Master Internship Offer

Machine learning for the geometrical identification of landmarks in shoot apical meristem images

Laboratory	**Inria Team Mosaic, Reproduction & Développement des Plantes, ENS de Lyon**
Duration	**6 months**
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Keywords	**Machine learning, 3D geometry, developmental biology, plant biology**
Tools	**Python, numpy, pandas, scikit-learn, jupyter**

General Context

In flowering plants, most of the development takes place post-embryonically as the aerial organs (leaves and flowers) are successively formed over the lifetime of the plant. In a large number of species, these organs arrange into strikingly regular, often spiraling patterns. This patterning process called **phyllotaxis** can be traced back to the activity of a small niche of stem cells located at the tip of the growing stem: the **Shoot Apical Meristem** (SAM).

Using the model plant species *Arabidopsis thaliana* we study how these patterns are created by looking in detail at the formation of new organs. They actually emerge as **primordia** (groups of differentiating cells) in a very specific zone of the SAM, at the periphery of the undifferentiated **central zone** (CZ). The primordia appear with a very regular timing and at spatial locations distant from a nearly constant angle. This strong spatio-temporal periodicity gives very interesting self-similarity properties to the system, and due to this, SAMs tend to present a high level of inter-individual similarity. The idea is to take advantage of this shape similarity to align different individual SAMs imaged using confocal microscopy onto a **common reference frame**. There, all individuals should superimpose almost perfectly, which makes it possible to perform population-scale statistics on quantitative measures of development.

The Problem

In a previous work (Galvan-Ampudia & Cerutti *et al.*, 2020), such an alignment could be performed by identifying key landmarks on the surface of the SAM, based on which it is possible to compute a geometrical transformation mapping the individual onto the common reference:

- The center of the meristem
- The main vertical axis of the meristem
- The lastly initiated primordium

However in this work, landmarks could only be identified through the use of genetically encoded fluorescent markers: the *CLV3* transcriptional reporter of CZ cells (Figure 1a-b) and the *qDII* ratiometric auxin biosensor (auxin accumulation being the earliest known marker of organ initiation). And it is still a challenge to perform the same kind of alignment on plants that have not been genetically modified to express the necessary reporters.

The aim of this project would be to answer the following question: can we **learn** how to position these landmarks based only on **invariant geometrical cues**, such as surface curvature (Figure 1c), geodesic distances or local symmetries, using the existing dataset where both geometry and reporter information is available.

In a first time, the main objective would be to design a method based on geometrical information to **identify the meristem center** using the existing *CLV3* data, where the position of the center has been determined, to systematically validate the method. A secondary objective would be to investigate if the same kind of method could be used to identify the other landmarks.

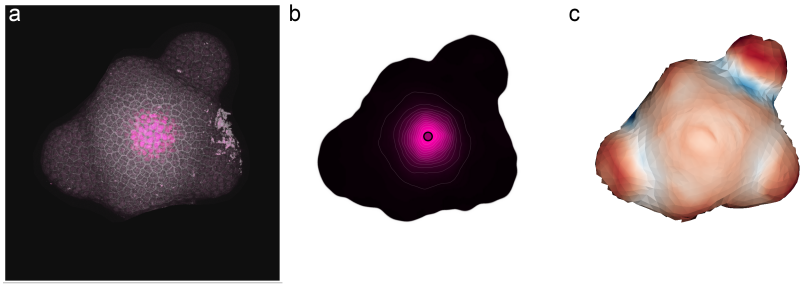

Figure 1: Identifying landmarks on shoot apical meristems. (a) Confocal microscopy image of a shoot apical meristem expressing the CLV3 reporter of CZ cells. (b) A continuous representation of the CLV3 signal allows to position very precisely the center of the meristem, a key landmark to perform SAM registration. (c) In lack of genetic information, could geometrical information (such as the mean curvature of a SAM surface triangular mesh) be sufficient to identify this landmark?

Considered Approach

The existing data consists of several 3D image sequences where the levels of the CZ reporter *CLV3* have been quantified and the meristem center has been identified (as a 3D point in image physical coordinates). On these images, we also extracted a certain number of geometrical features, using notably a 3D triangular mesh reconstruction of the SAM surface. Existing machine learning methods could be tested to predict the probability of each vertex of this mesh to be the meristem center, considering a set of geometrical features computed on this vertex as input. Via a cross-validation study over the available dataset, the idea would be to test if such an agnostic method can lead to a reliable identification of the meristem center. The geometrical information could be extended with additional features computed on the surface mesh, if necessary. Other methods relying more directly on the image signal could also be considered.

Expected Outcome

Such a method would be of great interest, as it can potentially be applied to all the confocal images of meristems where it is possible to extract the geometry of the meristem surface. Combined with other algorithms that identify the rest of the necessary landmarks, it would allow a robust alignment of virtually any SAM image onto a common reference frame. This would constitute the first step towards building an automatic tool to aggregate quantitative data from various experiments into a computational atlas of SAM development.

References

Galvan-Ampudia C., Cerutti G., Legrand J., Brunoud G., Martin-Arevalillo R., Azais R., Bayle V., Moussu S., Wenzl C., Jaillais Y., Lohmann J., Godin C., Vernoux T.: **Temporal integration of auxin information for the regulation of patterning**, *eLife*, 2020.