

ISME 14 Bioinformatics Workshop:

Using QIIME and MG-RAST to study microbial communities.

18 August 2012, Copenhagen University

Members of the QIIME and MG-RAST development groups, led by Greg Caporaso, Rob Knight, and Folker Meyer, will teach a full-day workshop on bioinformatics tools for microbial ecology. The morning will focus on lectures covering QIIME and MG-RAST, and in the afternoon students will work hands-on with these tools via Amazon Web Services (for QIIME) and the MG-RAST web server. Students will interact directly with core developers on the QIIME and MG-RAST projects to get a hands-on introduction to QIIME and MG-RAST. This workshop will provide the foundation on which students can begin using these tools to advance their own studies of microbial ecology.

For details on how to apply to the workshop visit:

http://www.qiime.org/workshops/isme14_bioinformatics.pdf

Because we expect more applications than we can accept, our goal is to give priority to applicants who will immediately be putting the skills developed at the workshop into practice.

The cost for the workshop will be **USD\$200 per participant**. Payment will be made after your application has been accepted. Copenhagen University is a short metro ride from the Bella Center, where ISME 14 will be held, so participants should plan to arrive at ISME 14 one day early for the Bioinformatics Workshop. **Applications are due April 22nd**, and all applicants will be notified by April 23th. **Note: Application deadline has been extended by seven days to April 22nd.**

To apply, please complete the application linked below and **submit it as a PDF by email** to Ulla.Westermann@colorado.edu. The subject of your e-mail must be "ISME 14 Bioinformatics Workshop Application". The information requested in the application is as follows:

- Name
- E-mail address
- Position (Graduate student, Postdoc, Professor, Research Scientist, etc.)
- Affiliation
- Citations for your two most relevant publications (if any)
- A 1-2 paragraph description of a data set that you are currently analyzing or will soon be analyzing. Include a description of the hypothesis you are testing, details on the experimental design (such as number of samples, sequencing platform, etc.), the current stage of the project (planning, sample collection in progress, sequencing in progress, data is in-hand, etc.), and the results of any preliminary studies. We will treat this information as confidential.

Application: http://www.qiime.org/workshops/isme14_bioinformatics_application.doc

