Coupling Physical Models to the Epithelial Cell Differentiation

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DISCLAIMER

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We are making use of techniques from applied mathematics and physics to develop a computational model of a mammalian acinus that is based upon mechanical principles. In our simulation, individual cells are modeled as interacting poroelastic bodies, containing both solid-like and fluid-like phases. We will describe the solid-like phase in detail, where internal stresses can be computed by making use of a reference map, which tracks the amount of deformation of a cell from its initial undeformed state. Each cell has its own deforming boundary; correctly tracking multiple interacting boundaries is a computationally challenging problem, and we will demonstrate some results of recently developed numerical methods that address this. Our model is being compared against two different sets of experiments. First, we are comparing against force measurements of fully grown acini. Second, our results are being compared to three dimensional confocal microscopy images of acini development. As part of this work, we are developing image analysis algorithms to automatically extract features that represent deformations of the cell during the mitotic process. First, we process the hyperstacks using edge-preserving smoothing bilateral filtering, which enhances the contrast between marked structures and background fluorescence. Next, a statistical region merging (SRM) segmentation algorithm is responsible for recovering nuclear mass, for later measurement of volumetric descriptions of the cell. Our framework scales to GB hyperstacks, particularly by splitting the hyperstacks into smaller portions of data, based on the extra-cellular matrix identification, so each subset enclose one acinus. Future work includes identification of consistent segments of similar curvature, aimed at recovering nuclei individually or cell adjacency due to proximity-only or in-mitosis.

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