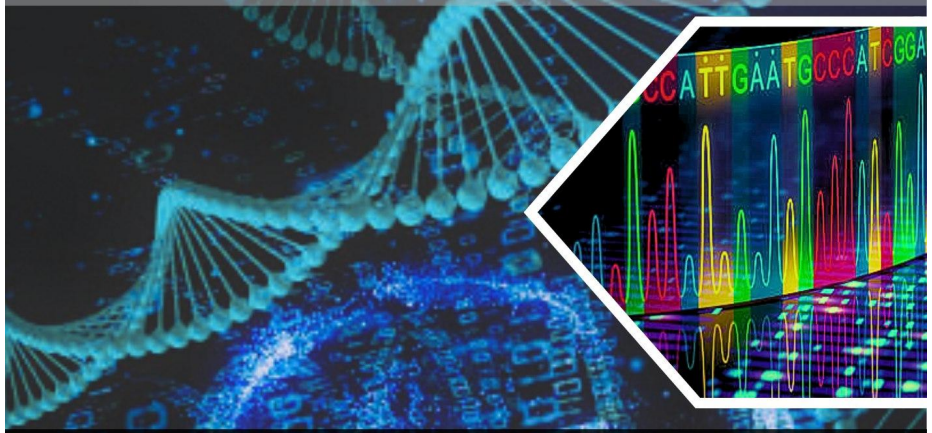
MICROBIAL GENOME & MICROBIOME ANALYSIS

MGMA2024
LONG READ MICROBIOME



MGMA2024 COURSE

MGMA_2024

MGMA 2024

Genomics.and.Epigenetics

Zalo Microbiome Research Group

SUNDAY

8:00 - 10:30 PM

06.10.2024
-
10.11.2024

Online & Free Course

Join us!

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Advanced VnPathoinformatics

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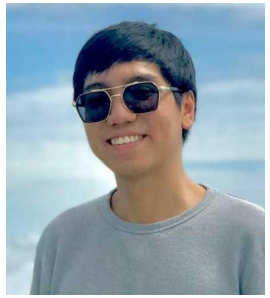

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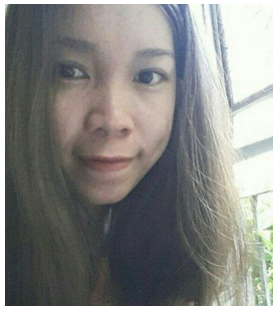

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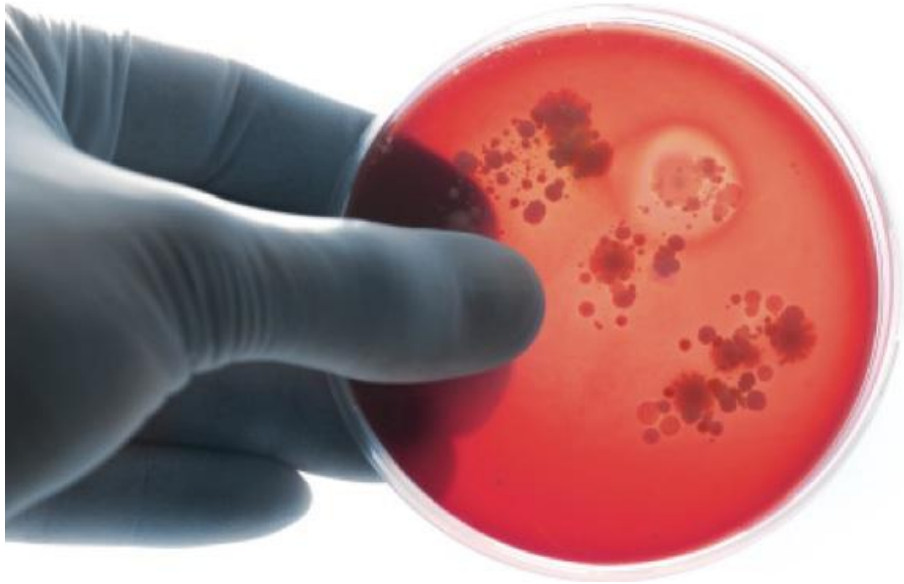
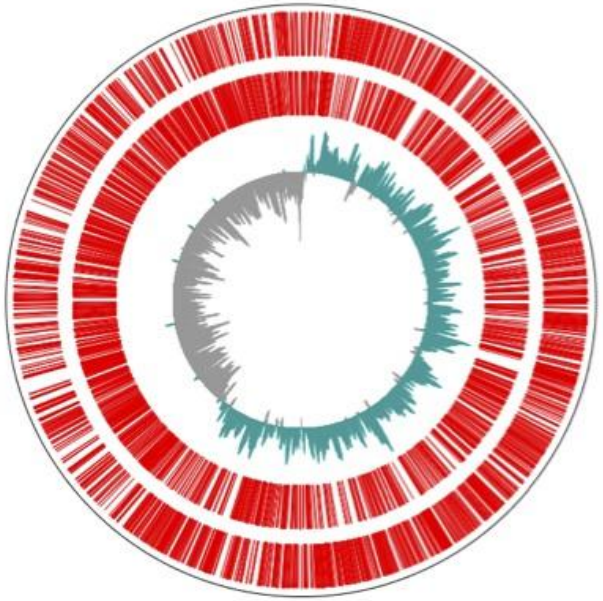
Content

- Review of MGMA2024
  - MODULE 1: MICROBIAL GENOME
  - MODULE 2: MICROBIOME ANALYSIS
- Introduction LONG READ platforms
- Overview of the course MGMA2024
  - MODULE 3: LONG READ MICROBIOME ANALYSIS
- 16S full-length ONT (Kim + Khải)

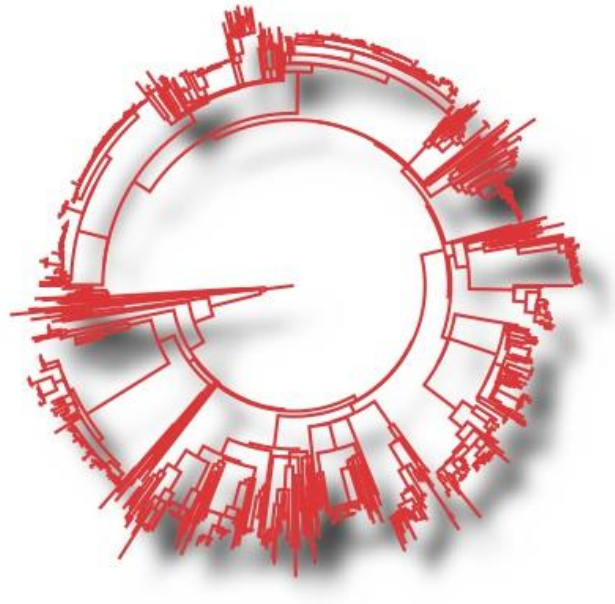
Microbial Genome Analysis: study one isolate at once



Culture microbe



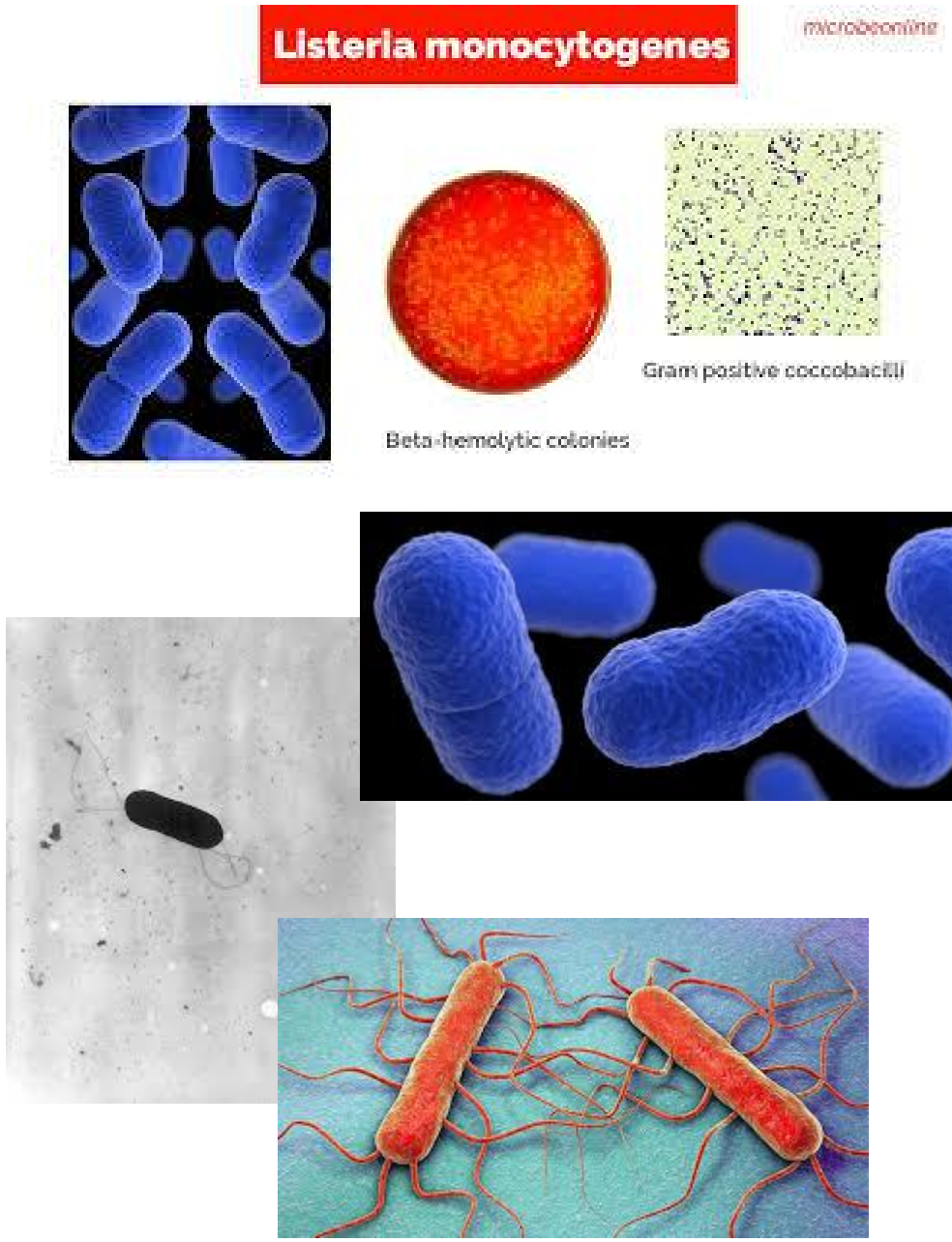
Genome Sequencing



Serotyping/genotyping

Microbe = Microorganism

Prokaryotes = Bacteria & Archaea



Listeria monocytogenes EGD-e, complete genome

GenBank: AL591824.1

GenBank Graphics

```
>AL591824.1 Listeria monocytogenes EGD-e, complete genome
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GGCTTGTAACCTACTTATCCACAAATCCACAGCGCCTATTACTATTACTACGATTTTTTATTAATTAATT
```

https://www.ncbi.nlm.nih.gov/nuccore/AL591824.1?report=fasta

Review of MGMA2024
MODULE 1: MICROBIAL GENOME

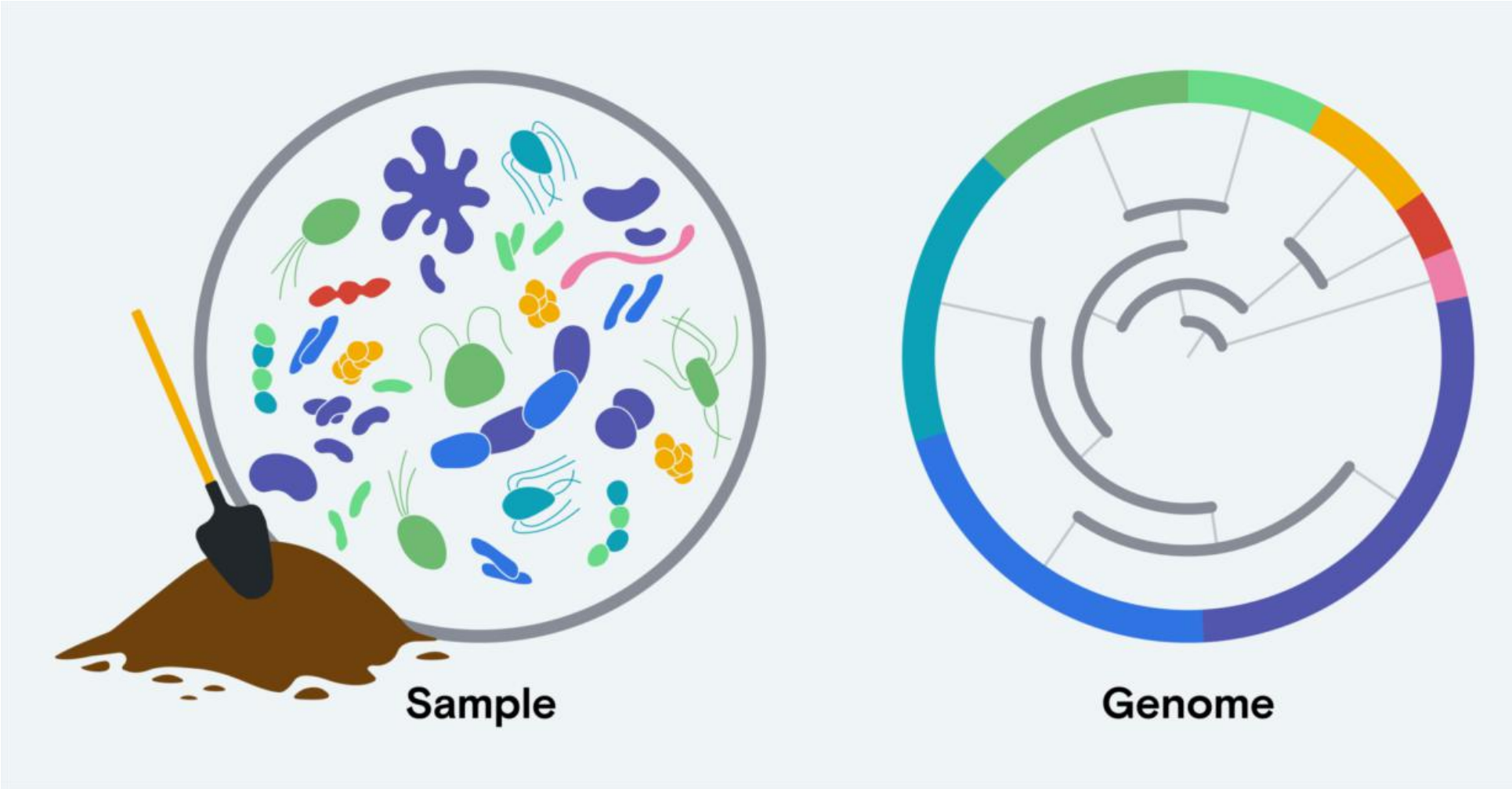
- Basic Ubuntu OS
- Basic Linux Commands
- Bash Scripting
- Basic Awk
- Programming with R
- Basic VScode, Colab and GitHub
- Sanger Sequencing and Next Generation Sequencing platforms

(Pacbio, Element Biosciences, Ion Torrent, GeneMind, ILLUMINA and MGI)

- Nucleotide sequence database: DNA and RNA
- Homology Search with BLAST
- Primer and Probe Design
- Multiple Alignment
- Phylogenetic Trees
- Pairwise and Multiple genome alignment with Mauve
- Gene and Genome Annotation
- Mapping for Whole genome sequencing analysis of Microbes
- Denovo assembly for WGS of Microbes
- Serotyping, genotyping and phenotyping for Microbes

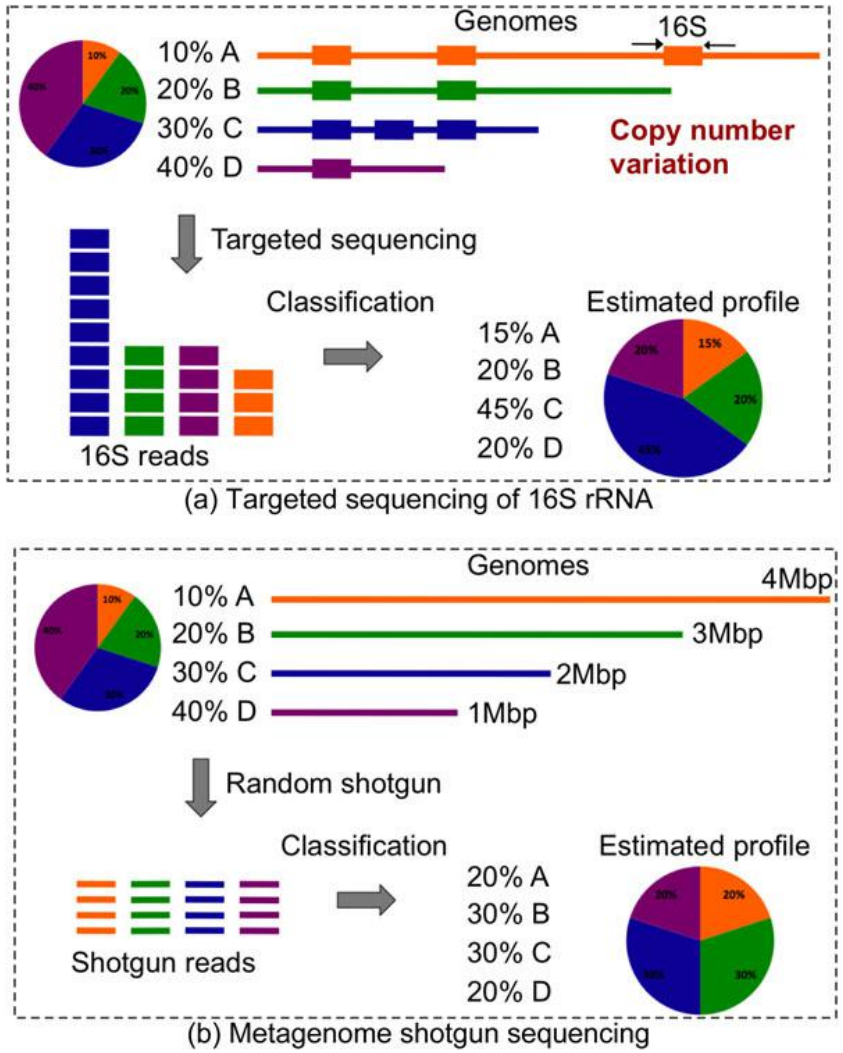
https://github.com/UeenHuynh/MGMA_2024

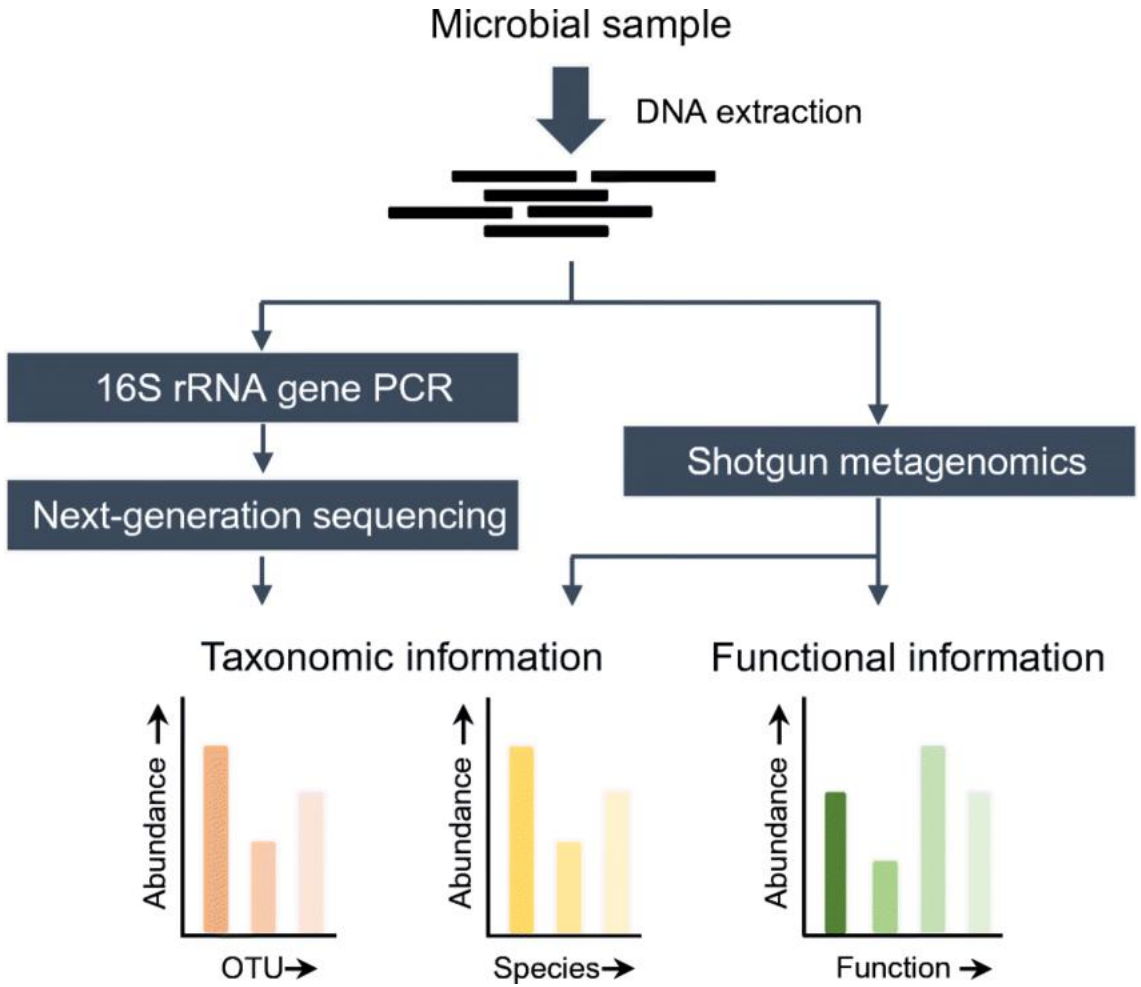
Microbiome Analysis or Metagenomics



https://www.elementbiosciences.com/blog/2-x-300-sequencing-all-the-reads-you-need-for-metagenomics

Target vs Shotgun Microbiome Analysis





10.1186/1471-2164-12-S2-S4

10.1007/s10096-019-03520-3

Review of MGMA2024
MODULE 2: MICROBIOME ANALYSIS

- R for Microbiome Data
- ggplot2
- Experimental Design for Microbiome studies
- Challenging when working with microbiome samples
- Bioinformatic Analysis of Microbiome Data (QIIME 2)
- Building feature table and feature representative sequences from raw reads
- Assigning Taxonomy & Building Phylogenetic Tree
- Clustering Sequences into OTUs
- OTU Methods in Numerical Taxonomy

- Alpha Beta diversity & Visualization
- Library prep and multiplexing for 16S and shotgun metagenomics
- Shotgun metagenomic Bioinformatic Analysis
- Microbiome Application

https://github.com/UeenHuynh/MGMA_2024

Introduction LONG READ platforms

PacBio

Revio system

Oxford NANOPORE Technologies

MinION

MGI

CycloneSEQ

Overview of the course MGMA2024
MODULE 3: LONG READ MICROBIOME ANALYSIS

- CN: 06/10 (20h-22h30)
  - Overview of the course
  - Review old lecture MGMA
  - Introduction new platform
  - 16S full-length **ONT** (Kim + Khải)
- CN: 13/10 (20h-22h30)
  - **shotgun ONT** (Quý + Như)
- CN: 20/10 (20h-22h30)
  - 20h - 21h30: **ONT** Platform introduction
  - 21h30 - 22h30: De novo assembly + mapping + variant calling ONT WGS (Huy + Phát)
- CN: 27/10 (20h-22h30)
  - 20h - 21h30: **Pacbio** Platform introduction (Mr. Ray)
  - 21h30 -22h30 : 16S full-length **PacBio** (Hùng + Thảo)
- CN: 03/11 (20h-22h30)
  - shotgun **Pacbio** (Sơn + Tuệ An)
- CN: 10/11 (20h-22h30)
  - De novo assembly + mapping + variant calling **PacBio** WGS (Hùng + Thảo)
- CN: 17/11 (20h-22h30)
  - **CycloneSEQ** Platform introduction

https://github.com/UeenHuynh/MGMA_2024