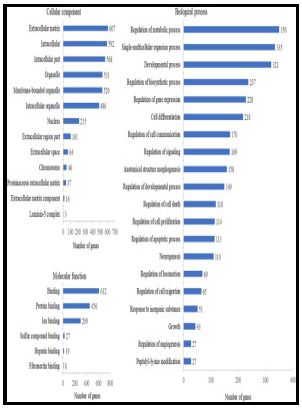
Molecular control of cell differentiation and morphogenesis - a systematic theory

M. Dekker - Quantitative proteomics and systems analysis of cultured H9C2 cardiomyoblasts during differentiation over time supports a 'function follows form' model of differentiation



Description: -
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Morphogenesis.
Cell differentiation -- Molecular aspects.Molecular control of cell differentiation and morphogenesis - a systematic theory
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Quantitative approach to life science ;Molecular control of cell differentiation and morphogenesis - a systematic theory
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Quantitative proteomics and systems analysis of cultured H9C2 cardiomyoblasts during differentiation over time supports a 'function follows form' model of differentiation

To explore the dynamics of lobule formation, the linking—unlinking frequency ν d of the fibers was investigated, which revealed that adjustments of this quantity could result in three distinctive morphologies. Finally, one should note that PI and RD are not mutually exclusive but in fact complementary e. Lee MM, Schiefelbein J 1999 WEREWOLF, a MYB-related protein in Arabidopsis, is a position-dependent regulator of epidermal cell patterning.

Tooth morphogenesis and cell differentiation

Here we exploited these available resources and conducted a comprehensive genome-wide analysis to expand our understanding of the genes involved in this process and to assemble them into a transcriptional regulatory network.

Quantitative proteomics and systems analysis of cultured H9C2 cardiomyoblasts during differentiation over time supports a 'function follows form' model of differentiation

Scheres B, Wolkenfelt H, Willemsen V, Terlouw M, Lawson E, et al. Nuclear mechanics during morphogenesis The nucleus is the largest organelle in most cells, and its position influences not only cellular mechanics and morphology, but also gene expression and signalling.

Testing Turing's theory of morphogenesis in chemical cells

Extensive exploration of various ABM implementations suggested that four rules, derived from four main regulatory events, were sufficient to recreate the structuring of the blastocyst. Further, we required that all of the included genes be regulated by the known early cell fate transcription factors, by demanding significant differential transcript accumulation in all three non-hair fate mutants wer myb23, gl3 egl3, and ttg relative to the hair fate mutant cpc try in two independent labs.

Erzberger Group

ABMs RD models employ relatively simple PDEs, which are sufficient for generic analyses of morphogen gradients and their interactions.

Testing Turing's theory of morphogenesis in chemical cells

CHEM 116 General Chemistry I 3-3-4 Prerequisite: CHEM 115 This is the second course in the General Chemistry series. However, the system evolves sufficiently slowly that it can adiabatically exhibit the dynamical instabilities predicted by Turing for open systems , ,.

A Dynamical Paradigm for Molecular Cell Biology

With respect to the root hair branching character, the composite Bayesian network identified two root-hair genes, bHLH66 and AT4G13390 encoding a proline-rich extensin-like wall protein , as the best predictors of the degree of root hair branching in an inverse correlation. For the analysis of root hair branching, 50 root hairs were examined per root in each of 9 seedlings 450 total hairs. These rather vague objectives can in retrospect be attributed to the fact that ABMs were relatively new in the field and that it was necessary to gain experience with exploring specific model features and the role of synergism among processes and rules.

Molecular control of cell differentiation and morphogenesis; a systematic theory.

Quantitative experimental results obtained using this artificial cellular system establish the strengths and weaknesses of the Turing model, applicable to biology and materials science alike, and pinpoint which directions are required for improvement. Although quantifiable validation is limited, the model is capable of creating tissue-scale morphological features that depend solely on single-cell decisions in response to environmental cues.

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