Shotgun Metagenomics Analysis with qiime2

one day workshop

Members of the QIIME 2 team from the Caporaso and Bokulich labs, led by Greg Caporaso, will visit the LUMC to give a one-day workshop, *Shotgun Metagenomics Data Analysis with QIIME 2* on 29th March 2024.

Shotgun metagenomics analysis is a major new feature of QIIME 2, and this will be the first workshop the team teaches on this topic. This is a great opportunity to learn cutting edge analytic techniques to simplify your shotgun metagenomics analysis with QIIME 2. And as usual, QIIME 2 doesn't try to reinvent the wheel: through new QIIME 2 plugins, you'll learn to apply top-performing tools from the CAMI benchmarks, including Kracken2, Bracken, and Megahit for processing your data without worrying about shuffling data between tools.

A unique feature of QIIME 2 is its data provenance tracking system, which ensures reproducibility of your bioinformatics results. To learn more about how this can improve your workflows, see the team's most recent article, *Facilitating bioinformatics reproducibility with QIIME 2 Provenance Replay* (PLOS Computational Biology, November 2023).

Prerequisites:

- All participants should bring a laptop and be able to install software on this laptop. Any laptop that can run a modern version of Google Chrome should work just fine!
- Please review the instructions here to install the requisite software on your laptop before the workshop.
- Then, review our overview of working with command line software.
- There are no specific prerequisites, but familiarity with molecular biology and microbiomes is expected.

Schedule:

09:00-10:30	Introduction to QIIME 2
10:30-10:45	Break
10:45-12:00	QIIME 2 tutorial (part I)
12:00-13:00	Lunch
13:00-15:00	QIIME 2 tutorial (part II)
15:00-15:15	Break
15:15-16:00	QIIME 2 tutorial (part III)
16:00-17:00	Summary and Q&A

Location:

LUMC (room V3-18/22, LUMC building 3)