Microbial communities can have an immense effect on their environment and are strongly affected by it. Using new methods for metagenomic sequencing analysis, we systematically identified microbial genomic structural variants and found them to be highly prevalent in the gut microbiome and to correlate with disease risk factors (Zeevi et al., Nature 2019). Our results suggest that these variants facilitate adaptation to environmental stress. Exploring genes that are clustered in the same variant, we uncover potential mechanistic links between microbiome and its host.

Inspired by our discovery of potential microbial adaptation to host pressures, I developed a strategy for mining marine microbiome samples for novel bioremediation genes. To this end, we devised a high-throughput evolutionary analysis, and revealed an unexpected insight into the structure of our genetic code (Shenhav and Zeevi, bioRxiv 2019). Our primary analyses uncovered overwhelmingly strong purifying selective pressure across marine microbial life. This selection was highly correlated with nutrient concentrations and has led us to explore robustness in the genetic code, common to nearly all life forms. We show that the structure of the genetic code, along with amino acid choices across all kingdoms of life, confers robustness to mutations that incorporate additional nitrogen and carbon into protein sequences. By accounting for this nutrient-conservation-driven purifying selection, we will be able to expose a new layer of selection associated with marine pollution.

David Zeevi, Ph.D.
Rockefeller University Center
Postdoctoral Fellow
Department of Physics and Biology

ABSTRACT:
Microbial communities can have an immense effect on their environment and are strongly affected by it. Using new methods for metagenomic sequencing analysis, we systematically identified microbial genomic structural variants and found them to be highly prevalent in the gut microbiome and to correlate with disease risk factors (Zeevi et al., Nature 2019). Our results suggest that these variants facilitate adaptation to environmental stress. Exploring genes that are clustered in the same variant, we uncovered potential mechanistic links between microbiome and its host.

Inspired by our discovery of potential microbial adaptation to host pressures, I developed a strategy for mining marine microbiome samples for novel bioremediation genes. To this end, we devised a high-throughput evolutionary analysis, and revealed an unexpected insight into the structure of our genetic code (Shenhav and Zeevi, bioRxiv 2019). Our primary analyses uncovered overwhelmingly strong purifying selective pressure across marine microbial life. This selection was highly correlated with nutrient concentrations and has led us to explore robustness in the genetic code, common to nearly all life forms. We show that the structure of the genetic code, along with amino acid choices across all kingdoms of life, confers robustness to mutations that incorporate additional nitrogen and carbon into protein sequences. By accounting for this nutrient-conservation-driven purifying selection, we will be able to expose a new layer of selection associated with marine pollution.

BIOGRAPHY:
David Zeevi is an independent postdoctoral fellow at the Rockefeller University Center for Studies in Physics and Biology. His research focuses on developing computational methods for studying the human gut and marine microbiomes, and their contribution to human and environmental health. David applies these tools in clinical settings in order to understand the relationship between nutrition, health, and gut microbes in humans; and in environmental settings in order to find new microbial mechanisms for combating pollution.

David has coauthored several publications in the human microbiome field, linking the microbiome to the effects of artificial sweeteners (Suez et al., Nature 2014) and host circadian rhythm (Thaiss et al., Cell 2015), inferring bacterial growth dynamics
(Korem et al., Science 2015), predicting the glycemic responses of individuals to complex meals (Zeevi et al., Cell 2015; Korem et al., Cell Metab 2017), and characterizing microbial genomic variability across individuals (Zeevi et al., Nature 2019).