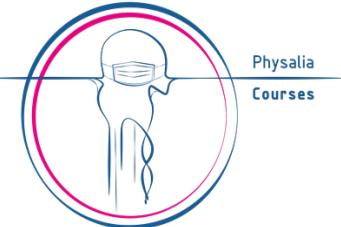
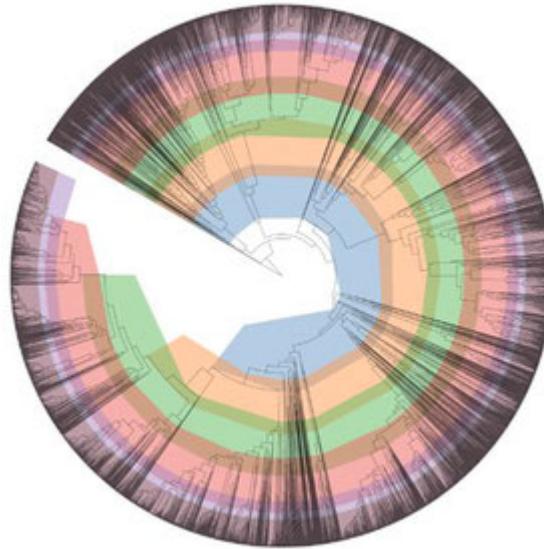


# ENVIRONMENTAL METAGENOMICS

Physalia course, online, 11-15 November 2024

Nikolay Oskolkov, Lund University, NBIS SciLifeLab  
Luis Pedro Coelho, Queensland University of Technology



NB: original course material courtesy:

Dr. Antti Karkman, University of Helsinki

Dr. Igor Pessi, Finnish Environment Institute (SYKE)



@NikolayOskolkov



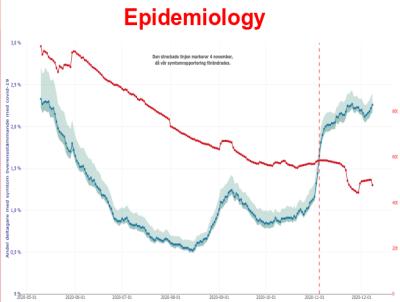
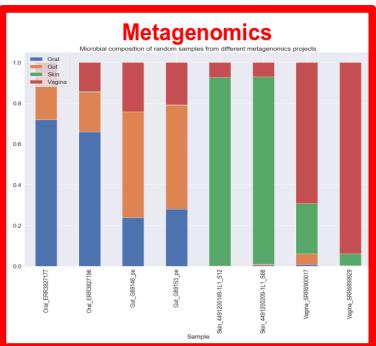
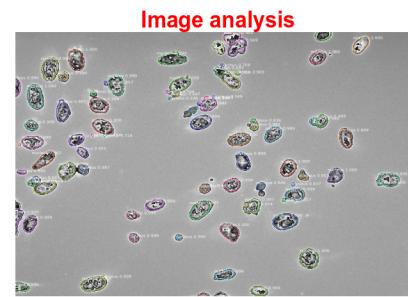
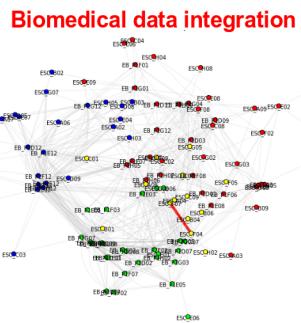
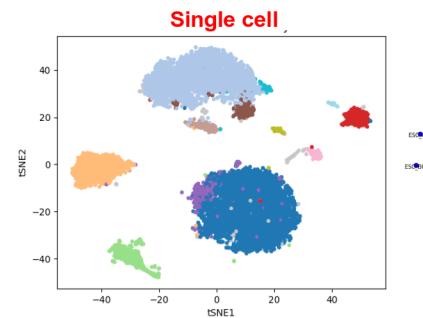
Personal homepage:  
<https://nikolay-oskolkov.com>

# Brief introduction: who am I

2007 PhD in theoretical physics

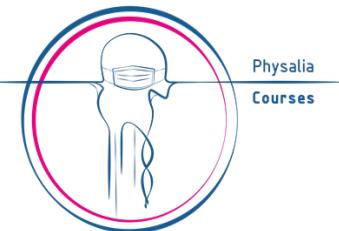
2011 medical genetics at Lund University

2016 working at NBIS SciLifeLab, Sweden



# About you

- Name
- University/Institute/Company
- Research interest(s)
- Previous experience(s) with microbial ecology, metagenomics, bioinformatics, etc.
- General hopes for this course



# Practical information: GitHub and Zoom

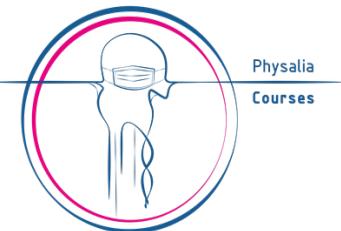
The course will take place **in Zoom from 9am to 1pm (CET)**

Links to the Zoom room will be posted in Slack

The course GitHub repository containing lectures and exercises is:

**[https://github.com/NikolayOskolkov/Physalia\\_EnvMetagenomics\\_2024](https://github.com/NikolayOskolkov/Physalia_EnvMetagenomics_2024)**

Please bookmark this address!



# Practical information: Amazon Cloud (AWS EC2)

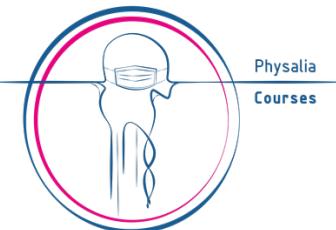


We will use the Cloud Computing service from Amazon, which we will access via **ssh** (secure shell protocol)

[https://github.com/NikolayOskolkov/Physalia\\_EnvMetagenomics\\_2024/blob/main/exercises.md#setting-up-the-cloud-computing](https://github.com/NikolayOskolkov/Physalia_EnvMetagenomics_2024/blob/main/exercises.md#setting-up-the-cloud-computing)

See [here](#) for information on how to connect, but remember:

- The IP address changes every day
- Everyone is given a username, with a **home** and **shared** folders
  - List of usernames can be found in Slack
  - The **shared** folder is copy-only: do not delete, move, rename, or write



# Practical information: conda



System for software management (python, R, JavaScript, C++, ...)

Allows easy installation of software in dedicated environments,  
separated from the main environment and other conda environments

- The environments that we will use have been already set up for everyone

## General conda commands

```
> conda env list  
> conda activate ambiente  
> conda deactivate
```





