Organogenesis is accomplished by a series of deformations which causes the planar cell sheet to form itself into a three-dimensional shape during embryogenesis. This drastic structural change is the integrated result of individual cell behaviors in response to spatio-temporally controlled mechanisms.

To better understand the programs underlying organ formation, it is necessary to quantitatively analyze individual cells’ morphology and dynamics. However, it is difficult to do so due to the massive size of the images generated by 4D microscopy as well as their ambiguity.

To unveil organogenesis from the point of view of distinct cell behaviors, we are developing application software that is capable of describing cell dynamics from 4D time-lapse imaging data sets by employing image processing techniques.

I. 4D cell segmentation/tracking system

Epithelial morphogenesis in developing embryos is considered to be an important model for collective cell migrations. Drastic cell rearrangements lead to drastic structural changes in building elaborate organs such as the tubular network of Drosophila trachea. To observe this, we are developing a software pipeline which will automatically recognize individual cell shapes out of 3D space and tracks them through time. This system extracts cell boundaries and reconstitutes cell shapes in the form of a skeletonized chain of voxels spanning 3D space. This abstract form of cell visualization makes it possible to describe morphometric quantities and kinetics of cells at a single-cell resolution (Figure 1). These morphometric quantities allow us to perform comparative studies on shapes and behaviors more precisely under several experimental conditions to gain a better understanding of the genetic programs underlying organogenesis. We are now applying this system to several experimental models to determine the practicality of the system (Shinoda et al.).

II. Image processing pipeline for 3D cell culture

To elucidate the relationship between mechanical forces underlying the tissue deformation out of large-scale imaging data, we have developed an image processing pipeline for 3D+T imaging datasets.

This pipeline is able to automate a segmentation/quantification process for a large number of images acquired under several experimental conditions for subsequent statistical analysis in addition to building a database of acquired quantities as its final output.

III. Software for manual image quantification

Biologically significant imaging features are not always significant to computational algorithms due to their structural instability. This level of difficulty requires inspection conducted by human eyes to extract features from the images gleaned. To simplify this, we have developed a GUI (Graphical User Interface) application which can easily visualize 4D imaging data and has made manual feature annotations easier (Figure 2).

This application is freely available at our website (https://bioimageanalysis.jp/).

Publication List:

[Original papers]