Formation of gene expression patterns in growing tissues

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Development of mouse embryo





@Recher, et al.., University of Cambridge



@Petersen, Miller. Marine Biological Laboratory in Woods Hole

Morphogen gradients through gene regulatory network specify cell fates



The GRN acts as an information decoder that specifies target pattern



Zagorski et al., Science, 2017 Petkova et al., Cell, 2019 Tkacik & Gregor, Development, 2021 Neural tissue in spinal cord undergoes changes in size and shape over time



Morphogen signaling gradients establish a striped pattern of neural progenitors



The striped pattern of gene expression domains is formed progressively



Research questions

- > How are morphogens interpreted to result in precise and reproducible patterns?
- How is pattern formation affected by tissue mechanical properties, cellular dynamics, and growth?
- > How is morphogen source formed in a growing tissue?
- > What are conditions for emergence of stable patterns in tissues?



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The morphogen signaling profiles do not scale with the embryo size



The initial morphogen positional error corresponds to the boundary imprecision at later stages



Zagorski et al., Science, 2017

Optimal decoder contains all the information that any cellular or computational mechanism could extract from input signals

Input signal
$$\{g_i(x)\} = \{g_1(x), g_2(x)\}, \quad K = 2$$

Signal distribution at every x

$$P(\{g_i\}|x) = \frac{1}{\sqrt{(2\pi)^K \det[\hat{C}(x)]}} \exp\left\{-\frac{1}{2} \sum_{i,j=1}^K (g_i - \bar{g}_i(x))(\hat{C}^{-1}(x))_{ij}(g_j - \bar{g}_j(x))\right\}$$

Optimal decoder from Bayes' rule

$$P(x^*|\{g_i\}) = \frac{1}{Z(\{g_i\})} P(\{g_i\}|x^*) P_X(x^*)$$

Tkacik et al., Genetics, 2015:formalismZagorski et al., Science, 2017:mouse spinal cord, K = 2Petkova et al., Cell, 2019:fruit fly, K = 4Tkacik & Gregor, Development 2021:review

Cells interpret the opposing morphogen signals using an optimal decoding strategy



Zagorski et al., Science, 2017

The decoding map predicts the correct shifts of gene expression domains in mutant with reduced Shh



Decoding map predicts bimodal *posterior* distribution of cell fates for high morphogen concentrations



The predicted bimodal distribution of cell fates is consistent with explant experiments



Zagorski et al., Science, 2017

The morphogens activate gene regulatory network to specify cell fate



Zagorski et al., Science, 2017

Computational screen resulted in a set of successful GRNs consistent with experimental observations



The target gene pattern established by GRNs resulted in a wide range of boundary imprecision



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Clonal cell populations disperse differently at different developmental stages



Bocanegra-Moreno et al., Nature Physics, 2023

MADM clones



Hippenmeyer et al., Neuron 2010

Green and red cells – single clone

The number of clone fragments is higher at early developmental stages than at later stages



Vertex model: movement of each cell is governed by movement of its vertices



Guerrero et al., Development 2019 Bocanegra-Moreno et al., Nature Physics, 2023 Vertex model ground state changes from fluid-like to solid-like with increasing tension and contractility



The classic formulation of vertex model could not reproduce experimental fragmentation



Including noise in the line tension and interkinetic nuclear movement (IKNM) increased fragmentation

+ noise in Λ_{ij} + cell area kinetics by $A^0_{\alpha}(t)$



Different levels of clone fragmentation were associated with different levels of cellular rearrangements (T1 transitions)

+ noise in Λ_{ij} + cell area kinetics by $A^0_{\alpha}(t)$ Fragmentation 0.15 0.15 0.1 0.1 0.05 0.05 0 0 -0.5 0 0.5 -1 Ā



Sub-region C is a novel region characterized by high levels of cell rearrangements

+ noise in Λ_{ij} + cell area kinetics by $A^0_{\alpha}(t)$





Vertex model simulation of tissue in sub-region B

Vertex model simulation of tissue in sub-region C

Vertex model simulation of tissue in sub-region A



Cell area variability is high only in sub-region C



Cell area variability is high only in sub-region C



Tissue simulated in sub-region C resembles the neural epithelium at E8.5





*Area CV, % Hexagons, normalized perimeter (p0), cell elongation, elongation CV, p0 CV, perimeter CV

Dynamics of cell area affects the rate of cellular rearrangements and cellular heterogeneity in sub-region C



Implementation of interkinetic nuclear movement (IKNM) in the vertex model





 $A^0_{\alpha}(\Delta t) = \frac{1}{2}(g_{\alpha}\Delta t + 1)(\rho_{\alpha}(\Delta t)^2 + 1)$

g_{α} growth rate of the cell $ho_{\alpha}(\Delta t)$ piecewise linear function representing nucleus position

Guerrero et al., Development 2019 Bocanegra-Moreno et al., Nature Physics, 2023
Apical cell area rapidly increases before mitosis in vivo



Kinetics of apical cell area growth induces T1 transitions in sub-region C



The number of clone fragments is higher at early developmental stages than at later stages



The growth rate of neural epithelium goes down at later developmental stages



Kicheva et al., Science, 2014 Bocanegra-Moreno et al., Nature Physics, 2023

Lowering proliferation rate decreased fragmentation in vertex model simulation



The decrease in the proliferation rate decreased fragmentation in E8.5 embryos



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The GRN acts as an information decoder that specifies target pattern



Ho et al., bioRxiv, 2024.03.01.582751

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Ho et al., bioRxiv, 2024.03.01.582751

Thermodynamical model coupled with reaction-diffusion equation

$$\frac{\partial[F]}{\partial t} = \alpha_F \frac{\kappa_F + c_{S \to F} \kappa_F [Shh]}{(1 + \kappa_{N \to F} [N])^{m_{N \to F}} + \kappa_F + c_{S \to F} \kappa_F [Shh]} - \gamma_F [F]$$

$$\frac{\partial[N]}{\partial t} = \alpha_N \frac{\kappa_N + c_{S \to N} \kappa_N [Shh]}{(1 + \kappa_{F \to N} [F])^{m_{F \to N}} + \kappa_N + c_{S \to N} \kappa_N [Shh]} - \gamma_N [N]$$

$$\frac{\partial[Shh]}{\partial t} = D_S \frac{\partial^2 [Shh]}{\partial x^2} + \alpha_S \frac{\kappa_{F \to S} [F]}{1 + \kappa_{F \to S} [F]} - \gamma_S [Shh]$$



Spinal cord grows as pattern is established



Kicheva et al., Science 2014 Zagorski et al., Science 2019 Bocanegra-Moreno et al., Nature Physics 2023 Computational screen: 169 979 successful solutions out of 400 000 visited



formed between 2.5 and 20h •

100

Lack of clear dependence of FP size on parameter values



Perturbing most of the parameters strongly affects FP size



Ho et al., bioRxiv, 2024.03.01.582751

FP formation can occur by different mechanisms, dependent or independent of FP-derived Shh



Distribution of parameters for Shh^{FP}-sensitive and insensitive classes of solutions



After formation the FP is scaling in size following tissue growth



After formation the FP is scaling in size following tissue growth



Ho et al., bioRxiv, 2024.03.01.582751

Removing Shh production by FP results in distinct solutions



Ho et al., bioRxiv, 2024.03.01.582751

Two time scales of FP formation: establishment and scaling



Ho et al., bioRxiv, 2024.03.01.582751

Initial flux regulates the size of FPs



The increase in Shh amplitude over time depends on floor plate growth



Removing Shh flux reduces Shh amplitude in the extent depending on the magnitude of flux



FP-derived Shh is not required for the formation of the floor plate



Early deletion of Shh results in a severe reduction of 85% of FP size



Late deletion of Shh does not alter FP size





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We explain the principles of gene expression pattern stabilization in systems of interacting, diffusible morphogens, with dynamically established source regions

PHYSICAL REVIEW LETTERS 130, 098402 (2023)

Stability of Pattern Formation in Systems with Dynamic Source Regions

M. Majka $^{(0)}$, R. D. J. G. Ho $^{(0)}$, and M. Zagorski $^{(0)}$

Institute of Theoretical Physics and Mark Kac Center for Complex Systems Research, Jagiellonian University, Łojasiewicza 11, 30-348 Kraków, Poland

$$\partial_t \psi_i = D_i \partial_{xx} \psi_i - \gamma_i \psi_i + H_i \theta (F_i(\psi_1, \psi_2))$$

 $F_i(\psi_1,\psi_2) \simeq \epsilon_{ii}\psi_i + \epsilon_{ij}\psi_j - C_i$



Under specific conditions stable gene expression patterns (GEPs) are formed



Indetermined GEP vs Travelling GEP vs Stable GEP



Majka et al., Physical Review Letters, 2023

GEP exhibit broad plateu of low-velocity drift



$$\lambda_i = \sqrt{\frac{D_i}{\gamma_i}}, \quad \tilde{\psi}_i = \frac{H_i}{\gamma_i}, \quad S_i = \frac{2C_i}{\epsilon_{ii}\tilde{\psi}_i}, \quad \chi_i = \frac{\epsilon_{ij}\tilde{\psi}_j}{\epsilon_{ii}\tilde{\psi}_i}$$

Gap gene expression pattern exhibits shifts in the posterior part



Estimated velocity of Kni-Gt is 17.5 μ m over 44 minutes, that corresponds to v = 24 μ m/h.

Verd et al., PLOS Comp Bio, 2017

Stability conditions for two-gene network motifs encountered in developmental GRNs



Majka et al., Physical Review Letters, 2023

Stable developmental patterns of gene expression without morphogen gradients in Drosophila-like system





M Majka, NB Becker, PR ten Wolde, M Zagorski, TR Sokolowski,, arXiv: 2306.00537

Summary (part 1)

> Morphogens are interpreted close to optimal limit of processing of noisy signals



> Patterning is affected by growth, cellular dynamics, and tissue properties



Summary (part 2)

> Initial FP size is determined by GRN strengths, and later on it scales with the tissue size



Stable patterns of interacting domains emerge under specific conditions




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Funding



The project is financed by the National Science Centre, Poland, no. 2021/42/E/NZ2/00188



The project is financed by the Polish National Agency for Academic Exchange

Ministry of Science and Higher Education

Republic of Poland



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PhD research scholarship



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