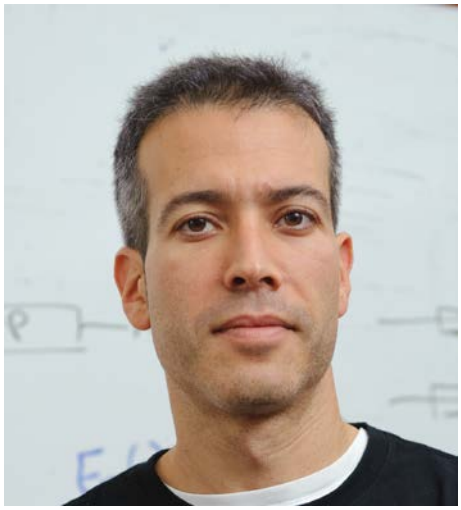
‘Special’ Seminar
Wednesday, April 25, 2018
12 noon, Mudd 100



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‘Personalizing treatments using microbiome and clinical data’

Accumulating evidence supports a causal role for the human gut microbiome in obesity, diabetes, metabolic disorders, cardiovascular disease, and numerous other conditions. I will present our research on the role of the human microbiome in health and disease, aimed at developing personalized medicine approaches that combine human genetics, microbiome, and nutrition.

In one project, we tackled the subject of personalization of human nutrition, using a cohort of over 1,000 people in which we measured blood glucose response to >50,000 meals, lifestyle, medical and food frequency questionnaires, blood tests, genetics, and gut microbiome. We showed that blood glucose responses to meals greatly vary between people even when consuming identical foods; devised the first algorithm for accurately predicting personalized glucose responses to food based on clinical and microbiome data; and showed that personalized diets based on our algorithm successfully balanced blood glucose levels in prediabetic individuals.

Using the same cohort, in another project we studied the relative contribution of host genetics and environmental factors in shaping human gut microbiome composition. Notably, although our cohort consists of individuals from several distinct ancestral origins who share a relatively common environment, we found no association between microbiome and genetic ancestry. In contrast, we show that over 20% of the gut microbiome variance can be explained by environmental factors related to diet, drugs and anthropometric measurements. We further show that 24-36% of the variance of several human traits and disease risk factors can be explained by the microbiome even after accounting for the contribution of human genetics. These results suggest that human microbiome composition is dominated by environmental factors rather than by host genetics.

Finally, I will present an algorithm that we devised for identifying variability in microbial sub-genomic regions. We find that such Sub-Genomic Variation (SGV) are prevalent in the microbiome across multiple microbial phyla, and that they are associated with bacterial fitness and their member genes are enriched for CRISPR-associated and antibiotic producing functions and depleted from housekeeping genes. We find over 100 novel associations between SGVs and host disease risk factors and uncover possible mechanistic links between the microbiome and its host, demonstrating that SGVs constitute a new layer of metagenomic information.