

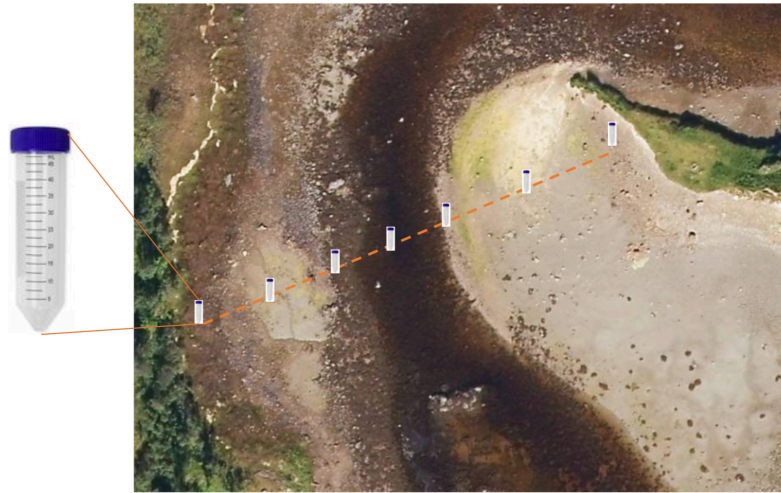


## Group work - Taxonomic and functional analysis of shotgun metagenomic data

Environmental samples were collected from the tidal zone in Finnvika, Tromsø, on October 9th, 2018. Total DNA was next isolated from 7 sediment samples, and subsequently subjected to shotgun sequencing using Illumina MiSeq technology.

In this exercise you will work in groups and explore the composition of five of these samples. You will be the first people to explore the composition in this environment, so we are very excited to look at the results 😊





Collect approx. 35 ml sediment  
Use spoon  
Surface layer (1 cm)  
Description of the sediment:  
Coarse sand, Medium sand,  
Fine sand, Very fine sand, Mud  
(Silt, Clay, Colloid)  
  
GPS location  
Temperature in sediment  
Photo of sampling site  
etc



### Your task will be to:

1. Describe the taxonomic composition of this environment
2. Try to extract complete genomes from the metagenomic sample (we have assembled the metagenome beforehand)
3. Perform functional analysis of the most abundant specie or most complete genome in the sample
4. Present the results (some slides with results e.g. taxonomic profiles) to all the other participants after lunch

You should apply all the knowledge you have acquired during the course to solve this task. Especially what you learned on day 2-4

### 💡 Suggestions:

We suggest that you split into smaller teams. For example that one team is working on the taxonomic profiling, and the other team is working on the binning of MAGs and functional part. Within a team, each participants can perform different tasks. For example in the "taxonomic team" one participant can do taxonomic profiling on the 16S rRNAs, while another participant can do the Kauju and Kraken approach.

But this is totally up to you 😊

### 💡 Suggestions:

In order to annotate the genome you select, have a look at the online annotation tools [EggNOG](#) and [RAST](#)

Also, the tool [Abricate](#) is installed on the virtual machine, and you can try to install [PROKKA](#) on the VM.

The data you will use is located in `/net/software/practical/7`

Copy the data corresponding to you project:

	Name	Name	Name	Name
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