Aalborg Universitet

Enabling detection of ecological patterns in 10.000 samples representing the Danish soil microbiome

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# MICROFLORA DANICA – THE MICROBIOME OF DENMARK

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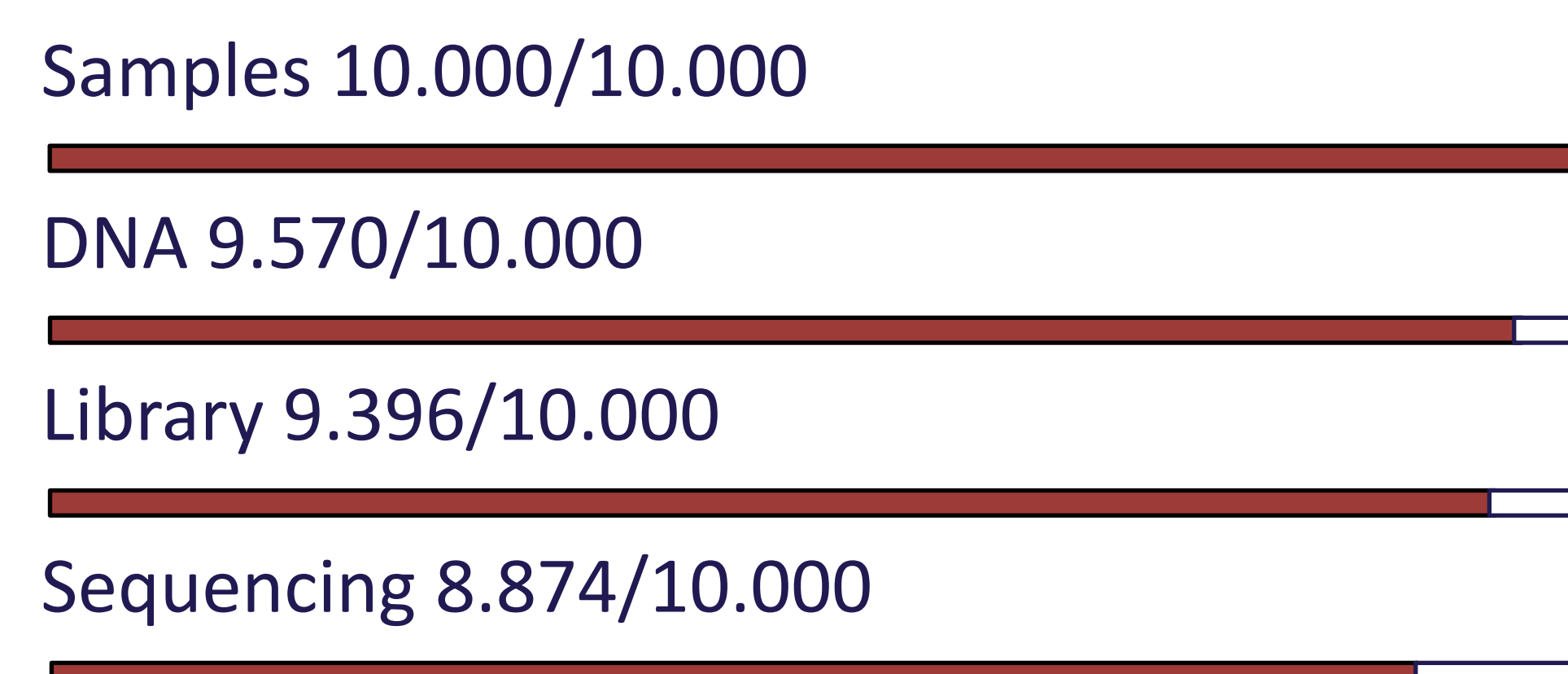
Introduction

By sampling soil, sediment, and water across both natural and cultural habitats and by applying novel DNA-based sequencing technologies, the aim of Microflora Danica is to generate an almost complete reference database of the microbiome of Denmark. The purpose of Microflora Danica is to establish a common reference database and to link the identified microbes to their functions and distributions across different habitats.
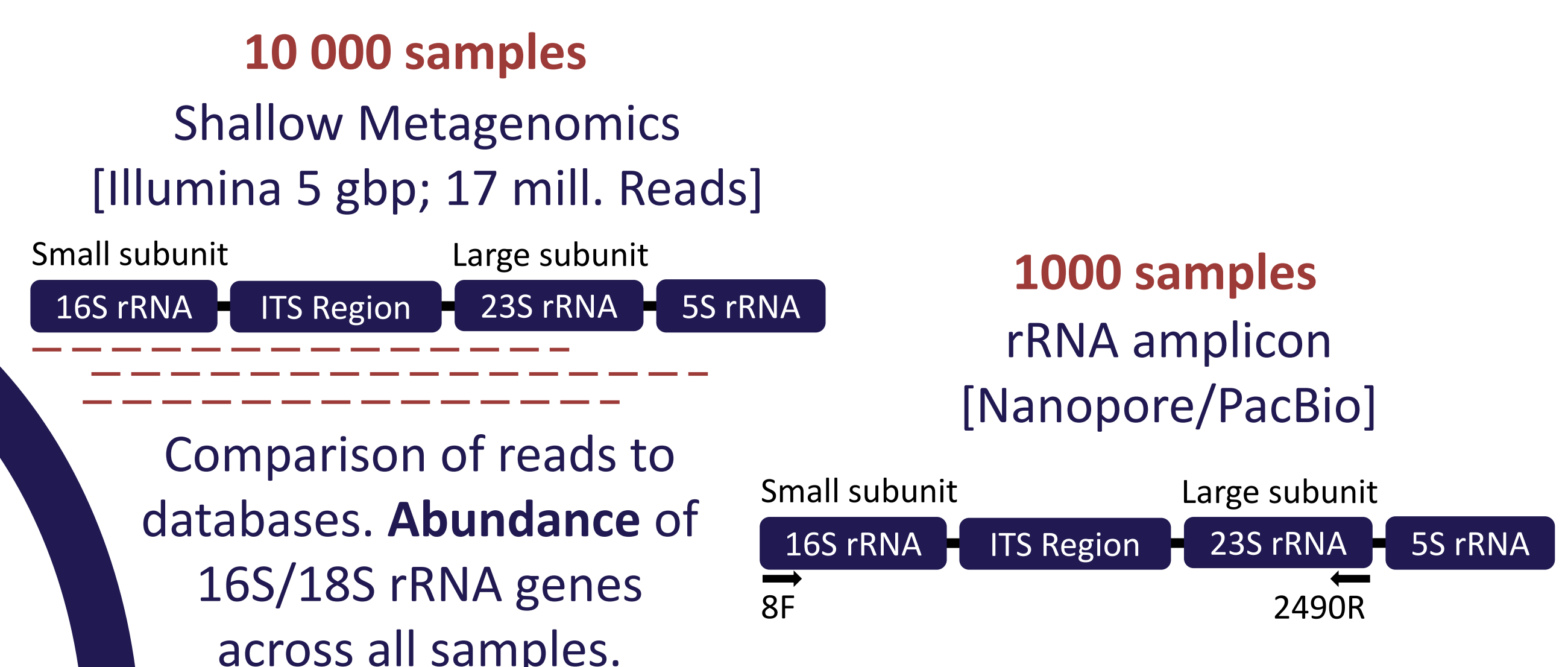
Coverage of Habitats

df.map - type
- biofilm
- sandfilter
- sediment
- sludge
- soil
- water
- water(dilute)
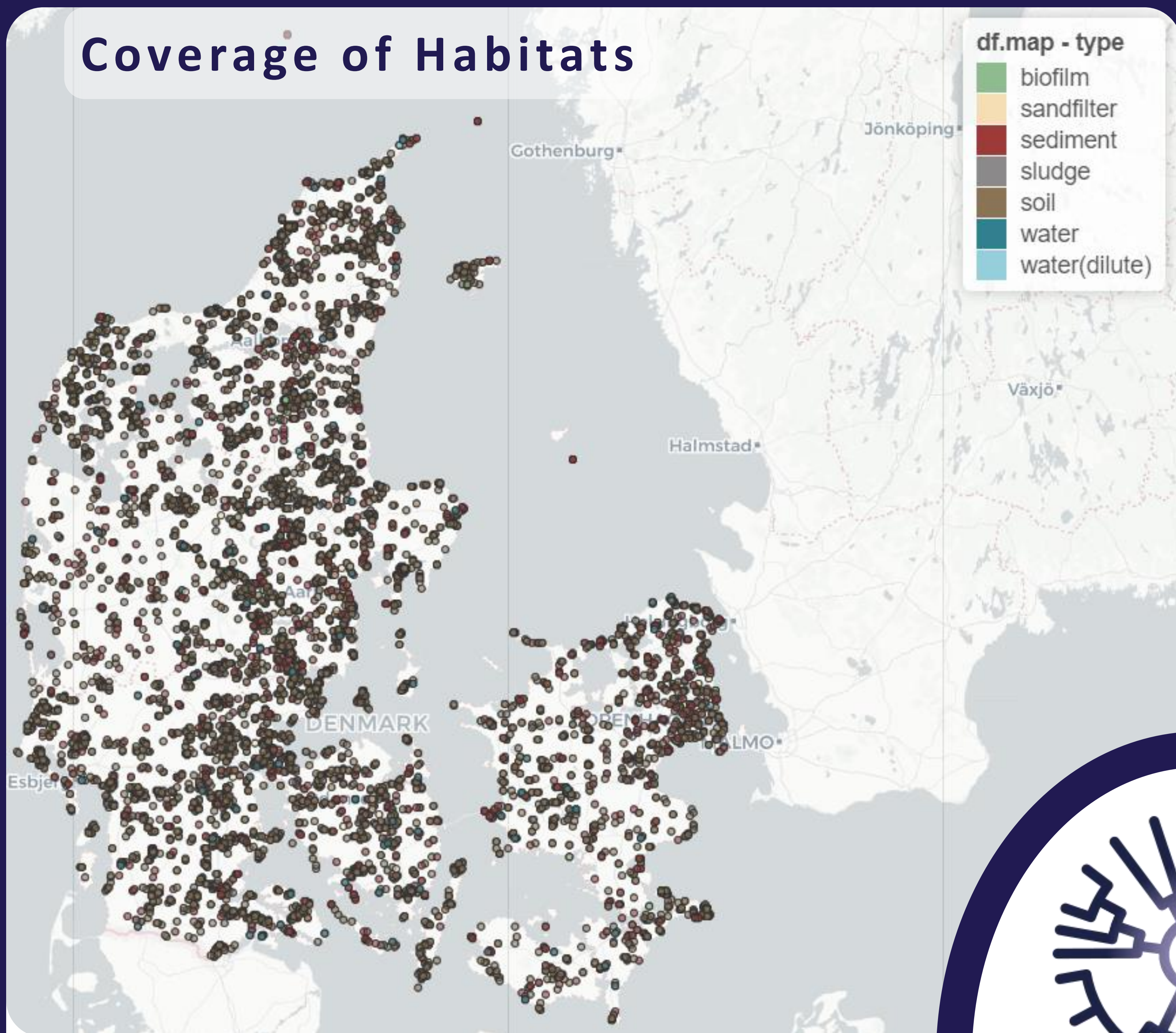
- 10.000 samples covering **natural and cultural habitats**

- **EMP500** samples included

Project Progress

Samples 10.000/10.000
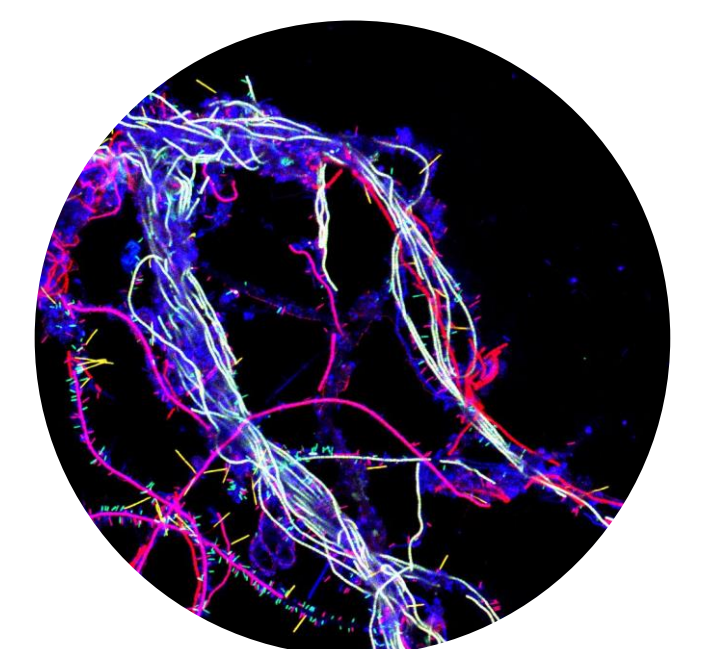
DNA 9.570/10.000

Library 9.396/10.000

Sequencing 8.874/10.000

Types of Data

10 000 samples
Shallow Metagenomics
[Illumina 5 gbp; 17 mill. Reads]

Small subunit — 16S rRNA — ITS Region — Large subunit — 23S rRNA — 5S rRNA

Comparison of reads to databases. **Abundance** of 16S/18S rRNA genes across all samples.

1000 samples
rRNA amplicon
[Nanopore/PacBio]

Small subunit — 16S rRNA — ITS Region — Large subunit — 23S rRNA — 5S rRNA
8F   2490R

Database of high-quality reference **16S/18S rRNA** sequences to build the tree-of-life.

100 samples
Deep Metagenomics
[Illumina + Nanopore]

DNA → Genome → Phylogenetic marker genes (ex. rRNA genes)

Retrieval of **genomes** from novel bacteria selected from samples of interest.

Interesting samples
FISH and FISH-Raman microspectroscopy

Visualization of **novel** and **uncultured** bacteria

Developed Methods

- Barcoding and **automated registration** of samples

- High throughput DNA extraction – **276 samples a day**

- **10x down-scaling** of sequencing library preparation through nanoliter dispensing

- Automated workflows using **liquid handlers**

- Automated **sequence processing pipeline**

Database

- Based on latest release of SILVA

- Addition of new full length 16S sequences

- De novo name generation when needed

- Expectation: final version based on < 15 million sequences

Research Questions
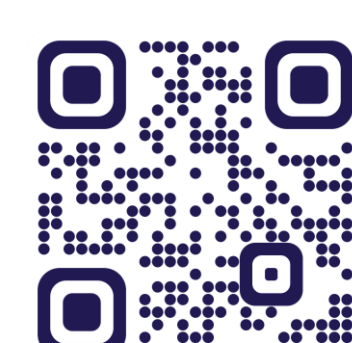

Unknown microbe
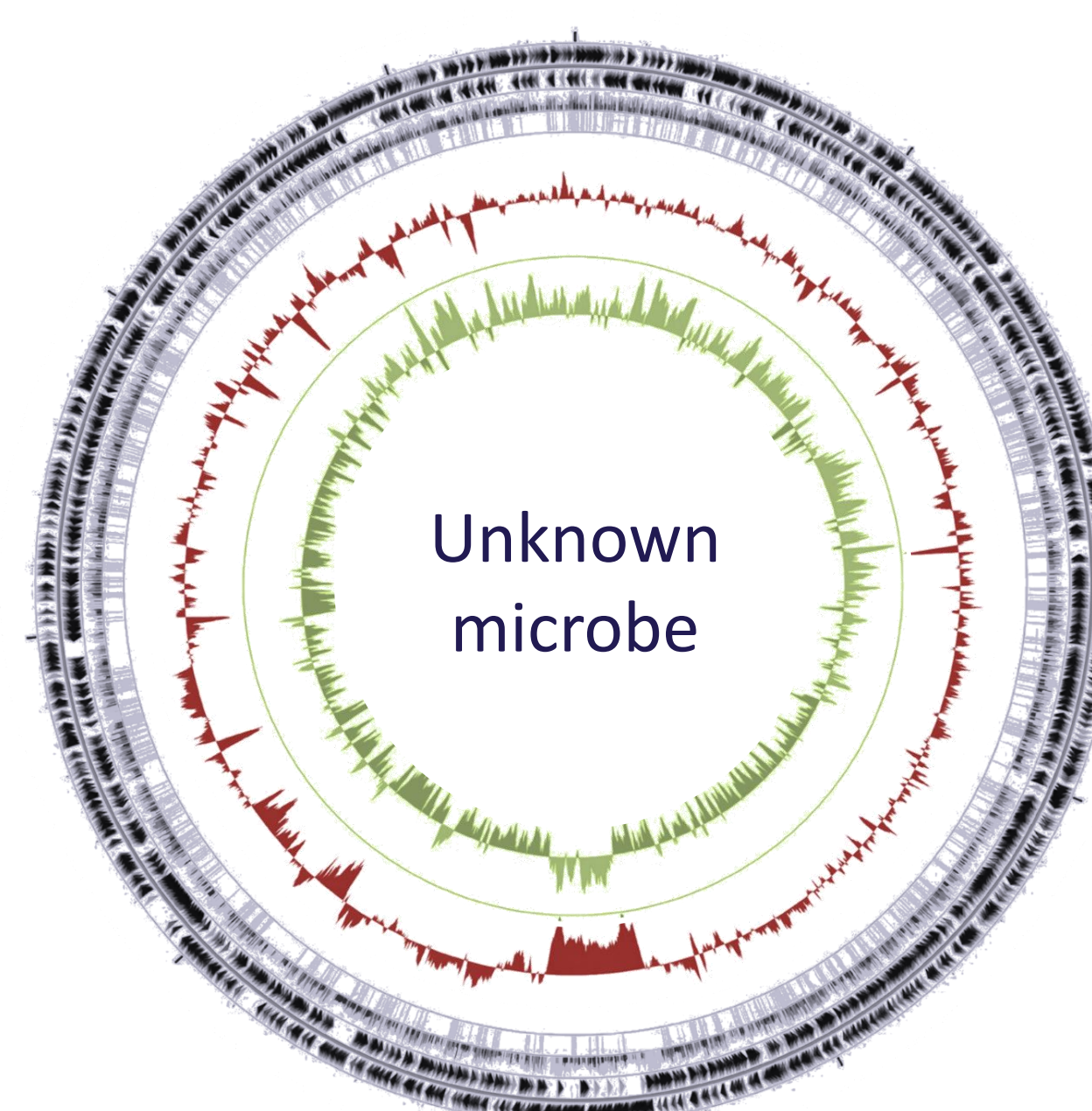
- Assessment of novelty and diversity

- Importance for habitat function

- Prediction of habitat preferences

- Naming of novel organisms

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