



Bioinformatics and a changing society

4 December at 9.00-16.00

in Pub1 auditorium, Publicum

Workshop descriptions

WORKSHOP 1

Public Health Microbiology

by Peter Simmonds & Heli Harvala

This workshop will introduce you to the basic sequence analysis utilizing a practical case study based on a real-life example and will demonstrate the importance of bioinformatics in public health microbiology investigations. **No prior experience is needed.**

At the end of day, you will be able to construct multiple alignment and phylogenetic tree using different software (i.e. SSE and MEGA), understand the basics behind alignments and phylogenetic analysis, to be able to access different databases, and to be aware of the importance and potential future issues relating to bioinformatics and phylogeny within clinical virology and public health microbiology.

For this workshop, you need to have your own laptop with the following two software installed (MAC users will need to install Wine or other Windows emulator in order to install SSE): SSE Version 1.4 (freely downloadable from GitHub: <https://github.com/psimmond/SSE> and MEGA 12.0 (freely downloadable, select Windows, Graphical (GUI), version 12: <http://megasoftware.net/>).

Do not hesitate to contact Heli Harvala (heli.harvala@utu.fi) or Peter Simmonds (peter.simmonds@utu.fi) if you have any questions or issues with installing the software.

WORKSHOP 2

Spatial Transcriptomics

by Lea Mikkola

This workshop focuses on analysis of spatial transcriptomics data of human atherosclerotic aorta and carotid artery tissues. The participants will run a basic analysis pipeline in R (RStudio) and will learn the most important steps in the workflow, its limitations, and how to map candidate genes on tissue sections.

Prerequisites are: R basics (we will not use time to learn how to use the program), and a work/personal laptop either with ready access to CSC's Puhti super computer's interactive R environment **and knowledge how to use it**, or with R and Rstudio already installed. The data isn't massive, but the laptop needs to have moderate processing capacity (at least 8 Gb RAM, preferably more).

Helpful reading: Sun et al. paper (2023) <https://doi.org/10.1016/j.jacc.2023.04.008>, which utilizes similar data, and the preprint from Mikkola et al. (2025), which uses the same data the students will be working with: <https://www.biorxiv.org/content/10.1101/2025.09.02.673686v1.full.pdf>.

More information from Lea Mikkola (lea.mikkola@utu.fi)





WORKSHOP 3

Basic R-Programming

by Nick Booth & Anni Kauko

This workshop is an introductory session to coding, covering the very basics of concepts that underpin practical computational science, using R as the example language. The session is ideal for those with **no prior experience of coding**, who perhaps have found the discipline too intimidating or confusing to approach and need a starting point. Researchers who have self-taught or used R programmes previously, but with no formal training, and would like to better understand how coding works will also find this session helpful.

Since this workshop will only be interacting with the basic functionalities of R, access to a simple installation of R and R Studio are the only requirements.

More information from Nick Booth (nicholas.booth@utu.fi)

WORKSHOP 4

Gut Microbiome

by Tuomas Borman & Matti Ruuskanen

Because of the complex nature of microbiome data, robust and reproducible computational approaches are essential. This workshop introduces the latest advances in microbiome analysis within Bioconductor, focusing on the mia (Microbiome Analysis) framework. Participants will gain hands-on experience with data handling, visualization, and analysis through a practical case study. The workshop will also introduce the Orchestrating Microbiome Analysis with Bioconductor online book (<https://microbiome.github.io/OMA>), a freely available resource that promotes best practices and supports adoption of the ecosystem. Together, these resources enable scalable, transparent, and community-driven microbiome data science.

Participants are expected to have some basic programming experience, for example, having written code in R or another programming language. No advanced programming or bioinformatics knowledge is required.

More information from Tuomas Borman (tuomas.v.borman@utu.fi)

WORKSHOP 5

Legal Aspects of Bioinformatics

by Juha Vesala & Sini Mickelsson

This workshop addresses bioinformatics through the lens of certain legal issues. We will discuss topics such as data anonymization, conditions for using health data in AI development, and consent as a basis for using sensitive data from the perspective of how the legal framework can hinder or enable research and R&D. The workshop is intended to bring together experts from different fields, and **no prior legal knowledge is expected**. Participants can also propose topics for discussion when registering for the event.

More information from Juha Vesala (juha.vesala@utu.fi) and Sini Mickelsson (sini.mickelsson@utu.fi)

