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Visualizing the response of a gut bacterial population to antibiotic perturbations BRANDON SCHLOMANN, Department of Physics, University of Oregon, TRAVIS WILES, KAREN GUILLEMIN, Institute of Molecular Biology, University of Oregon, RAGHUVEER PARTHASARATHY, Department of Physics, University of Oregon — Each of our intestines is home to a vast ecosystem composed of trillions of bacteria in a dynamic environment. Bacterial communities face fluctuations in nutrient influx, invasions by new microbes, physical disturbances from peristalsis, and, perhaps, the arrival of antibiotic drugs. Metagenomic profiling has shown that antibiotic treatments can cause major changes in the composition of species present in the gut, at timescales shorter than a day. How this happens is unknown, as these dynamics have never been observed directly. I'll present recent work that addresses this by using well-defined microbial communities in a model organism, the zebrafish. Light Sheet Fluorescence Microscopy is used to image a commensal species of *Vibrio* responding to antibiotic perturbations in the guts of live, larval fish. We find that sub-lethal concentrations of different classes of antibiotics induce similar physical responses in *Vibrio*, namely filamentation and reduction of motility. The arrested bacteria then aggregate and can be ejected via peristalsis, resulting in large population collapses. These observations suggest that antibiotics can cause large disruptions to gut ecosystems even in low concentrations, and that physical processes may be important drivers of response dynamics.

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