# DOCTORAL POSITION AT THE UNIVERSITY CÔTE D'AZUR

## 4D MORPHOMETRIC STUDY OF CELL AND TISSUE SHAPE CHANGES TO COMPUTATIONALLY UNRAVEL THE PROCESS OF SEA URCHIN EMBRYO GASTRULATION

Computational morphometric analysis has become an essential tool in modern biology to better understand how cell and tissue change shape during embryo development. Therefore, exciting collaborations among computer scientists and biologists have arisen to pierce the mystery of how life take shape. In recent years, new microscopy techniques (e.g., SPIM) have enabled the digital image acquisition of developing embryos with unprecedented 3D spatial and temporal resolution allowing a fine reconstruction of all the morphogenetic processes concurring to shape the embryo [1].

The acquisition of 3D+t high resolved image series results in huge amount of data (also referred to as BIG data sets). Basic image processing approaches fail to provide the necessary tools for multi-dimensional image analysis. We have developed sophisticated image analysis tools to extract multi-dimensional information from BIG data sets [2]. Our image analysis tools were successfully applied to embryos constituted of tens of cells [3]. Very recently, in a joint collaboration between the Morpheme team and the Rauzi team, this computational tool has been extended to temporal 3D image series of the developing sea urchin embryo constituted by more than 1000 cells. These BIG data sets together with our image analysis tools give access for the first time to detailed morphometric information of shape changes of each single cell (tracked over time in 3D) forming the sea urchin embryo [4].

We are at present interested in better understating the mechanisms driving gastrulation in the sea urchin embryo. During this developmental phase, the tissue located at the vegetal pole buckles initiating gut formation. Such changes in tissue shape are driven by stereotypic cell shape and topological changes. The goal of this doctoral project is to characterize in 4D the cell shape/topology and cytoskeletal protein variations, and to perform cell population analysis to eventually unveil the key stereotypic processes driving tissue buckling.

We are seeking a very motivated and talented candidate with advanced expertise in computer science, mathematics or physics. We expect the candidate to have skills in several of the following fields: 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.

Applicants must send as soon as possible a CV, a statement of interest, and 2 or 3 reference letters to Grégoire Malandain (gregoire.malandain@inria.fr) and to Matteo Rauzi (matteo.rauzi@univ-cotedazur.fr).

**Deadline: 17th of May 2020**

Location: Inria-I3S Morpheme team, I3S, Sophia-Antipolis, France

*[1] PJ Keller, "Imaging Morphogenesis: Technological Advances and Biological Insights," Science, vol. 340, no. 6137, pp. 1234168+, June 2013. [2] R Fernandez, P Das, V Mirabet, E Moscardi, J Traas, JL Verdeil, G Malandain, and C Godin, "Imaging plant growth in 4-d: robust tissue reconstruction and lineaging at cell resolution,"Nat Meth, vol. 7, pp. 547–553, 2010.*
*[3] Guignard, L., Fiuza, U.-M., Leggio, B., Laussu, J., Faure, E., Michelin, G., Biasuz, K., Hufnagel, L., Malandain, G., Godin, C., and Lemaire, P. (2020). Contact-area dependent cell communications and the morphological invariance of ascidian embryogenesis. Science, accepted for publication.*
*[4] Moullet, A. (2020) "Automated segmentation of sea urchin embryos", Ms thesis.*

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