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11:00-12:00, 7F Seminar Room, DB Building A

Objective identification of homogeneous regions inside heterogeneous tissue

Summary

Within developing tissues, cell proliferation, cell motility, and other cell behaviors vary spatially, and it results in variability of tissue local deformation, giving a complexity of the morphogenesis.

Recently, novel formalisms have been developed to quantify epithelial tissue local deformation and underlying cellular processes. However, many tissues were found to be heterogeneous but without obvious boundary between such regions, leaving analysis limited to arbitrary regions drawn as a grid parallel to tissue axes, or regions expressing already known differentiation maker genes. Therefore, a major challenge for the study of morphogenesis now is to objectively define tissue sub-regions exhibiting different dynamics. Here we propose a method to automatically divide a tissue into regions where a given quantity of morphogenesis, such as local deformation or cell dynamics, is homogeneous. This was achieved by integrating several approaches including image segmentation, clustering, and cellular Potts model simulation. We illustrate the use of the pipeline using a large dataset obtained during the metamorphosis of the *Drosophila* pupal notum. Resultant sub-regions showed distinctive patterns of deformation and cellular processes with higher homogeneity than a conventional grid segmentation along tissue axes. Interestingly, the tissue segmentations based on the local deformation rate and on the cellular processes included some similar regions, suggesting that the cellular processes were regulated similarly inside the regions, and it resulted in unique tissue deformations. This pipeline will contribute substantially to the analysis of complex tissue shaping and the biochemical and bio-mechanical regulations driving tissue morphogenesis.