

Deterministic and Stochastic Models of Bicoid Protein Gradient Formation in Drosophila Embryos

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Drosophila



Essential Cell Biology, 3rd Edition, 2009 By Bruce Alberts, Dennis Bray, Karen Hopkin, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts, Peter Walter



Bicoid Morphogen

- Drosophila body plan and position information.
- Providing the concentration mechanism to active other gap gene in drosophila embryo
- Contributing to set up the anterior posterior axis.
- Controlling cells fate along 70% of this axis.

Bicoid Morphogen Concentration



Constant Source

• Usual assumption





Surdej, P., Jacobs-Lorena, M.: *Developmental regulation of bicoid mRNA stability is mediated by the first 43 nucleotides of the 3' untranslated region*. Molecular and Cellular Biology 18(5) (1998) 2892-2900

Reaction Diffusion Equation

• The reaction-diffusion equation of singlemorphogen concentration system is below:

$$\frac{\partial}{\partial t}M(x,t) = D \frac{\partial^2}{\partial x^2}M(x,t) - \tau_p^{-1}M(x,t) + S(x,t)$$

- *M*(*x*, *t*) is morphogen concentration
- S(x, t) is a general source term at the anterior pole
- *D* is diffusion constant
- τ_p is half-life of the morphogen protein

Turing, A.: *The chemical bass of morphogenesis*. (1952) Bergmann,S : *Pre-Steady-State Decoding of the Bicoid Morphogen Gradient*. (2007)

Reaction Diffusion Equation in Flow model

• The reaction-diffusion equation of single-morphogen concentration system with cytoplasmic flow:

$$\frac{\partial}{\partial t}M(x,t) = D\frac{\partial^2}{\partial x^2}M(x,t) - \tau_p^{-1}M(x,t) - v\frac{\partial}{\partial x}M(x,t) + S(x,t)$$

- *M*(*x*, *t*) is morphogen concentration
- S(x, t) is a general source term at the anterior pole
- *D* is diffusion constant
- \$\mathcal{\alpha}_p\$ is half-life of the morphogen protein
 \$\mathcal{\bar{v}}\$ is flow velocity

Hecht, I. : Determining the scale of the Bicoid morphogen gradient. (2009)

Stochastic Model

Bicoid proteins chemical reaction diffusion





Bicoid proteins production

Bicoid proteins degradation

Bicoid proteins diffusion

Solution to Model with Constant Source



Solution to Model with Combined Source



Solution to Stochastic model



Measured Data



Integrated 2D patterns – reconstructed image 14A-2



Measured Data



● 1D integrated data - cycle 14A (1-8 classes)

1) ℤ 2) ℤ 3) ℤ 4) ℤ 5) ℤ 6) ℤ 7) ℤ 8) ℤ



Matching Models to Data



Time (mins)

Comparison Between Model Output and Database in Cycle14A with 8 Classes



Comparison Between Model Output and Database in Cycle14A with 8 Classes



Estimating Parameter Values

 Squared error between model output and measured intensities to evaluate error.

$$E = \sum_{t=T_1}^{T_2} \sum_{x=1}^{L} \{M(x,t) - M_d(x,t)\}^2$$

- Parameters estimation:
 - Diffusion constant $D = 1.8 \,\mu m^2 / s$,
 - The time mRNA starts to decay $t_0 = 118$ mins,
 - mRNA half-life $\tau_m = 29$ mins
 - Bicoid protein half-life $\tau_p = 120$ mins.

Matching Parameter Values to Data

• The errors in the joint space of diffusion constant and maternal mRNA decay onset time.



Conclusion

- Widely used model with a constant source is unrealistic.
- Three models with realistic source.
- Matching models output to database.
- Developing data driven model for embryo spatiotemporal data i.e. Kriged Kalman Filter

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THANKS !

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Letters to Nature

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Dynamic control of positional information in the early Drosophila embryo

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