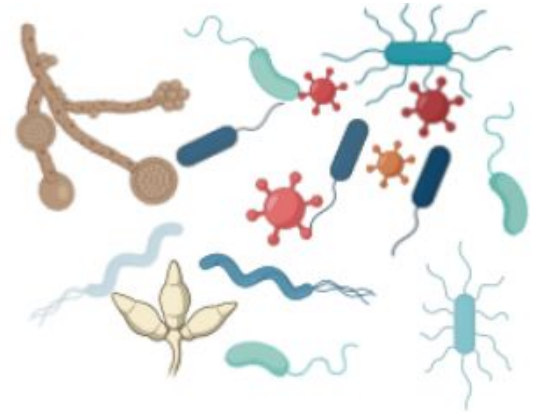


# MetaPhlan3

MetaPhlAn is a computational tool for profiling the **composition** of microbial communities (Bacteria, Archaea and Eukaryotes) from **metagenomic shotgun** sequencing data (**not 16S**) with species-level.

MetaPhlAn relies on **unique clade-specific marker genes** identified from ~17,000 reference genomes

~13,500 bacterial and archaeal  
~3,500 viral  
~110 eukaryotic



# Installation

```
salloc -A open --nodes=1 --ntasks-per-node=1 --mem-per-cpu=64gb --time=02:00:00
```

Allocate resources for a job on a cluster interactively  
Assigns requested resources and starts a shell with them

Number of nodes. Might contain multiple CPUs/cores

Allocates 64 GB of memory per CPU for that single task

Specifies the total time the job is allow to run

-A (account under which the job will run)  
Open = default or general access

Tasks per node. Specifies that only 1 process should run in the requested node

# Installation

conda create --name mpa -c bioconda metaphlan

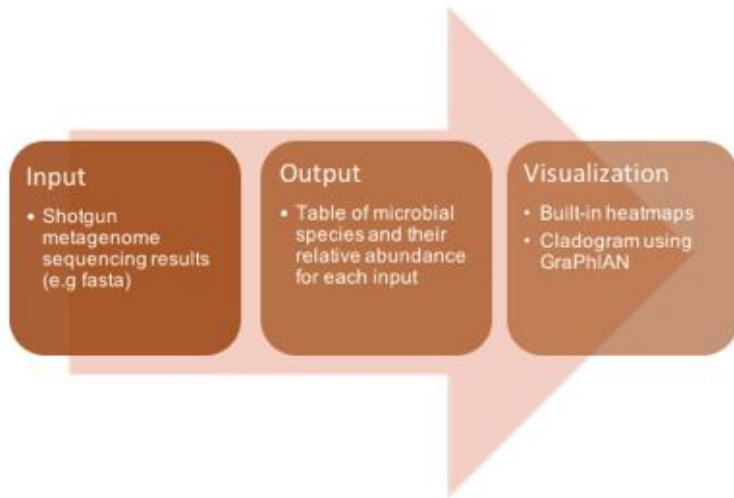
*conda create --name mpa -c conda-forge -c bioconda python=3.7 metaphlan*

conda activate mpa

metaphlan -h

```
usage: metaphlan --input_type {fastq,fasta,bowtie2out,sam} [--force]
      [--bowtie2db METAPHLAN_BOWTIE2_DB] [-x INDEX]
      [--bt2_ps BowTie2 presets] [--bowtie2_exe BOWTIE2_EXE]
      [--bowtie2_build BOWTIE2_BUILD] [--bowtie2out FILE_NAME]
      [--min_mapq_val MIN_MAPQ_VAL] [--no_map] [--tmp_dir]
      [--tax_lev TAXONOMIC_LEVEL] [--min_cu_len]
      [--min_alignment_len] [--add_viruses] [--ignore_eukaryotes]
      [--ignore_bacteria] [--ignore_archaea] [--stat_q]
      [--perc_nonzero] [--ignore_markers IGNORE_MARKERS]
      [--avoid_disqm] [--stat] [-t ANALYSIS_TYPE]
      [--nreads NUMBER_OF_READS] [--pres_th PRESENCE_THRESHOLD]
      [--clade] [--min_ab] [-o output file] [--sample_id_key name]
      [--use_group_representative] [--sample_id value]
      [-s sam_output_file] [--legacy-output] [--CAMI_format_output]
      [--unknown_estimation] [--biom biom_output] [--mdelim mdelim]
      [--nproc N] [--install] [--force_download]
      [--read_min_len READ_MIN_LEN] [-v] [-h]
      [INPUT_FILE] [OUTPUT_FILE]
```

# Usage



Basic usage: 1 sample

```
metaphlan SRR6468499.unmapped.fastq.1  
--input_type fasta > SRR6468499_profile.txt
```