Deeper understanding of microbiomes as a benefit of forgetting microbial names

Abstract: Microbes run the world... but they don't care for the names we give them. Molecular functional abilities of individual microbes in micriobiomes living in different environmental conditions are clearly different. Thus, the question of "who is there?" is not as relevant as "what are they doing?"
Focusing on microbial molecular functionality, instead of names or classes, allows for a better description of microbial and microbiome-ial abilities and similarities. The recent emergence of high-throughput genomic sequencing, coupled with the growing analytical capacities, has unlocked new horizons in our understanding of the microbial world. However, making sense of this deluge of data requires efficient and accurate computational techniques. The identification of microbial clades resident in a particular niche is only an estimate of the microbiome's functional potential. We developed a sequencing read-based approach that can be applied to individual microbes and microbiomes to facilitate assessment of functional diversity. By adopting this point of view in analyzing metagenomic data we hope to map emergent functionalities of condition (or niche) -specific microbiomes.

Papers:

1. Zhu, C., Miller, M., Marpaka, S., Vaysberg, P., Rühlemann, M.C., Wu, G., Heinsen, F.A., Tempel, M., Zhao, L., Lieb, W., Franke A., **Bromberg, Y.** (2017**)** Functional sequencing read annotation for high precision microbiome analysis. *Nucleic Acids Research, gkx1209.*

2. Zhu, C., Mahlich, Y., Miller, M., **Bromberg, Y**. (2017) *fusion*DB: assessing microbial diversity and environmental preferences via functional similarity networks. Database: http://services.brombarglab.org/fusiondb. *Nucleic Acids Research,* gkx1060.

3. Zhu, C., Delmont, T.O., Vogel, T.M., **Bromberg, Y.** (2015) Functional basis of microorganism classification. *PLoS Comput Biol.* **11***(8): e1004472*.

BIO: Dr. Yana Bromberg is an associate professor at the Department of Biochemistry and Microbiology, Rutgers University. She also holds an adjunct position at the Department of Genetics at Rutgers University and is a fellow at the Institute of Advanced Studies in the Technical University of Munich. Dr. Bromberg is a member of the Board of Directors of the International Society for Computational Biology and actively participates in the organization of the ISMB/ECCB conferences.
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 genes, genomes, and metagenomes in the context of specific environments and diseases. The lab also studies evolution of life's electron transfer reactions in Earth's history (and as potentially applicable to other planets). This work has been recognized by awards from various agencies including the NSF, NIH, and a number of private foundations. Dr. Bromberg is frequently invited to talk about her research in conferences all over the world and has, to-date, co-authored over fifty peer reviewed scientific articles.