University of Georgia
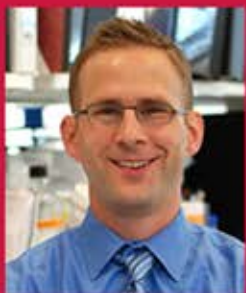# Institute of Bioinformatics

2017 SYMPOSIUM
Parsing the Microbiome

September 25th | 2017

University of Georgia Center for Continuing Education & Hotel

The 2017 Institute of Bioinformatics annual symposium focuses on the microbiome, a collective term for the multitude of microbial communities that form critical components of biological systems important in human health, agriculture, and the environment. Microbiome research frequently involves complex datasets, with a wide variety of organisms interacting at different spatial, temporal, and taxonomic scales. *Parsing the Microbiome* will feature several prominent experts who are developing or applying bioinformatics tools to understand these data and condense them into interpretable results. This one-day symposium will be useful to students, postdocs, and faculty interested in microbiome research and the current leading methods in this field.

Keynote Speakers

Daniel Beiting

University of Pennsylvania, School of Veterinary Medicine, Philadelphia, Pennsylvania

Dr. Beiting is an immunologist using -omics approaches to interrogate the host-pathogen interface. He is the co-developer of MicrobiomeDB (http://microbiomeDB.org) a new database for interrogating microbiome data based on associated sample metadata.

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Daniel Jacobson

Oak Ridge National Laboratory, Oak Ridge Tennessee

Dr. Jacobson develops new mathematical, statistical, and computation methods to gain new insight into complex biological systems. His work focuses on bioenergy sciences and plant-microbe interfaces, and utilizes high-scale computing with network analysis, linear algebra, Bayesian statistics, and systems analytics to parse a range of -omics datasets (genomics, transcriptomics, proteomics, microbiomics, etc.).

Gipsi Lima Mendez

Department of Microbiology and Immunology, University of Leuvan, Belgium

Dr. Lima-Mendez led the bioinformatic analysis of microbial interactions in the Tara Oceans Expedition metagenome, and has worked on human gut microbiomes and the development of bioinformatic tools for viral communities.

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Katherine Pollard

Gladstone Institute, University of California San Francisco

Dr. Pollard develops statistical and computational methods for massive genomic dataset analysis, focusing on questions of genome evolution in organisms ranging from microbes to humans.

Peter D. Karp

Director of the Bioinformatics Research Group within the Artificial Intelligence Center at SRI International

Dr. Karp has authored 160 publications in bioinformatics and computer science in areas including metabolic pathway bioinformatics, computational genomics, scientific visualization, and scientific databases.

This event is kindly sponsored, in part, by

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