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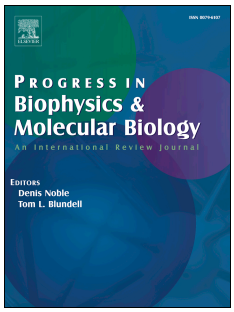

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Mathematical Models of Dorsal Closure

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Abstract

Dorsal closure is a model cell sheet movement that occurs midway through *Drosophila* embryogenesis. A dorsal hole, filled with amnioserosa, closes through the dorsalward elongation of lateral epidermal cell sheets. Closure requires contributions from 5 distinct tissues and well over 140 genes (see Mortensen et al., 2018, reviewed in Kiehart et al., 2017 and Hayes and Solon, 2017). In spite of this biological complexity, the movements (kinematics) of closure are geometrically simple at tissue, and in certain cases, at cellular scales. This simplicity has made closure the target of a number of mathematical models that seek to explain and quantify the processes that underlie closure's kinematics. The first (purely kinematic) modeling approach recapitulated well the time-evolving geometry of closure even though the underlying physical principles were not known. Almost all subsequent models delve into the forces of closure (*i.e.* the dynamics of closure). Models assign elastic, contractile and viscous forces which impact tissue and/or cell mechanics. They write rate equations which relate the forces to one another and to other variables, including those which represent geometric, kinematic, and or signaling characteristics. The time evolution of the variables is obtained by computing the solution of the model's system of equations, with optimized model parameters. The basis of the equations range from the phenomenological to biophysical first principles. We review various models and present their contribution to our understanding of the molecular mechanisms and biophysics of closure. Models of closure will contribute to our understanding of similar movements that characterize vertebrate morphogenesis.

Keywords: computational; actin; myosin; cell junctions; cell sheet morphogenesis; oscillation.

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