

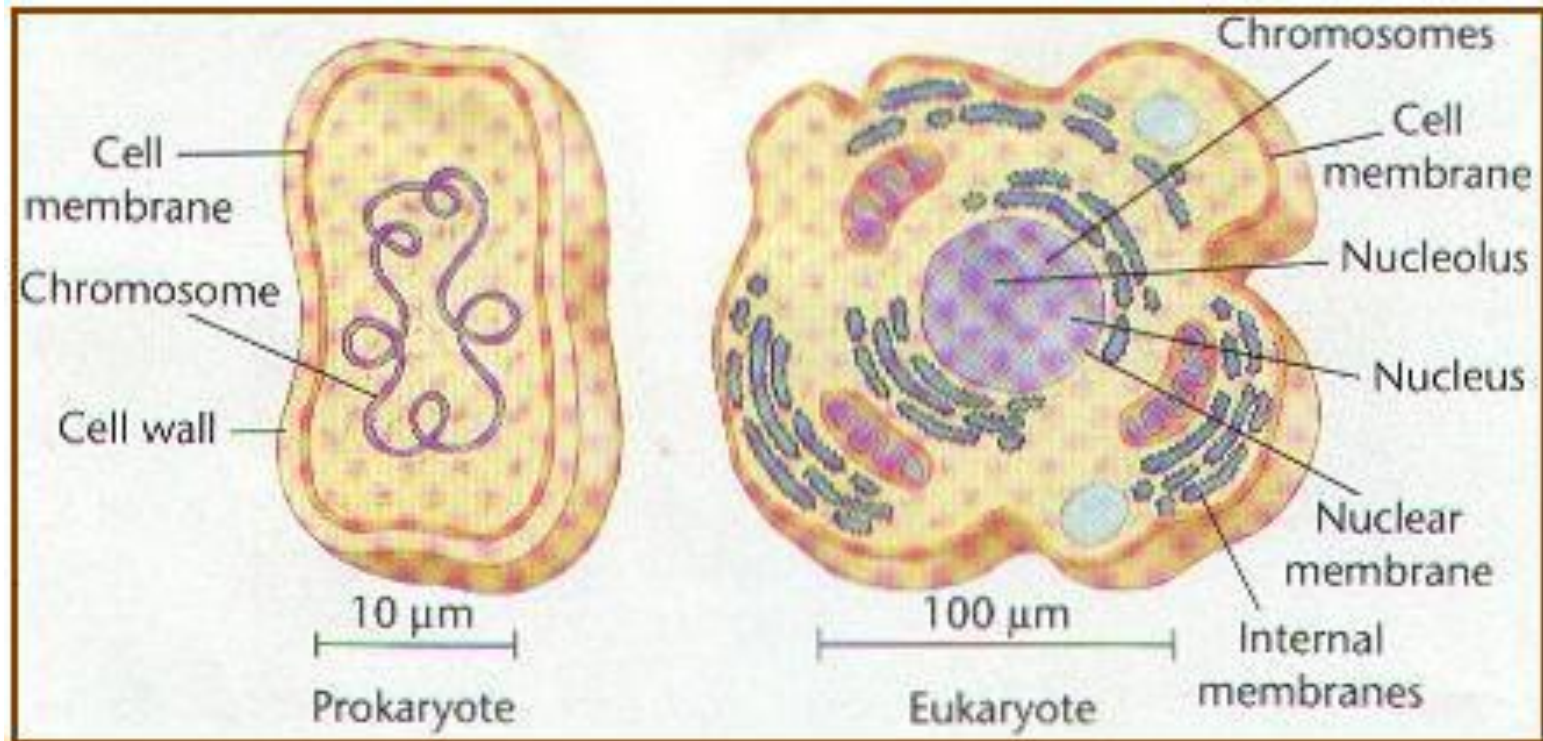
Bioinformatics

Overview

Prokaryote - Eukaryote

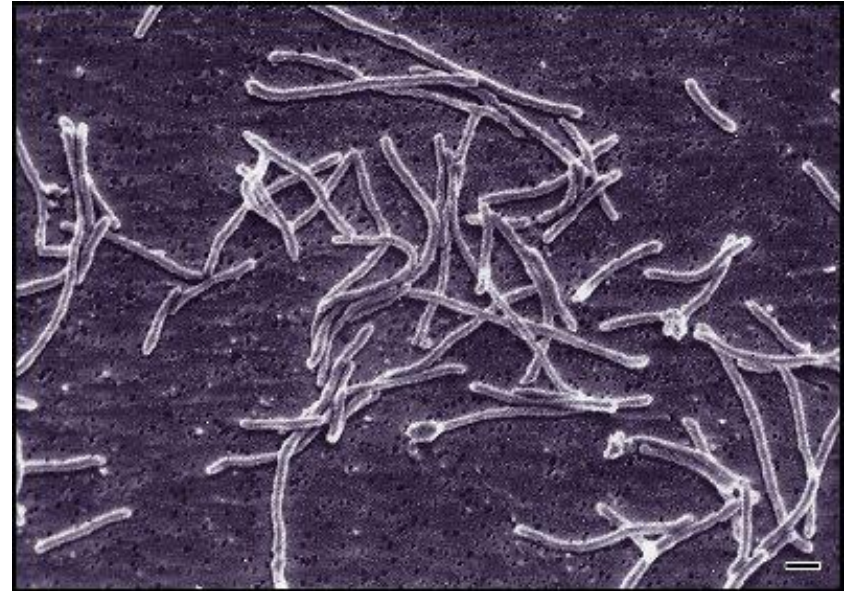
Prokaryote	Eukaryote
Older and less evolved	Younger and more evolved
Construction: - Has no nucleus - Has no Endoplasmatic reticulum - DNA in a single circular molecule	Construction: - Has a nucleus - Has a Endoplasmatic reticulum - DNA in form of chromosomes
E.g.: Bacteria, Archaeas	E.g.: Plants, Animals, Protozoas

Prokaryote - Eukaryote

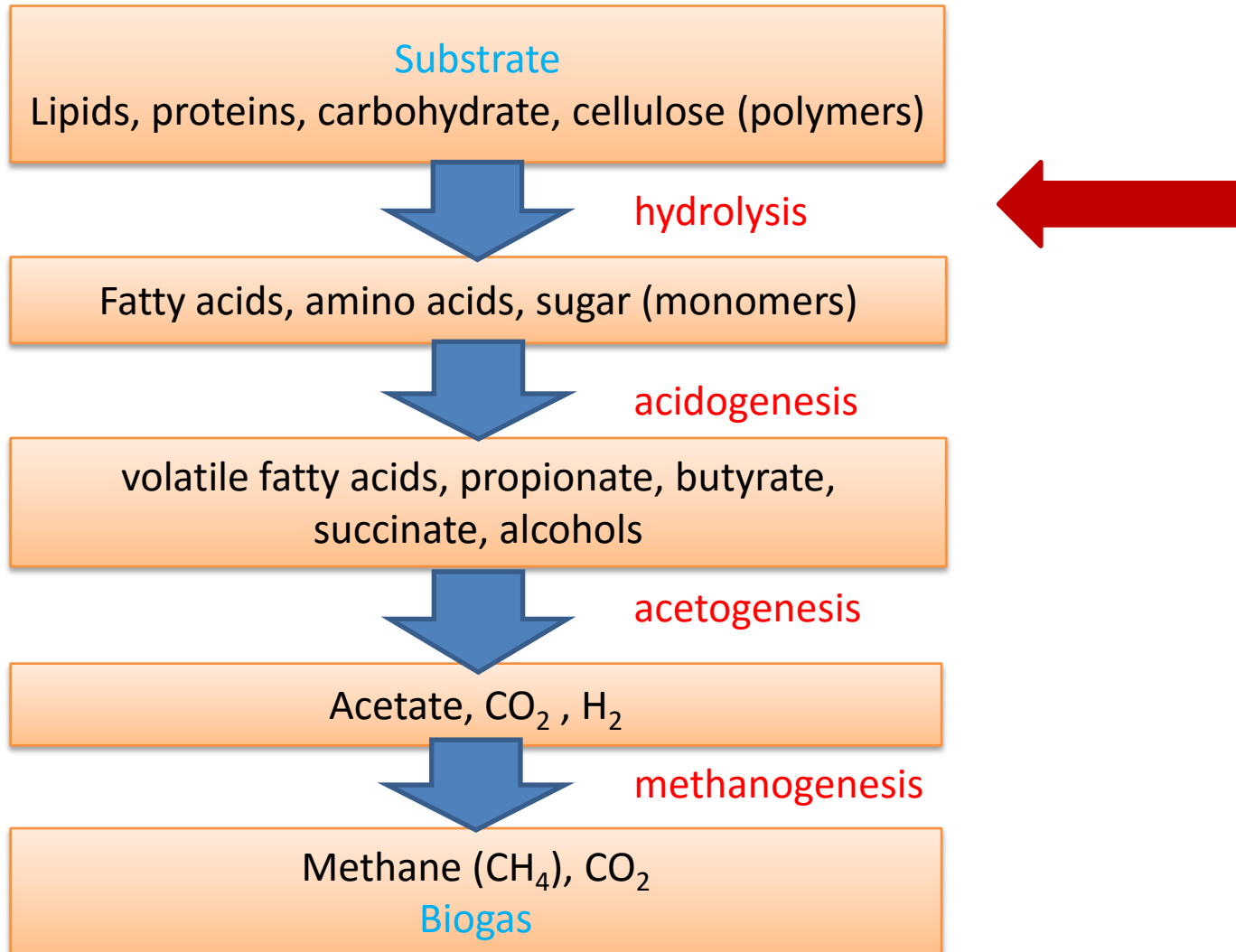


Archaeas

- Constructed like prokaryote
- Anaerobic
- Incidence in extreme conditions e.g. deep depths
- Example for Archaeas:
Thermus Aquaticus - taq-polymerase in the PCR

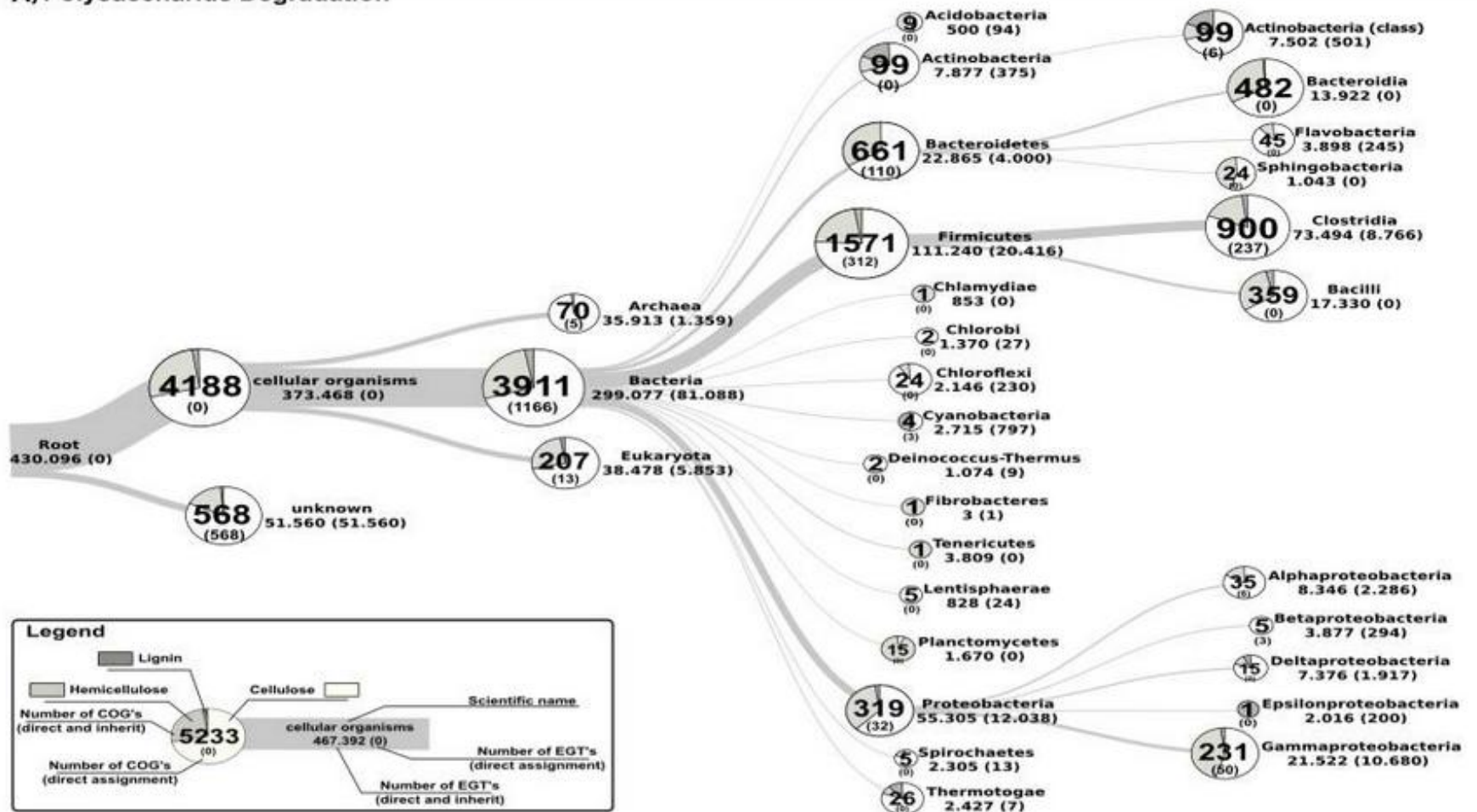


Phases of the Process and their relevant Microorganisms

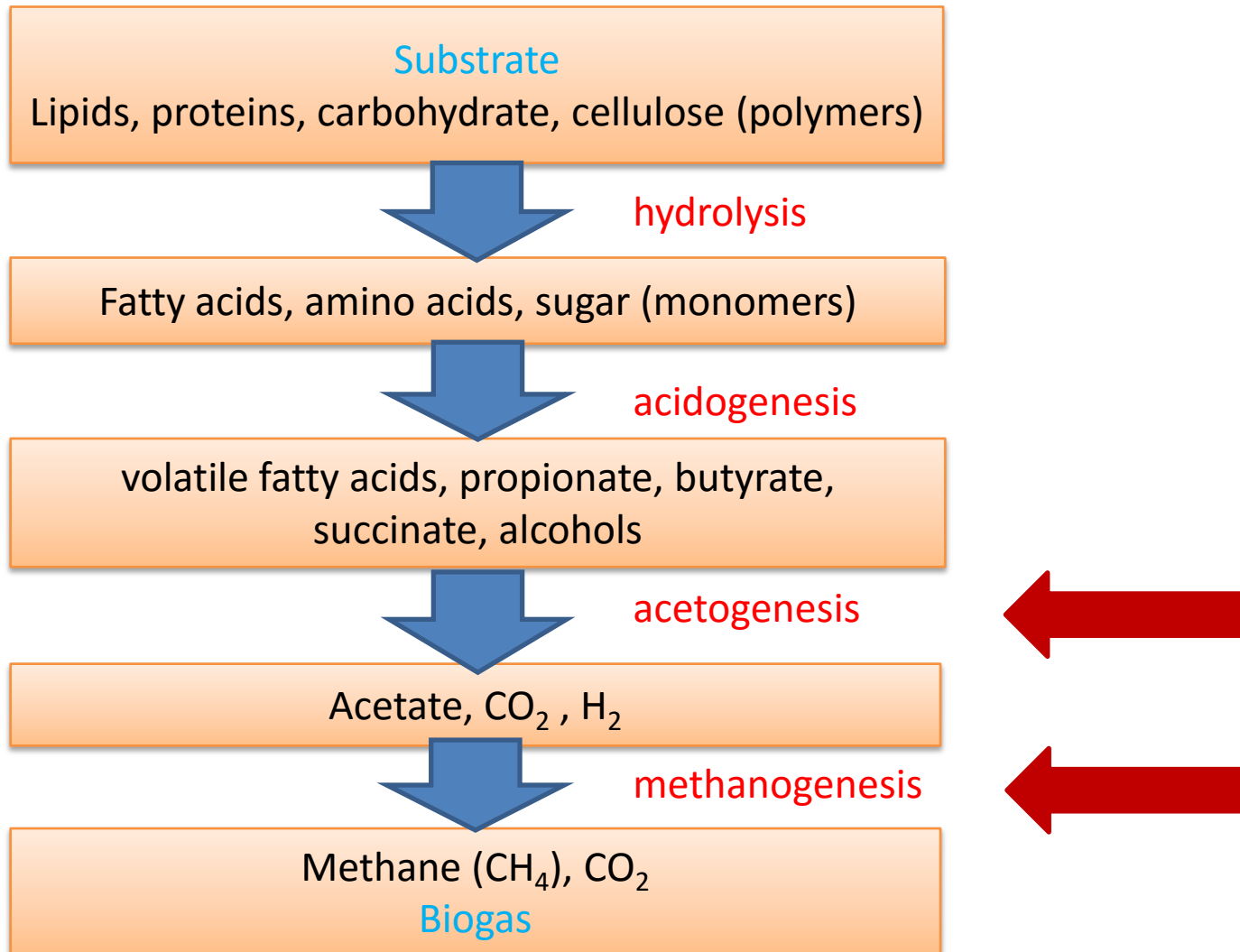


Polysaccharide Degradation

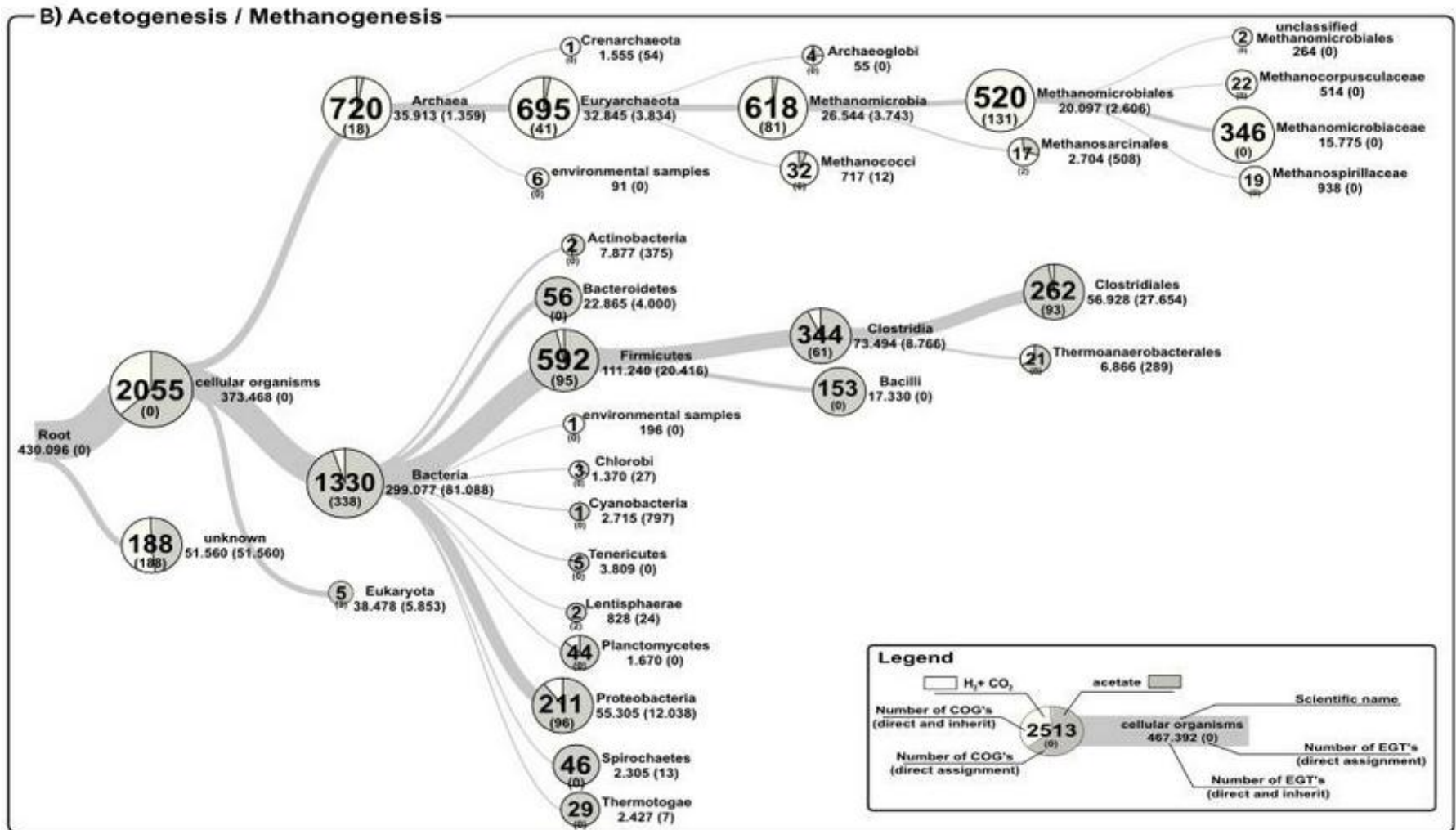
A) Polysaccharide Degradation



Phases of the Process and their relevant Microorganisms



Acetogenesis and Methanogenesis



P

Process and their Microorganisms

Lipids, prote

(ers)

Clostridium thermocellum,
Bifidobacterium longum,
Bacteroides thetaiotaomicron, ...

Fatty ac

Clostridium saccharolyticum,
Clostridium acetobutylicum,
Clostridium kluyveri, ...

volatile f

sis

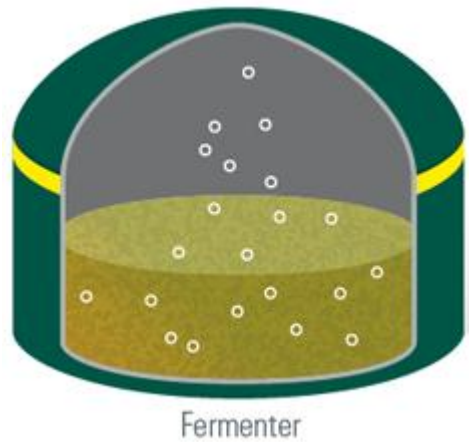
Carboxidothermus
hydrogenoformans, *Moorella*
thermoacetica, *Pelotomaculum*
thermopropionicum, ...

sis

Methanosarcina acetivorans,
Methanosarcina barkeri,
Methanoplanus petrolearius, ...

genesis

Why do we use Bioinformatics?

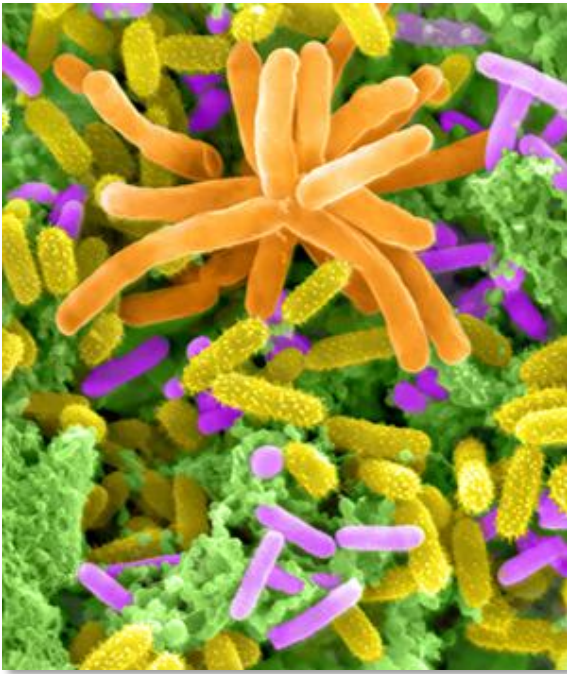


Who's on the
crime scene?
Can a genetic
fingerprint
help us?



The composition of nucleic acids of the
microbe community can give us information
about the happenings.

What are the aims of Bioinformatics?

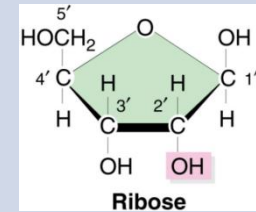
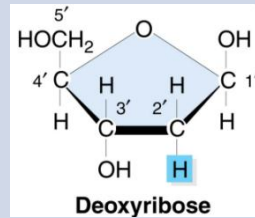


mRNA-Analysis
DNA-Analysis
+
Bioinformatics

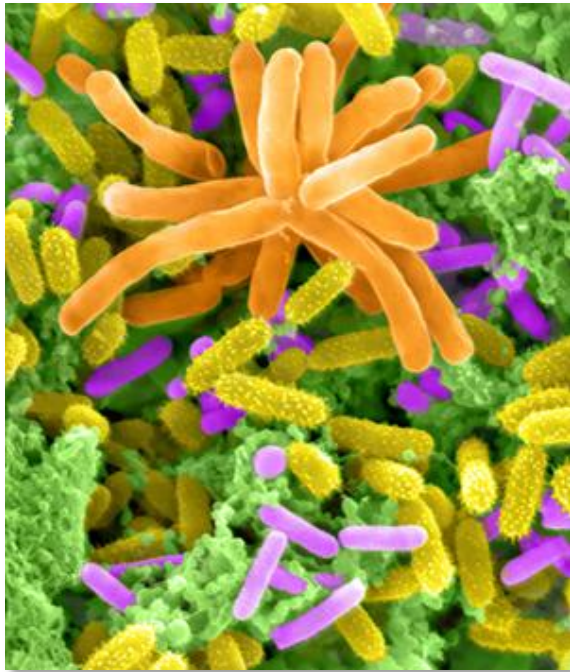
DNA and RNA

(Deoxyribonucleicacid and Ribonucleicacid)

DNA	RNA
Contention: - Deoxyribose - Base - phosphate	Contention: - Ribose - Base - phosphate
Bases: - Adenin - Guanine - Cytosin - Thymin	Bases: - Adenin - Guanine - Cytosin - Uracil
Structure: - Double strand helix	Structure: - Usually single strand
Location: - Nucleus (in eukaryotic cells also in mitochondrias and chloroplasts, in prokaryotic cell in cytoplasm)	Location: - Nucleus, ribosomes, cytoplasm
Amplification: - Replicates itself - Replication	Amplification: - Needs to be transcribed from DNA - Transcription



What are the aims of Bioinformatics?



mRNA-Analysis
DNA-Analysis
+
Bioinformatics

- Analysis of the taxonomic composition
- Analysis of the metabolism
- Discovery of new microorganisms
- Identification of new genes/functions/enzymes
- Comparison of different processes
- Analysis of the gene-content
- Optimisation of the processes

Aim: Total optimisation of the biogas process chain for the increase of the operational, metabolic, energetic and ecological efficiency.

NCBI

- NCBI = **N**ational **C**enter for **B**iot**e**chnology **I**nformation
- Public database with DNA, RNA and Protein Sequences
- <http://www.ncbi.nlm.nih.gov/>



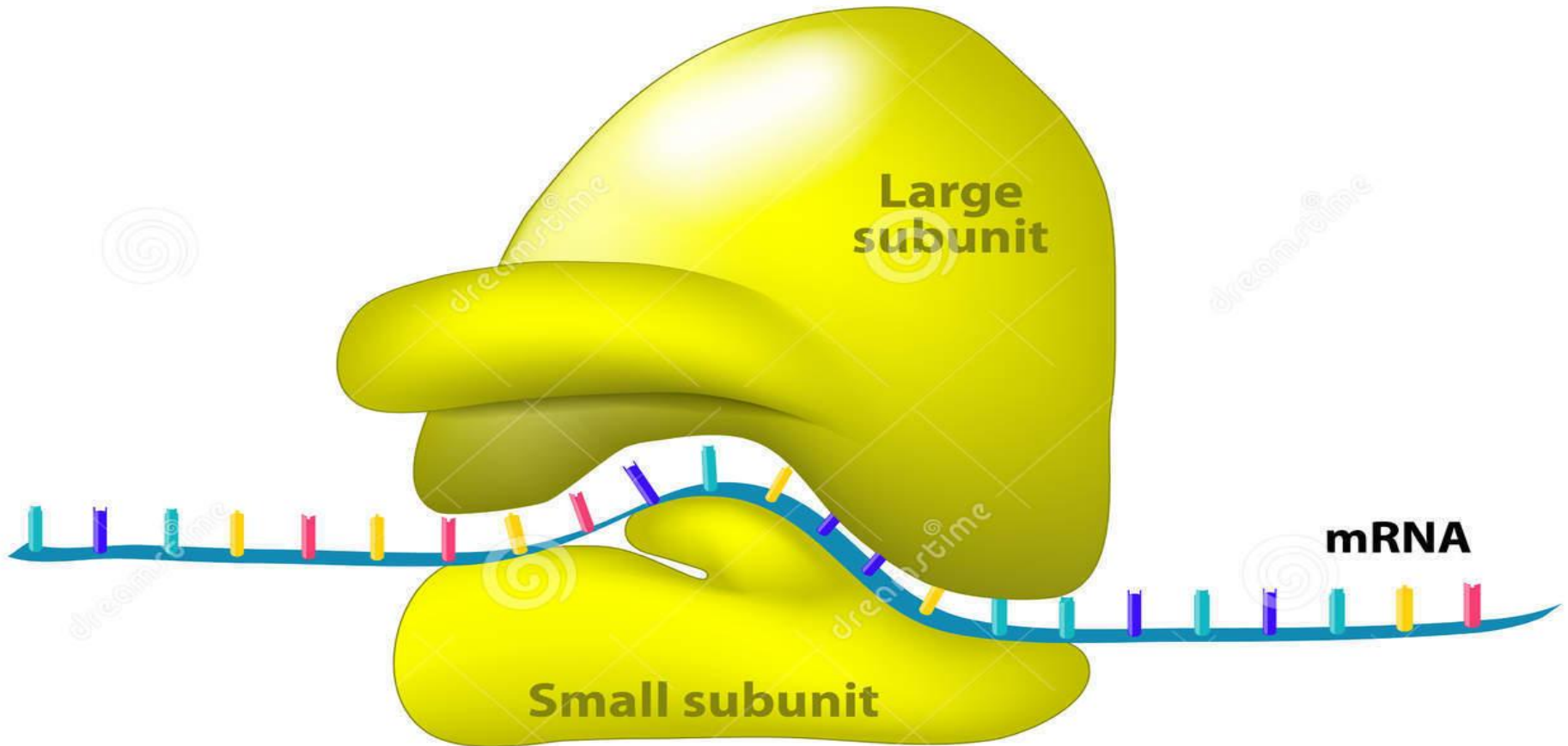
Identification of an unknown DNA-Sequence with BLAST

- Exemplified on a sequence which is the code for the 16S rRNA

What is 16S ribosomal RNA and why do we use it?

- It is a part of Ribosomes

RIBOSOME



What is 16S ribosomal RNA and why do we use it?

- It is a part of Ribosomes
- S is a unit for molecules for their weight and their size
- rRNA is part of Ribosomes
- We work with 16S rRNAs because they have a suitable number of nucleotides

What is BLAST?

- BLAST = **B**asic **L**ocal **A**lignment **S**earch Tool

What is an Alignment?

- It is a comparison of two sequences and their parallelism is shown by vertical lines

```
Query 4      GTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGGG 63
             |||||||||||||||||||||||||||||||||||||||||||||←
Sbjct 1      GTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGGG 60

Query 64     GAACTTCGGTTCCCAGCGGCGGACGGGTGAGTAACACGTGGGTAACCTACCTCATAGTGG 123
             |||||||||←
Sbjct 61     AAACCTTCGGTTTCCAGCGGCGGACGGGTGAGTAACACGTGGGCAACCTGCCTCACAATGA 120
```

What is BLAST?

- BLAST = **B**asic **L**ocal **A**lignment **S**earch Tool
- Verify unknown sequences with known sequences from databases
- Unknown sequence is called “Query”
- Located similar sequences is called “Subject”
- Results are shown in a hit-list
- It is a part of NCBI

How does it works? - Overview

- Step 1: Open the file with the sequence
- Step 2: Copy the DNA – Sequence with its titleline
- Step 3: Open the NCBI-BLAST-Website:
<http://blast.ncbi.nlm.nih.gov/Blast.cgi>
- Step 4: Choose the program **nucleotide blast**
- Step 5: Insert the file content into the window
- Step 6: Selection of the datas „16S ribosomal RNA sequences (Bacteria and Archaeobacteria)“