

# An Interactive System for Analyzing Plant Embryo Cell Division

Jiayi Hong\*  
Université Paris-Saclay,  
CNRS, Inria, LRI, France

Ferran Argelaguet\*  
Inria, Univ. Rennes,  
CNRS, IRISA, France

Alain Trubuil†  
Université Paris-Saclay,  
Inrae, France

Tobias Isenberg\*  
Université Paris-Saclay,  
CNRS, Inria, LRI, France

## ABSTRACT

We provide an interactive system for biologists to assist them in analyzing the development of plant embryos. With this tool they could reconstruct the development history of an embryo, based on a single segmented 3D image from the confocal microscopy. Compared to their traditional manual procedure, our approach supports reasoning about the development of both wild type and mutant plant embryos. For this purpose we use reconstructed surface models of the individual cells, allow the researchers to interactively assign sister cells per development cycle, and complete an inheritance tree. In addition to this manual assignment, we also add an automatic assignment based on the area of the cell interfaces (shared surfaces between cells). For the interactive assignment or correction, we explore different selection strategies of the cells in the dense dataset.

**Index Terms:** Human-centered computing—Visualization—Visualization systems and tools

## 1 INTRODUCTION AND BACKGROUND

A correct history of the cell division of a given plant embryo can help to understand the embryo’s development, in particular when trying to understand the differences between wild type and mutant embryos. For this purpose, plant biologists use a confocal microscopy to get a 3D dataset of the embryo’s state at a given time, segment this dataset, and then manually derive the inheritance of the cells. They do so by analyzing neighboring cells and, using their expertise, the visual depiction, and data such as the area of the interface (i. e., the shared surface between two cells) to determine the children cells which divided from the same parent cell. They continue this process until all cells have been assigned to sisters, and then continue this process in the next hierarchy level until the complete tree is derived. While this process is simple for small embryos, practical datasets containing 100 to 200 cells or more will make this process tedious. Moreover, traditionally they need to use several tools such as Avizo, Fiji, and OsiriX at the same time for the analysis.

We are working to assist with this process by creating a single system that supports the inheritance analysis. For this purpose, we combine a 3D visualization of the embryo with abstract data about the cells, interactive navigation and selection techniques. The challenges in this project arise from the unique properties of the datasets: practical cases contain numerous cells (100–200 and more) which are densely packed in 3D space, and dedicated selection techniques are needed. Moreover, we also face the challenge of having to combine 3D visualization with the visualization of abstract data properties and the hierarchical development tree.

In previous work, researchers have visualized cell data to help biologists get knowledge about cell development [3, 6], but they did not cover to our knowledge the cell division process. For example, MorphoNet [4] visualizes diverse cell data on a website and allows biologists and others to visually explore cell shapes. However, the tool is mainly a combination of live-imaging techniques and its selection process is slow. Also, this work has mainly focused on computational approaches that calculate cell-related information. For the inheritance analysis, however, the most fundamental

step is to accurately pick the target cell, based on our discussions with plant biologists. Nonetheless, traditional 3D object selection techniques like ray-casting [1, 2] are not applicable in this scenario because the plant embryo datasets, while consisting of dedicated elements (the cells), are too tightly packed with virtually no space in-between. Moreover, the specific application requires the biologist to correctly identify and select the target cell, as opposed to selecting an approximate neighborhood of cells.

## 2 INTERFACE DESIGN

We started by analyzing the traditional approach that the biologists take to derive the inheritance tree. For each target cell, they traverse all of its neighboring cells analyzing the shared surfaces, area between the neighbor and target cell, and the relative position of the cell in the whole embryo. Based on their expertise, they then make a decision and mark the cells as sisters. To support this process in our tool, we thus provide three techniques to discover and select target cells, four views to list all the neighbors of the target cell, as well as provide additional information such as the area of the interfaces.

### 2.1 Graphical Interface

Our graphical interface contains four views: the main view, the tree view, a neighbor list view, and a cross-section view (see Fig. 1(a)). The main view provides the 3D visualization of the whole plant embryo and allows the biologists to interact with it using traditional 3D navigation techniques such as panning, rotating, and scaling. Next, the tree view records information including all cell names and the user’s assignment, and supports interaction such as left-click selection and right-click special operations. By keeping assigning, they could see the hierarchy tree developing in the tree view. The operation menu of the tree widget also allows the biologists to add tags to the cell for further analysis (e. g., external and internal cells). They can also permanently hide cells such as those that do not belong to the embryo (called the suspensor). Then, the neighbor list will present all the neighbors of the target cell as its name indicates. Hovering on the neighbors gives a preview of the two cells merging together, while selecting one neighbor will display the target cell, selected neighbor cell and their shared area. Finally, we added a cross-section view to allow the biologists to analyze the internal structure of the embryo without needing to manipulate the spatial arrangement of the cells. All these elements are linked to each other so that one can use them in the cell assignment process.

### 2.2 Selection Techniques

To better support the biologists in the cell assignment, we explored and implemented three different selection techniques for precisely selecting a target cell. The challenge, as noted before, is the dense packing of the cells and the resulting occlusion of internal cells. Traditional ray-pointing or picking techniques cannot be used directly.

Thus, we firstly support selection by means of list items as shown in the tree view and in the neighborhood list view. This method has the advantage that all cells are immediately accessible (i. e., not subject to occlusion by other cells), albeit requiring much scrolling in the lists for larger embryos. Moreover, this approach does not show information about the relative positioning or the spatial properties of the cells, aside from the numerically derived data that is shown.

\*e-mail: {jiayi.hong | ferran.argelaguet | tobias.isenberg} @inria.fr

†e-mail: alain.trubuil@inrae.fr

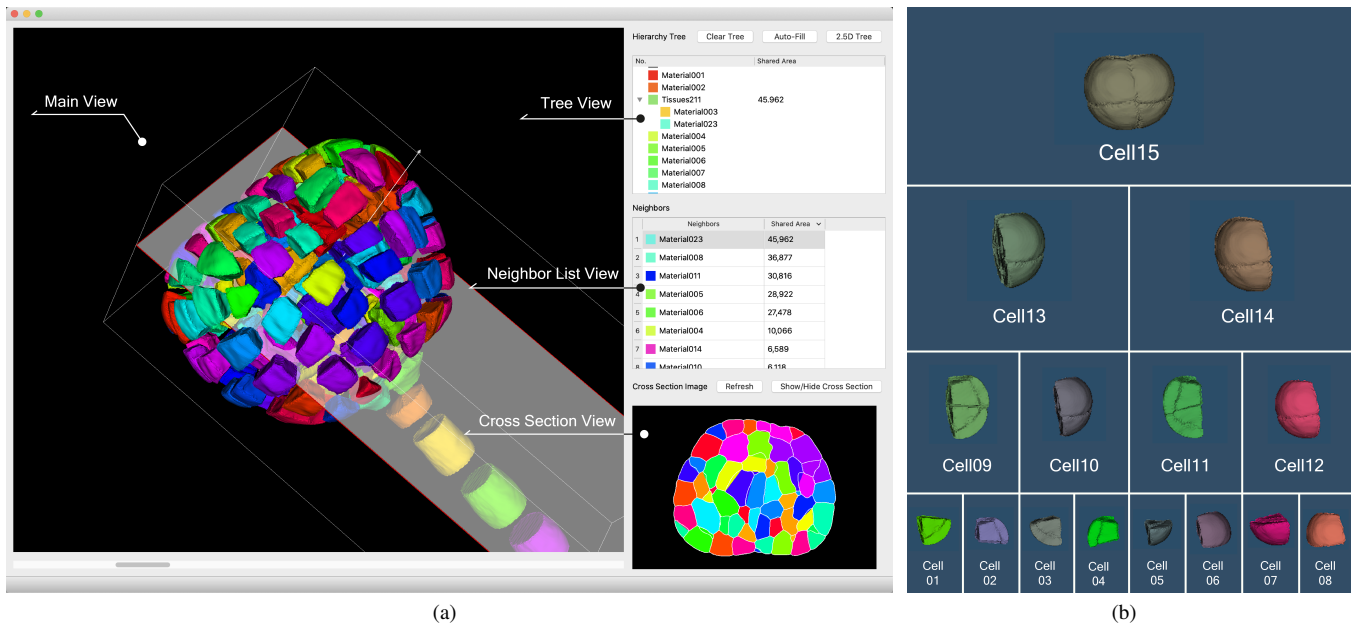


Figure 1: Our system: (a) the main interface and (b) the hierarchy tree for 8-cell embryo.

We thus also explored spatial selection. To be able to deal with the occlusion in the dense dataset, we implemented an explosion selection method that uses exploded view depictions for 3D models based on traditional illustration [5, 7]. Using a slider, the user can control the degree of object separation and thus make the individual cells accessible for selection (exploded view shown in Fig. 1(a)).

As a last technique, we also allow the biologists to select cells in the cross-section view. They are free to re-arrange the cutting plane as needed by manipulating the 3D coordinate axes in the main view. The intersection of the embryo with the cutting plane will show in the cross-section view. In this way, biologists could easily access the enclosed inside cells.

### 2.3 Hierarchy Tree

Based on biologists' working preference, we added a hierarchy tree to provide an overview of the assignment. To demonstrate the development of the embryo, we created a 2.5D hierarchy tree that uses the assignment structure as well as 3D renderings of the given tree node sub-elements as shown in Fig. 1(b). All nodes are linked to each other such that rotating any cell in the hierarchy tree also rotates all the other cells accordingly.

### 3 DISCUSSION AND FUTURE WORK

In our current implementation, we support to locate the target cells, manually assign sisters and construct a hierarchy tree. The most fundamental step for biologists is to accurately select the target cell, and we are currently comparing the different selection techniques in a controlled experiment. From discussions with experts and own tests, we already found that the cross-section view is not ideal for selecting, but provides good neighborhood information.

To test the whole cell classification system, we also invited one plant biologist to use it. He stated that our system works great in organizing the information and assists him in analyzing the development of an embryo with numerous cells. He also stated that it could be improved by applying machine learning to help him with the decision making, rather than marking cells manually. In this way, the decision time could be largely reduced. Our next steps will thus include conducting an observational study of this tool in

use to investigate the performance of the system, especially in assisting to study differences between wild type and mutant embryos. Second, we plan to provide the automatic suggested construction of the hierarchy tree by machine learning to help the propagation of decisions and accelerate cell assignments. Finally, we plan to refine the whole interaction for biologists to intuitively build the tree by these two approaches (manual assignment and assignment with machine learning).

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