

Drug Resistance Evolution in Spatially Structured Populations

Jona Kayser

University of California, Berkeley, USA

Abstract:

For many naturally occurring populations, ranging from microbial biofilms to solid tumors, it has been argued that their spatial organization can drastically influence their evolutionary dynamics. This is especially relevant in the context of adaptation to deteriorating environments, such as antibiotic or chemotherapeutic attacks, where the emergence of resistant clones can lead to treatment failure. Comparing results from whole-genome sequencing of microbial colonies to those obtained from well-mixed cultures, I will show that spatial structure considerably promotes the emergence of large clones. Introducing a newly developed microbial model system, featuring trackable engineered mutations with tunable fitness effects, I will demonstrate how the underlying evolutionary dynamics result in spatial trapping of the majority of mutant clones and how secondary driver mutations can lead to their escape. Finally, I will discuss the potential of multi-recombinase strategies and CRISPR/Cas9 technology to extend the current assay and speculate on the consequences of our results for the mitigation of drug resistance evolution.

Friday, April 8th, 2015, 13:00

Room PH 127