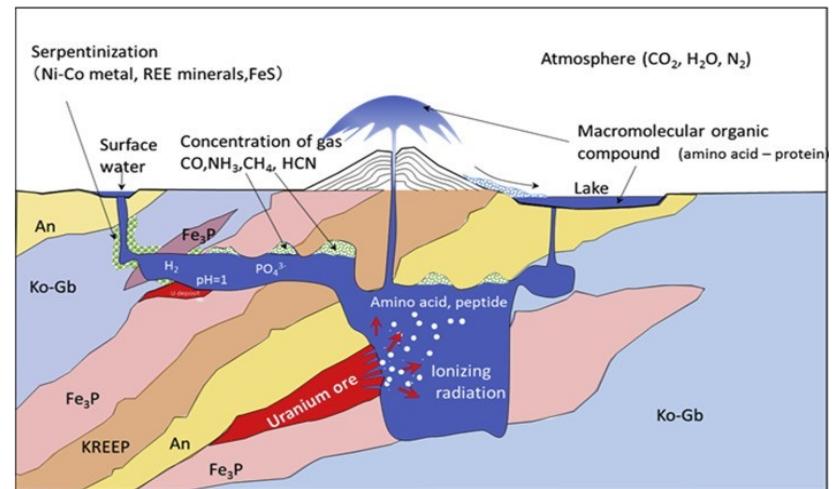
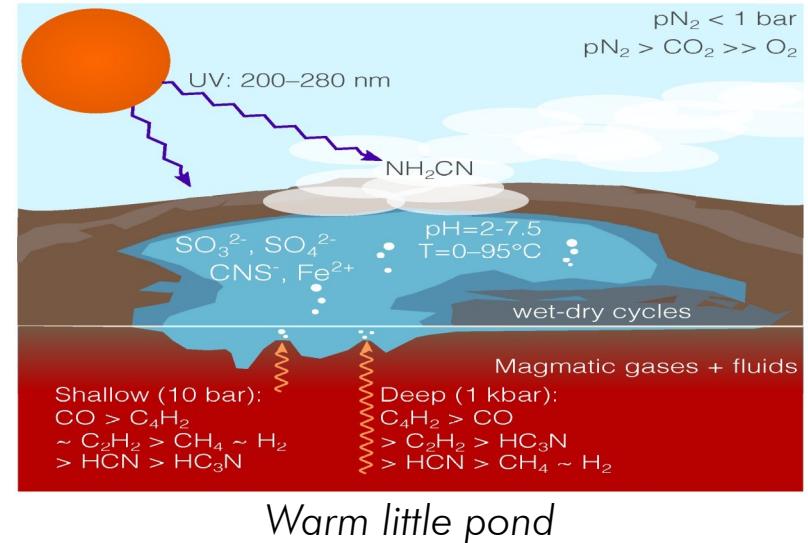
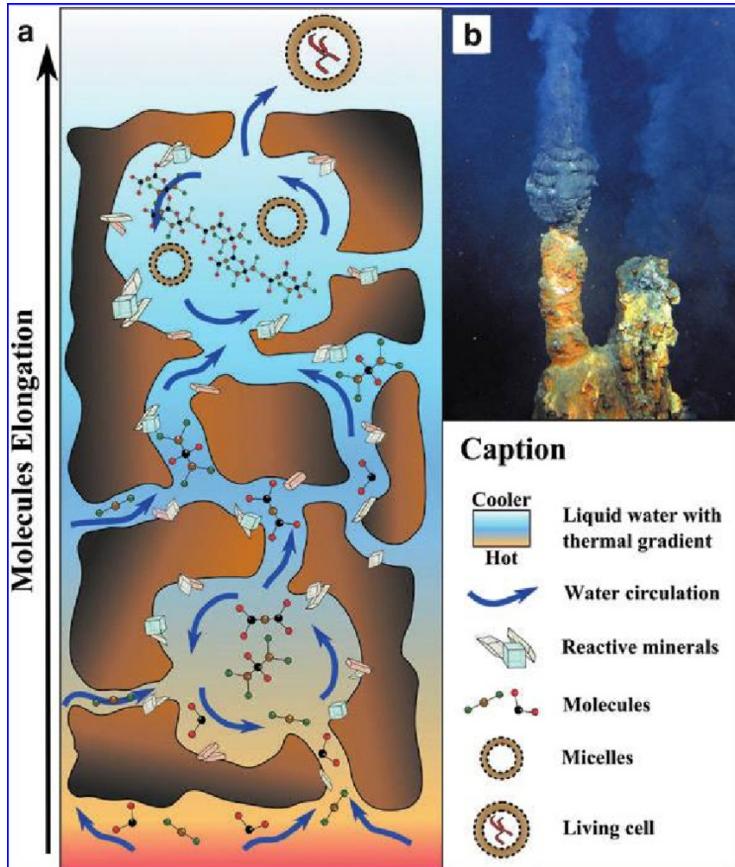
Origin of Life



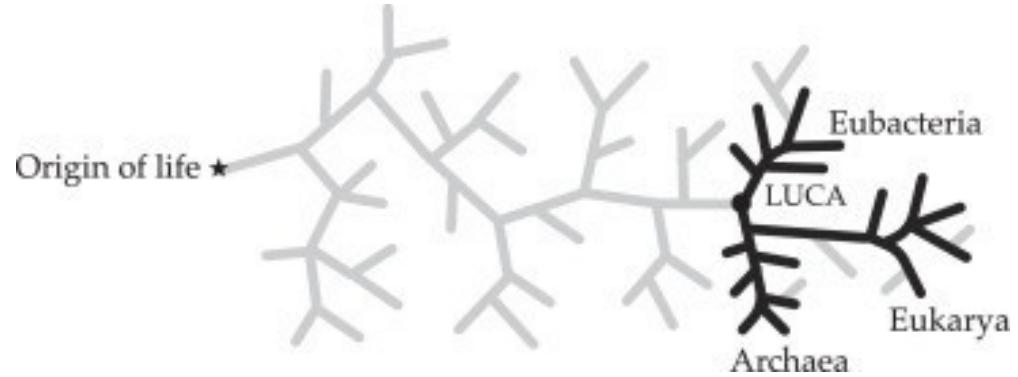
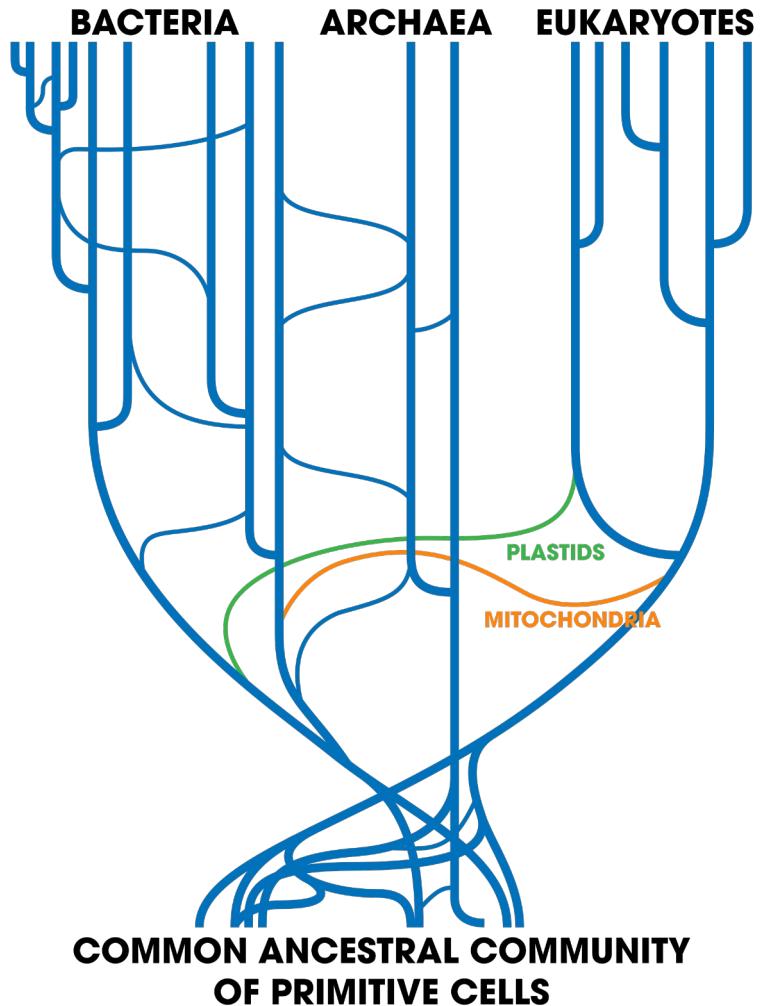
Origin of Life



Origin of Life Scenarios

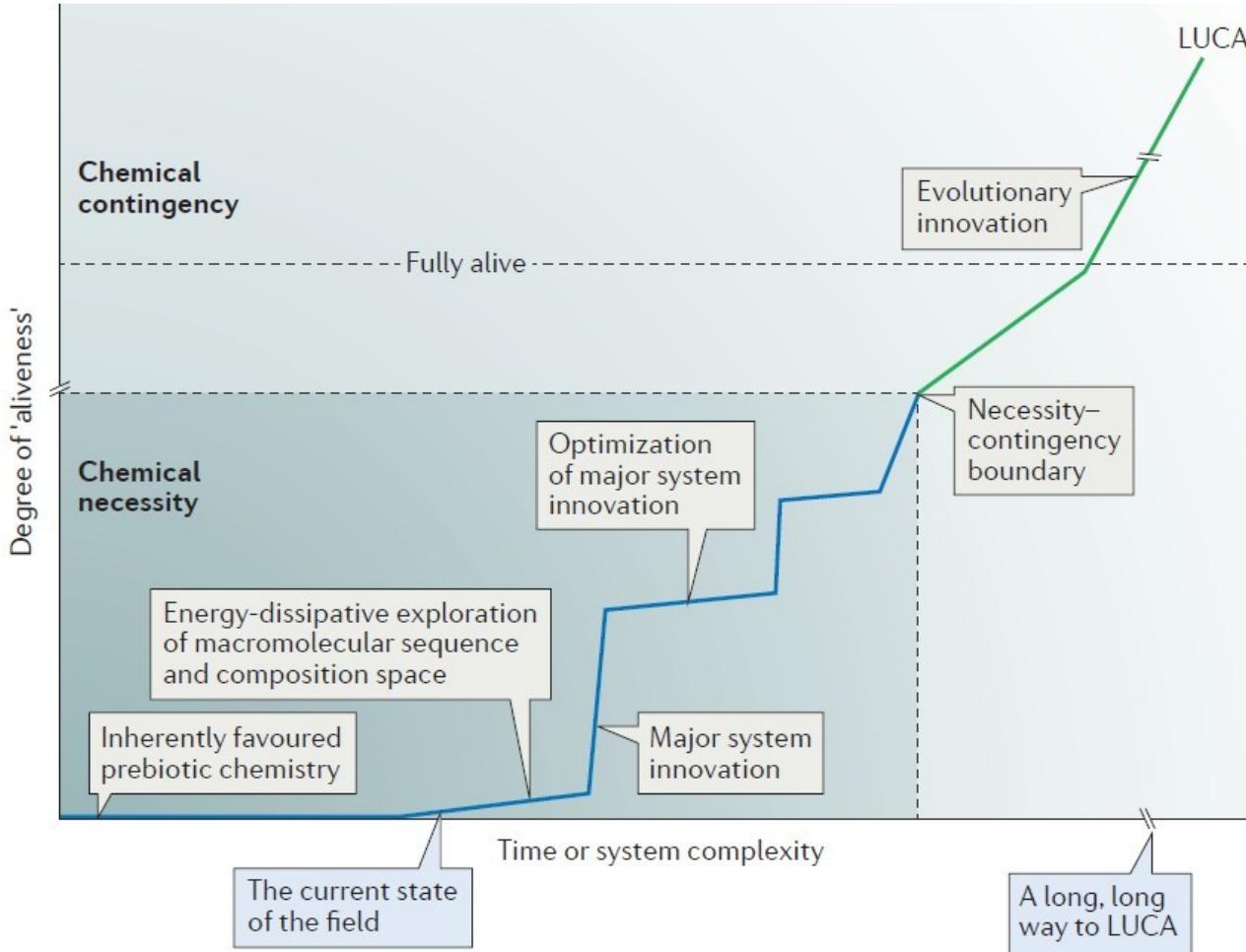


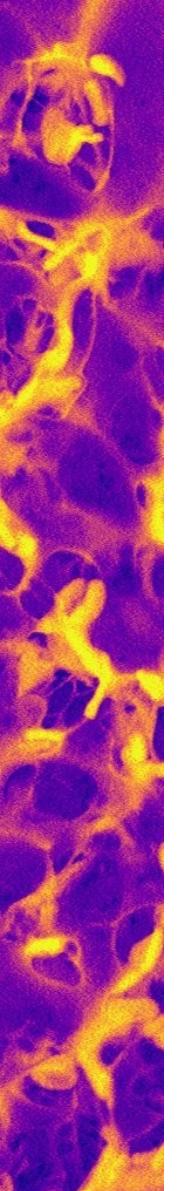
Last Universal Common Ancestor (Survivor?)



LUCA, the Last Universal Common Ancestor, is an operational definition that assumes a single type of organisms of bottleneck for all life. What about Viruses? What about other possible life form? Should we speak about Last Universal Common Survivors (LUCS) instead?

Last Universal Common Ancestor (Survivor?)



A vertical strip of a microscopic image showing various microorganisms, possibly bacteria or fungi, with a color palette ranging from purple to yellow.

MICROBIAL ECOLOGY: A VERY BRIEF GUIDE

Ecosystems

ecosystem

/'i:kəʊsɪstəm/

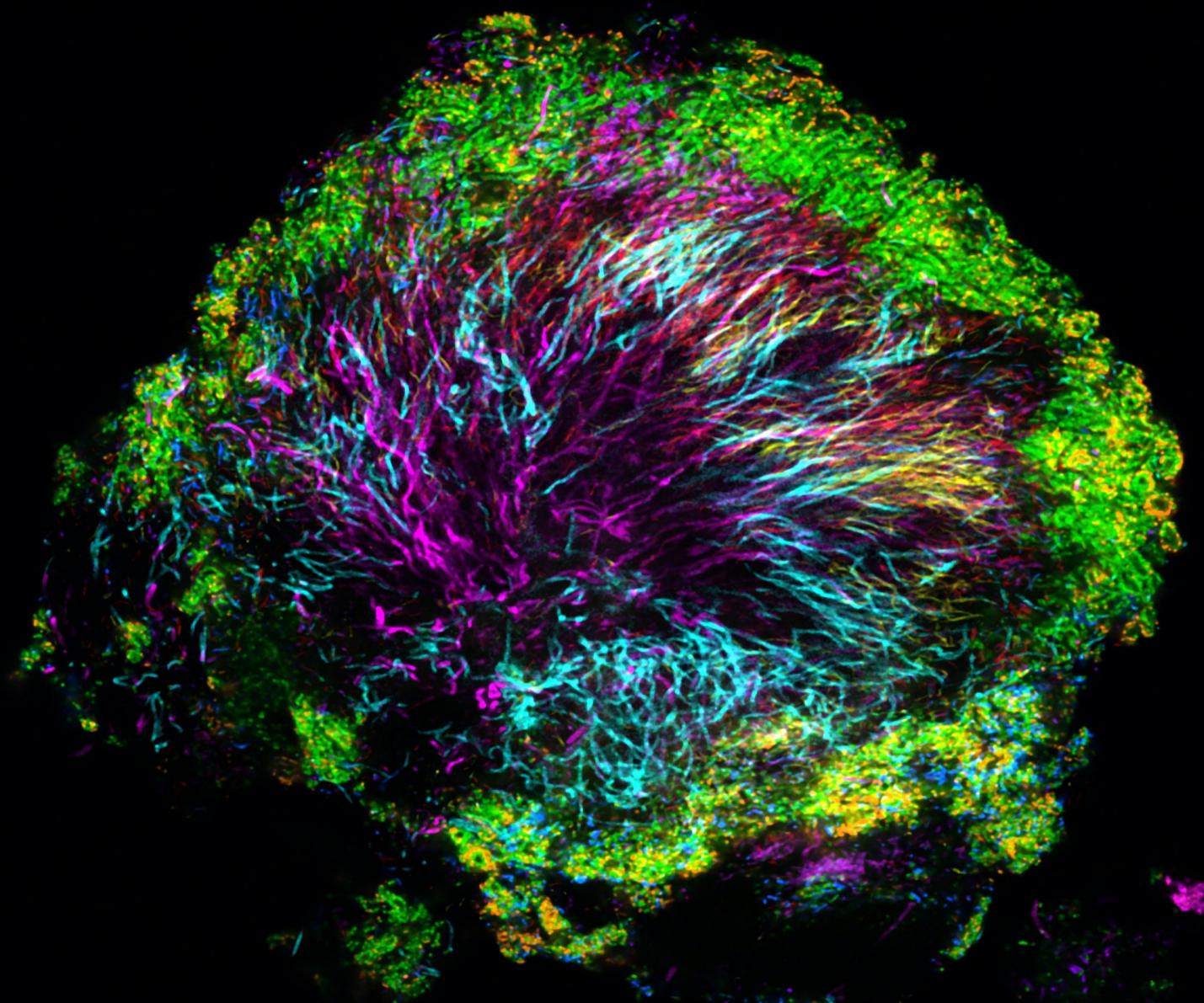
Noun

composite from greek oikos (οἶκος, family, family property, house) and the english system. Oikos was the basic unit of greek society.

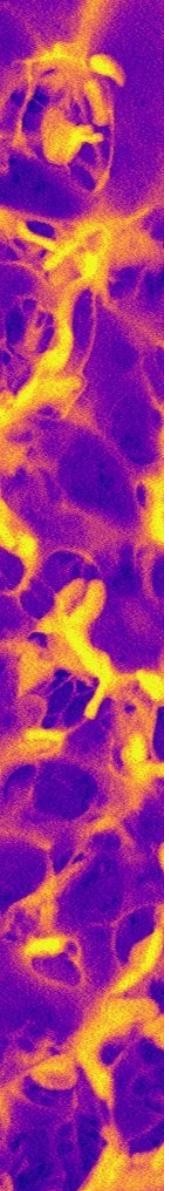
- a biological community of interacting organisms and their physical environment
- (in general use) a complex network or interconnected system

First used in 1935 by Sir Arthur George Tansley, ecosystem







A vertical strip on the left side of the slide showing a microscopic view of microorganisms, possibly bacteria or yeast, with various shapes and colors including yellow, orange, and purple.

Ecosystems

The definition of an ecosystem is arbitrary, and its boundaries can be artificially altered to match the desired research question.

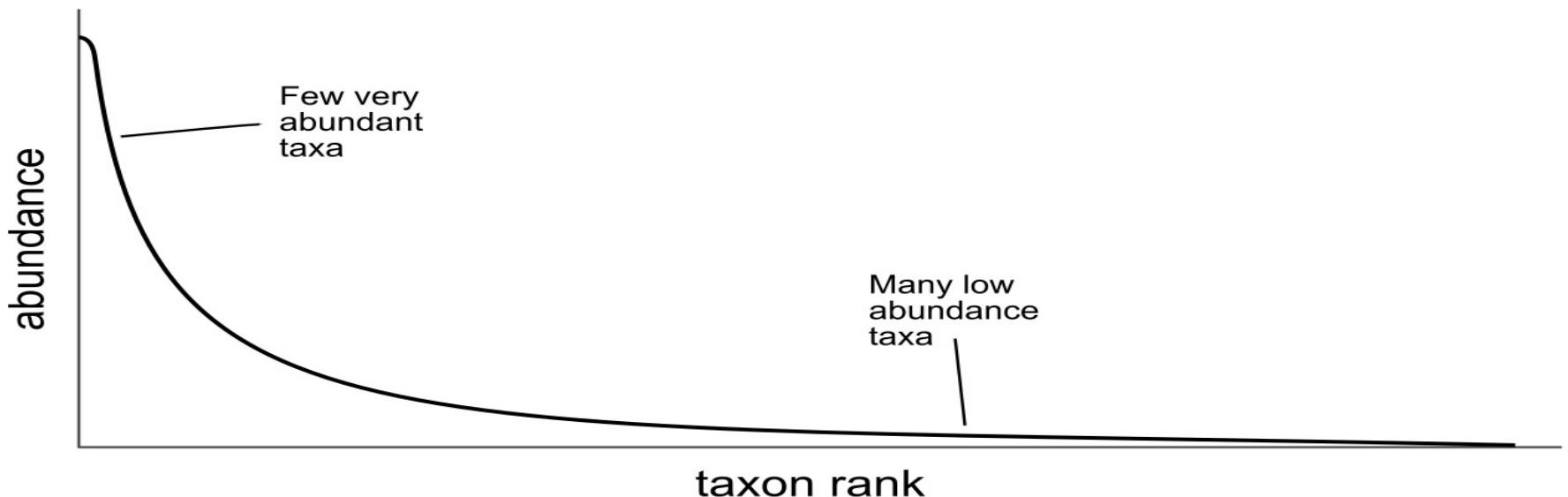
When investigating the microbial world, we need to keep into account what the microbes experience in the environments with respect to our perception of an ecosystem.

Life at “low Reynolds numbers” presents a completely different set of problems and necessary adaptations.

When taking macroscopic and microscopic drivers into account for the definition of the basic characteristics and processes of an ecosystem, the “microscale” becomes an important starting point.

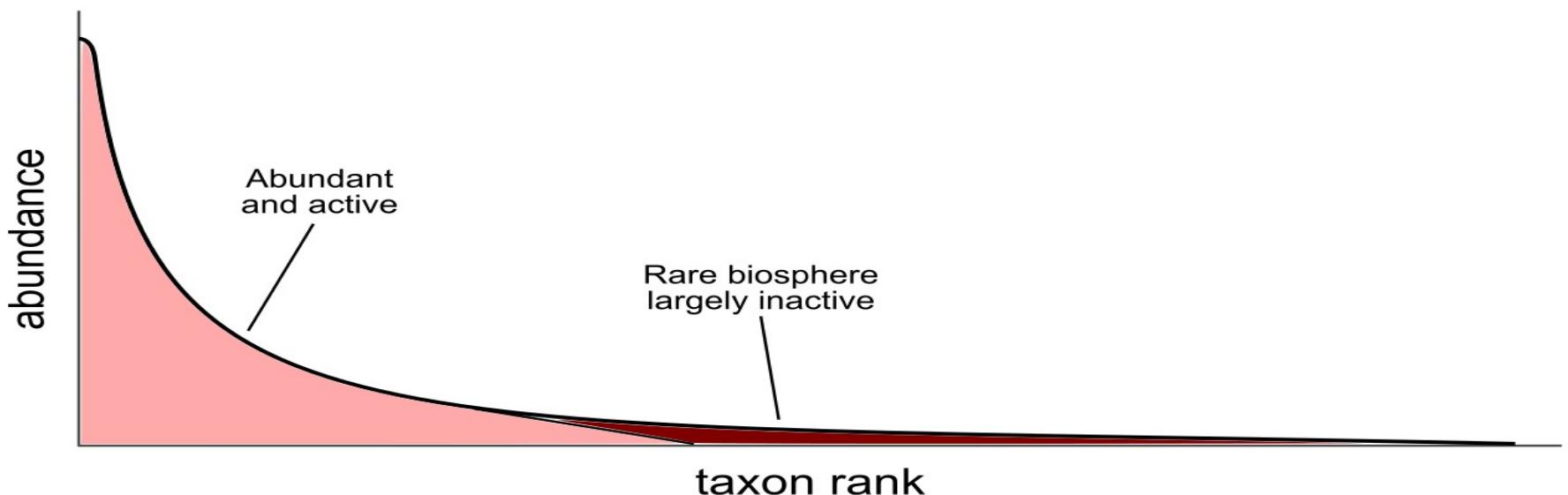
Community structure

Microbial seed-banks theory. Relatively few microbial taxa are abundant and active, while the large majority of the diversity is constituted by a large number of low abundance taxa, often in a dormancy state. Dormancy is a bet-hedging strategy. Dormant microorganisms generate a seed bank capable of being resuscitated following environmental change



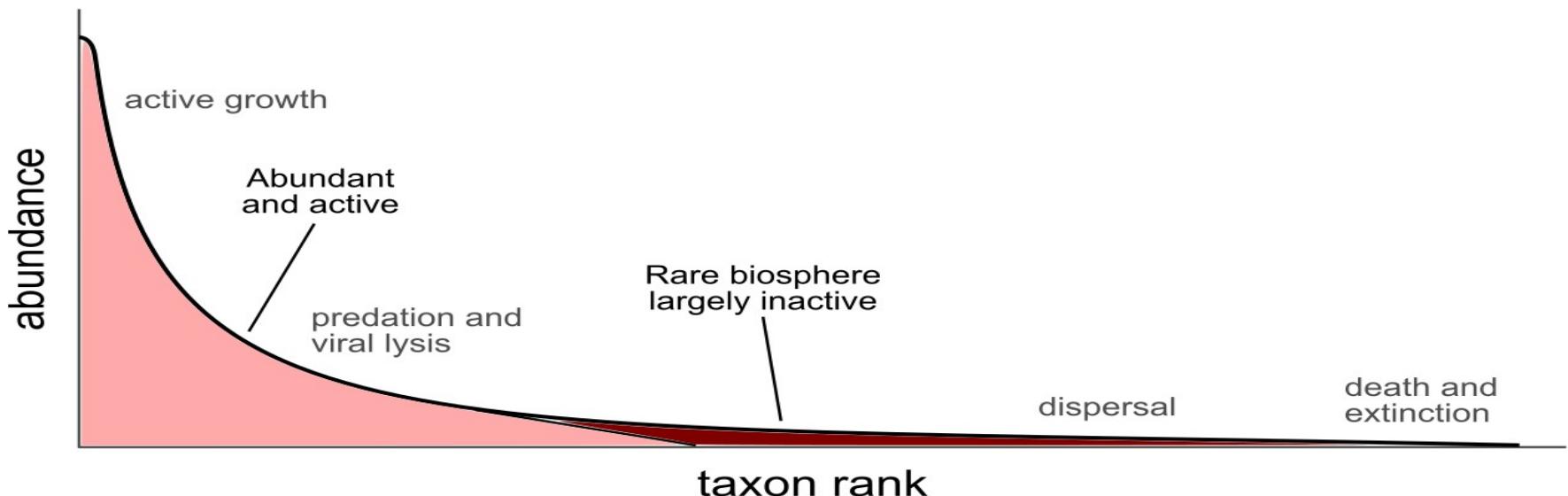
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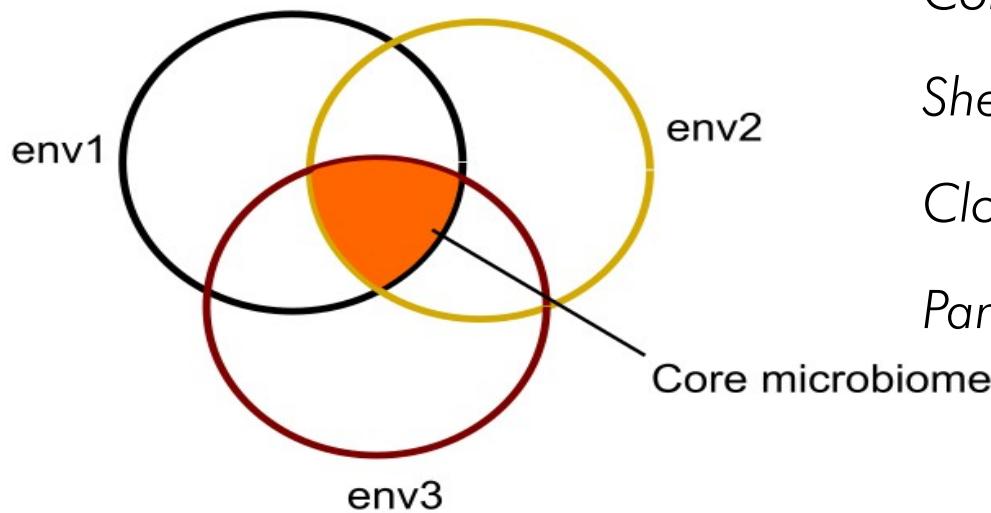


Community structure

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Common taxa: the core microbiome



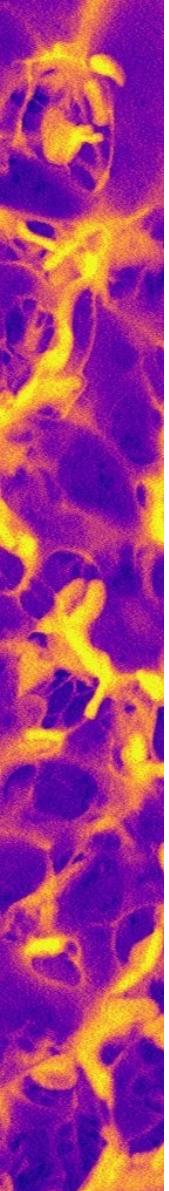
$$\text{Core} = A \cap B \cap C$$

$$\text{Shell} = A \cap B + A \cap C + B \cap C$$

$$\text{Cloud} = (A \cup B + A \cup C + B \cup C) - (A \cap B \cap C)$$

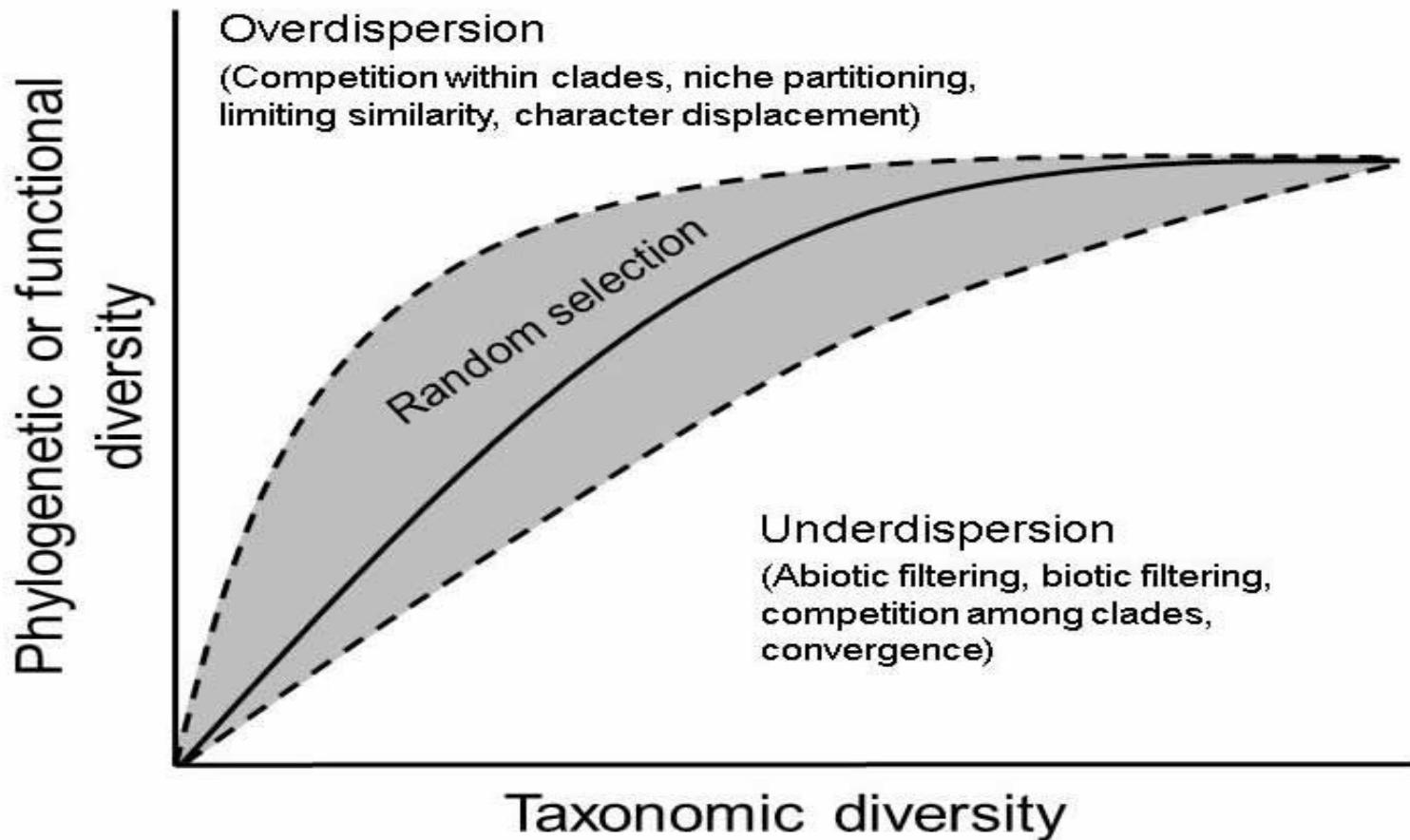
$$\text{Pan} = A \cup B \cup C$$

The **core microbiome** (or microbiota) is the taxa present in all the observed samples. It can be defined **across an environment** (core microbiome in surface sediments), for a **selected area** (the core microbiome of the Antarctic waters) or for a **specific functions** (the core microbiome carrying out nitrogen fixation). A similar concept can be used for functional diversity (the core functions instead of taxa). It can be seen as the deterministic portion of the community.



Ecosystem Functions (microbial)

Functional redundancy



Ecosystem Functions

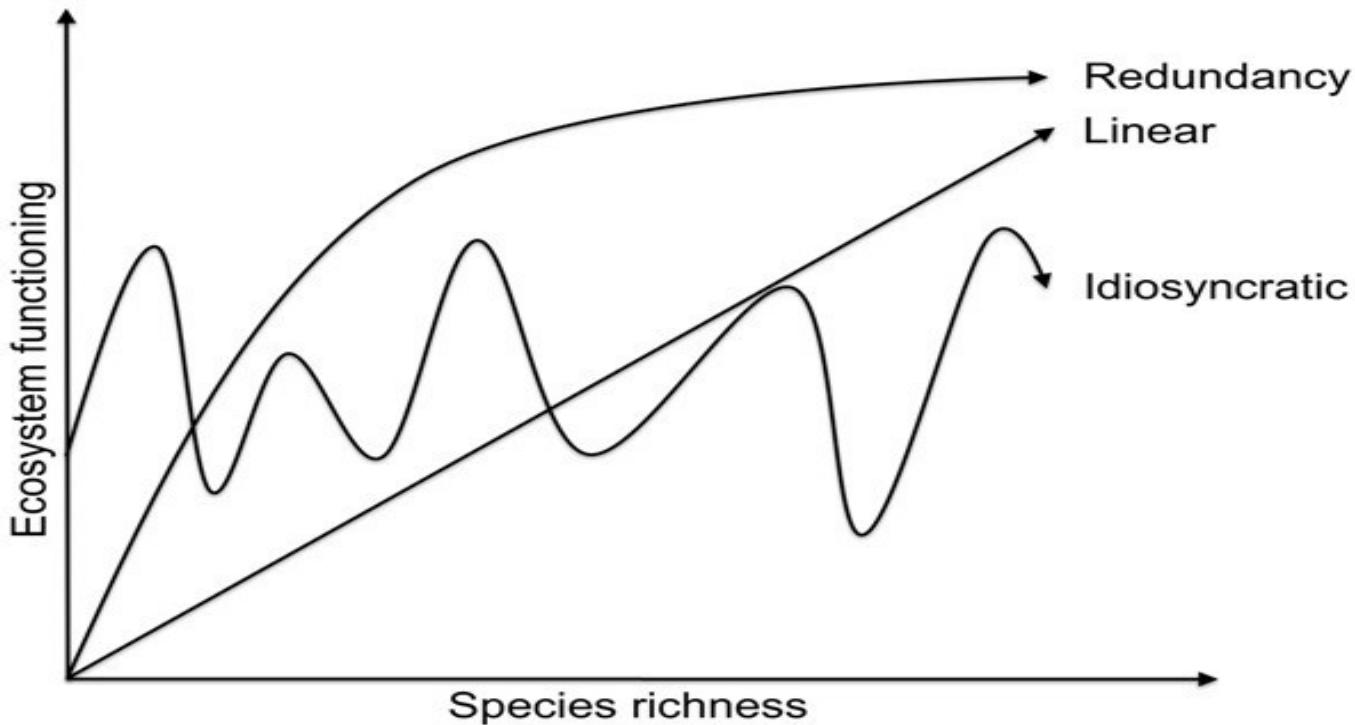
'Ecosystem function' is the technical term used in the framework to define the biological, geochemical and physical processes and components that take place or occur within an ecosystem

Or more simply put, ecosystem functions relate to the structural components of an ecosystem (e.g. vegetation, water, soil, atmosphere and biota) and how they interact with each other, within ecosystems and across ecosystems

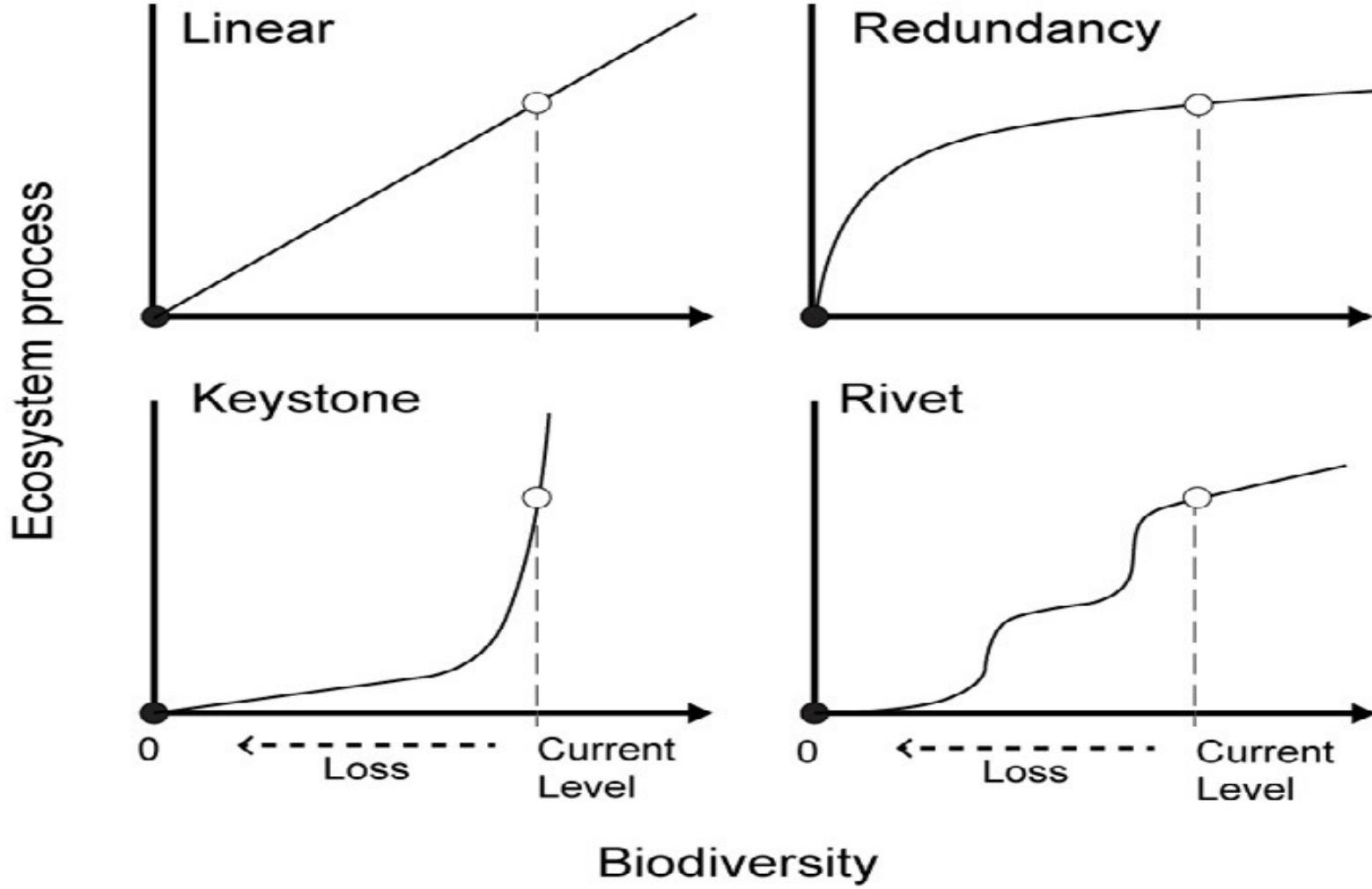
Sometimes, ecosystem functions are called ecological processes. Different ecosystem functions provide ecosystem services to humans and the environment alike.

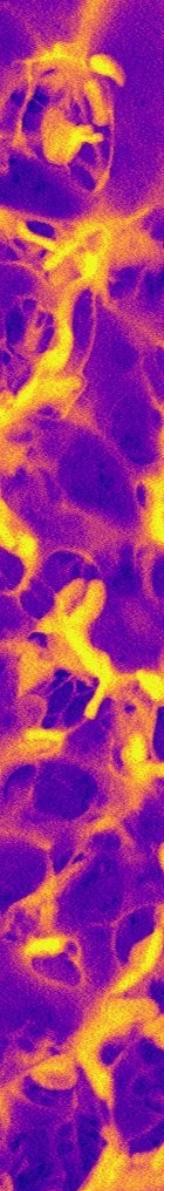
Given the key role of microorganisms in element and nutrient cycling the ecosystem functions provided by the microbial community (and by specific groups of microbes) are fundamental for the functioning of the ecosystem.

Biodiversity-ecosystem function relationship



The relationship between **biodiversity** and **ecosystem functioning** (called **BEF** relation) are widely studied to understand the role of different taxa and the overall functioning and vulnerability of an ecosystem

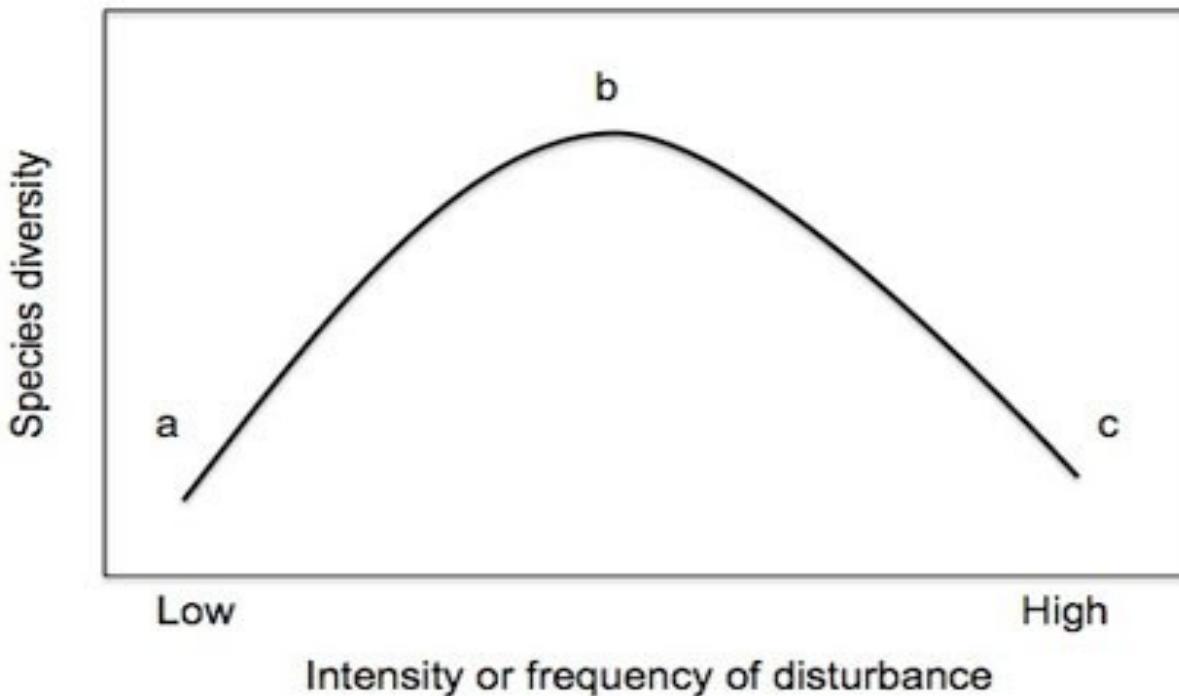


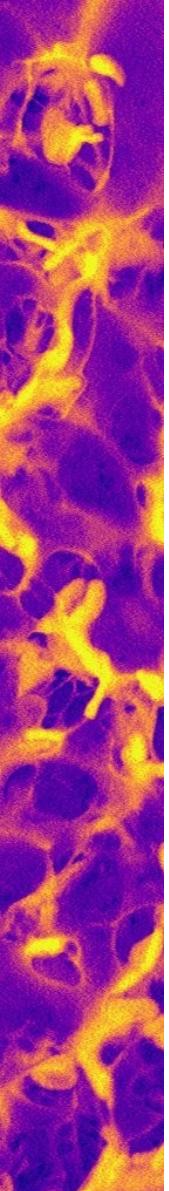


Disturbance theory and ecosystem recovery

Intermediate disturbance hypothesis

The intermediate disturbance hypothesis (IDH) suggests that local species diversity is maximized when ecological disturbance is neither too rare nor too frequent

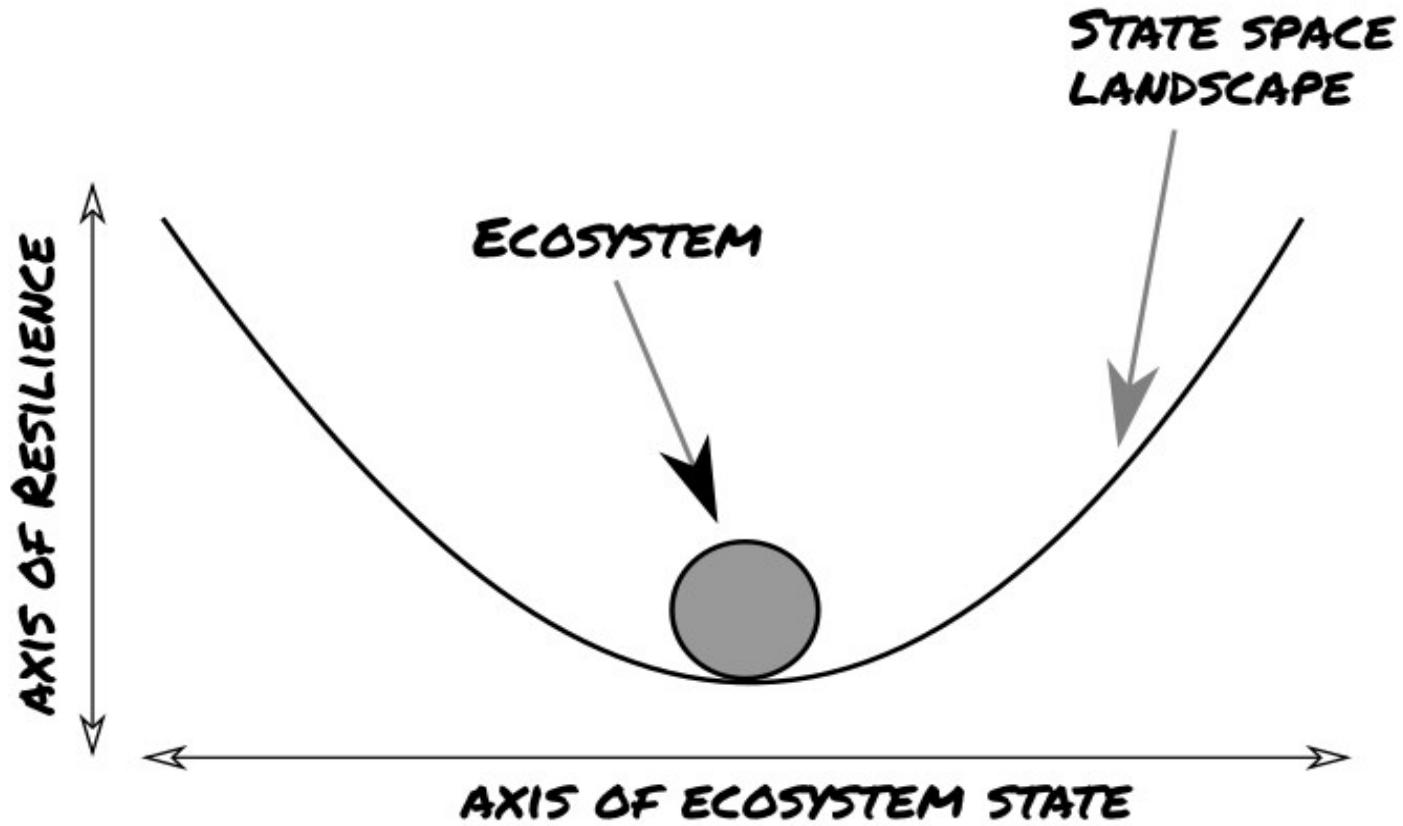


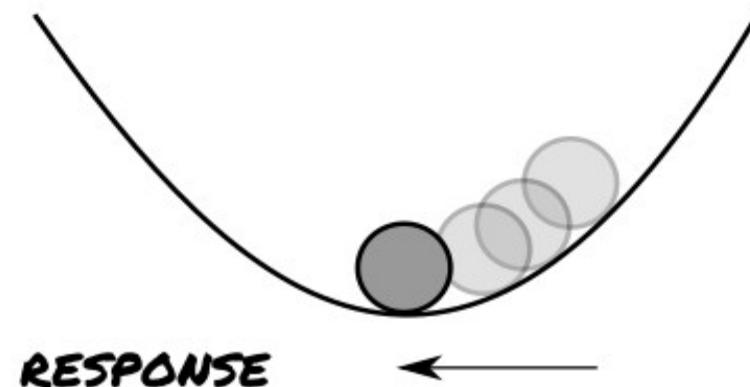
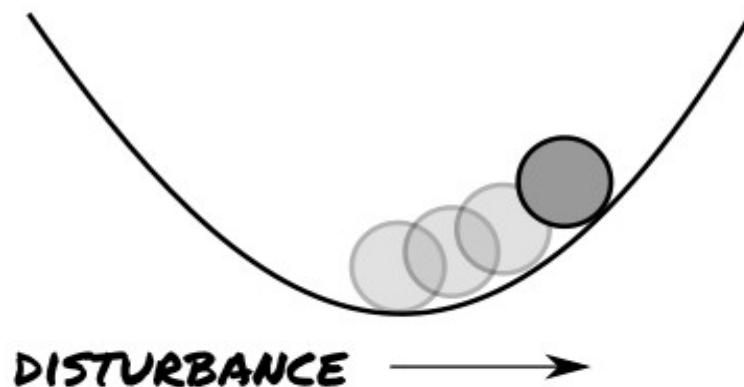


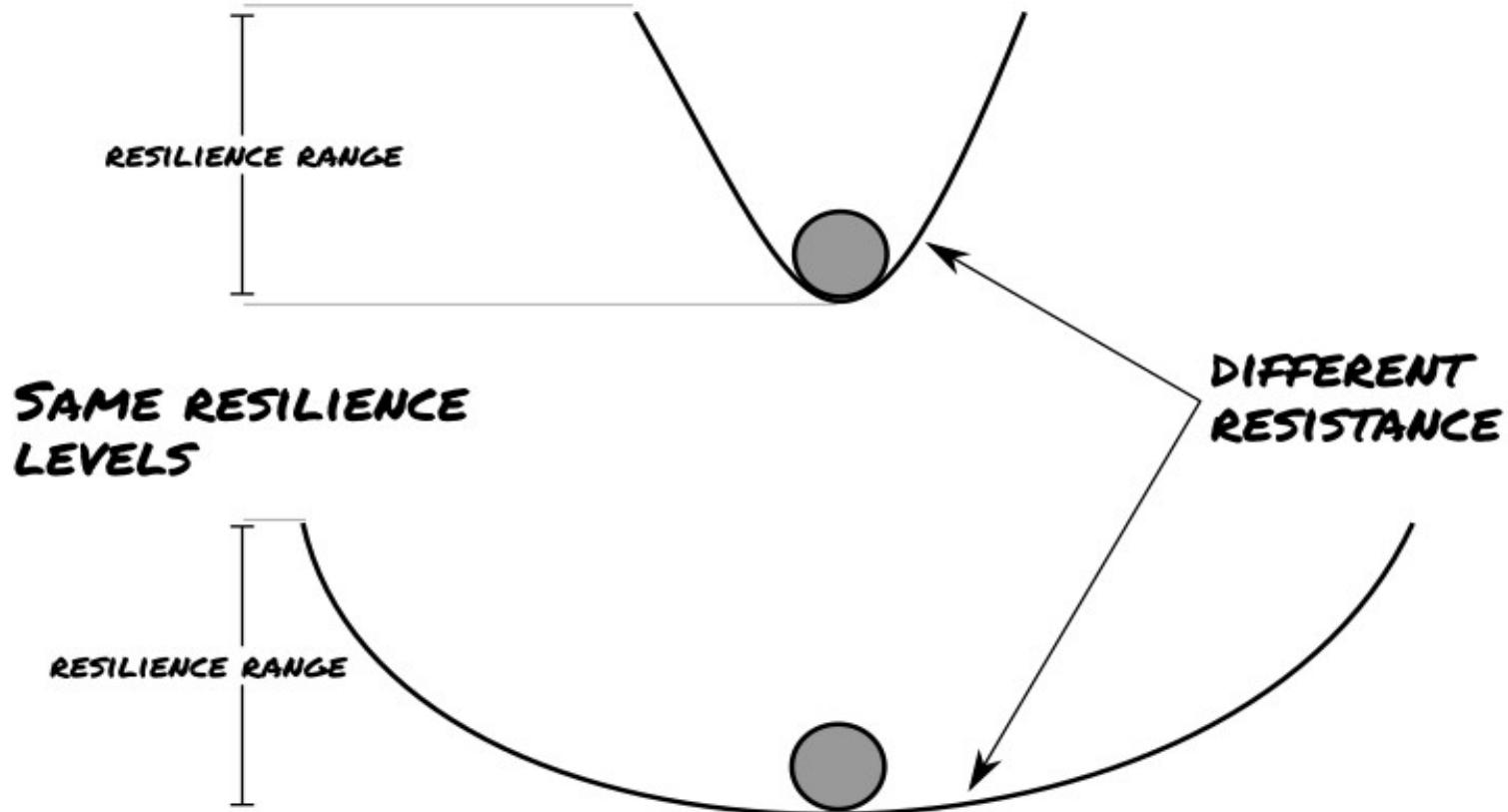
For each ecosystem we can define two basic properties that describe how an ecosystem responds to forcing factors (i.e. change):

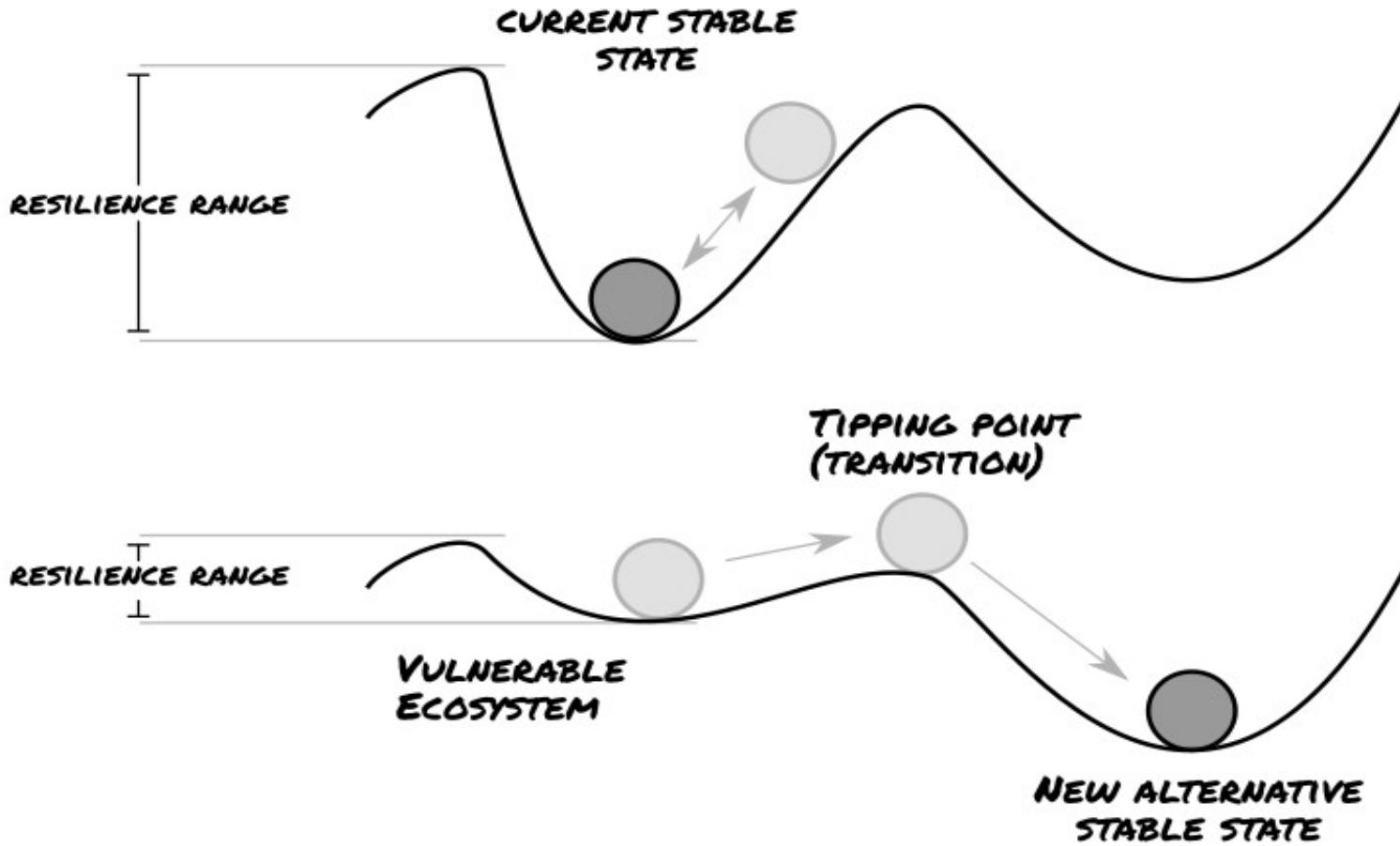
Resistance is the ability for an ecosystem to remain unchanged when being subjected to a disturbance or disturbances. Some ecosystems are better at resisting change than others, and therefore have high resistance

Resilience is the ability and rate of an ecosystem to recover from a disturbance and return to its pre-disturbed state. Some ecosystems can shift greatly from their previous state and still return to pre-disturbance conditions. The measure for how far an ecosystem can be shifted from its previous state and still return to normal is called its amplitude









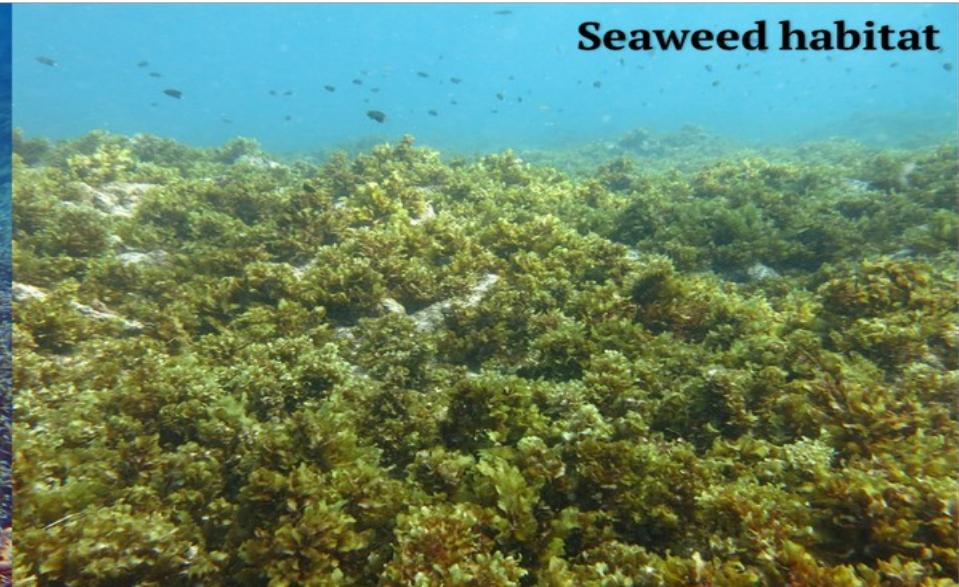
Most ecosystem states are metastable, and can be pushed to a number of alternative (meta)stable states that depend on the nature of the ecosystem itself

alternative stable states

Recovering coral habitat



Seaweed habitat



Risk factors for *C. difficile* colonization

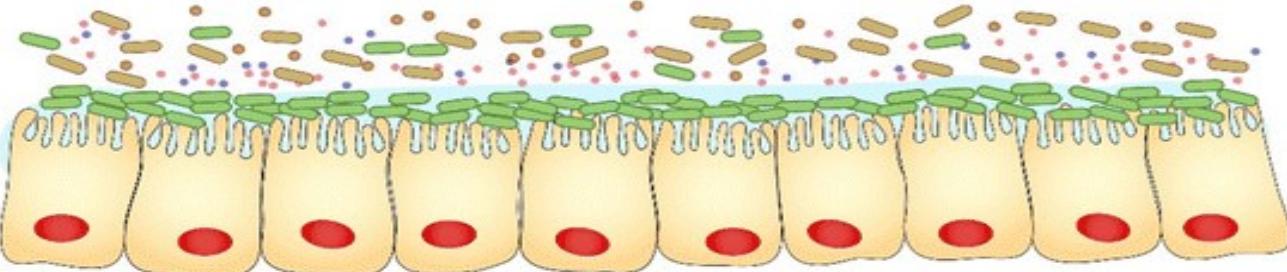
- Previous hospitalization
- Exposure to antibiotics
- Chemotherapy treatment
- Corticosteroid use
- Haemodialysis / renal disease

Exposure to *C. difficile* spores leading to asymptomatic *C. difficile* colonization



Risk factors for symptomatic CDI

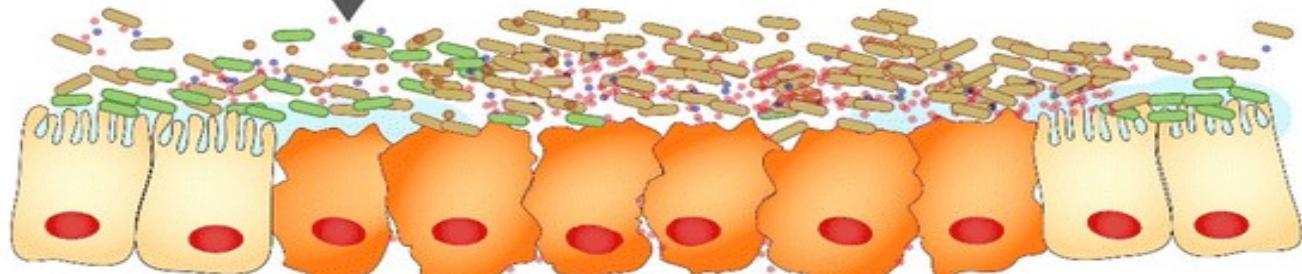
- Increased age
- Exposure and duration of antibiotics
- Presence of nasogastric tube
- Severe underlying disease
- Prolonged hospital admission
- Exposure to drugs that reduce stomach pH



Healthy intestinal epithelial cells with intact microbiome in an individual with asymptomatic *C. difficile* colonization

Factors that protect against progression to symptomatic CDI

- Increased levels of IgG and IgA
- Intact indigenous microbiome
- Colonization by less virulent *C. difficile* strain



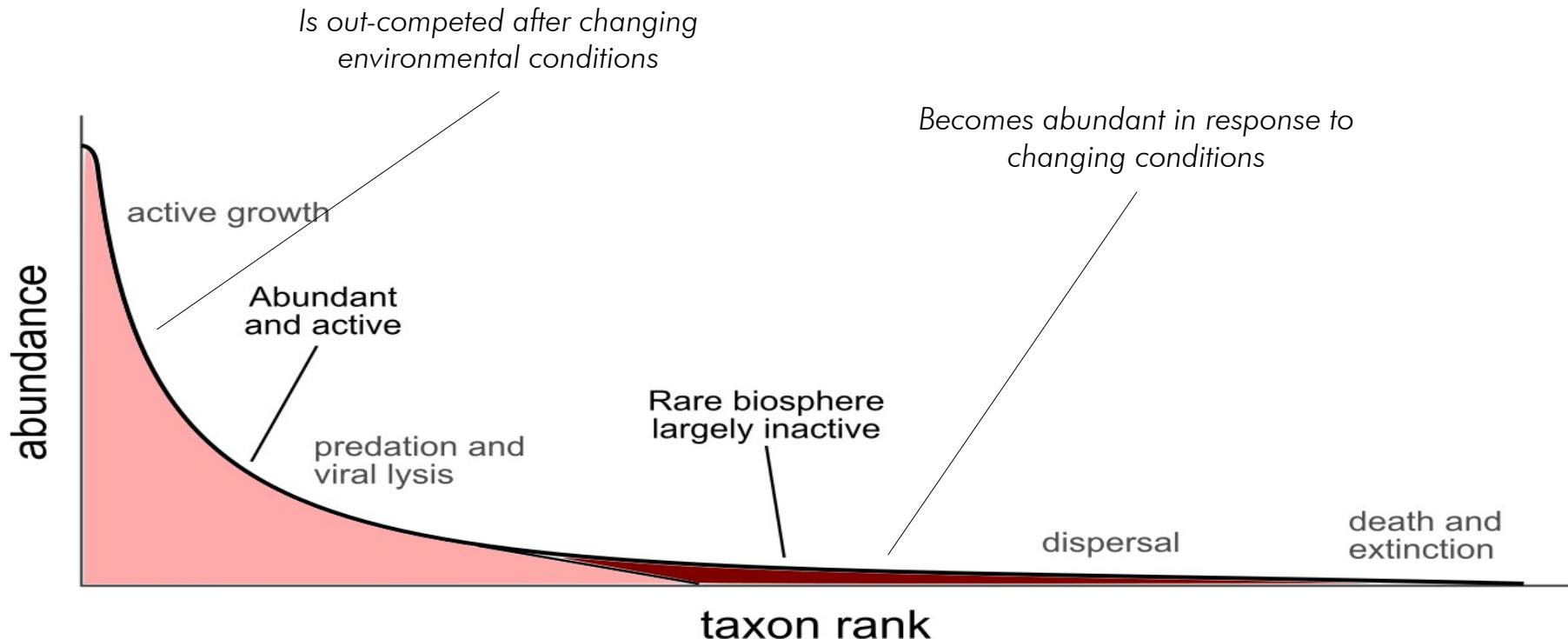
Damaged intestinal epithelial cells in an individual with symptomatic CDI

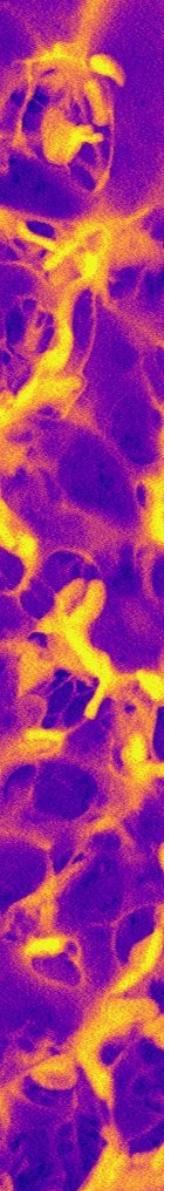
Legend

- Clostridium difficile* cell
- Normal colonic flora
- Clostridium difficile* spore
- Toxin A
- Toxin B



Role of rare and dormant species as a reservoir of functions and adaptations in response to environmental disturbance





Community Controls

Types of Control

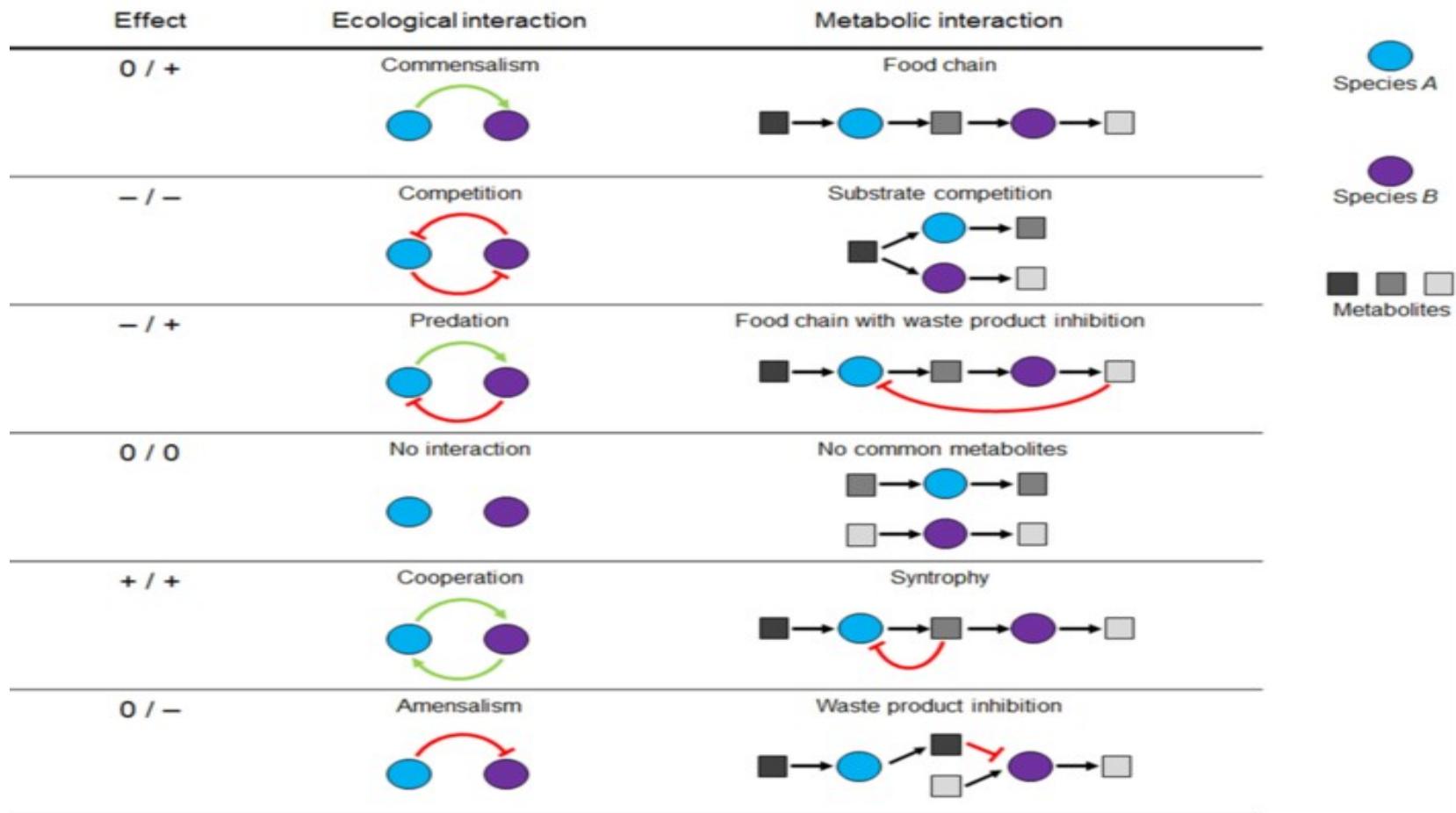
Resource or **bottom-up control** refers to the limitation of a prokaryotic community by **carbon and nutrients** derived from allochthonous inputs, primary production, and heterotrophic production

Top-down control refers to the **predatory limitation** of a prokaryotic community below levels supportable by resources alone. Top-down control refers to situations where the abundance, diversity or biomass of lower trophic levels depends on effects from consumers at higher trophic levels

A **trophic cascade** is a type of top-down interaction that describes the indirect effects of predators. In a trophic cascade, predators induce effects that cascade down food chain and affect biomass of organisms at least two links away

Sideways control refers to within community interaction, such as **competition and chemical warfare**

Community interactions



This week read

Welch, R.A., Burland, V., et al. (2002). Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*. *Proceedings of the National Academy of Sciences*, 99(26), pp. 17020-17024 doi: 10.1073/pnas.252529799

Woese, C. R., and Fox, G. E. (1977). Phylogenetic structure of the prokaryotic domain: The primary kingdoms. *PNAS* 74, 5088–5090. doi:10.1073/pnas.74.11.5088.

Pace, N. R., Sapp, J., and Goldenfeld, N. (2012). Phylogeny and beyond: Scientific, historical, and conceptual significance of the first tree of life. *PNAS* 109, 1011–1018. doi:10.1073/pnas.1109716109.

Spang, A., Saw, J. H., Jørgensen, S. L., Zaremba-Niedzwiedzka, K., Martijn, J., Lind, A. E., et al. (2015). Complex archaea that bridge the gap between prokaryotes and eukaryotes. *Nature advance online publication*. doi:10.1038/nature14447.