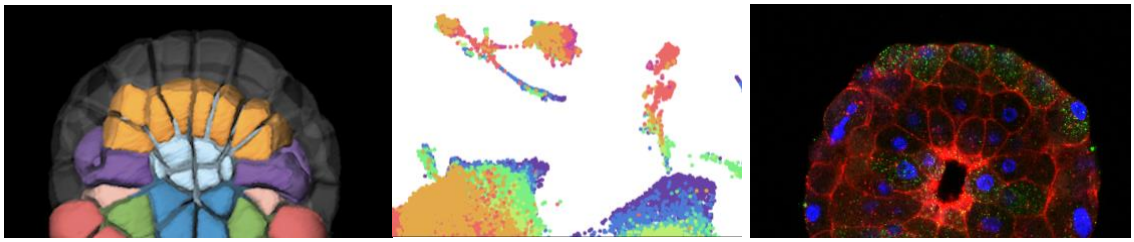

Construction of a provisional gene expression to phenotype map for embryonic development

A funded 3-year PhD project to be carried out in the Tunicate team of the Centre for Research in cell Biology of Montpellier (CRBM, Montpellier, France)

Context

The embryonic development of ascidians, a group of marine invertebrates, is remarkably invariant, at the single cell level, between individuals of a given species and between species, even if they diverged up to 400 MY ago (Lemaire, 2011). Ascidian genomes, however, evolve particularly rapidly. To understand this paradox, we are combining experimental, mathematical and physical approaches to explain the remarkable precision and evolutionary stability of ascidian embryonic morphologies (e.g., Guignard, Fiuza et al., 2020).

Main aims

The aim of this interdisciplinary developmental biology PhD project is to explore the natural variation in quantitative gene expression profiles across individuals of a given species and between species, and to relate this variation to changes in embryonic morphological phenotypes.

The selected PhD candidate will first adapt and develop experimental methods to construct individually- and spatially-resolved transcriptomics atlases of embryogenesis in several ascidian species, using multiplexed scRNA-seq (e.g., Saunders et al., 2022, Gehring et al., 2020), followed by a reconstruction of the spatial position of each sequenced cell back onto the embryo (e.g., Satija et al., 2015, Nitzan et al., 2019, Moriel et al., 2021). The accuracy of these atlases will be assessed using single-molecule fluorescent in situ hybridisation (smFISH) (Choi et al., 2021) of spatially/functionally informative genes (Melton and Ramanathan, 2021).

In collaboration with the team's partners, she/he will then explore different statistical approaches to identify gene sets potentially involved in the cell-autonomous or intercellular control of morphogenesis. For instance, the expression of cell-autonomous morphogenetic regulators is expected to prefigure major morphogenetic transitions, while gene sets involved in intercellular morphogenetic control are expected to show statistically-correlated expression between neighbouring cells across individuals and/or species.

This descriptive statistical approach will be complemented by an analysis of the morphogenetic consequences of quantitative perturbations (sublethal doses of morpholinos or pharmacological inhibitors) of the function of some of the identified genes.

Profile and skills required

We welcome applications from highly motivated candidates in search for an interdisciplinary environment at the crossroads of experimental biology, computer science and statistics. Statistical analyses will be carried out in tight collaboration with the statistical physics lab of Prof. Madhav Mani in Evanston, USA and the French computer science labs of Dr. Grégoire Malandain in Sophia Antipolis and of Dr. Emmanuel Faure in Montpellier.

Ideal candidates are young scientists holding a **master's degree in molecular genetics, cell and developmental biology or bioinformatics, with a strong interest for methodological developments in single cell omics**. Knowledge in the statistical analysis of large datasets would be a plus. Our team has an equal opportunities employment policy.

Application procedure

Interested students should contact Dr. Patrick Lemaire (patrick.lemaire[at]crbm.cnrs.fr) at their earliest convenience and before July 1st 2023 by sending a detailed CV, a motivation letter for the project and the names of 2 academic referees. The position will remain open until filled. Starting date is September 1st, 2023.