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Dynamic processes of the microbiota - from metagenomics to biofilms

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The extent, origin, and impact of microbial diversity is a central question in biology. We expect that physical processes contribute to this diversity, but we are only beginning to explore the nature of these interactions. I will briefly discuss two approaches to this question, one based on metagenomics the other on observation of bacterial biofilms. First, I will address the challenge of identifying the constituents of microbial systems by presenting a new approach to analyzing community sequencing data that identifies microbial subpopulations while avoiding problematic clustering-based methods. Using data from a time-series study of human tongue microbiota, we were able to resolve within the standard definition of a "species" up to 20 ecologically distinct subpopulations with tag sequences differing by as little as one nucleotide (99.2% similarity). This fine resolution allowed us decouple sequence similarity from dynamical similarity, and to resolve dynamics on multiple time scales, including the slow appearance and disappearance of strains over months. Second, I will present recent results on the growth and competition of bacteria within biofilms. We imaged the growth of *living* biofilms of *Vibrio cholerae* from single founder cells to ten thousand cells at single cell spatial resolution and with temporal resolution of one cell cycle. We discovered a transition from a branched 2D colony to a dense 3D cluster, in which cells at the biofilm center exhibit collective vertical alignment and local nematic packing. Our results suggest that biofilm cells exploit mechanics to simultaneously achieve strong surface adhesion, access to 3D space, resistance to invasion, and dominance over surface territory.