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Hands-on activities

Wednesday, 10 September 2025 09:00 (8:00)

Content

Hands-on A Exploring Metabolic Cross-Feeding in a Synthetic Pseudomonas Consortium Vittorio Venturi (ICGEB), Mihael Špacapan (ICTP), William R. Shoemaker (ICTP) 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.

Hands-on B A primer on evolutionary inference from cancer sequencing datasets Giulio Caravagna, Riccardo Bergamini, Nicola Calonaci (University of Trieste) Understanding the evolutionary history of cancer is essential for interpreting its progression, therapeutic resistance, and clonal architecture. In this hands-on session, participants will be introduced to the fundamental concepts and practical tools used to infer evolutionary dynamics from sequencing data of human tumours. The session is designed for researchers with a background in quantitative methods and will combine concise theoretical introductions with guided exploration of real data. We begin by examining the types of sequencing data commonly used for evolutionary inference, focusing on variant allele frequencies (VAFs) and somatic copy number alterations (CNAs). Participants will learn to process variant calls and CNA files to derive inputs for downstream analysis and visualise the mutational landscape of tumours through interactive plots. Building on this foundation, we will explore methods for clonal decomposition using unsupervised learning tools. Attendees will utilise clustering algorithms to identify clonal populations. We will then use these to reconstruct evolutionary models, introducing core principles such as the clonal evolution model and the distinction between trunk and branch alterations. During this session, we will also make use of a synthetic tumour growth model, which will allow students to simulate a solid tumour that grows in space. The session will include a discussion of common pitfalls, limitations of current models, and suggestions for further exploration. Participants will leave with a set of notebooks and tools that can be readily adapted to their research, as well as a practical understanding of how to extract evolutionary insights from cancer sequencing datasets.

Summary

Session Classification : notitle