World of Microbiome
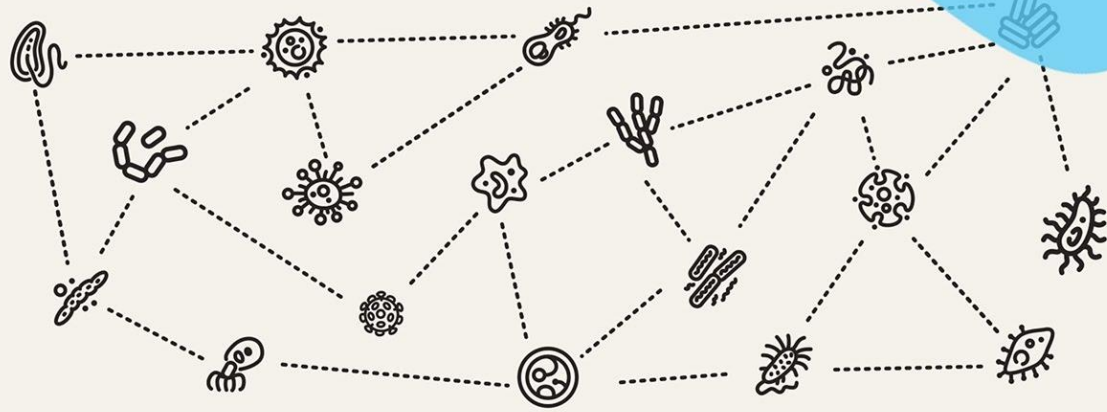
November 10, 2022

WHAT IS A MICROBIOME?

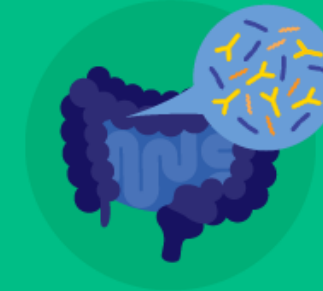## microorganisms

tiny organisms living in all kinds of environments

microbiota

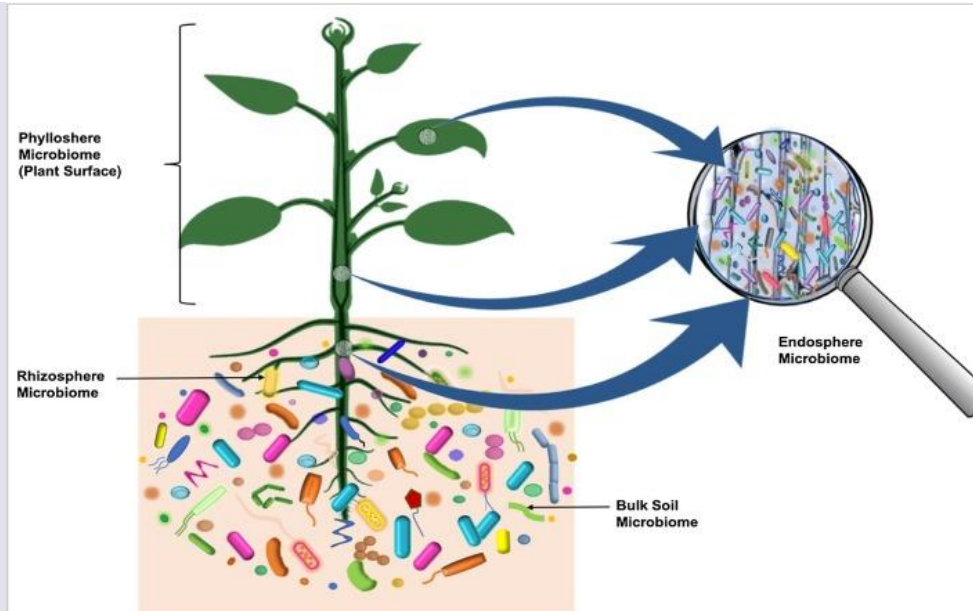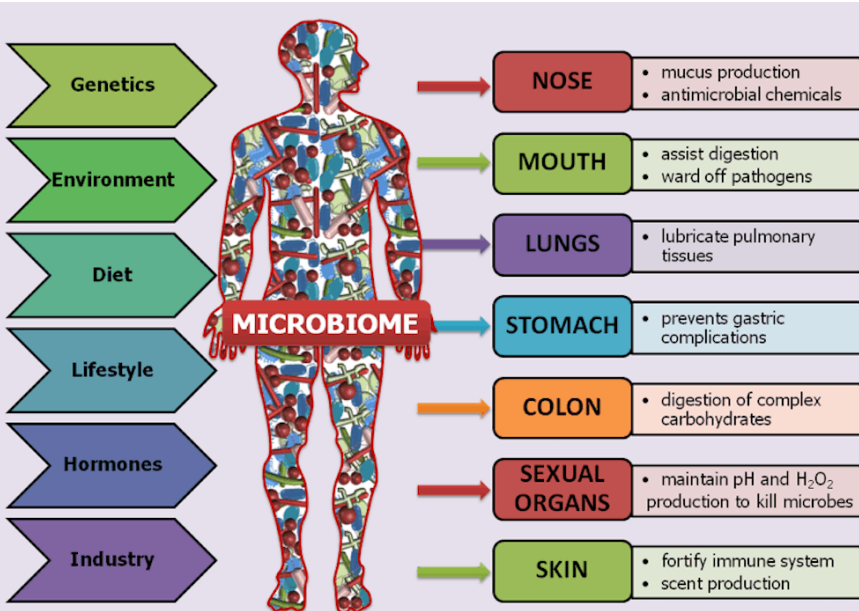a community of microorganisms in a specific environment

microbiome

a community of microorganisms & their role within a specific environment, considering environmental conditions & interactions with each other

eufic

Genetics
Environment
Diet
Lifestyle
Hormones
Industry

MICROBIOME

- **NOSE**
  - mucus production
  - antimicrobial chemicals
- **MOUTH**
  - assist digestion
  - ward off pathogens
- **LUNGS**
  - lubricate pulmonary tissues
- **STOMACH**
  - prevents gastric complications
- **COLON**
  - digestion of complex carbohydrates
- **SEXUAL ORGANS**
  - maintain pH and H_2O_2 production to kill microbes
- **SKIN**
  - fortify immune system
  - scent production

Phylloshere Microbiome (Plant Surface)

Endosphere Microbiome

Rhizosphere Microbiome

Bulk Soil Microbiome

OCEAN MICROBIOME
Photoautotrophs
Chemolithoautotrophs
Heterotrophs
Mixotrophs
Diazotrophs
Parasites
Pathogens
Predators
Symbiotic interactions

Plankton

What is Microbiome?

- The microbiome is the community of **microorganisms (such as fungi, bacteria and viruses) that exists in a particular environment (**Types of Microbiome: 1. Soil Microbiome (Most complex) 2. Marine microbiome 3. Plant microbiome 4. Animal Microbiome (Ex. Chicken gut microbiome) 5. Human microbiome (Ex. Human gut microbiome**)**

- In **humans**, the term is often used to describe the **microorganisms that live in or on a particular part of the body, such as the skin or gastrointestinal tract**. These groups of microorganisms are dynamic and change in response to a host of environmental factors, such as exercise, diet, medication and other exposures.

- Microbiome research mostly looks at bacteria and fungi and rarely into archaea, viruses and other types.

Human microbiome
Archaea, bacteria, fungi and viruses

Mouth

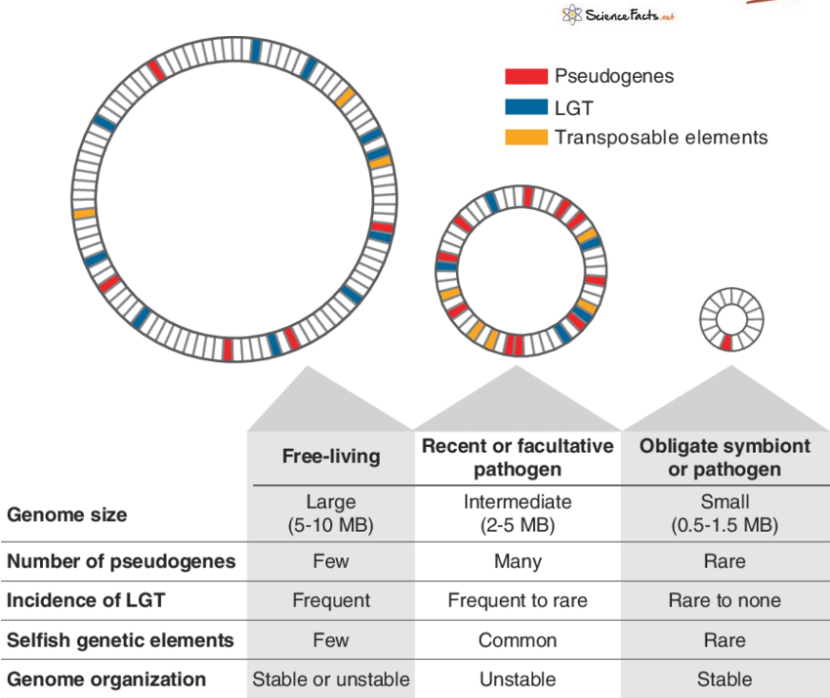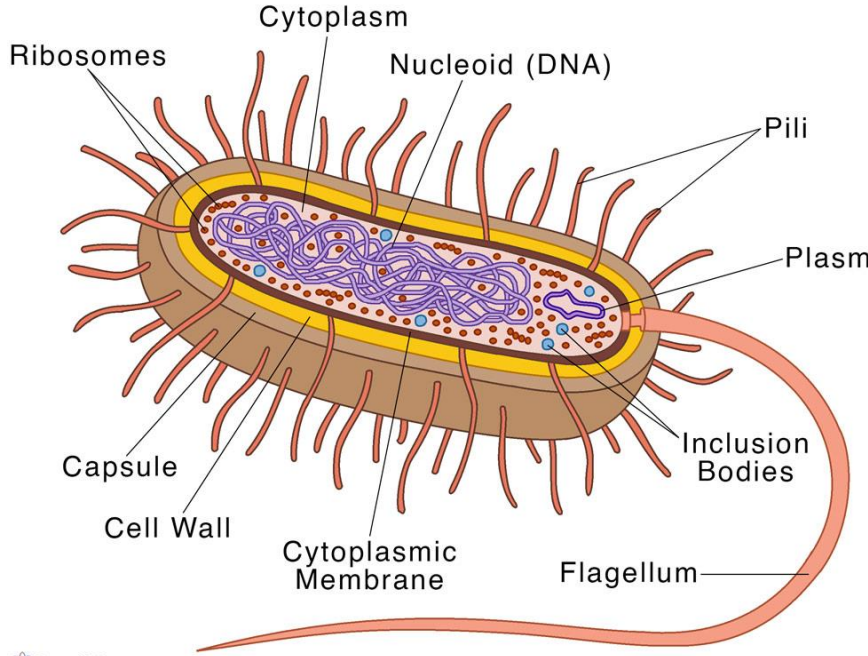Skin

Digestive

Urogenital
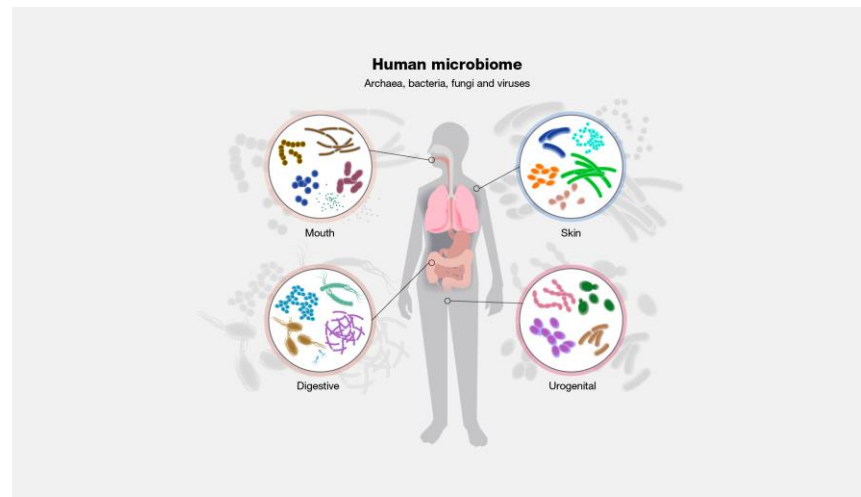
Why study Microbiome?

- **We know the microbiome is important for maintaining human health**, and when things go wrong it can contribute to disease. In order to understand how microbes, influence human disease, we first need to understand the microbial make up of a healthy person—what types of microbes are present, and what are they doing?
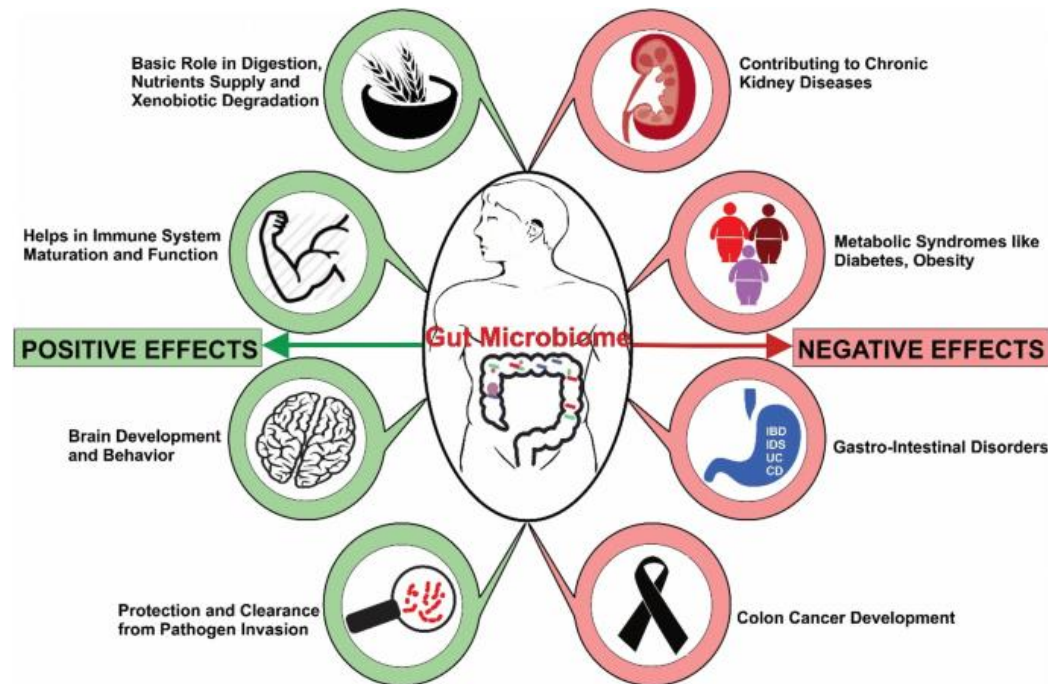
What is a bacteria ?

Bacterial Genome:
1. Single chromosome
2. 2. Mostly circular
3. 3. Contains about 500-7500 genes
4. 4. Genome size ranges from 400kbp – 13 million base pairs.

Bacteria Cell

	Free-living	Recent or facultative pathogen	Obligate symbiont or pathogen
Genome size	Large (5-10 MB)	Intermediate (2-5 MB)	Small (0.5-1.5 MB)
Number of pseudogenes	Few	Many	Rare
Incidence of LGT	Frequent	Frequent to rare	Rare to none
Selfish genetic elements	Few	Common	Rare
Genome organization	Stable or unstable	Unstable	Stable

Legend:
- Pseudogenes
- LGT
- Transposable elements

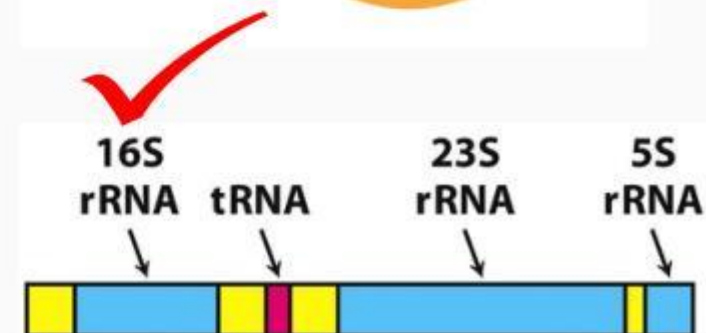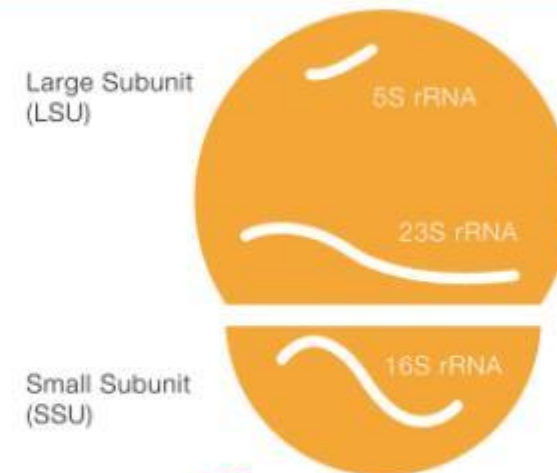# Prokaryote Ribose and 16SrRNA

16S rRNA

rRNA——molecular clock:

1. Universality
2. Activity in cellular functions
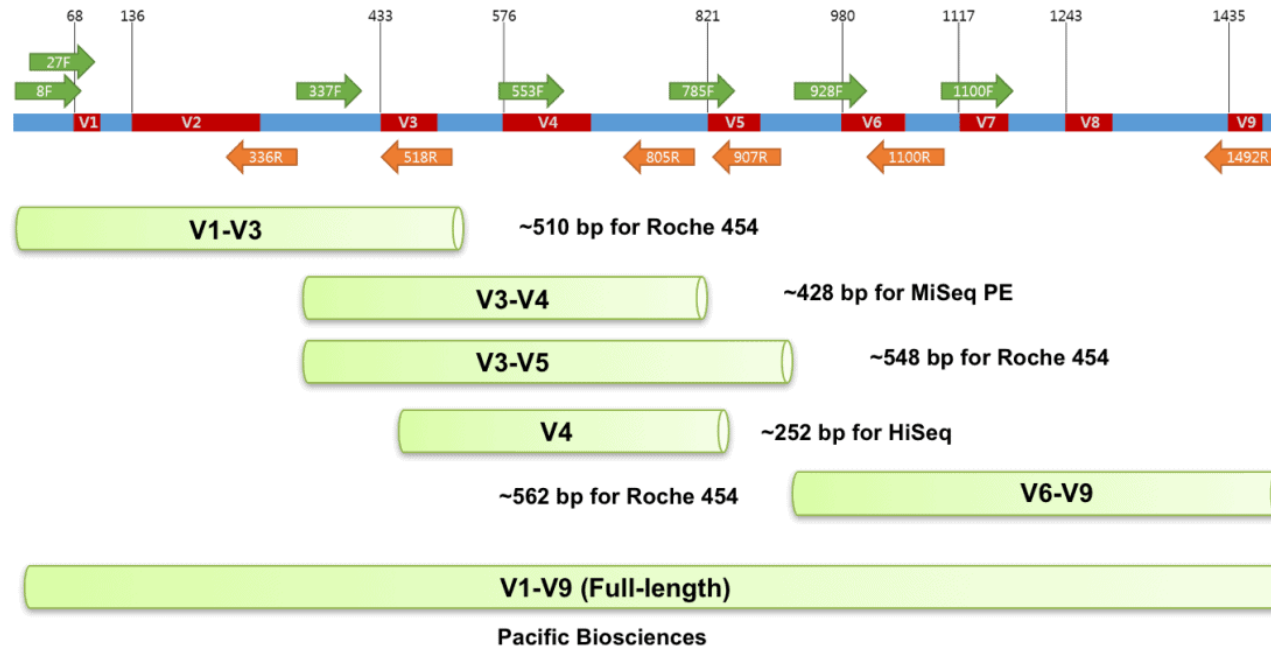3. Extremely conserved structure and sequence

Three types of rRNA in prokaryotic ribosomes:

- 23S (3300 bp)
- 16S (1550 bp) —— a standard in bacterial taxonomic classification
- 5S (120 bp)

CD Genomics
The Genomics Services Company

Prokaryotic Ribosome

Large Subunit (LSU) — 5S rRNA — 23S rRNA

Small Subunit (SSU) — 16S rRNA

| 16S rRNA | tRNA | 23S rRNA | 5S rRNA |

16rRNA sequence

The 16S rRNA gene is used for phylogenetic studies as it is highly conserved between different species of bacteria and archaea. Provides very good resolution till genus level and to some extent species level. There could be one or more copies of 16SrRNA in a bacterial genome.
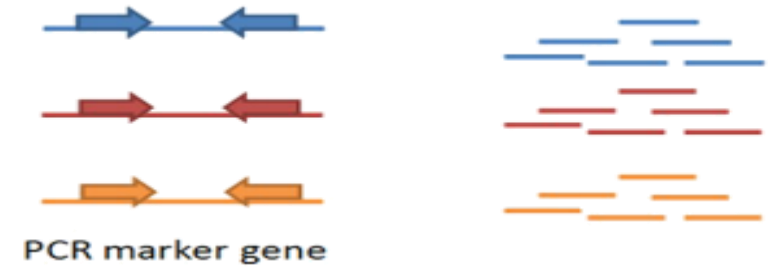
Comparison metagenomics VS. 16SrRNA

METAGENOMICS

Bacterial Genome

16SrRNA SEQUENCING

PCR marker gene
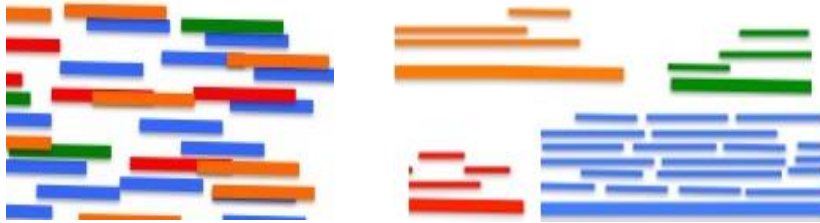
Entire communities (viruses and fungi)
Relatively expensive
Highly variability, higher resolution
Direct assessment of genes and pathways
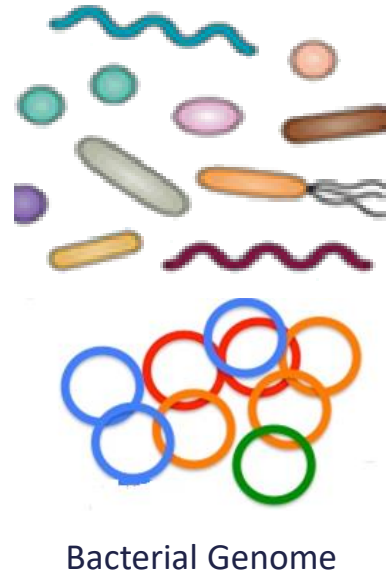
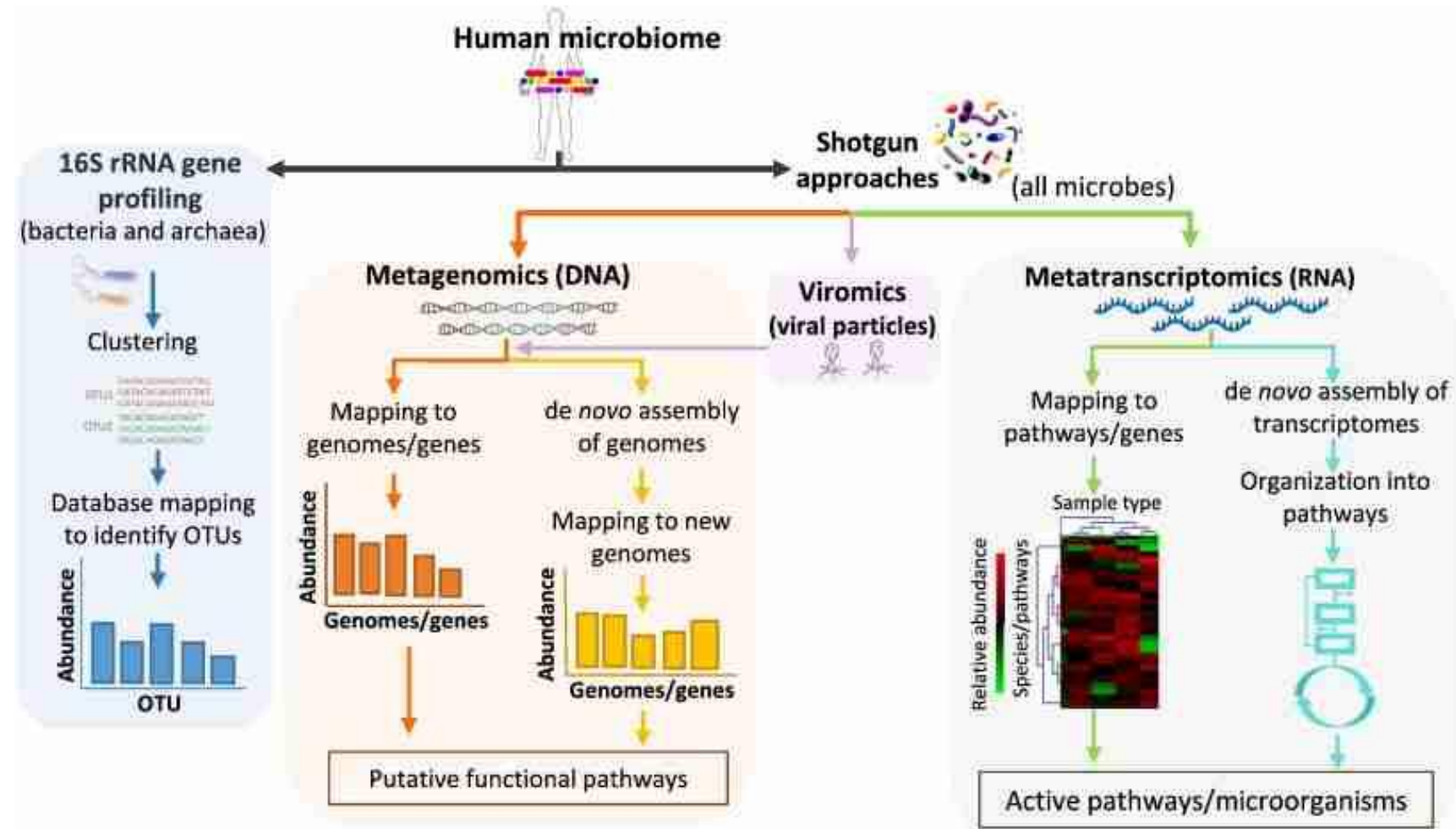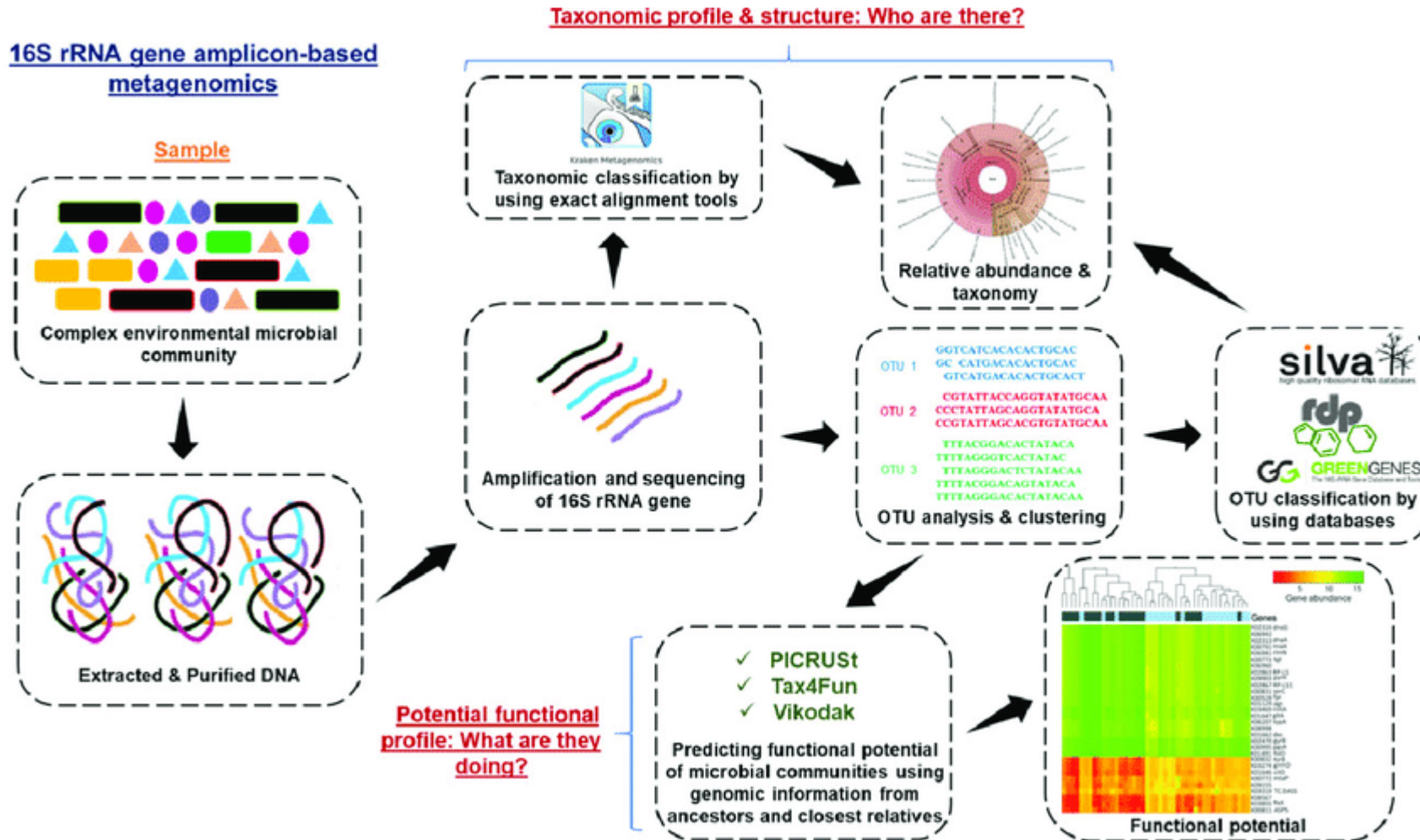Only bacteria and Archaea
Relatively cheap – large sample sizes
Taxonomic classification to Genus level?
Genes and pathways based on classification

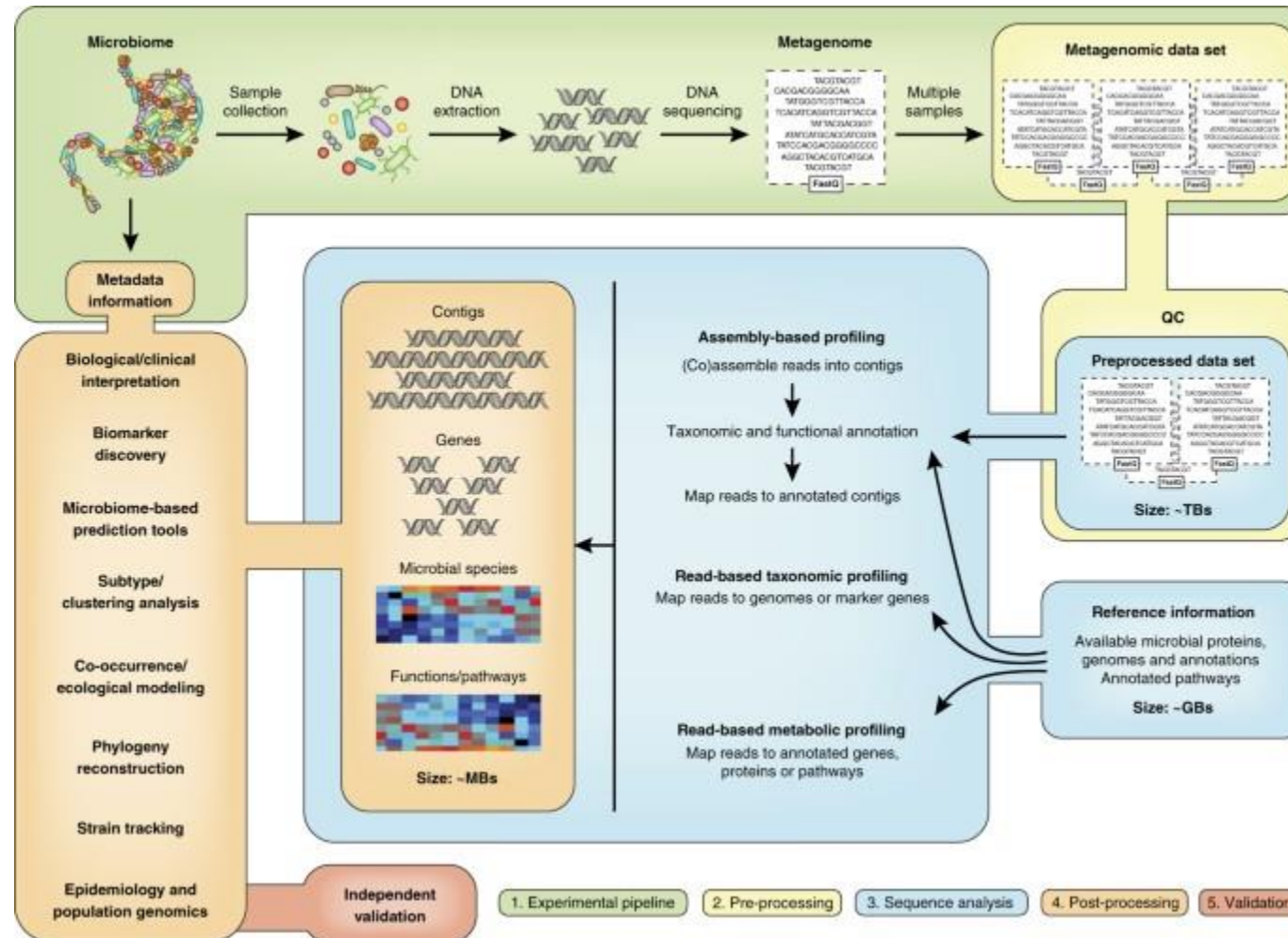# Comparison metagenomics VS. 16SrRNA

16s rRNA processing pipeline

Shotgun Metagenomics Pipeline

Suites of analysis tools

Quantitative Insights Into Microbial Ecology

qiime

16SrRNA

mothur

| Download | Wiki | Forum | facebook |

R packages dada2, phyloseq, DESeq2

Check for updates

RESEARCH ARTICLE

Bioconductor workflow for microbiome data analysis:
from raw reads to community analyses [version 1;
referees: 3 approved]

Ben J. Callahan[1], Kris Sankaran[1], Julia A. Fukuyama[1], Paul J. McMurdie[2], ✉ Susan P. Holmes[1]

⊞ Author affiliations

⊞ Grant information

STUDY DESIGNS

Experimental and analytical tools for
studying the human microbiome

Justin Kuczynski[1], Christian L. Lauber[2], William A. Walters[1], Laura Wegener Parfrey[3],
José C. Clemente[3], Dirk Gevers[4] and Rob Knight[3,5]

GENOME
RESEARCH

MaAsLin

Microbial community profiling for human microbiome projects:
Tools, techniques, and challenges

Micah Hamady and Rob Knight

Genome Res. 2009 19: 1141-1152 originally published online April 21, 2009
Access the most recent version at doi:10.1101/gr.085464.108

Suites of analysis tools

MetaGenomics

Meta'omic Analysis with
MetaPhlAn, HUMAnN, and LEfSe

QIAGEN

BIOI

SOLUTIONS   PRODUCTS   INSIGH

Home > Plugins > MetaGeneMark

MetaGeneMark

Gene finding for microbial genome and metagenome assemblies

Gene finding expertise for CLC Genomics Workbench

PLoS COMPUTATIONAL BIOLOGY

Metabolic Reconstruction for Metagenomic Data and Its Application to the Human Microbiome

Sahar Abubucker[1], Nicola Segata[2], Johannes Goll[3], Alyxandria M. Schubert[4], Jacques Izard[5,6], Brandi L. Cantarel[7], Beltran Rodriguez-Mueller[6], Jeremy Zucker[8], Mathangi Thiagarajan[3], Bernard Henrissat[9], Owen White[7], Scott T. Kelley[10], Barbara Methé[3], Patrick D. Schloss[4], Dirk Gevers[8], Makedonka Mitreva[1], Curtis Huttenhower[2,8]*

1 The Genome Institute, Washington University School of Medicine, St. Louis, Missouri, United States of America, 2 Department of Biostatistics, Harvard School of Public Health, Boston, Massachusetts, United States of America, 3 J. Craig Venter Institute, Rockville, Maryland, United States of America, 4 Department of Microbiology and Immunology, University of Michigan, Ann Arbor, Michigan, United States of America, 5 Department of Molecular Genetics, Forsyth Institute, Cambridge, Massachusetts,

The taxonomic and functional compositions of a microbiome
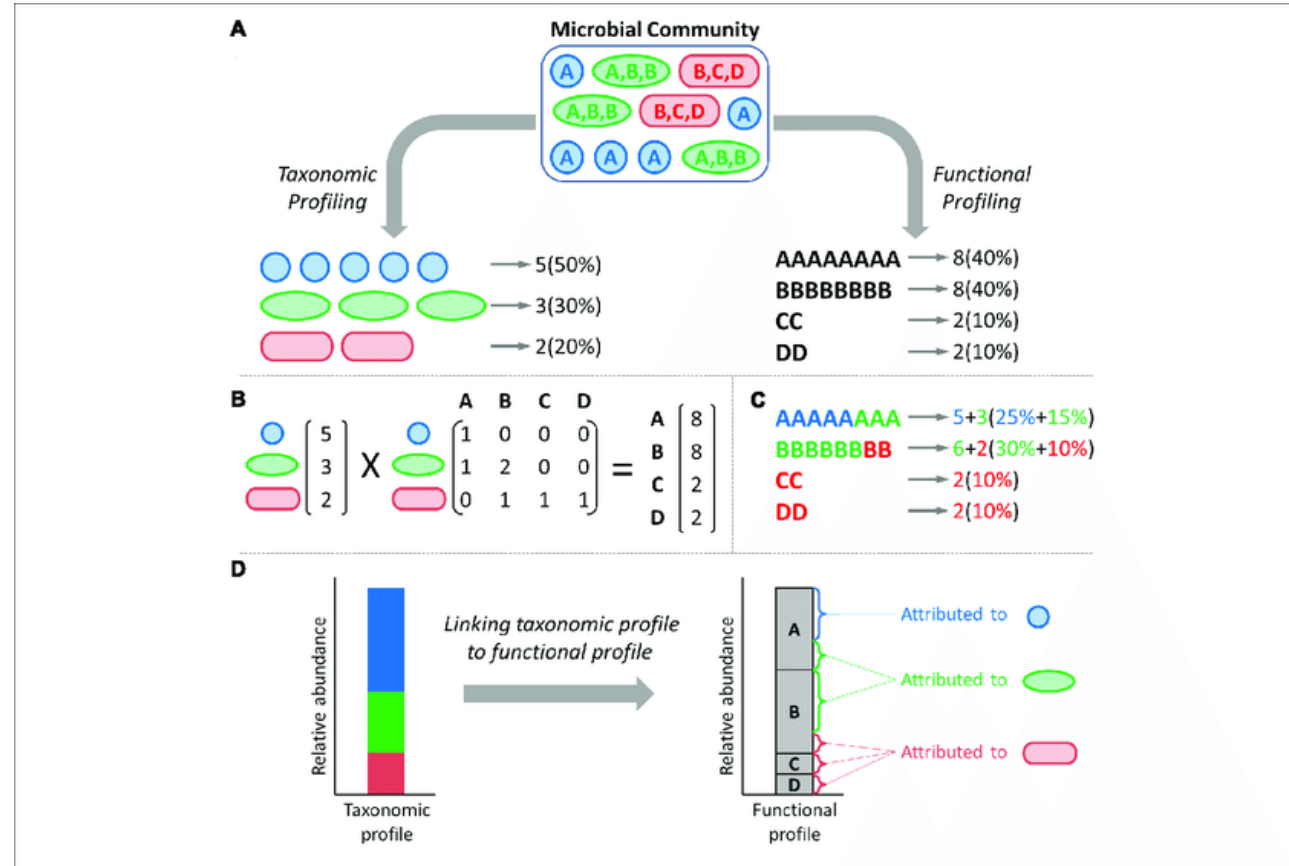
(A) Typical microbiome studies quantify and report the taxonomic (colored shapes) and functional (letters) profiles of a given community as separate entities. (B) The functional profile of a community is a linear combination of the taxonomic composition and the genomic content of each taxon. (C) Functional profiles can be deconvolved into taxon-specific functional profiles, denoting which share of the abundance of each function is attributed to each taxon. (D) Such deconvolved functional profiles can be visualized, illustrating the total abundance of each function as a stacked bar of taxon-specific attributions.

The taxonomic and functional compositions of a microbiome
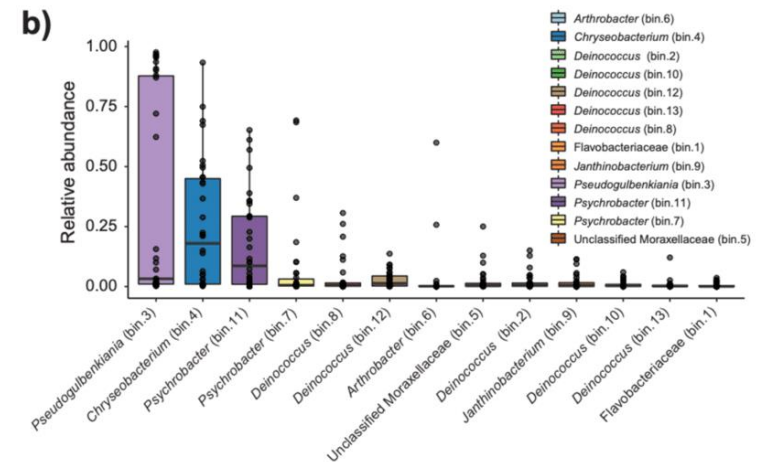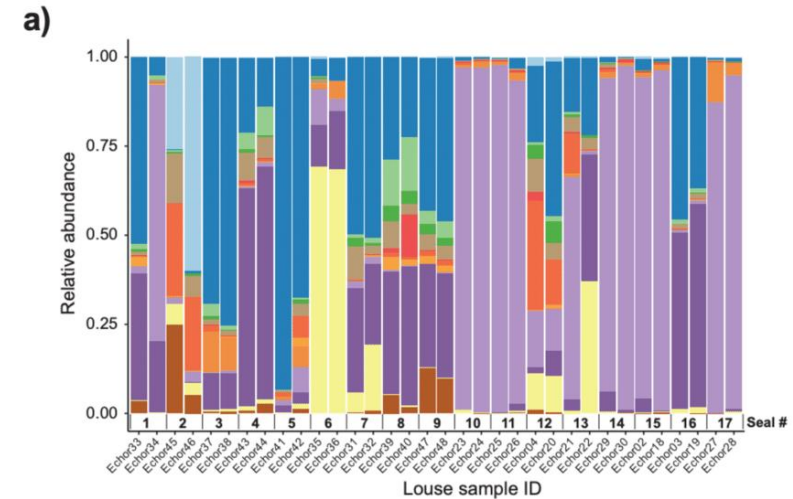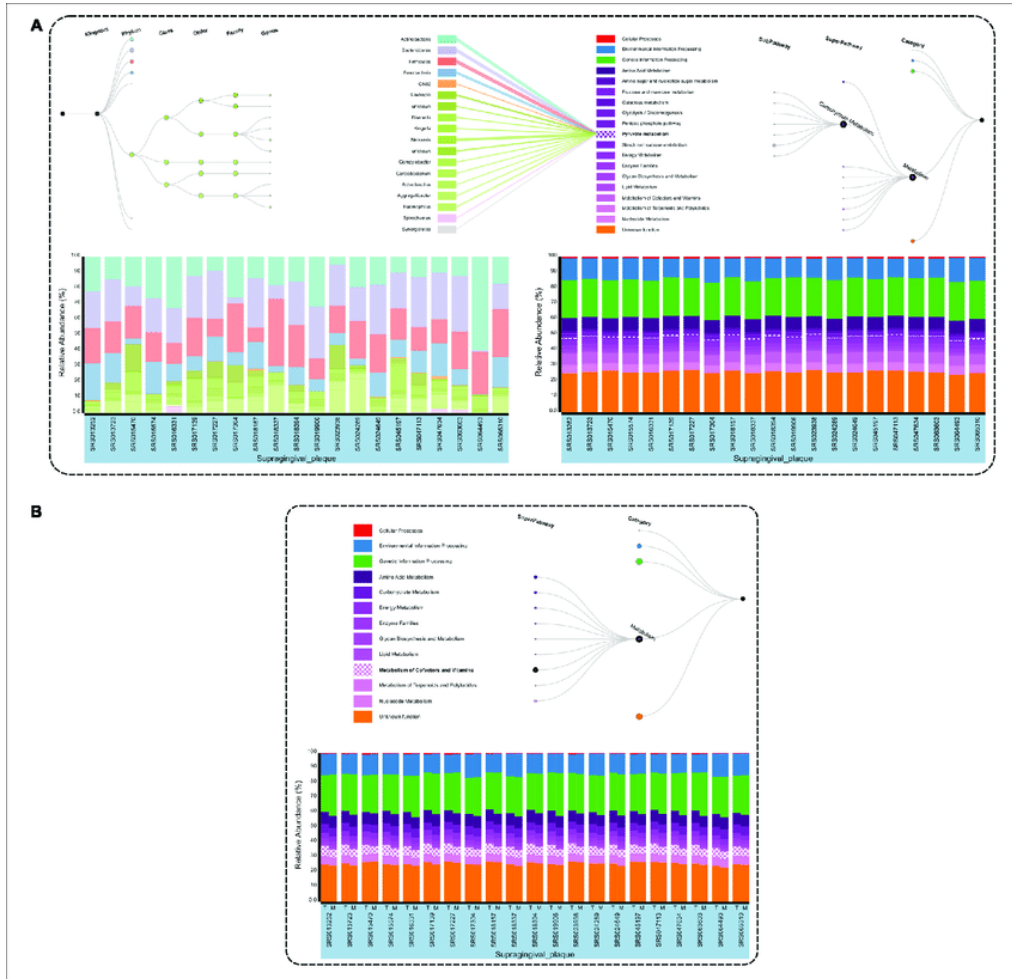
Diversity estimates are a central topic in microbiome data analysis.

- Alpha, Beta and Gamma diversity

- The α-diversity is just the diversity of each site (local species pool).

- The β-diversity represents the differences in species composition among sites.

- The γ-diversity is the diversity of the entire landscape (regional species pool).

- Shannon index α-diversity Test Shannon index measures how evenly the microbes are distributed in a sample. It answers the question "How different?" How are the microbes balanced to each other? Do we have species evenness (similar abundance level) or do some species dominate others?

# Diversity estimates are a central topic in microbiome data analysis.

Site A — Alpha diversity: 3

Site B — Alpha diversity: 3

Site C — Alpha diversity: 2
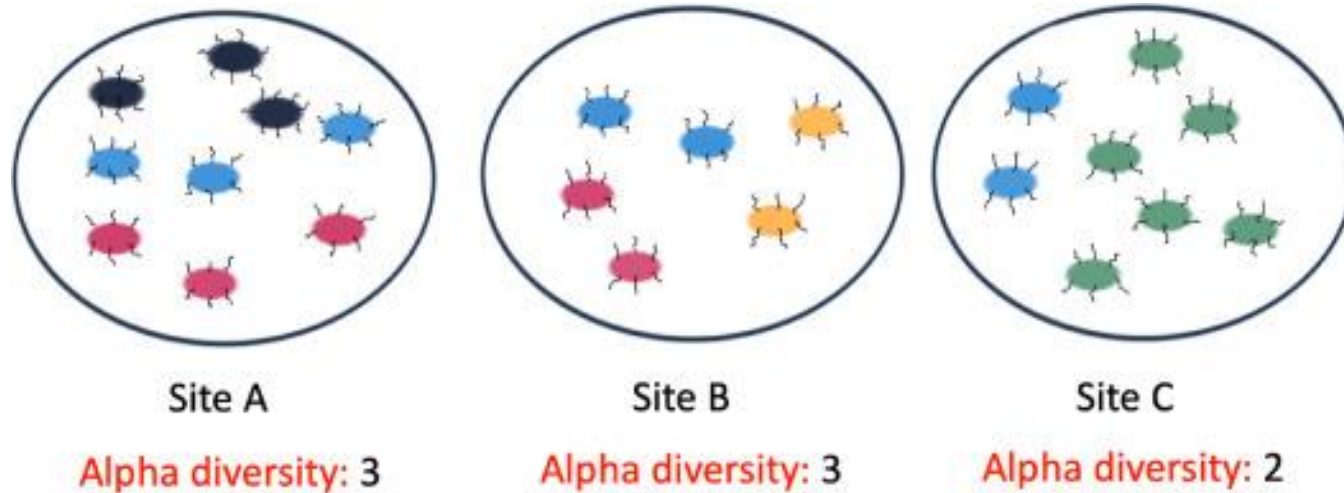
Beta diversity between Site A and Site B: (3-2)+(3-2)=2

Beta diversity between Site B and Site C: (3-1)+(2-1)=3

Gamma diversity between Site A, Site B and Site C = 5
This indicates the number of different species present in the entire ecosystem.

The developing gut microbiome and major influencing environmental factors
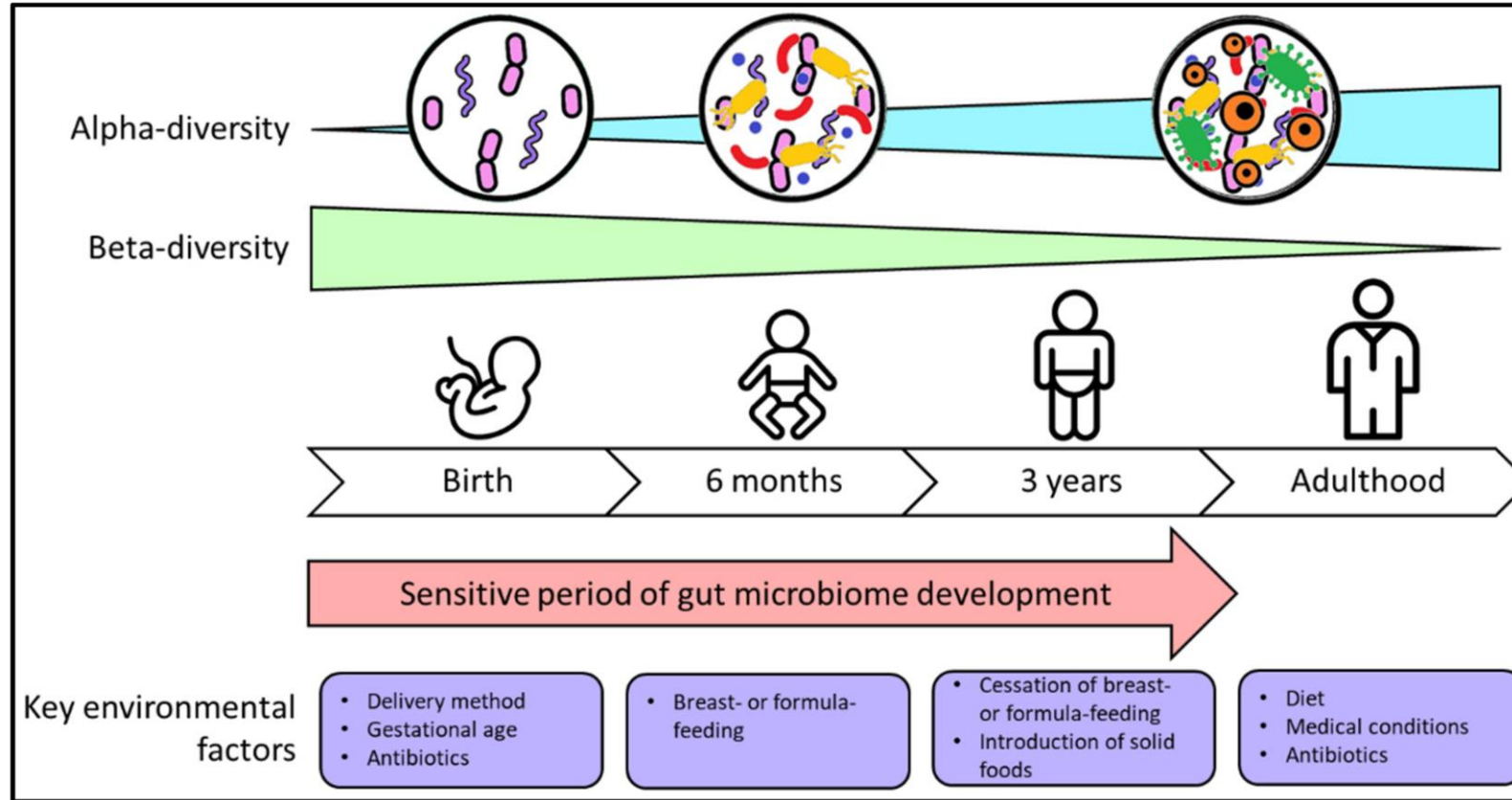
Alpha-diversity (diversity within one sample) increases as the gut microbiome develops. The beta-diversity (diversity between samples) decreases with age, indicating that gut microbiome differences are most variable between people during infancy, and become more similar n adulthood. The first three years of life represent a period of heightened plasticity where gut microbiome development is easily impacted by environmental factors.

Bibliography

- Tools for Analysis of the Microbiome → https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7598837/

- Best practices for analysing microbiomes → http://users.encs.concordia.ca/~gregb/home/PDF/best-practices-analysing-microbiomes-nat2018.pdf

Thank You