Combi Seminar

Wednesday, 2.28.18 | 1:30 | Foege Auditorium

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"Towards a highly efficient diversity census of the microbial biosphere: a group testing approach"

Abstract:

Exploring the microbial biosphere has grown exponentially in recent years, although we are far from understanding its entirety. We present the "diversity census" problem of exploring all species in a large cohort of specimens, and detecting a specimen that contains each species. The naive approach to this problem is to sequence each specimen, thus requiring costly sample preparation steps.

We suggest an orders of magnitude more efficient approach for diversity censusing. Specimens are pooled according to a predefined design and standard sequencing is performed over each pool. For each species, from the ultra-rare to the most common, the algorithm detects a single specimen that contains the species. The approach can be applied to large cohorts of monomicrobial cultures or to complex samples containing a mixture of organisms. The approach can be applied to create a comprehensive repository of biological samples covering the natural repertoire of a specific genotype, *e.g.*, detect samples that contain all variants of a certain pathogen, or samples that contain each allelic variant of a specific gene.

We model the experimental procedure and show via *in silico* simulations that the approach enables censusing more than 95% of the species while taking 10-70 fold less resources. Diversity censusing presents a novel problem in the mathematical field of group testing that may also be applied in many biological problems and in other domains.

Joint work with Bar Shalem and Ely Porat from Bar-Ilan University, and Amnon Amir from UCSD.