Contribution ID : **3** Type : **not specified**

Hands-on activities in groups

Tuesday, 9 September 2025 14:00 (2:30)

Content

Hands-on 1 **Image-based analysis of drug-induced cell competition dynamics** Luca Braga, Giannino del Sal

Cell competition is increasingly recognized as a critical mechanism shaping tissue homeostasis, tumor evolution, and therapeutic response. In the context of cancer, pharmacological pressure can shift the balance between competing cell populations, selectively promoting survival or elimination based on genotype-specific vulnerabilities. Participants will be introduced to the principles and basic techniques of cell-based high-throughput functional screenings. These approaches will be applied to explore how different drugs modulate cell competition dynamics using fluorescence-based quantitative imaging. Participants will quantitatively analyze the interaction between two genetically distinct cell populations exposed to a panel of small molecules, focusing on how drug-induced shifts in proliferation or survival drive clonal dominance. By integrating time-lapse imaging with endpoint assays, the course aims to build a framework for interpreting competitive interactions as a functional and measurable readout of drug responsiveness. The program combines theoretical modules with hands-on activities in imaging, quantification, **and data interpretation.** Attendees will gain insights into how image-based approaches can be leveraged to investigate cell behavior in complex, heterogeneous systems.

Hands-on 2 **Exploring Metabolic Cross-Feeding in a Synthetic Pseudomonas Consortium** Vittorio Venturi, Mihael Špacapan

In this experiment, a synthetic consortium of two *Pseudomonas* strains is designed to degrade ferulic acid via a metabolically complementary pathway. Ferulic acid, a common phenolic compound in the rhizosphere, is initially degraded by *Pseudomonas* Strain A, which expresses key enzymes such as feruloyl-CoA synthetase and vanillin dehydrogenase to convert ferulic acid into vanillic acid. This intermediate is then utilized by *Pseudomonas* Strain B, which carries enzymes like vanillate O-demethylase and protocatechuate dioxygenase to further degrade vanillic acid into protocatechuic acid. Protocatechuic acid subsequently enters the β-ketoadipate pathway, ultimately feeding into central carbon metabolism via TCA cycle intermediates. The consortium reflects metabolic cross-feeding, with each strain performing a distinct step in the degradation pathway. Growth dynamics and substrate conversion can be monitored through OD_{600}, CFU counts, FACS and metabolite profiling (i.e. presence of ferulic and/or vanillic acid in the minimal medium), allowing inference on the interdependence, efficiency, and stability of this two-strain system under defined conditions.

Summary

Session Classification : notitle