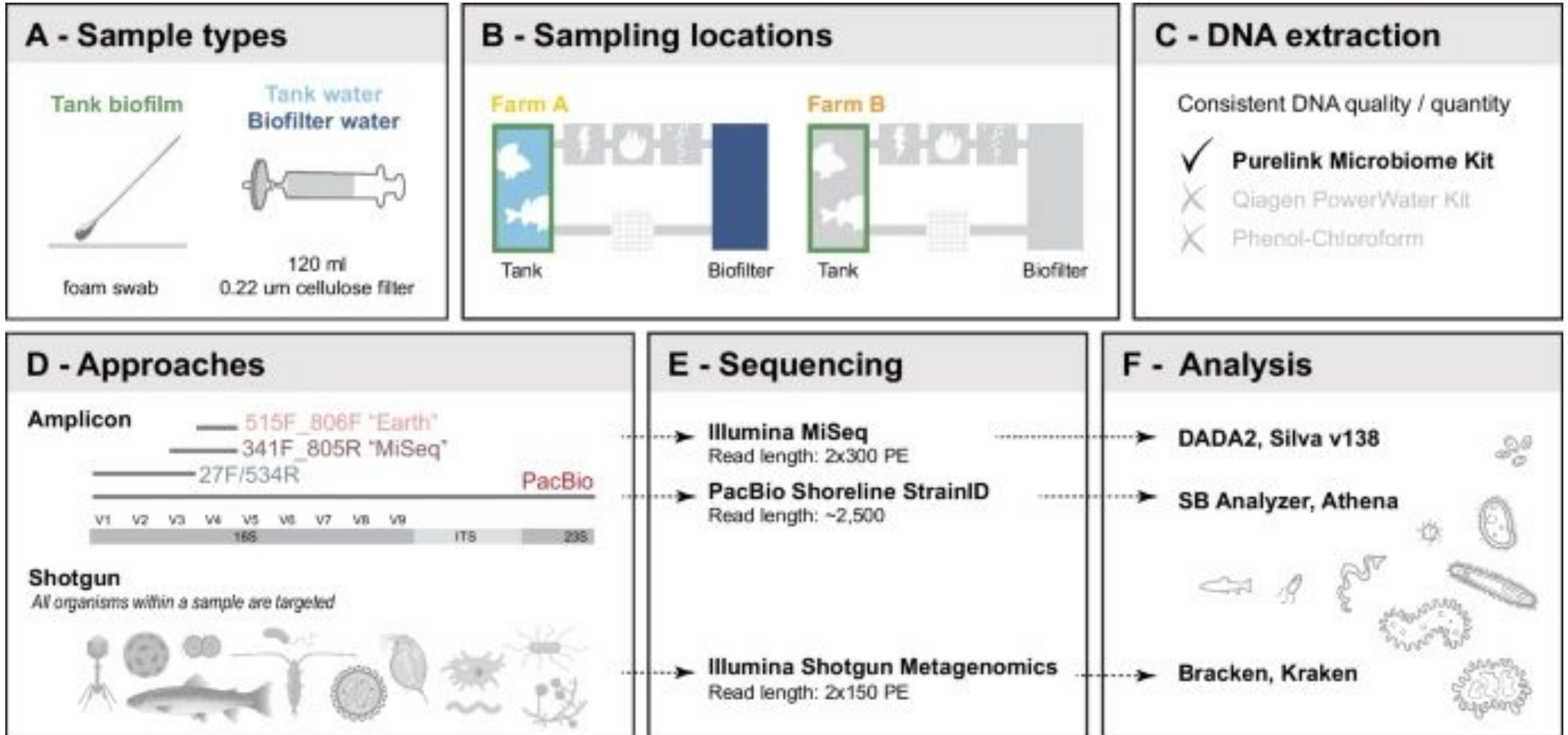


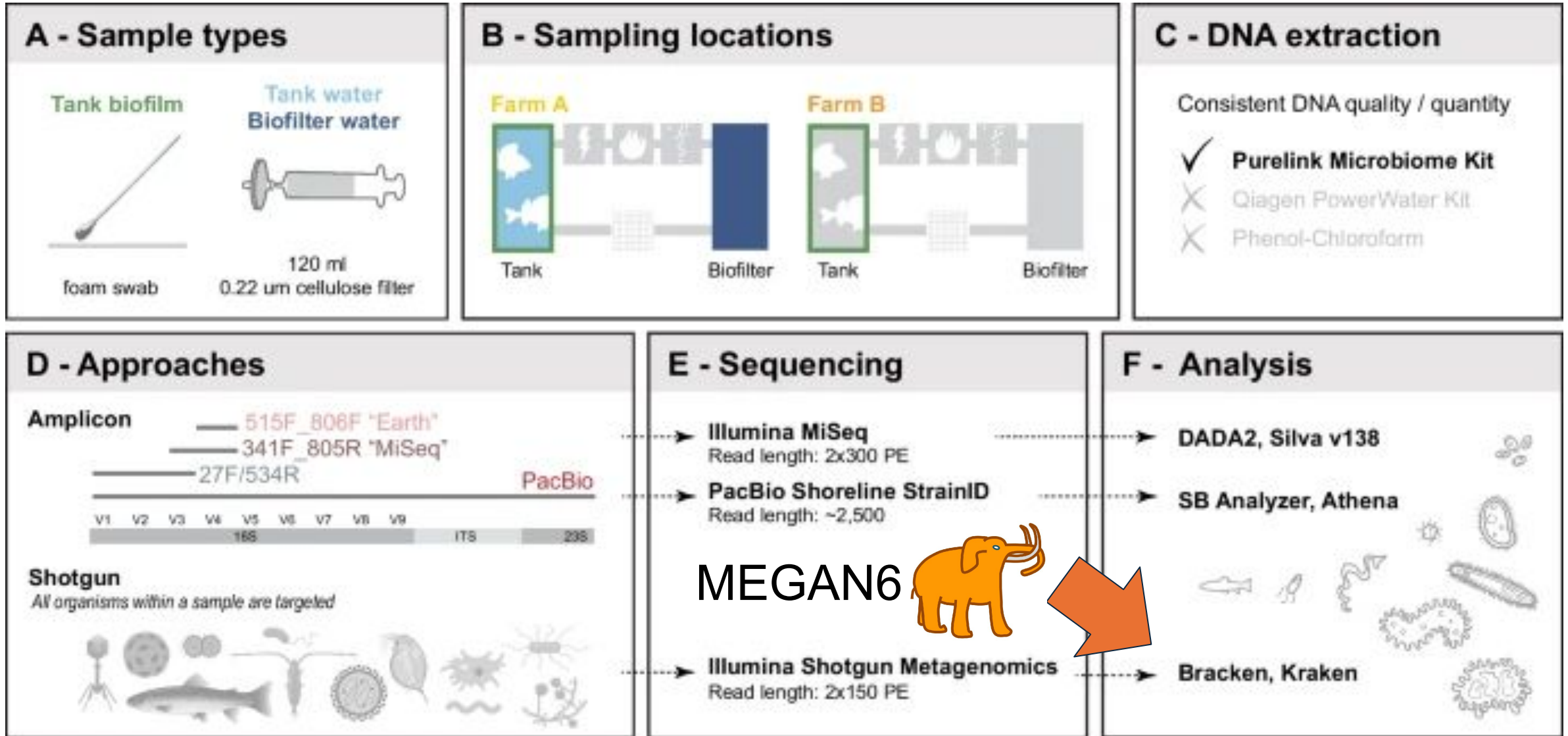
MEGAN6

Metagenome Analyzer

What are some different sequencing approaches?

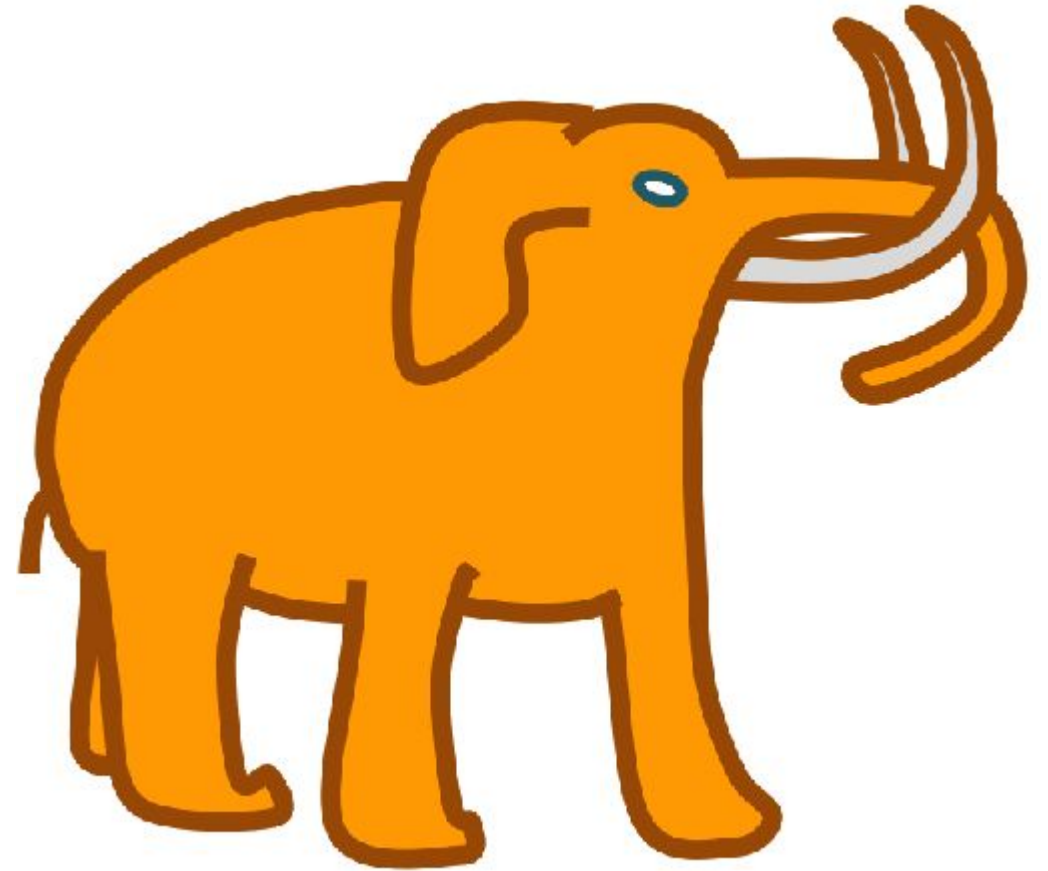


What are some different sequencing approaches?



MEGAN6

- MEGAN or “MEtaGenome ANalyzer” allows for the analysis of large metagenomic datasets.

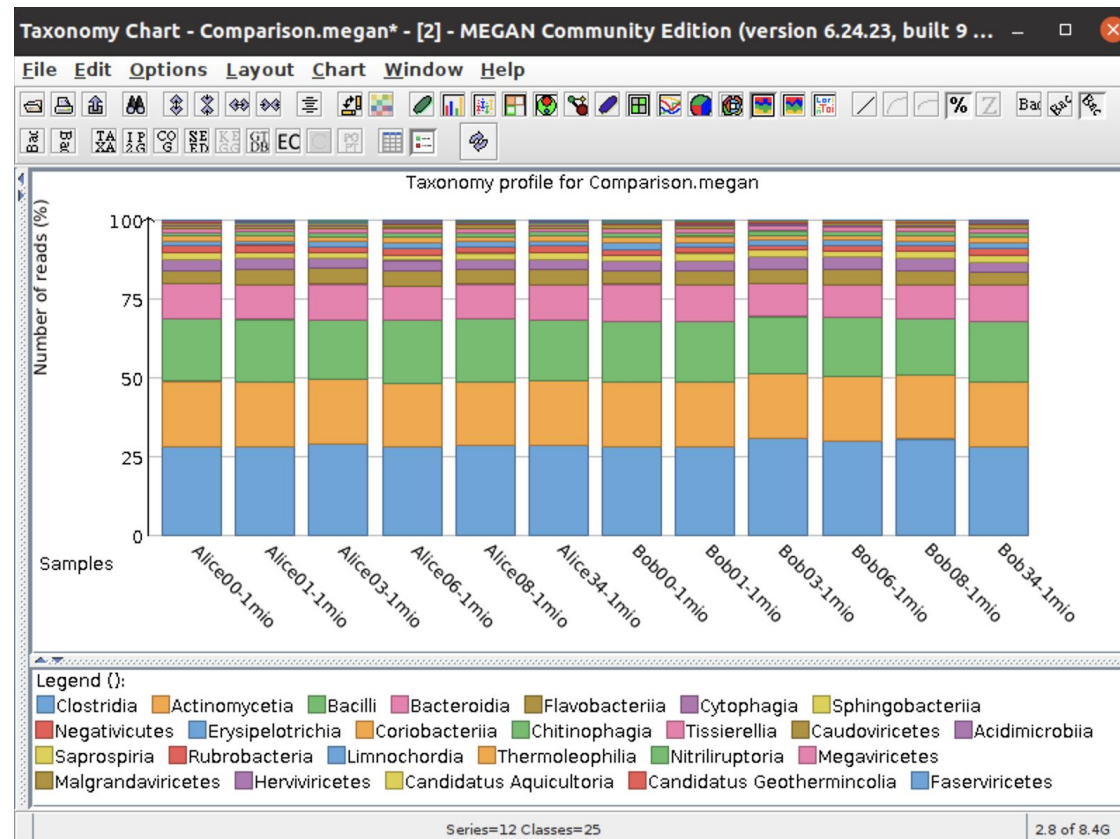


MEGAN History

- First version, MEGAN released in 2007 focusing on analyzing taxonomic content
- Later versions like MEGAN6 also allow for functional profiling

Research Questions that MEGAN6 can help you answer

- What species are in my samples?



Research Questions that MEGAN6 can help you answer

- What are they doing/What is the functional content of the communities?

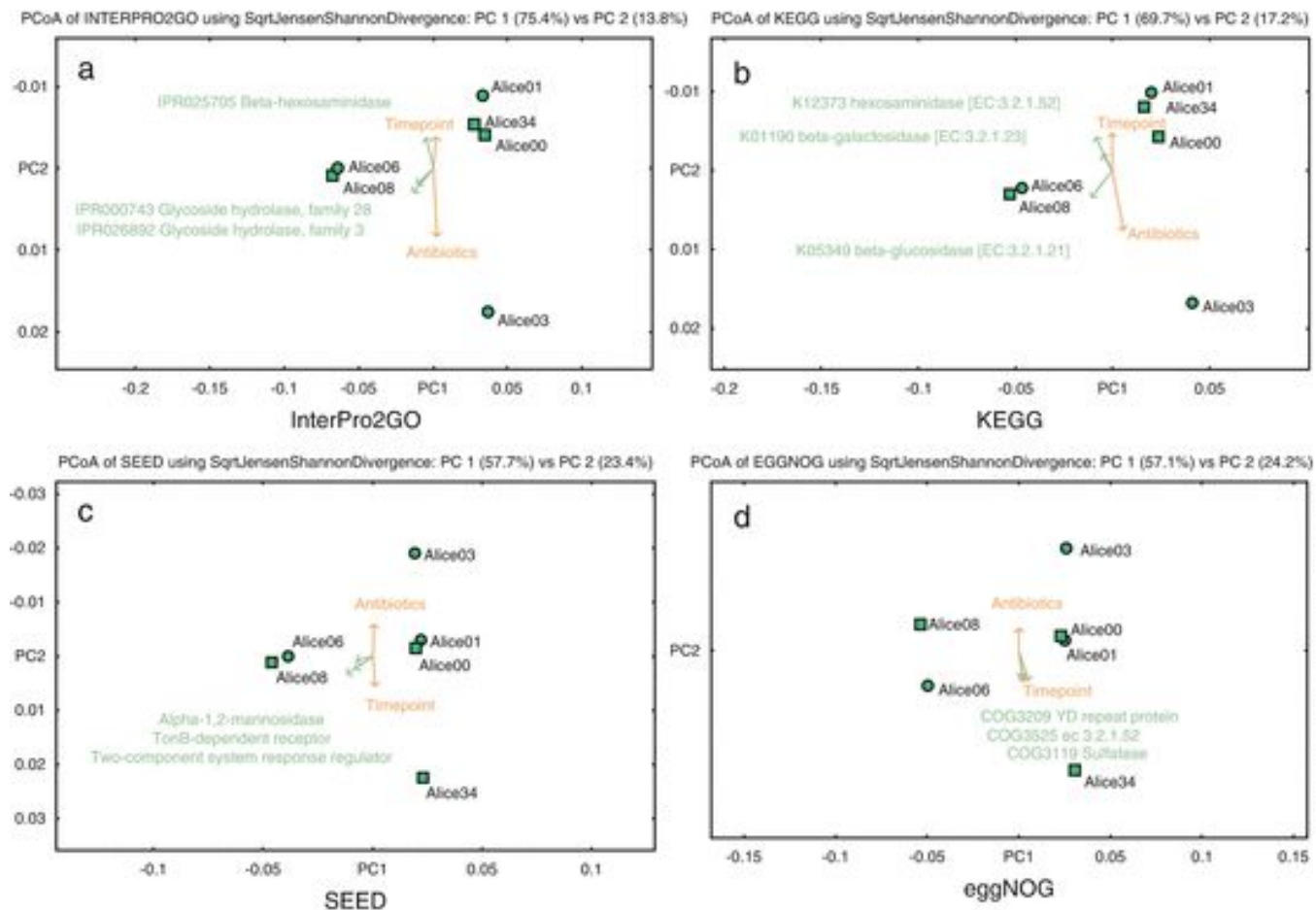
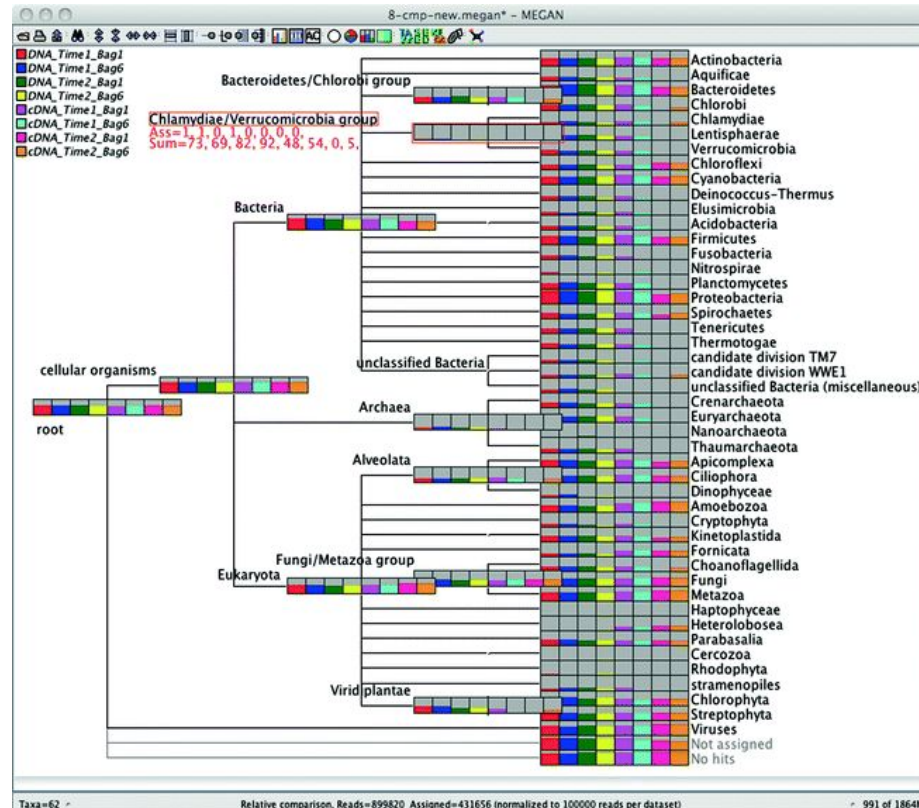


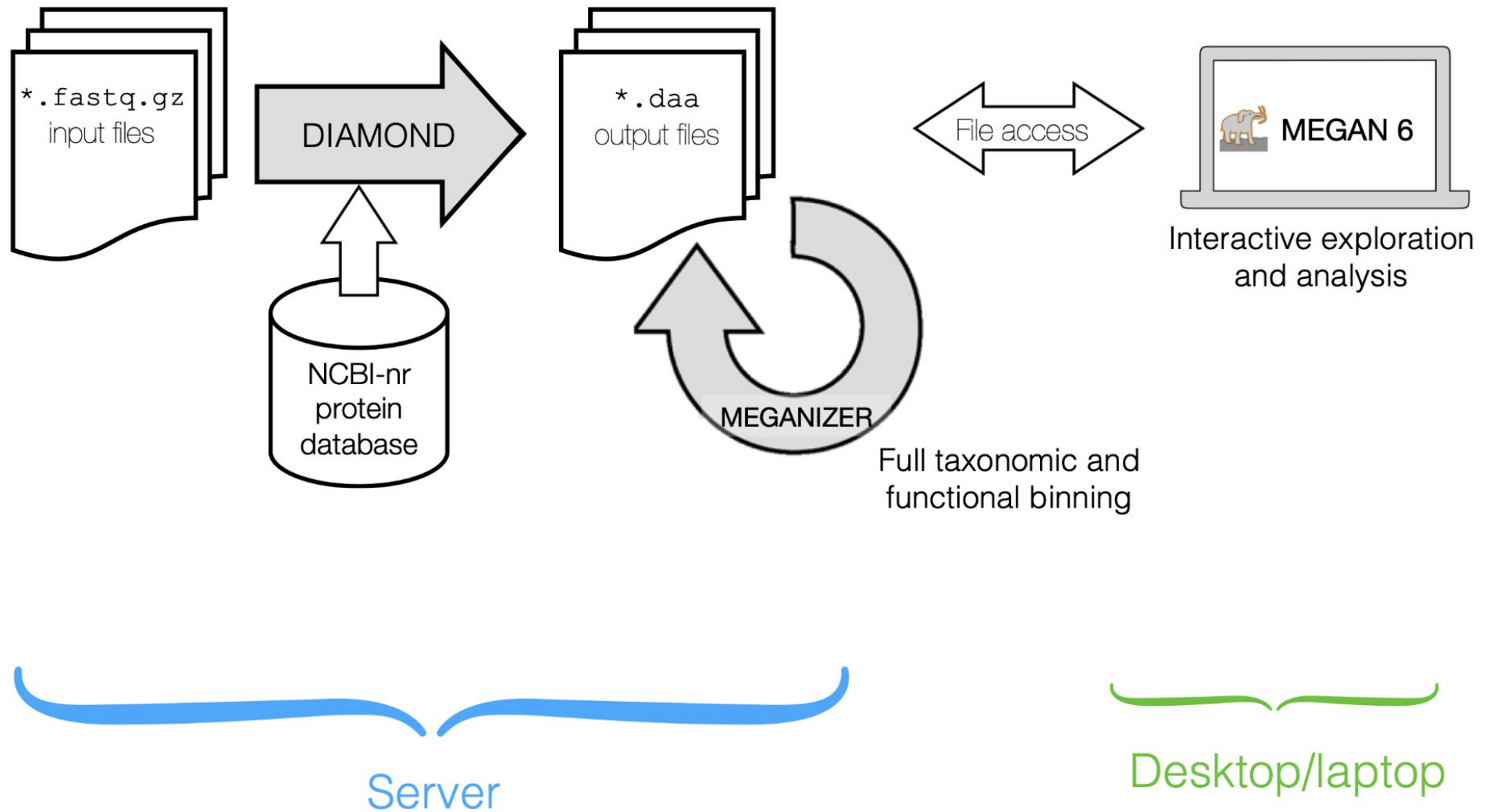
Figure Credit: Functional Metagenomics: Tools and Application (Chapter Functional Analysis in Metagenomics Using MEGAN6)

Research Questions that MEGAN6 can help you answer

- How does the taxonomic content and functional potential compare across various sample types or conditions?



How Does MEGAN6 Work?



Download MEGAN/DIAMOND files needed

DIAMOND

```
mkdir MEGAN
```

```
cd MEGAN
```

```
wget https://github.com/bbuchfink/diamond/releases/download/v2.0.9/diamond-linux64.tar.gz
```

```
tar xzf diamond-linux64.tar.gz
```

```
wget ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/taxdmp.zip
```

```
wget ftp://ftp.ncbi.nlm.nih.gov/pub/taxonomy/accession2taxid/prot.accession2taxid.gz
```

```
wget ftp://ftp.ncbi.nlm.nih.gov/blast/db/FASTA/hr.gz
```

EVERYTHING CAN BE FOUND HERE TOO

/storage/home/dkb5890/scratch/MEGAN_workshop/

This folder is 205 G → make sure you create your folder where you have enough space

DIAMOND

Build database

```
salloc -A open --nodes=1 --ntasks-per-node=1 --mem-per-cpu=16gb --time=12:00:00
```

```
./diamond makedb --in nr.gz -d nr_nov --taxonmap prot.accession2taxid.gz --taxonnodes nodes.dmp  
--taxonnames names.dmp
```

DIAMOND

blastx

```
~/MEGAN/diamond blastx -f 100 \  
-d ~/MEGAN/hr_nov.dmnd \  
-q ~/raw_metagenomes/240131_VH00707_131_AAF2G52M5_MG/D1_DC2_1_bulkDNA_S1_R1_001.fastq \  
-o ~/MEGAN/alignments/D1_DC2_1_bulkDNA_S1_R1_001.daa
```

EVERYTHING CAN BE FOUND HERE TOO

/storage/home/dkb5890/scratch/MEGAN_workshop/

Download MEGAN

From the MEGAN website: <https://software-ab.cs.uni-tuebingen.de/download/megan6/welcome.html>

The following file maps NCBI-nr accessions to taxonomic and functional classes (NCBI, GTDB, EC, eggNOG, InterPro2GO, SEED), unzip before use:

megan-map-Feb2022.db.zip

`wget` <https://software-ab.cs.uni-tuebingen.de/download/megan6/megan-map-Feb2022.db.zip>

`wget` https://software-ab.cs.uni-tuebingen.de/download/megan6/MEGAN_Community_unix_6_25_10.sh

`unzip` MEGAN_Community_unix_6_25_10.sh

Install the GUI and command line tools by running:

`./MEGAN_Community_unix_6_25_10.sh`

EVERYTHING CAN BE FOUND HERE TOO

`/storage/home/dkb5890/scratch/MEGAN_workshop/`

MEGANIZATION

```
/storage/home/dkb5890/megan/tools/daa2rma -i ~MEGAN/alignments/D1_DC2_1_bulkDNA_S1_R1_001.daa \  
-mdb ~MEGAN/megan-map-Feb2022.db \  
--out ~MEGAN/alignments/D1_DC2_1_bulkDNA_S1_R1_001.rma6
```

EVERYTHING CAN BE FOUND HERE TOO

/storage/home/dkb5890/scratch/MEGAN_workshop/

→ rma file to MEGAN!!

