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# A 3D vertex model to map contraction patterns to epithelial shape and mechanics

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## Abstract

Epithelial tissues play key roles in the function of animal organisms. They usually consist of one or more layers of cells with a clear apico-basal polarization. Epithelia performing different functions during morphogenesis and physiology show a great diversity in form. Epithelial shape is thought to depend on the ability of the actomyosin cytoskeleton within cells to generate active forces, and for instance epithelial folding can result from apical constriction (1). However, we lack a quantitative understanding of the relation between contractility patterns and tissue shape. To address this question, a number of experimental systems have been proposed, including quasi-2D intestinal organoids, where cellular and tissue shape can be recorded along with tractions on the substrate (2). It is also possible to culture tissues of controlled footprint and induce contractility patterns in space and time using optogenetics (3). To analyze and understand these kinds of experiments, here we develop a 3D computational vertex model to simulate the effect of general active contractile patterns on cellular and tissue shape and on substrate tractions. After validating our implementation with simple examples where the outcome can be predicted analytically, we focus on patterned apical constriction. In a first study, we revisit a previous study in intestinal organoids (2), analyzing how the mechanical compartmentalization controls cellular pressure patterns, which in turn can affect the proliferation rate. In a second study, we identify the key model parameters that control the tissue-scale outcome of a localized pattern of apical constriction.

References:

(1): <https://doi.org/10.1242/dev.102228>

(2): <https://doi.org/10.1038/s41556-021-00699-6>

(3): <https://doi.org/10.1038/s41467-022-33115-0>

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