

Using PDE models to describe *mRNA* expression pattern dynamics

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CE 291F – ME 236 –EE291 Class Project

May 2010

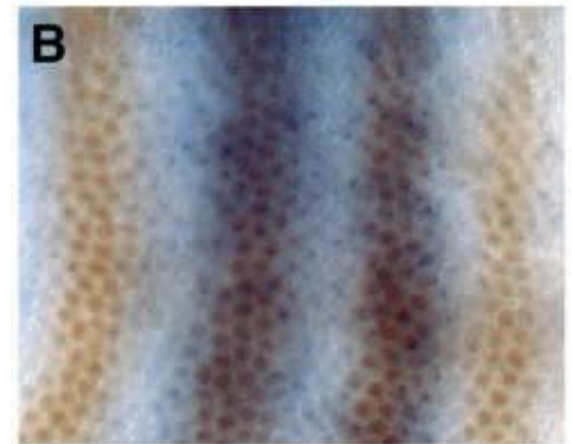
[Berkeley Drosophila Transcription Network Project]

mRNA transcription in *Drosophila* Embryo



Drosophila

Embryo with **eve** stripes



[Muhammad Mahdi Karim]

Transcription factors **activate** or **repress**
mRNA transcription



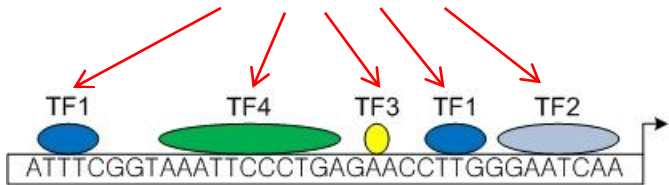
Pattern generation
(*mRNA* concentration gradient)

[Levine et al., *PNAS* 102, 14, 4936-4942, 2005]

[Ludwig et al., *Development* 125, 949-958, 1998]

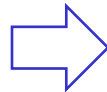
Problem formulation

Transcription factors
bound to DNA



Configuration (c)
: control input

[Segal, et al., *Nature* 451, 535-541, 2008]

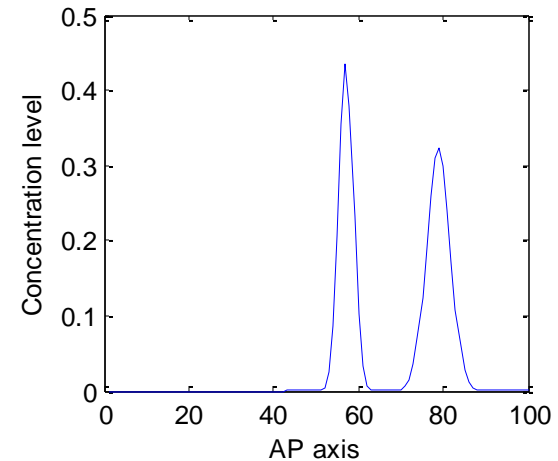
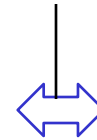


**Spatiotemporal
model**
(PDE w/ distributed
controller ϕ)

$u(x, t)$
Solution



Error



Concentration of *eve*
: experimental data

*Parameters are
unknown*

Parameter estimation of a diffusion PDE

$$\begin{aligned}u_t &= D\Delta u + g \\ &= \underline{D}\Delta u - \underline{d}u + \phi\end{aligned}$$

u: concentration of *eve* mRNA

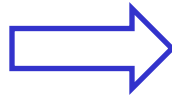
g: rate of increase of *eve* mRNA per volume

ϕ : transcription rate

D: mass diffusivity

d: feedback gain

Estimate
Parameters
using an *adjoint-
based* method.



Describe the
dynamic propagation
of *eve* mRNA
expression pattern.

Q) How can we model ϕ ?

Nuclei: Distributed over an embryo

Input:

- configuration (c)

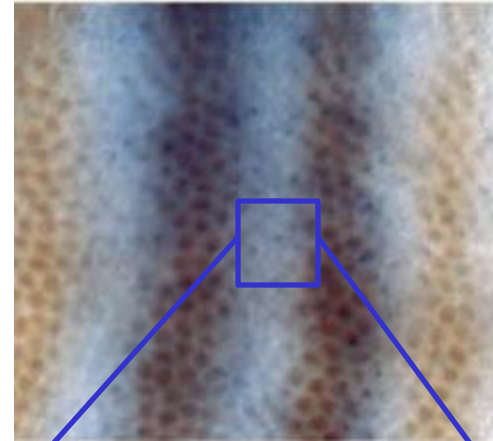


Controller ϕ
(a nucleus at (x, t))



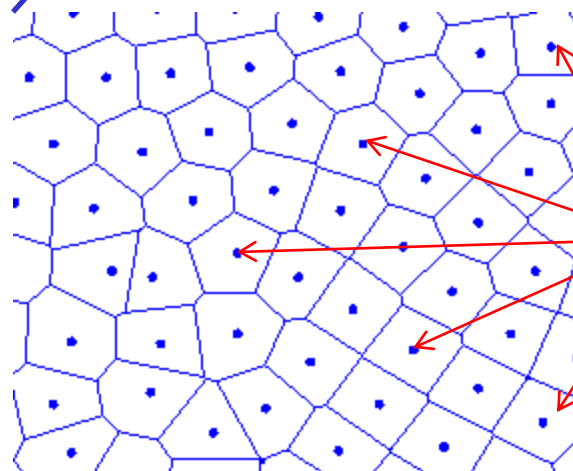
Output:

- *eve* mRNA transcription rate at (x, t)



[Ludwig, et al., *Development* 125, 949-958, 1998]

Embryo
: domain



Nuclei
: distributed machines with a controller

Combinatorial controller modeling

$$\begin{aligned}\phi &= eP(E | x, t) \\ &= e \sum_{c \in C} P(E | c, x, t) P(c | x, t)\end{aligned}$$

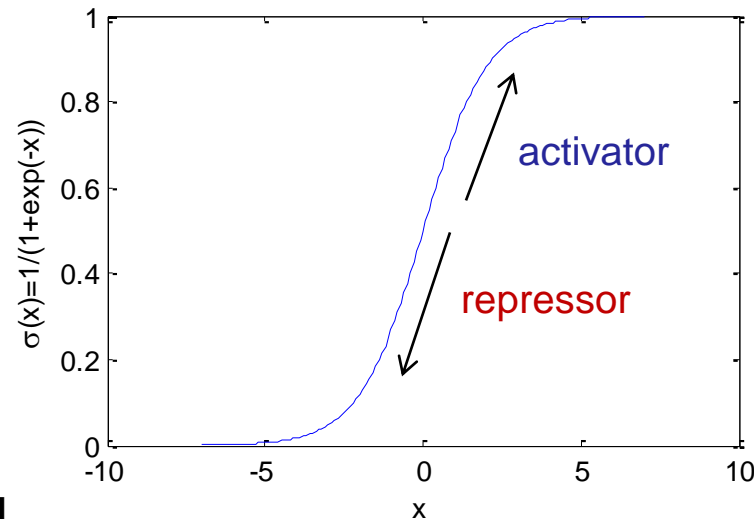


Configuration (c): control input

$$P(E | c, x, t) = \sigma \left(w_0 + \frac{1000}{|S|} \sum_{i=1}^{l(c)} w_{\tau_i} \right) = \sigma \left(\frac{w_0}{|S|} + \frac{1000}{|S|} \sum_{\tau=1}^m \underbrace{z_{\tau}(c)}_{\substack{\# \text{ of TF}_{\tau} \text{ in } c}} w_{\tau} \right)$$

Transcription contribution

$\sigma(x)$: logistic function



TF $_{\tau}$: activator $\Leftrightarrow w_{\tau} > 0$

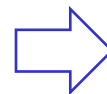
TF $_{\tau}$: repressor $\Leftrightarrow w_{\tau} < 0$

[Segal, et al., Nature 451, 535-541, 2008]

Model development



Configuration(c): control input



$$\phi$$

Transcription rate

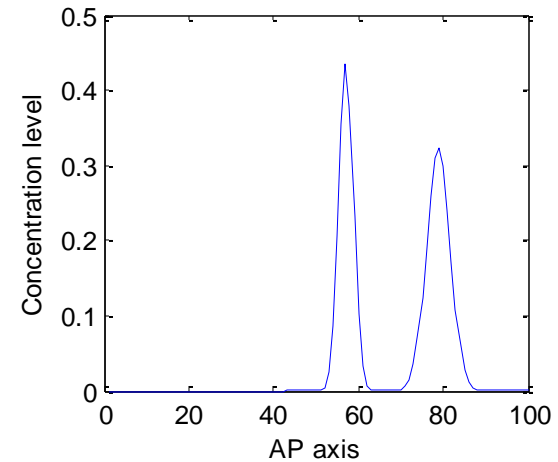
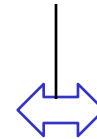
$$u_t = Du_{xx} - du + \phi$$



$$u(x, t)$$

Solution

Error



Concentration of *eve*
:experimental data

Adjoint-based parameter estimation

minimize: $J = \frac{1}{2} \int_{\Omega} \sum_{i=1}^T \|u(x, t_i) - o(x, t_i)\|_2^2 dx$

subject to: $u_t = Q(u, \theta) + S(\theta)\Delta u$

$$\nabla_x u_j(x, t) \cdot n = 0 \quad \forall x \in \partial\Omega \quad j = 1, 2, \dots, d_u$$

$$u(x, t_0) = o(x, t_0) \quad \forall x \in \Omega$$

Equation of first variation:

$$\hat{u}_t = \frac{\delta Q(u, \theta)}{\delta u} \hat{u} + S(\theta)\Delta \hat{u} + \frac{\partial Q(u, \theta)}{\partial \theta} \hat{\theta} + V(u, \theta)\hat{\theta}$$

where $V(u, \theta) = \begin{bmatrix} \sum_{j=1}^{d_u} \frac{\partial S_{1j}}{\partial \theta} \Delta u_j \\ \vdots \\ \sum_{j=1}^{d_u} \frac{\partial S_{d_u j}}{\partial \theta} \Delta u_j \end{bmatrix}$

Adjoint-based parameter estimation

Adjoint PDEs:

$$-\mu_t = \frac{\delta Q(u, \theta)^T}{\delta u} \mu + S^T(\theta) \Delta \mu \quad \text{on } (t_{i-1}, t_i] \quad \text{for } i = 1, \dots, T$$

$$\nabla_x \mu_j(x, t) \cdot n = 0 \quad \forall x \in \partial\Omega \quad j = 1, 2, \dots, d_u$$

with terminal conditions:

$$\mu(x, t_T) = u(x, t_T) - o(x, t_T)$$

$$\mu(x, t_i) = \mu(x, t_i^+) + u(x, t_i) - o(x, t_i) \quad \text{for } i = 1, \dots, T-1$$

Adjoint-based parameter estimation

Gateaux derivative (in the direction \hat{u}):

$$\begin{aligned} dJ(\theta; \hat{\theta}) &= \lim_{h \rightarrow 0} \frac{J(\theta + h\hat{\theta}) - J(\theta)}{h} = \int_{\Omega} \sum_{i=1}^T (u(x, t_i) - o(x, t_i))^T \hat{u} dx \\ &= \int_{\Omega} \sum_{i=1}^T \int_{t_{i-1}}^{t_i} \mu^T \left(\frac{\partial Q(u, \theta)}{\partial \theta} + V(u, \theta) \right) \hat{\theta} dt dx \end{aligned}$$

Gradient:

$$\nabla_{\theta} J = \int_{\Omega} \sum_{i=1}^T \int_{t_{i-1}}^{t_i} \left(\frac{\partial Q(u, \theta)}{\partial \theta} + V(u, \theta) \right)^T \mu dt dx$$

Adjoint-based method algorithm

Step 1. Guess (initial) parameter θ

Step 2. Solve PDE numerically $\Rightarrow u(x, t)$

Step 3. Solve Adjoint PDE numerically $\Rightarrow \mu(x, t)$

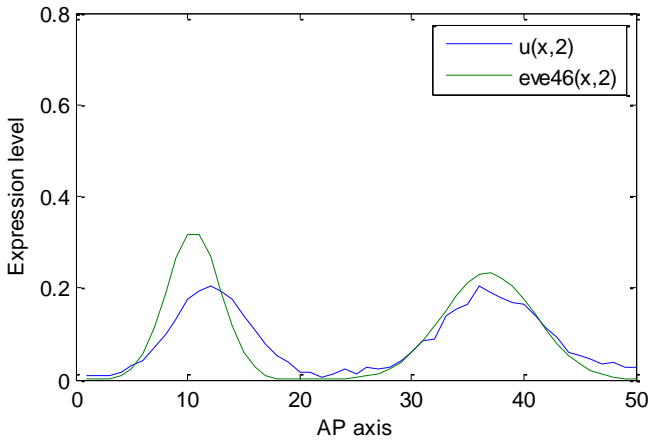
Step 4. Update parameter: $\theta = \theta - \alpha \nabla_{\theta} J$

where

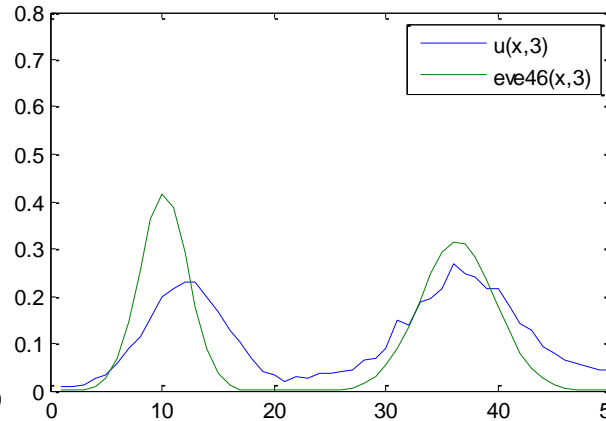
$$\nabla_{\theta} J = \int_{\Omega} \sum_{i=1}^T \int_{t_{i-1}}^{t_i} \left(\frac{\partial Q(u, \theta)}{\partial \theta} + V(u, \theta) \right)^T \mu dt dx$$

Parameter estimation results

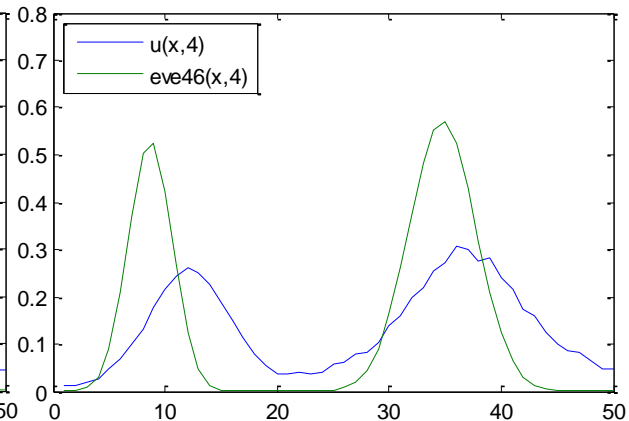
Time 2



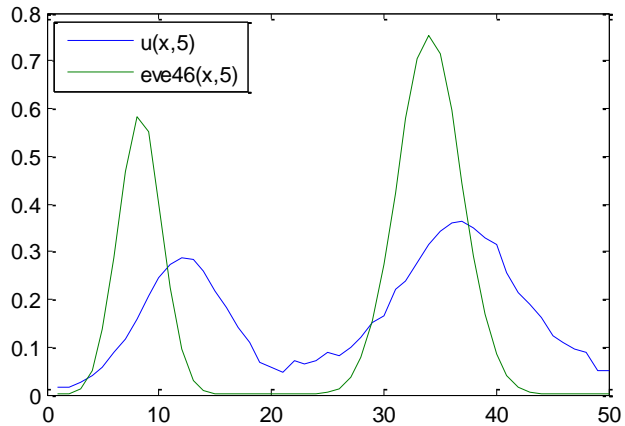
Time 3



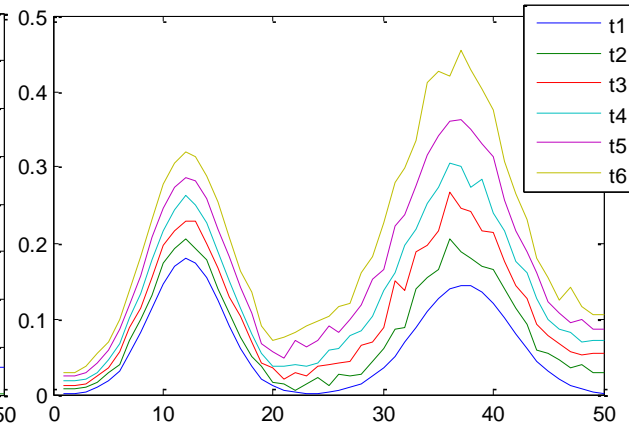
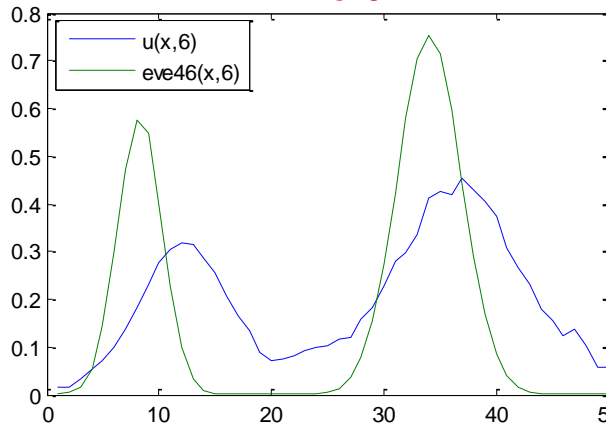
Time 4



Time 5

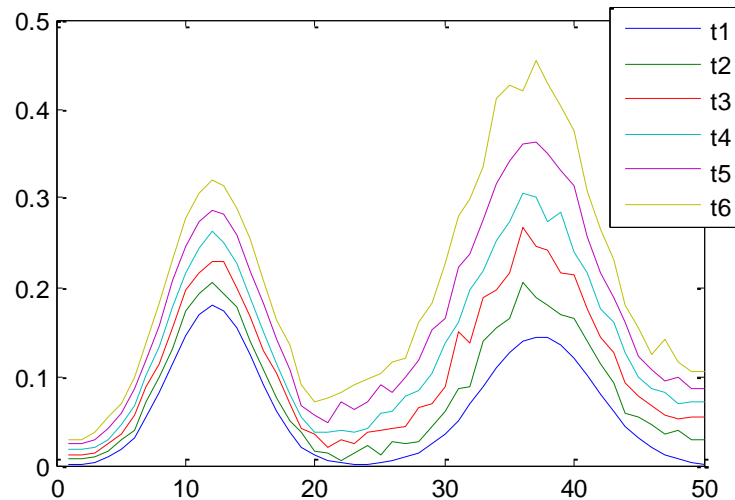


Time 6



$$\theta = (0.3210, -0.1298, -1.5619, 9.1793, -3.8370, -1.4426)$$

Conclusions and future goals



- + Describe fast enhancement of the right stripe
- Cannot describe late stage of pattern dynamics

Future Work (in summer):

- 2D PDE
- More transcription factors & *mRNAs*
- Study algebra
 - : find a group structure of configuration

Thank you!

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