



Yana Bromberg

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Maple Room 1:00 PM

Functional basis of microbial annotation: theory to practice

ABSTRACT:

How does the environment drive selection of its inhabitants? Molecular functional abilities of individual organisms living in different conditions, *e.g.* temperature or salinity, are clearly different. We previously built *fusion* (functional similarity-based organism network), a computational method that groups fully sequenced organisms according to their similarity in potential functional abilities, as encoded by their genomes. We then developed *mi-faser* a sequence-based means of identifying the molecular functions encoded in metagenomes via mapping raw genetic reads to the functions of their corresponding “parent” genes. We estimate the microbiome functional diversity by mapping the functions identified from metagenome reads onto a manually curated set of enzymes. We further intend to use *mi-faser* to map to a much broader set of functions defined in *fusion*. By thus analyzing metagenomic data we can identify the diversity of, both, functions and organisms that occupy a particular environmental niche. Our approach recapitulates the functions encoded in the genomes that can be assembled, as well as an additional large set of functions present in the microbiome, but not identifiable via current techniques. By adopting this point of view in analyzing metagenomic data we hope to identify emergent functionality of metagenomes specific to condition (disease, pollution, *etc.*) versus normal individual samples.

BIO:

Dr. Yana Bromberg is an associate professor at the Department of Biochemistry and Microbiology, Rutgers University and adjunct professor at the Department of Genetics at Rutgers. She is also a fellow at the Institute of Advanced Studies in the Technical University of Munich. Dr. Bromberg received her Bachelor degrees in Biology and Computer Sciences from the State University of New York at Stony Brook and a Ph.D. in Biomedical Informatics from Columbia University, New York. She is known for her seminal work on a method for screening for non-acceptable polymorphisms, or SNAP for short, which evaluates the effects of single amino acid substitutions on protein function. Currently, research in the Bromberg lab is focused on the molecular functional annotation of microbiomes, aiming to identify emergent functionality specific to individual environmental niches. The lab also analyses human variomes for disease predisposition and the studies evolution of life’s electron transfer reactions. Dr. Bromberg is a member of the Board of Directors of the International Society for Computational Biology and actively participates in organizing the ISMB/ECCB conferences (ISMB stands for Intelligent Systems for Molecular Biology, and ECCB is its European equivalent). She chairs conference proceedings, conducts workshops, and organizes a special interest group aimed at the study of genomic variation — VarI-SIG. Dr. Bromberg’s work has been recognized by several awards, including the NSF CAREER award, the TSS young investigator award from the American Society for Microbiology, the Rutgers Board of Trustees Research fellowship for Scholarly Excellence, the PhRMA foundation young investigator research starter award and the Hans-Fischer award for outstanding early career scientists from the Institute of Advanced Studies in Technical University of Munich. Dr. Bromberg also serves as an editor and a reviewer of several top journals, including BMC Genomics and PLoS Computational Biology. To date, she has authored or co-authored over 50 peer reviewed scientific articles and has been invited to give over 80 talks.

