Image-based perspective of morphogenesis: from individual to population

The goal of this project is to study and quantify the development variability in ascidian embryos.

On the one hand, the embryo development may be highly reproducible (ie stereotyped) within one given species: in some of them, cells can be even unambiguously named through the whole development (e.g. C. elegans) or during the first stages of the embryogenesis (e.g. ascidians [Lemaire 2011]). Such models are then highly attractive for developmental studies. On the other hand, current live microscopy techniques allow the acquisition of temporal sequences of 3D images with a spatio-temporal resolution high enough to follow embryo development at sub-cellular scale [Keller, 2013]. Among them, the light sheet microscopy [Krzic, 2012] allows to image developing embryos of ascidians from the very early stages to the gastrulation stage. It offers an unique opportunity to not only study the development of individuals but also to study the development variability within a population.

A first study [Guignard, 2020] has already permits to extract cell characteristics and lineages for a dozen of embryos (of wild type ascidians), each acquisition being made of more than a hundred of 3D images. In addition, cells can be named in the first developmental stages, based on [Conklin, 1905]. Unpublished results demonstrate a strong reproducibility of cell naming with respect to geometrical (cell position), and topological (cell neighbourhood) considerations. This suggests that cell naming can be learnt from exemplars.

The goal of this thesis is to investigate several questions:

1. How stereotyped is the embryo development? First, at the cell level, geometrical and topological variability has to be quantified. It has been noticed (unpublished results) that some cells exhibit different division orientation between embryos. Characterization and recognition of such different division patterns will also be of great interest. Second, at the tissue (group of cells having the same fate) level: is the variability intra-tissue different from the variability inter-tissue? Third, at the embryo level, how can be the inter-individual variability quantified?
2. From the question #1, automated naming schemes can be proposed and investigate, to get ride from user intervention. How to deal with different division patterns at this stage should also be addressed.
3. Still from question #1, could be build an average developing embryo, and/or recognize different developmental schemes within a database of developing embryo?
4. From above questions, could we leverage the development stereotypy to guide the segmentation of an embryo image sequence, so as to minimize manual curation?
5. Last, but not least, naming from exemplars is limited by the names to be found in the exemplars (generally not exceeding the 10^{th} generation). However, some of them are imaged beyond this 10^{th} generation: can automated naming rules, consistent with Conklin's rules, be proposed to further name these embryos?

This thesis will take place within a collaboration between P. Lemaire's lab (CRBM, Montpellier) and Morpheme team (I3S/INRIA, Sophia-Antipolis), and will be located in Sophia-Antipolis. The ideal candidate must have a master degree in computer science, mathematics or physics, with an interest in developmental biology, or may have a master degree in biology with a strong knowledge in computer science and/or mathematics. S/he should have skills in several of the following areas: Image Processing and Analysis, Data Sciences, and Machine Learning. S/he should be proficient in programming in C/C++ and Python languages. Previous experience in biological or medical imaging will be considered as an asset.

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