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DEVELOPMENT

Budding potential

Developmental biology is moving towards systems approaches, which seek to build comprehensive and quantitative models of how tissues form. These approaches require integrated means of viewing cell movement and mixing during organogenesis, and this paper provides one such tool: a novel two-dimensional model of mouse limb bud growth that can chart cell movements and patterns of regulatory gene expression in time and space.

To generate the model, Marcon and colleagues first looked at limb bud morphologies across the 72 hours of limb bud development and computed the possible velocity vector fields that could explain the morphological changes. This enabled them to generate virtual maps of the fates of individual tissue regions over time. Next, they performed experimental clonal analysis, in which single cells in the limb bud were marked at embryonic day 8 (E8) and the resulting clones observed at E12. They then compared the virtual and experimental fate maps and selected the computational model that best matched the experimental data.

The authors demonstrate how their model can be applied to questions regarding organogenesis. For example, there is a long-running debate about when the segments of the proximodistal axis of the limb bud are specified; by running the growth model in reverse, Marcon *et al.* suggest that proximodistal identities are not specified early. They also show — using *Hoxd13* as an example — that the model can help to distinguish changes in a gene expression domain that are accounted for by tissue movements from those that result from up- or downregulation of the gene.

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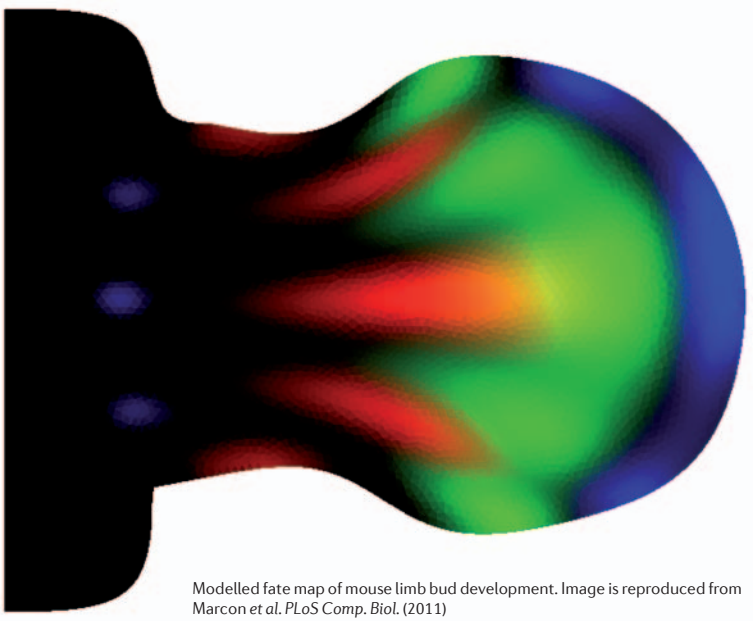
ORIGINAL RESEARCH PAPER Marcon, L. *et al.* A computational clonal analysis of the developing mouse limb bud. *PLoS Comp. Biol.* **7**, e1001071 (2011)



Modelled fate map of mouse limb bud development. Image is reproduced from Marcon *et al. PLoS Comp. Biol.* (2011)