



Modeling tissues using CompuCell3D

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Modeling tissues with cellular and subcellular resolution requires clever representations of single cell complexity. Too much detail can saturate even most powerful computers while too simplistic approaches have usually limited predictive power. As it is usual in sciences the demands and capabilities are orthogonal to each other.

To solve simple cell-sorting problem, in 1992 Graner and Glazier [1] introduced cellular Potts Model (CPM) which currently is one of the most popular ways to model tissues, organs or even organisms with single-cell resolution. CPM represents cells as spatially extended domains and allows relatively faithful model representation of basic cellular behaviors such as adhesion, growth, death, mitosis, chemical secretion, absorption etc. Over the years CPM evolved to become one of the most popular methods used in single-cell-based tissue simulation.

In this talk I will present CompuCell3D (CC3D) simulation environment [2] that allows building running and testing CPM-based models of tissues. CC3D is an open source project with fairly rich set of tools that facilitate model construction, visualization and post-processing. CC3D has Python interpreter that gives modelers great flexibility in customizing their models without requiring code recompilation. In fact bulk of the typical CC3D model is written in Python. I will present brief demo of the CC3D package and conclude the talk by addressing most pressing software-related issues facing multi-cell tissue modeling community.

[1] Maciej Swat, Gilberto L. Thomas, Julio M. Belmonte, Abbas Shirinifard, Dimitrij Hmeljak, James A. Glazier (2012). "Multi-Scale Modeling of Tissues Using CompuCell3D," In Anand R. Asthagiri, Adam P. Arkin ed. *Methods In Cell Biology*, Vol 110, pp. 325-366.

[2] Francois Graner, James A. Glazier (1992). "Simulation of biological cell sorting using a two-dimensional extended Potts model," *Phys Rev Lett.* 69. p. 2013-2016.