



University
of Basel

Department
Biozentrum



Basel Computational Biology Seminar

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High-resolution dynamics of lineage diversity during adaptation to weak antibiotic pressure

Tracking low-frequency lineages in large microbial populations is key to fully elucidating their evolutionary dynamics, especially for weak selection pressures and short time scales. However, resolution is often limited by methods for labeling lineages or whole-genome sequencing. To overcome this challenge, we introduce a large library of random DNA barcodes into *E. coli*, allowing us to track lineages down to tens or hundreds of cells. We demonstrate the utility of this method by subjecting barcoded populations to serial passaging over ~420 generations in the presence of sub-inhibitory concentrations of common antibiotics. High-resolution analysis of the barcoded lineages reveals that each antibiotic regimen exhibits a unique pattern of lineage diversity loss, suggesting different adaptation dynamics. The relative contribution of standing genetic variation and de novo mutations also varied. Our results demonstrate the power of low-frequency barcoding in the study of bacterial evolution..

Date: **Monday, February 18th, 2019**
Time: **16:00 h**
Room: **Lounge, level E13, Klingelbergstrasse 61**
(vis-à-vis Pharmazentrum)
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