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Stress Controlled Analysis of Morphogenesis

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ABSTRACT

Although genetic pathways in *Drosophila melanogaster* embryo development have been thoroughly studied and determined, the mechanics underlying morphogenetic movements has not been well understood yet. Such an awareness motivated a study that led us to the finite element formulation of a first model in which we distinguished two types of deformation. Namely, the active deformations caused by the active forces acting in the epithelial tissue of the embryo (i.e. apical constriction and apical-basal elongation); and the passive elastic deformations of the epithelial cells [1]. The resulting kinematic model allowed us to perform a set of numerical experiments that led to the determination and classification of an ensemble of plausible mechanisms that can achieve realistic invagination of the ventral furrow in *Drosophila melanogaster* embryo [2] (see figure 1).

In this first model, the active deformations were considered as independent of the passive elastic ones, and were imposed by ad hoc parameters. Although this parametric set of local cellular behaviours permitted us to retrieve useful mechanical information, experimental evidence shows that gene expressions are also regulated by mechanical variables [3].

Moreover, the model only deals with purely elastic stress fields and therefore is path-independent and reversible. As a result, active forces must be maintained after the completion of mesoderm internalisation to prevent a complete reversal of the imposed movement. In contrast, cells are able to remodel their cytoskeletons dynamically, making embryonic tissues appear materially viscous.

In order to implement these features in the model, we have introduced a system of active elastic rods into the structure of the model (see figure 2a). In addition to the elastic deformation, the rods on the apical side of each cell unit (pink rods in figure 2a) can also undergo an active deformation $l_{\mathbf{A}}$ (lengthening if $l_{\mathbf{A}} > 0$, or shortening if $l_{\mathbf{A}} < 0$). However, in contrast to the continuum approach considered above, the active deformations of the rods depend now on their own elastic stresses σ according to the following evolution law:

$$\frac{dl_a}{dt} = \beta(\sigma - \sigma_f),$$

where β is a material parameter and σ_f is target stress value [4].

In order to mimic the remodelling of the cytoskeleton, stress relaxation of σ and the value $\sigma_f = 0$ may be considered, which is in agreement with the non-accumulation of elastic energy within the cell. The final deformation of each cell is determined by imposing the equilibrium of the elastic forces, arising from an elastic potential Π_{el} that is complemented with a constant volume constraint Π_{vol} within each cell unit (conservation of the volume of the cytoplasm). A set of preliminary numerical tests have shown that such an approach can reproduce two-dimensional invagination of the epithelium (see Figure 2b).

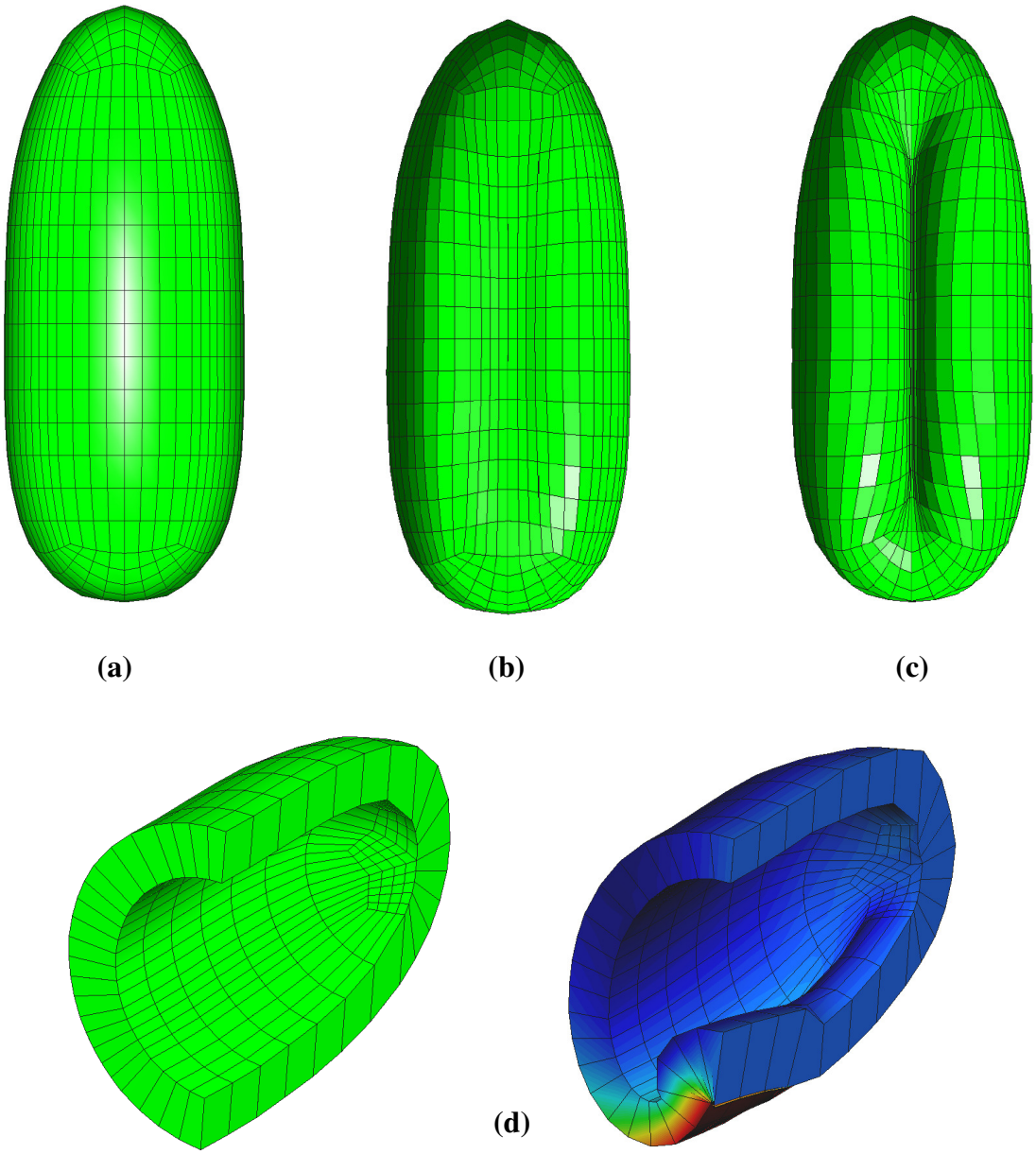

Figure 1. 3D analysis with the kinematic approach: Ventral view of: **(a)** the initial undeformed configuration, **(b)** an intermediate 3D deformation, **(c)** the final deformed configuration. **(d)** Cross-sections view, with contour plots of the circumferential Cauchy stresses.

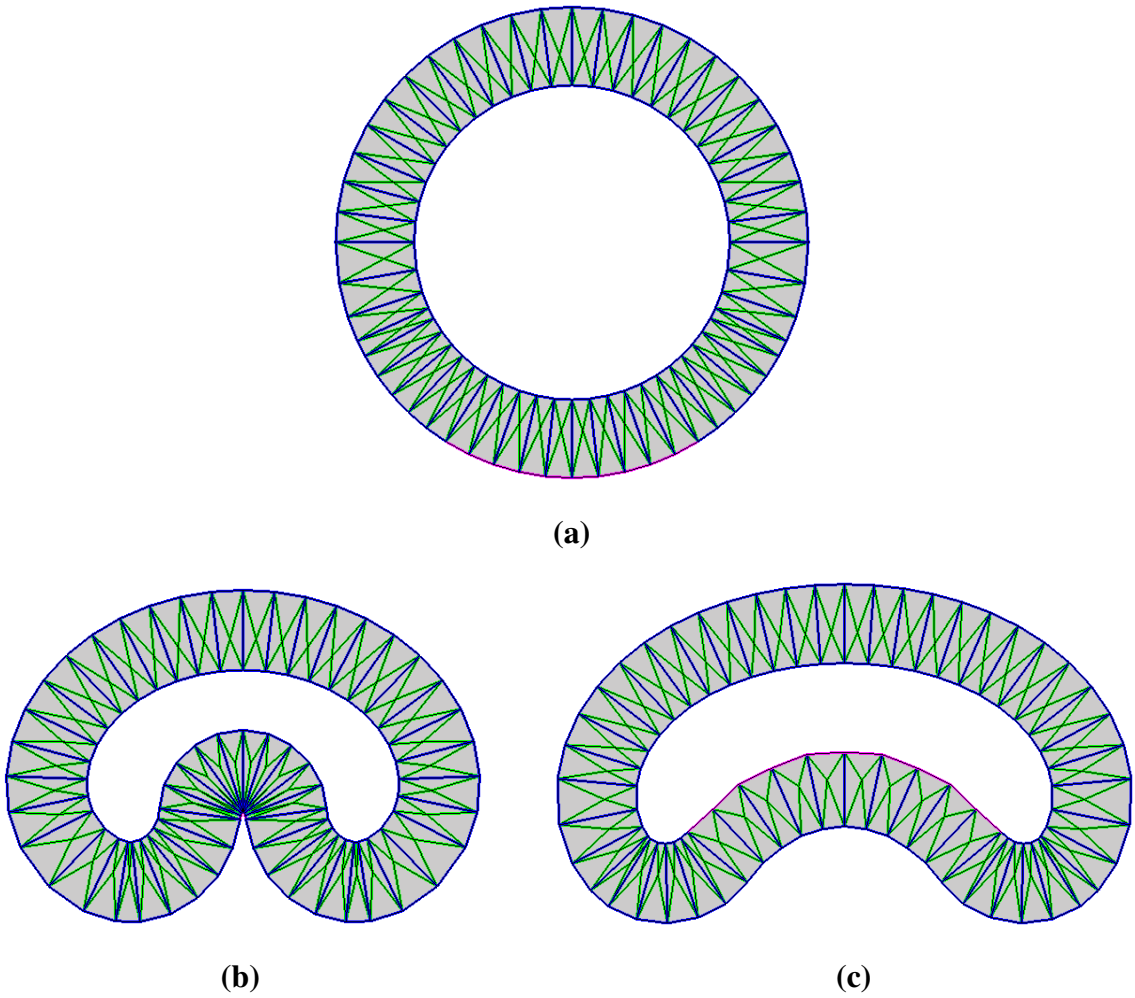

Figure 2. 2D analysis with the stress regulated approach. The pink line simulates the actin-myosin network which can produce the apical-constriction or the basal expansion, whereas the isochoric cytoplasm is in grey. **(a)** System of 52 cell units in its initial undeformed configuration (apical and basal side respectively toward the external and internal; **(b)** final deformed configuration of the system of 52 cells due to constriction of the apical sides (magenta line in subfigure (a)); **(c)** final deformed configuration of the system of 52 cells when the active movement is set as an expansion of the basal sides of the cells (magenta line).

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