UCI Microbiome

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Contacts & Information

http://microbiome.uci.edu

Consulting hour sign-ups: UCI Microbiome Initiative Consulting Hour Sign-Up

Microbiome Centers Consortia: https://microbiomecenters.org/

https://twitter.com/UCI_Microbiome

@UCI_Microbiome

Proud member of MICROBIOME CENTERS CONSORTIUM

Description for inclusion in grant applications

UCI Microbiome seeks to create cross-discipline collaboration to discover universal principles about microbiomes across all systems. It started as the UCI Microbiome Initiative in 2017, led by Prof. Jennifer Martiny (Ecology and Evolution) and Assoc. Prof. Katrine Whiteson (Molecular Biology and Biochemistry) and is now a two-school based center in the School of Biological Sciences and the School of Medicine. They offer advice on experimental design, sample collection/storage conditions, and sequence or metabolomic analysis. They also host training workshops, weekly consulting hours, and monthly meetings to facilitate interactions and promote microbiome science among the UCI research community. UCI has excellent resources for conducting microbiome analyses on campus. The Genomics High Throughput Facility led by Director Dr. Melanie Oakes and Prof. Suzanne Sandmeyer provides sequencing for whole genomes, amplicon libraries, and metagenomic and metatranscriptomic libraries with several Illumina sequencing instruments, Pac Bio and 10X genomics instruments. They can also prepare libraries for sequencing, from nucleic acid extraction to quality control checks using the Covaris and Pippin Prep instruments. The Mass Spectroscopy facility led by Director Dr. Felix Grun has new Waters LC-MS/MS capacity and training available to enable users to run their own samples, along with help to establish new protocols and analysis strategies. Regular workshops led by the UCI Microbiome Initiative offer training in relevant multivariate statistical analyses.

Support letter text: UCI Microbiome offers resources to help determine the optimal study design and sample collection/storage conditions, as well as obtain culture independent sequencing or metabolomics data using the facilities here at UCI. We will include the researchers from the proposed project in our training workshops. Furthermore, we will provide consultation on a weekly basis and we now offer a bioinformatics service to analyze and interpret microbiome sequence data, and provide publication quality figures.

Microbiome Initiative Presentations / Workshop Slides

1. Workshop slides
    - General overview of microbiome research
    - Basic Microbiome methods in the lab like DNA extraction and Amplicon library preparation
    - Overview of sequence analysis

2. Presentation slides
    - Sequence Analysis presentation including Anvio and qiime2 workshop presentations (Day1, Day2)
    - June 2022 Metagenomics workshop, folder with materials: UCIMicrobiome_MetagenomicsWorkshop_2022

Resources for Microbiome Data Analysis

If you would like to start with a nice blog post to get a general overview of Microbiome Data Analysis of Amplicon data you can check out Alex Chase's Blog

1. Bioinformatic Support Presentations and help sheet

2. Getting access to the HPC3 on Campus

3. Accessing qiime2 on the HPC3
   - To use the installed qiime2 module on the hpc type

     # > `module load anaconda/2020.07`
     # > source activate `qiime2-2020.8`
     # To deactivate an active environment, use:
     # > source deactivate

4. Getting started with analyzing your data in R slides & folder containing analysis workshop materials

5. Online Courses
   - Free coursera course about the microbiome led by Prof. Jessica Metcalf and Prof. Rob Knight

   - Annual Gut Microbiome conference Educational Resources

   - Prof. Dan Knight's University of Minnesota Microbiome Course:

     https://www.youtube.com/watch?v=Ok5h24KZbAE

6. Consultation hour with the UCI Microbiome Initiative
   - Get help with project design and/or data analysis

Software and Microbiome Analysis

1. R and R studio; R is a powerful open access analysis platform with packages for many relevant tasks. UCI's Data Science Initiative and many online resources are a good way to get started. The packages Vegan, Random Forest and phyloseq are all relevant for us

2. Quantitative Insights Into Microbial Ecology (Qiime) The new version is Qiime2.

3. Many labs are actively writing relevant software. A few examples:
    a. Dan Knights (check out Shogun, and course on You Tube)
    b. Curtis Huttenhower (many of their packages are available on Galaxy)
    c. Rob Edwards (several useful tools including Prinseq for sequence analysis and cleanup)
    d. Pat Schloss (developer of 16S analysis package mothur)
    e. Elhanan Borenstein
    f. Meren and Anvi'o
    g. https://astrobiomike.github.io/

4. Primer-E is a very powerful multivariate analysis program. It is not free and works only on PC, but it is very user friendly and powerful.

5. Web-based software: MetaboAnalyst and MicrobiomeAnalyst

6. Tools from the Human Microbiome Project

7. Earth Microbiome Project

8. Physician's Guide to Microbiome analysis (review paper)

9. Recent paper about standards and the microbiome: Knight et al.

10. Helpsheet with an overview to understand the terminology used in microbiome research

Note: Many of these packages are available on [UCI's HPC3]

Reading Resources

1. Ed Yong's well-written book, "I contain Multitudes", which has an associated blog
2. Article in The Guardian about the Human Microbiome and Health, along with suggestions for high fiber foods!
3. An article about fecal transplants from The New Yorker, The Excrement Experiment.
4. An article about the microbiome in the New Yorker, Germs are us.
5. Michael Pollen on the microbiome in the NY Times
6. A supplement in Nature focused on the microbiome
7. Collection of microbiome stories on NPR, including a nice 5 minute video
8. National Microbiome Initiative Fact Sheet
9. Forest Rohwer and SDSU in the New Yorker about the celebration of the 100th anniversary of the discovery of phage, and the associated book, Life in Our Phage World