The Faculty of Biotechnology and Food Engineering

Seminar

Dr. David Zeevi

Towards mining the marine microbiome for remediation targets: lessons from the human microbiome

Abstract

Microbial communities can have an immense effect on their environment and are strongly affected by it. I will present new methods that mine the rich data source of metagenomic sequencing for insights of microbial activity and adaptation. We developed a method to measure the growth of gut microbes using only a single metagenomic sample (Korem et al., Science 2015). We also developed tools to systematically identify 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). Exploring genes that are clustered in the same variant, we uncovered potential mechanistic links between microbiome and its host.

The microbiome responds and adapts to its environment. Better insights regarding its activity could therefore be used when studying this environment. In one such work, we used the human microbiome to inform health-related choices by accurately predicting host glycemic responses to meals, and using these predictions to design dietary interventions that effectively reduce hyperglycemia (Zeevi et al., Cell 2015).

Microbiomes could also inform environments other than the human host. Our primary analyses uncovered overwhelmingly strong purifying selective pressure across marine microbial life (Shenhav and Zeevi, bioRxiv 2019). This selection, that is highly correlated with nutrient concentrations, 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 of marine microbes, 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. I will present this strategy for mining marine microbiome samples for novel bioremediation genes by studying purifying selection in protein-coding sequences.

Monday, 3/2/2020, 13:00 – 14:00, Auditorium

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