

Lipidomics Data Analysis – Sphingolipids and T2DM Risk

Who

Anyone interested in the organization and interpretation of large-scale clinical lipidomics datasets

When

March 4th, 2021, 2:00 - 5:00 PM (Singapore, GMT+8)

Where

- On-site: National University of Singapore, Center for Life Sciences, 28 Medical Drive, Singapore
- Online

Moderators

- Hyungwon Choi, Cardiovascular Research Institute, NUSmed
- Bo Burla, Singapore Lipidomics Incubator, Life Sciences Institute, NUS

Prerequisites

We will be using R for conducting the data analyses. We therefore encourage you to bring a computer with R and RStudio installed, or with RStudio Cloud (<https://rstudio.cloud/>) running in a web browser. However, you are also very welcome to attend this workshop without any computer and/or knowledge in R.

Overview

In the first part, we will look at the structure of lipidomics datasets and discuss lipid nomenclature systems. We then look at some aspects and challenges of the analytical data processing and quality control workflow. The practical part will include reading of lipidomics data and metadata into R, parsing of the data into different formats for visualization and downstream statistical analyses (see below), converting lipid nomenclature, and creating selected quality control plots.

In the second part, we practice how to reorganize and inspect the overall data trends from both sample meta data and lipidomics data via visualization and dimension reduction. We probe the correlation structure between the sphingolipids and other competing risk factors collected at baseline, and test associations between the lipids and the risk of DM incidence, using logistic regression (binary outcome) and Cox regression analysis (time-to-event analysis).