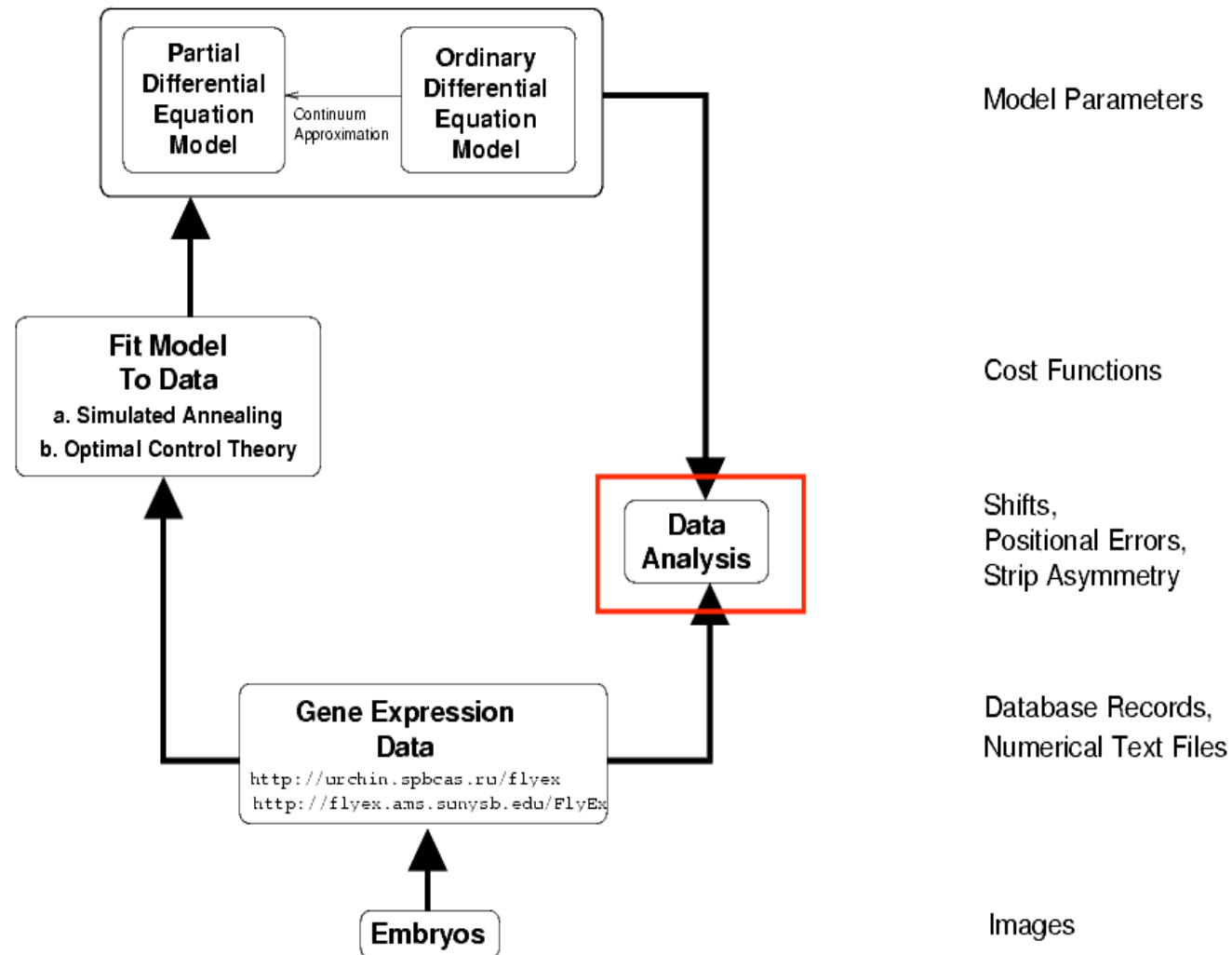


# System biology of development

*Maria Samsonova*

*(St.Petersburg Polytechnic University, SPb,  
Russia)*

# System Biology of Segment Determination



**Synthesis**

$$\frac{dv_i^a}{dt} = R_a g_a \left( \sum_{b=1}^N T^{ab} v_i^b + m^a v_i^{bcd} + h_a \right)$$

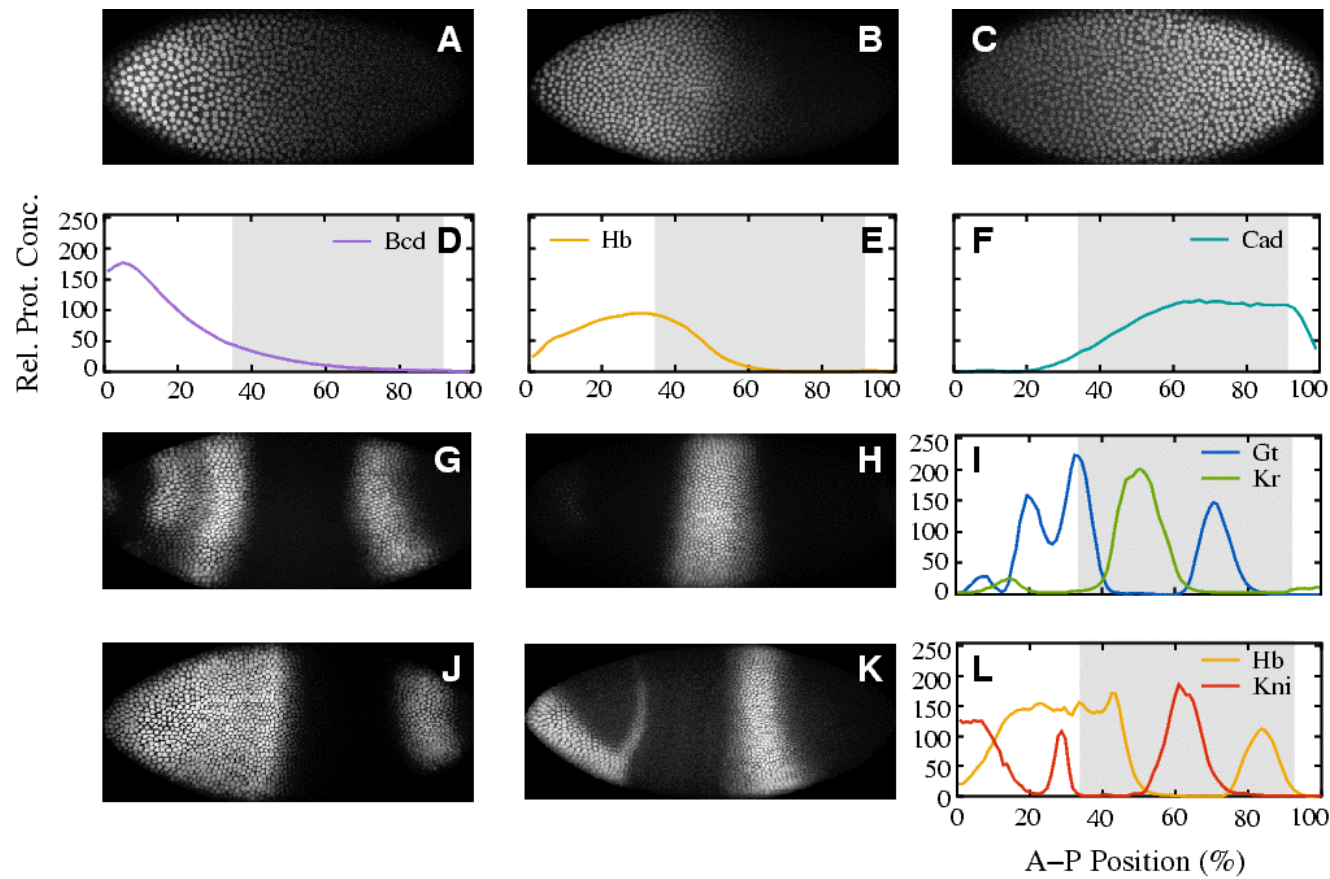
**Transport**

$$+ D^a(n) \left[ \left( v_{i-1}^a - v_i^a \right) - \left( v_{i+1}^a - v_i^a \right) \right]$$

**Decay**

$$- \lambda_a v_i^a$$

# Expression patterns of gap genes

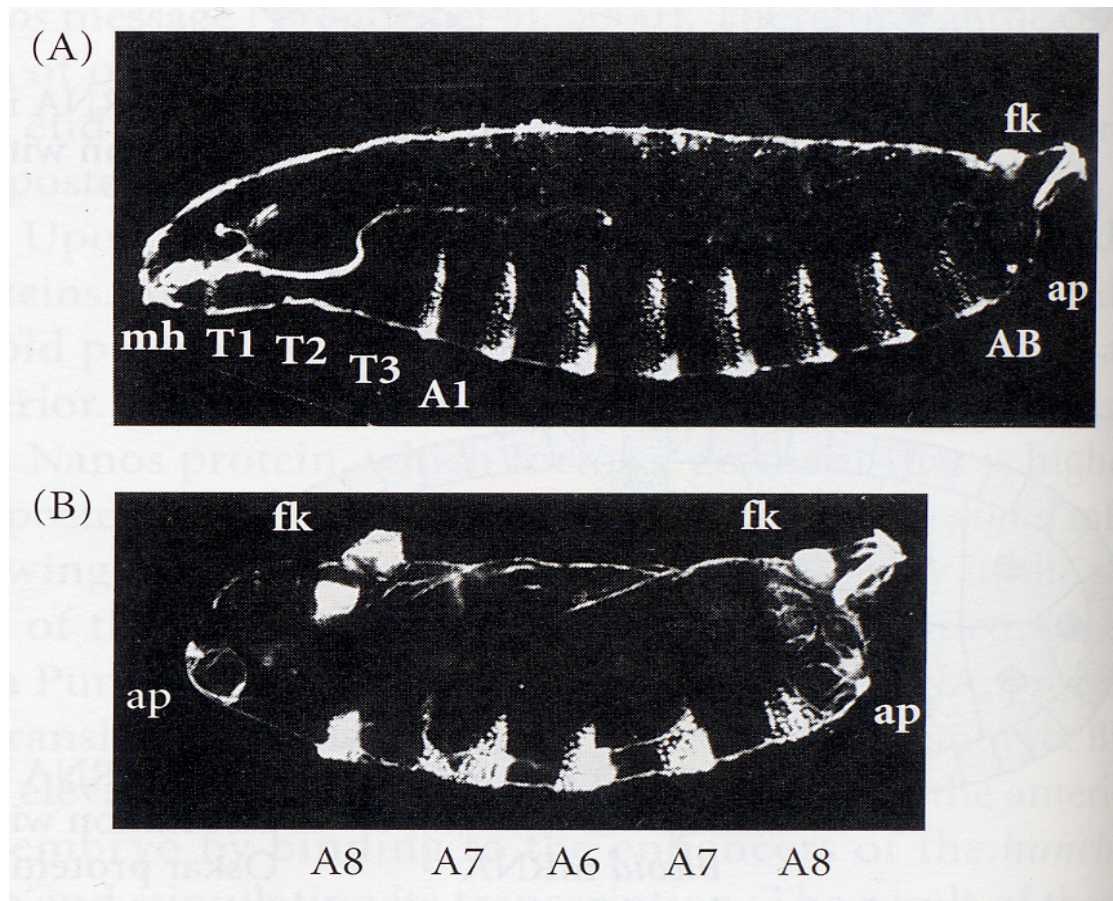




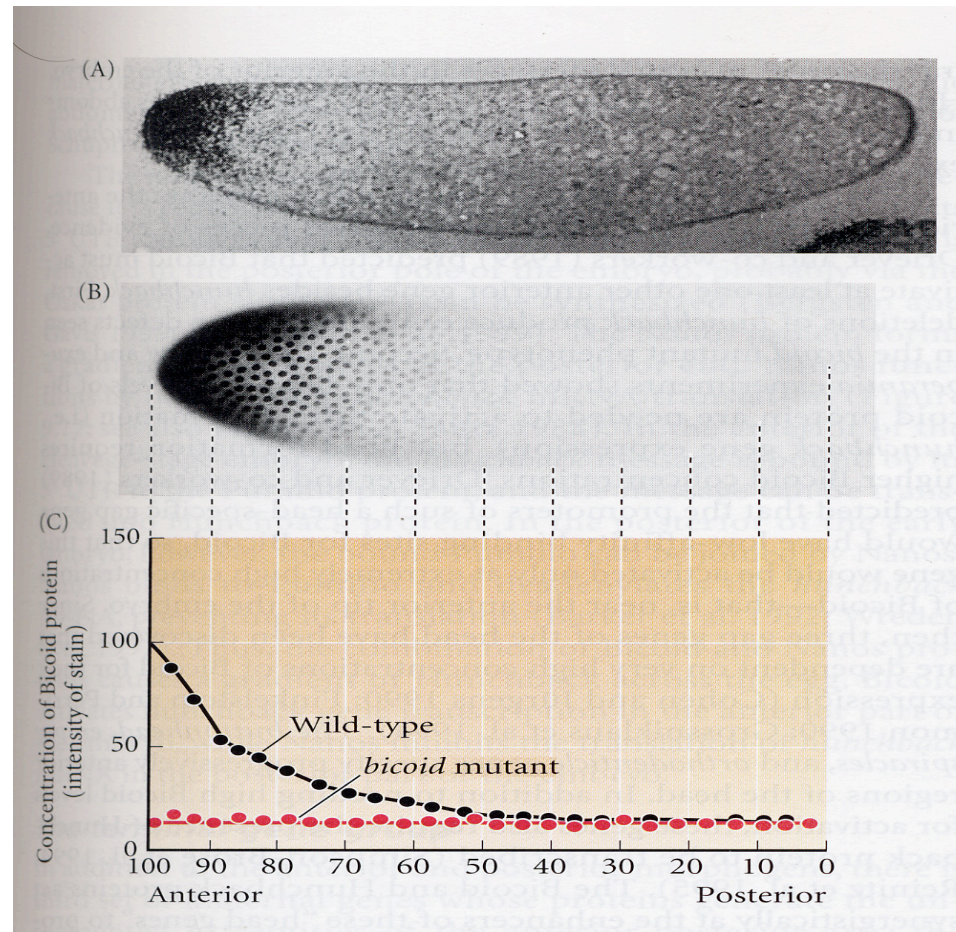
# Criteria for morphogen action

- ❑ Released from localized source;
- ❑ form a concentration gradient over a population of nearby and distant cells that respond to signaling molecule in concentration-dependent way;
- ❑ Cells in the pathway of the gradient should show two or more qualitatively different responses;
- ❑ Over- and underexpression experiments should change the cell fate in the predicted directions;
- ❑ Morphogen action should be direct.

Phenotype of the strongly affected embryo from a female fly deficient in the *bicoid* gene

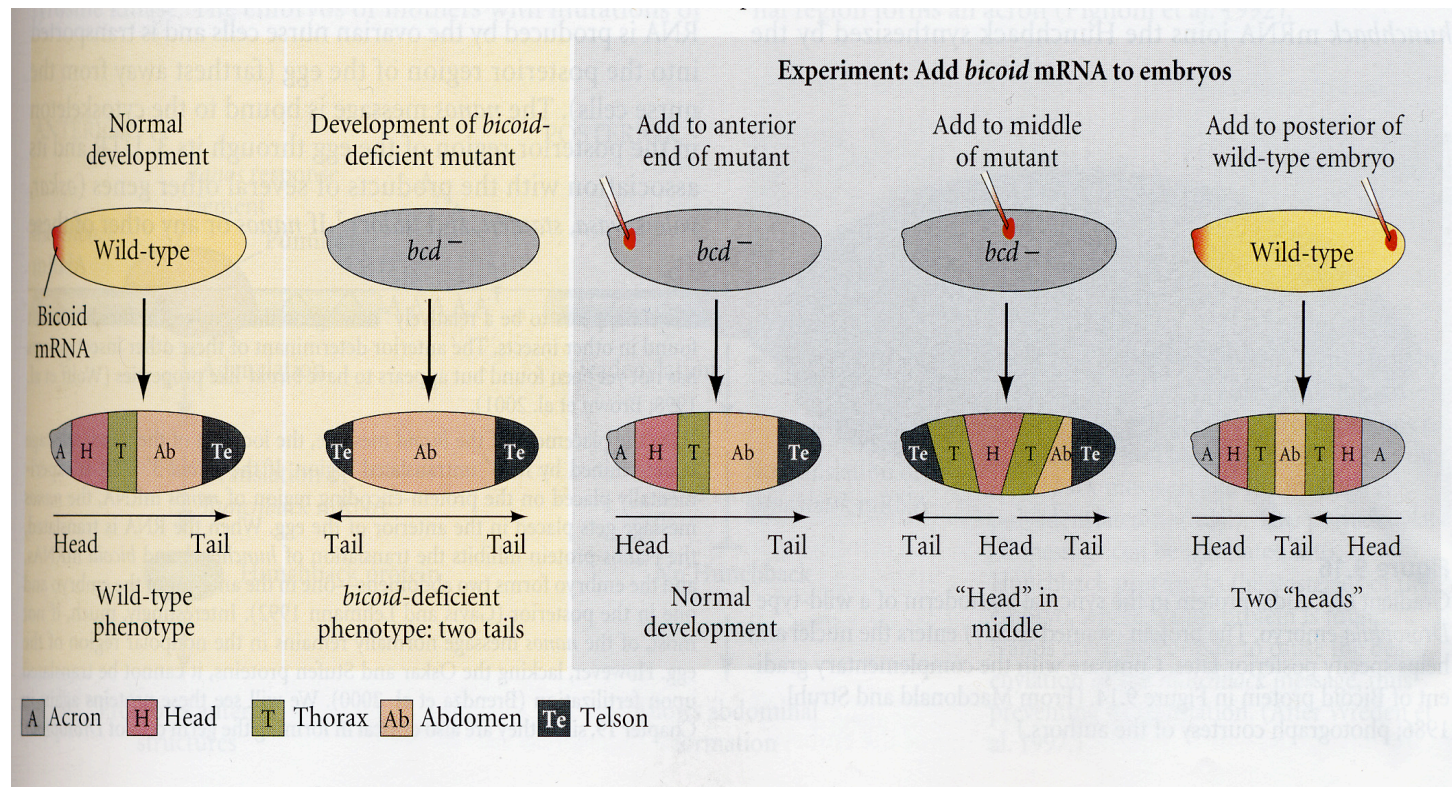


# Gradient of Bicoid protein in the early *Drosophila* embryo



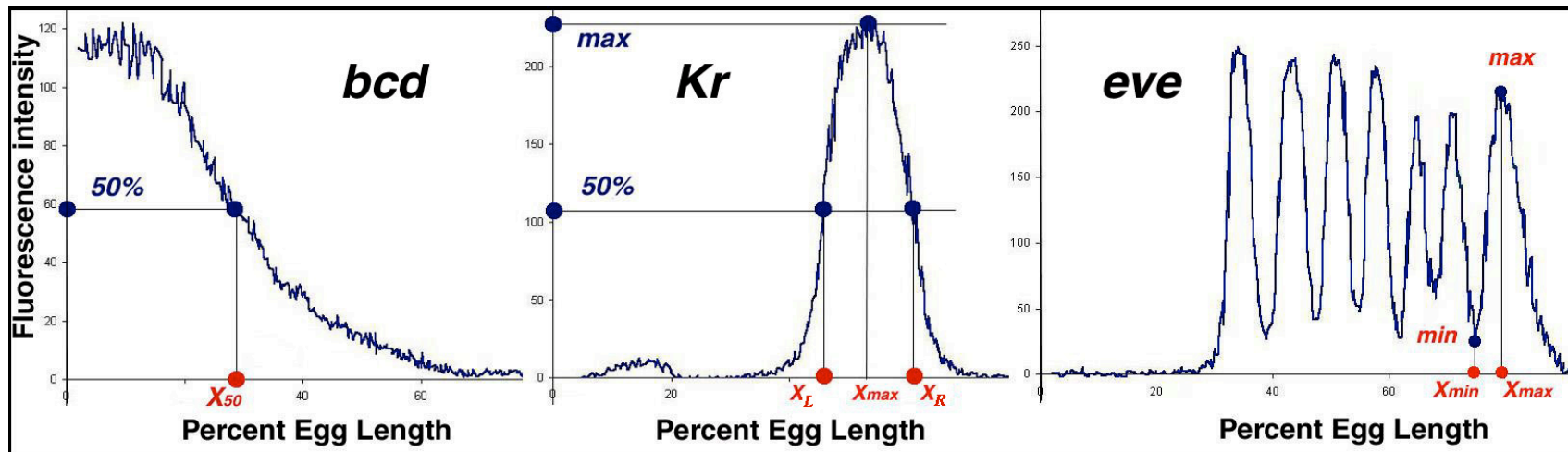
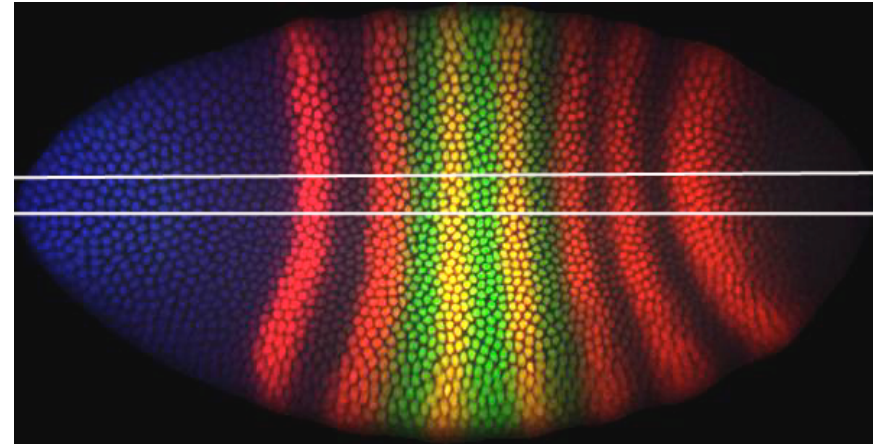


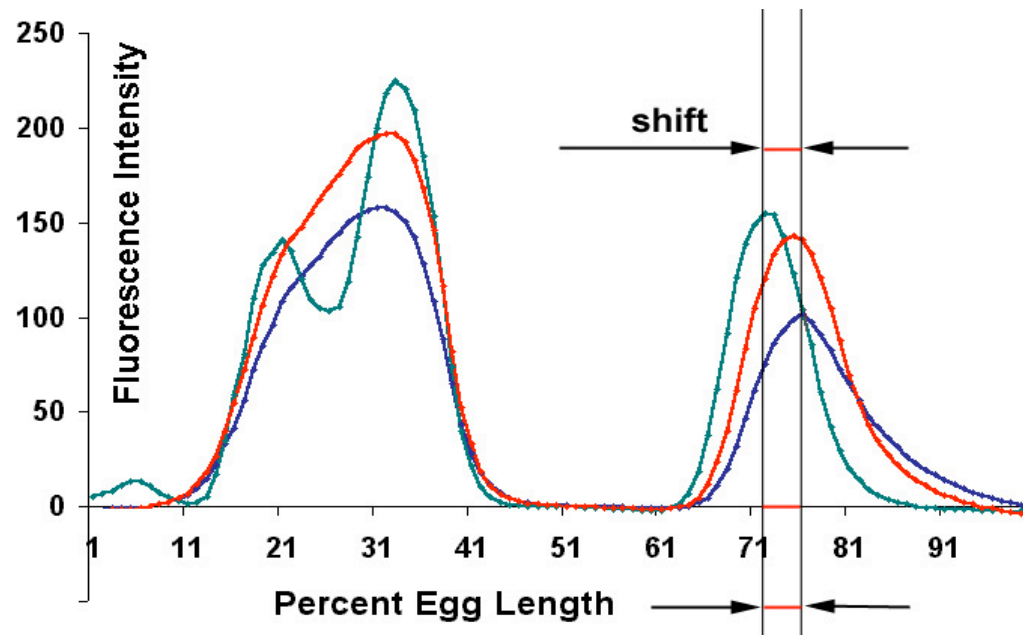
# *bicoid* encodes the morphogen responsible for head structures



# Features used to characterize expression patterns

Embryo stained for expression of  
*bcd*, *Kr* and *eve*

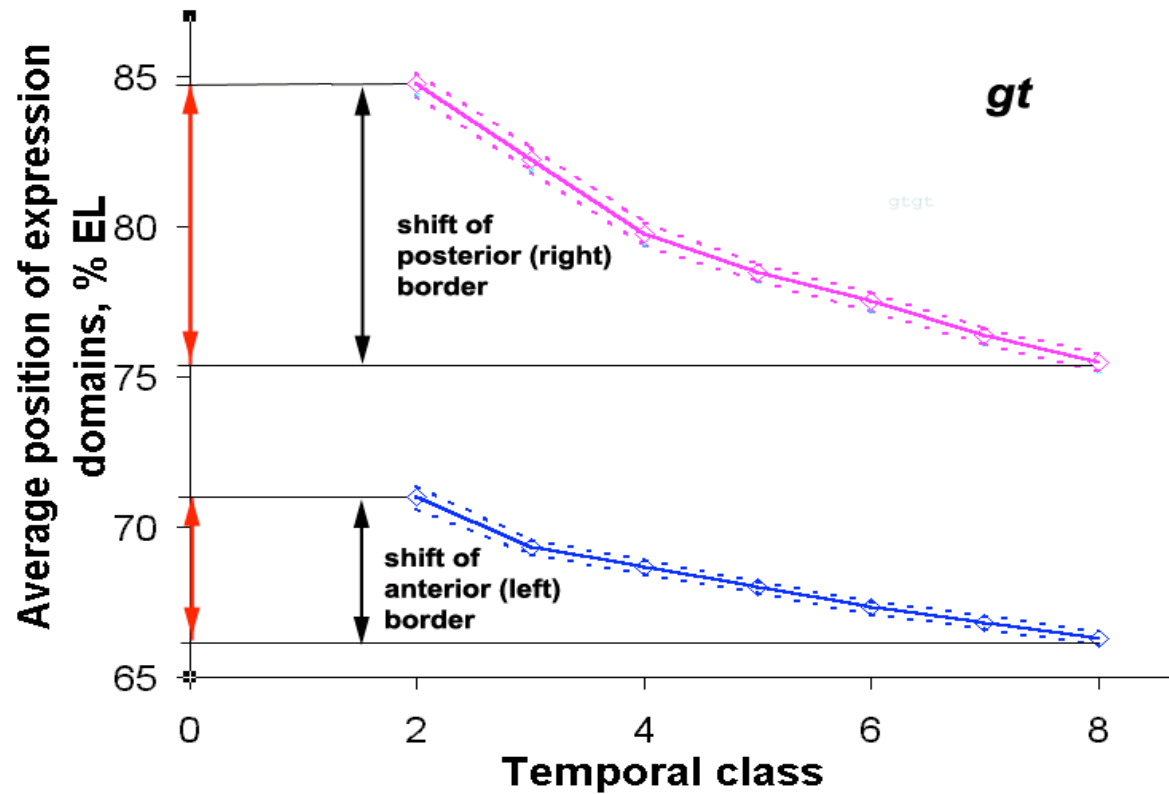




**Computation of  
shifts: the  
highly dynamic  
pattern of *gt*  
as an example**

- 1. Extract characteristic features of expression domain.**
- 2. Calculate the average position of a given characteristic feature over the embryos of each time class.**
- 3. Compute the difference between average positions of the feature in different time classes.**

# Shifts of domains of gap genes



gene	<i>Kr</i> {n=261}		<i>kni</i> {n=134}		<i>gt</i> {n=137}	
	A-border	P-border	A-border	P-border	A-border	P-border
shift (%EL)	1.02	5.23	1.60	6.32	4.72	11.04

# Analysis of the Gap Gene System

Using the new dataset and the ODE model with nuclear divisions, we ask:

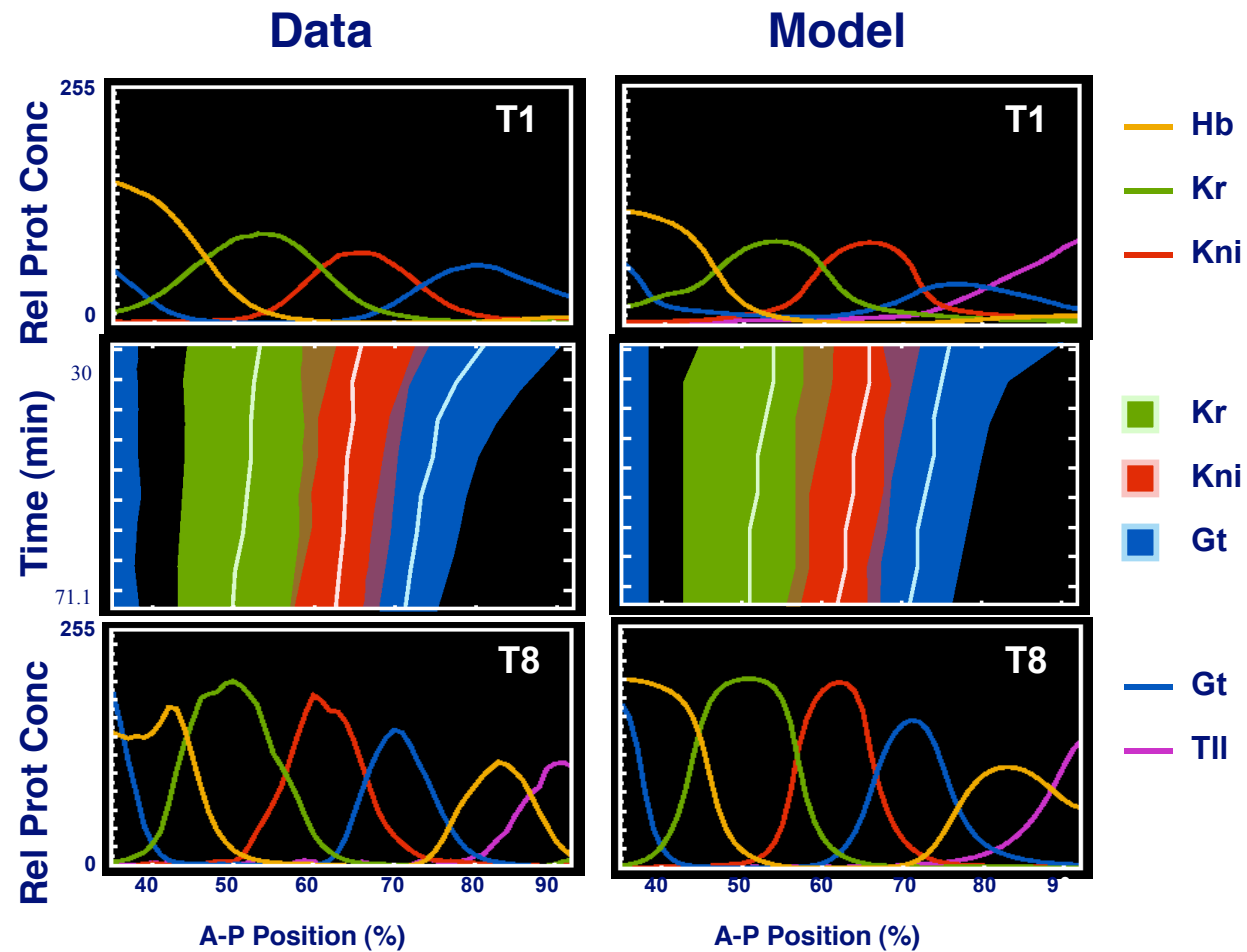
How are gap gene domains maintained and refined?

Why do they move?

Is Bcd a morphogen?



# Gap Gene Expression



# Constraints on the T Matrix

	<i>bcd</i>	<i>cad</i>	<i>hb</i>	<i>Kr</i>	<i>gt</i>	<i>kni</i>	<i>tll</i>
<i>hb</i>	0/1/9	3/1/6	2/2/6	4/6/0	2/4/4	10/0/0	3/5/2
<i>Kr</i>	0/0/10	0/1/9	7/3/0	1/2/7	10/0/0	10/0/0	10/0/0
<i>gt</i>	1/0/9	2/1/7	8/2/0	10/0/0	2/6/2	3/7/0	10/0/0
<i>kni</i>	1/1/8	1/1/8	9/1/0	6/4/0	10/0/0	0/2/8	8/2/0



Activation



No Interaction  
(cutoff = 0.01)



Repression



Weak Constraint

N = 10

$$\frac{dv_i^a}{dt} = R_a g_a \left( \sum_{b=1}^N T^{ab} v_i^b + m^a v_i^{bcd} + h_a \right)$$

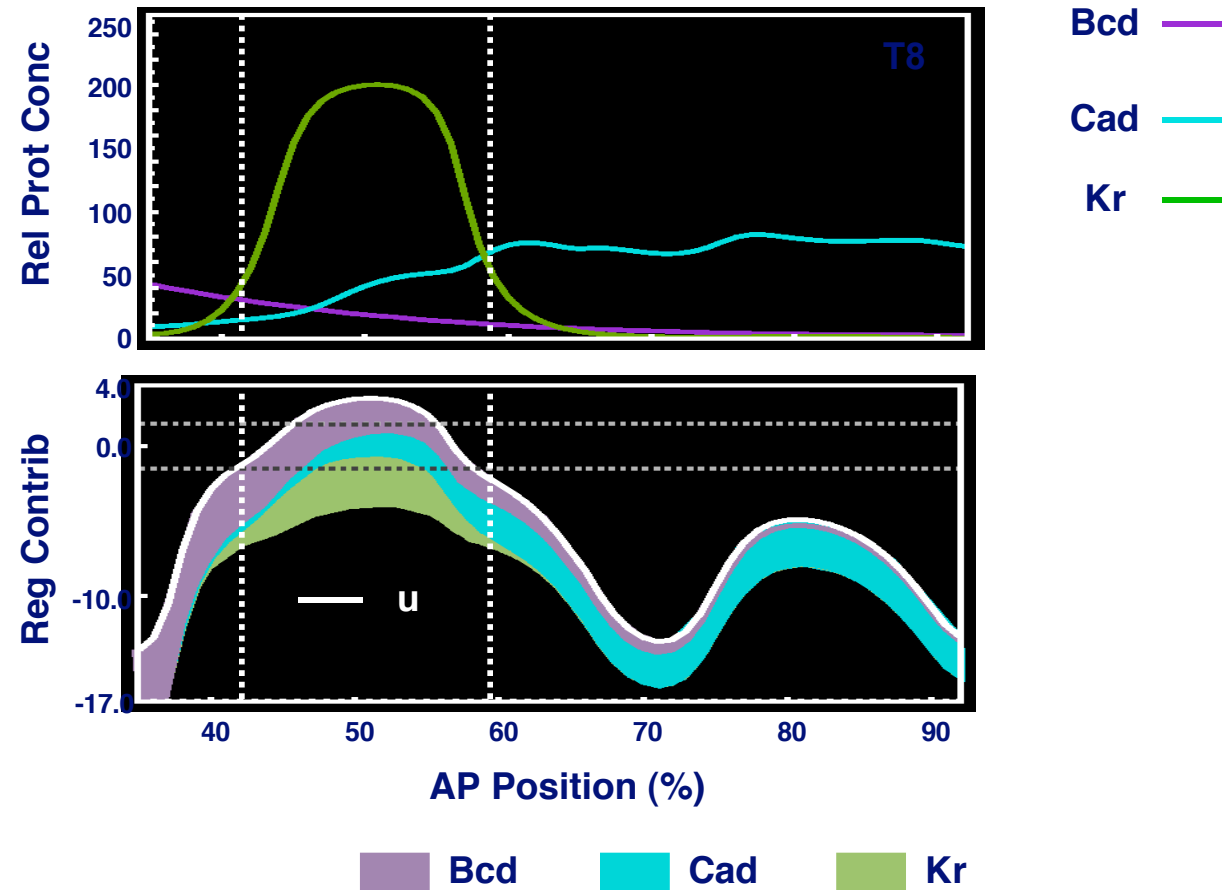
## Dynamic dissection:

We can look at individual parts of this sum to ‘dissect’ the various regulatory contributions on a specific gene.

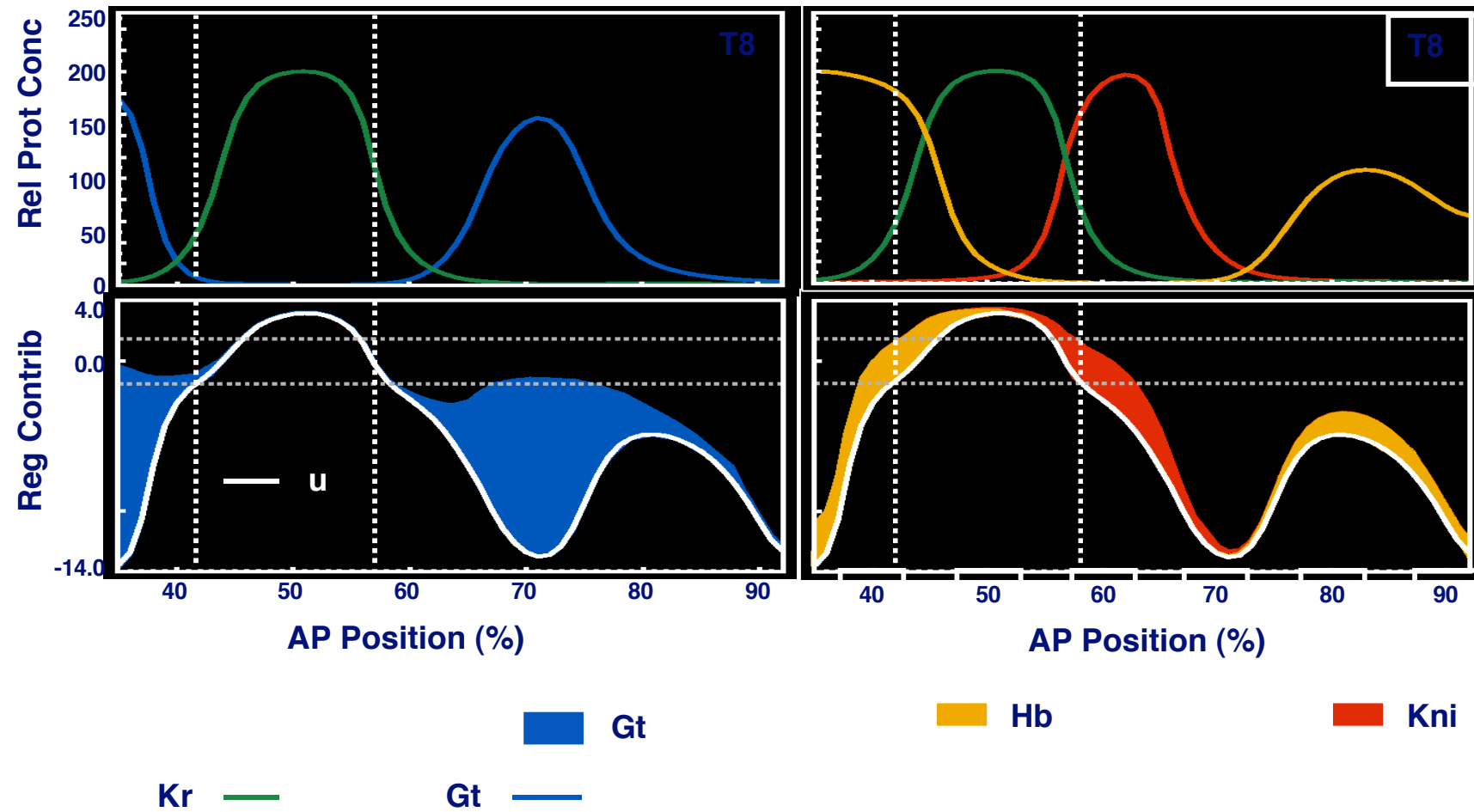
For example:

$T^{Kr \rightarrow hb} v^{Kr}$  represents Kr’s regulatory input on *hb*

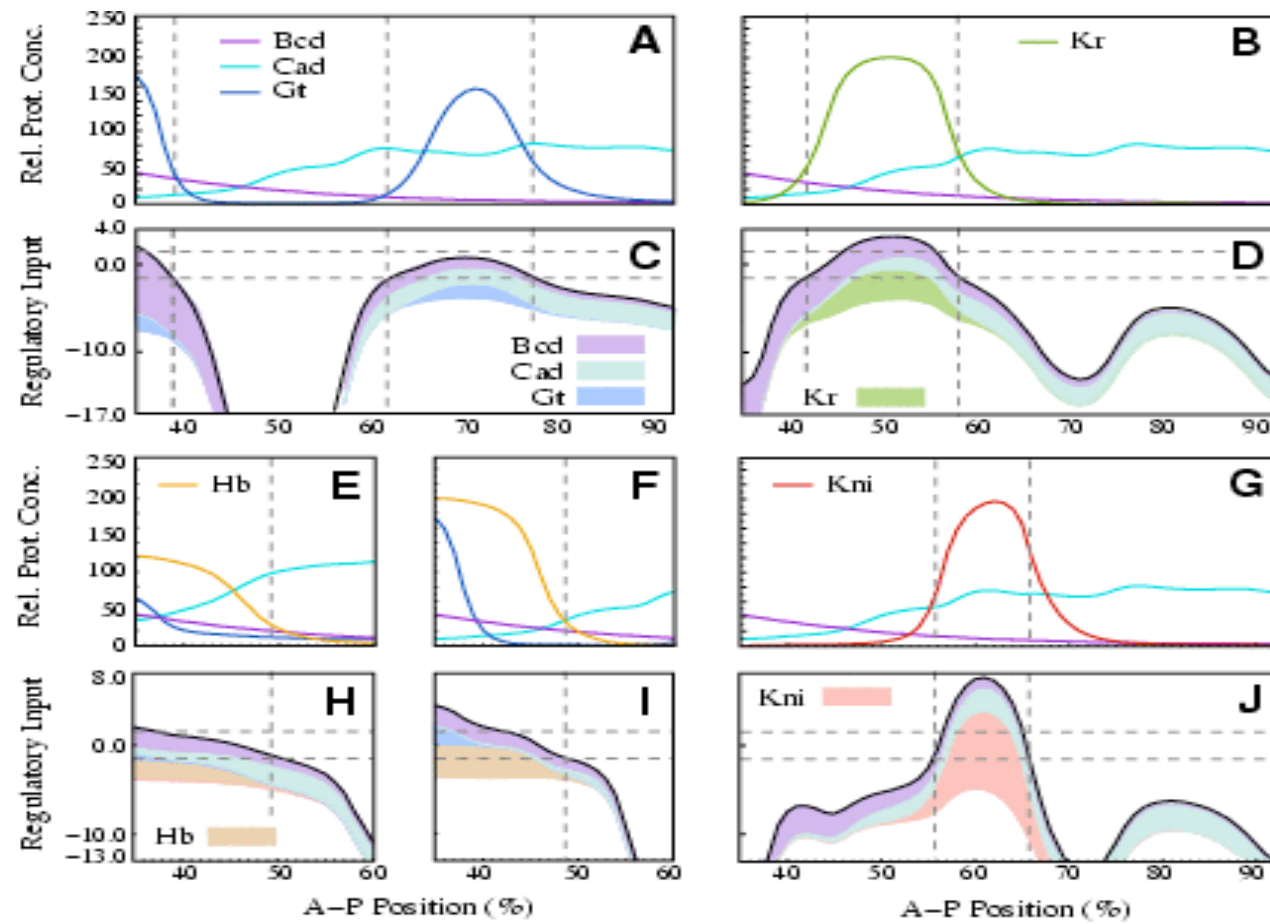
# Graphical analysis of gap gene regulation: boundary control by activation



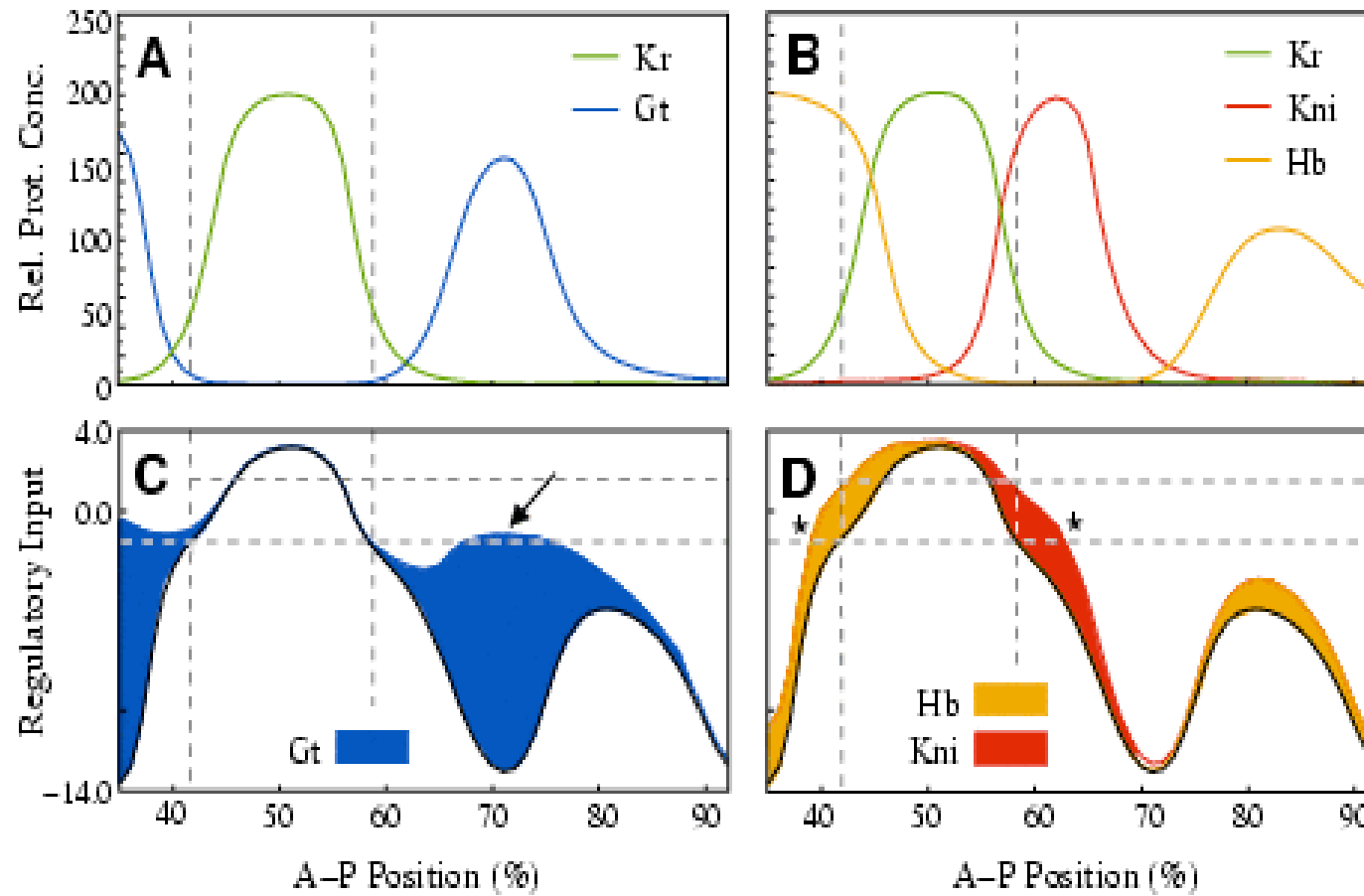
# Graphical analysis of gap gene regulation: boundary control by repression



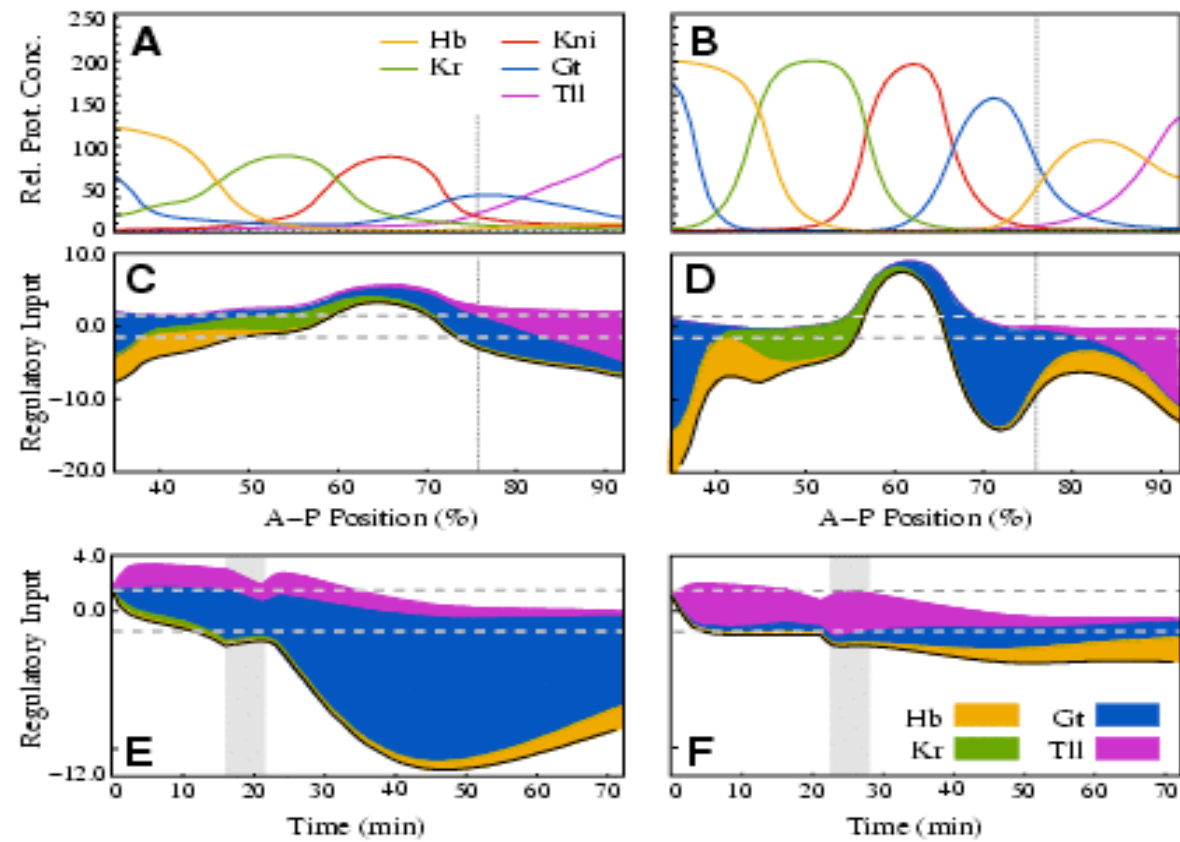
# Gap gene activation



## Kr repression



# Kni repression





# Constraints on the T Matrix

	<i>bcd</i>	<i>cad</i>	<i>hb</i>	<i>Kr</i>	<i>gt</i>	<i>kni</i>	<i>tll</i>
<i>hb</i>	0/1/9	3/1/6	2/2/6	4/6/0	2/4/4	10/0/0	3/5/2
<i>Kr</i>	0/0/10	0/1/9	7/3/0	1/2/7	10/0/0	10/0/0	10/0/0
<i>gt</i>	1/0/9	2/1/7	8/2/0	10/0/0	2/6/2	3/7/0	10/0/0
<i>kni</i>	1/1/8	1/1/8	9/1/0	6/4/0	10/0/0	0/2/8	8/2/0



Activation



No Interaction  
(cutoff = 0.01)



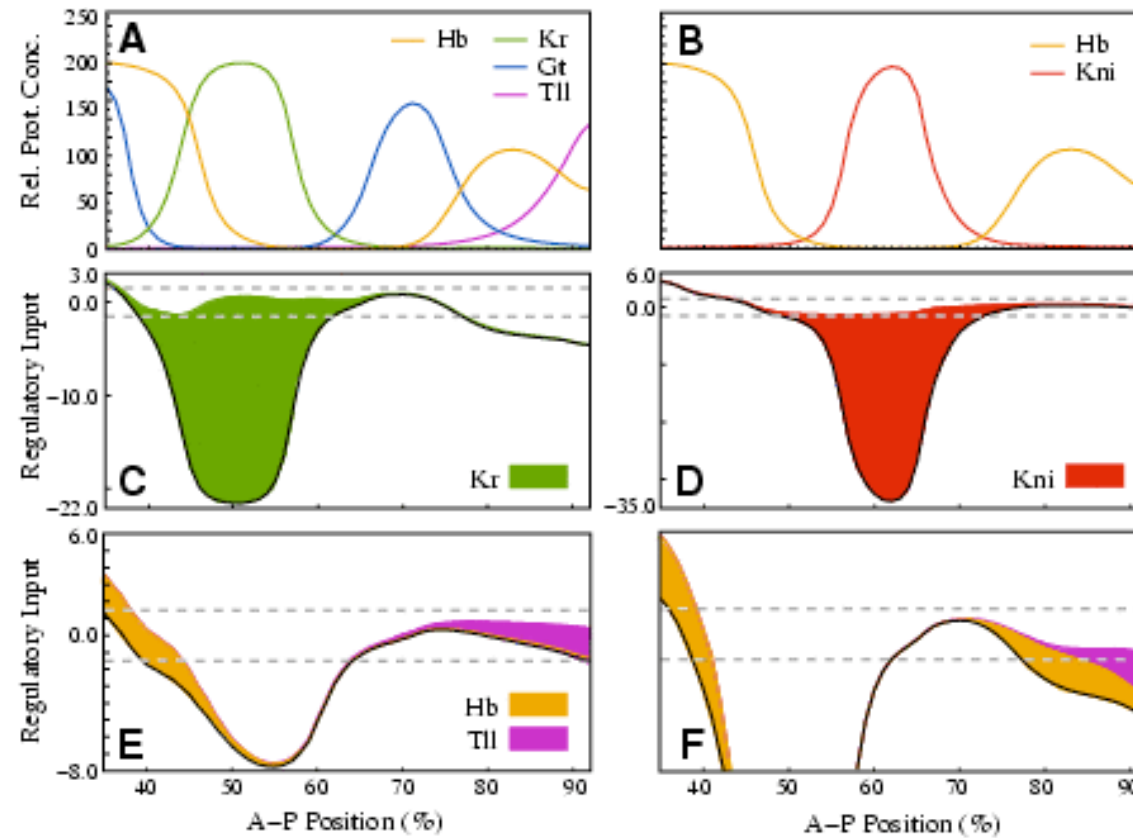
Repression

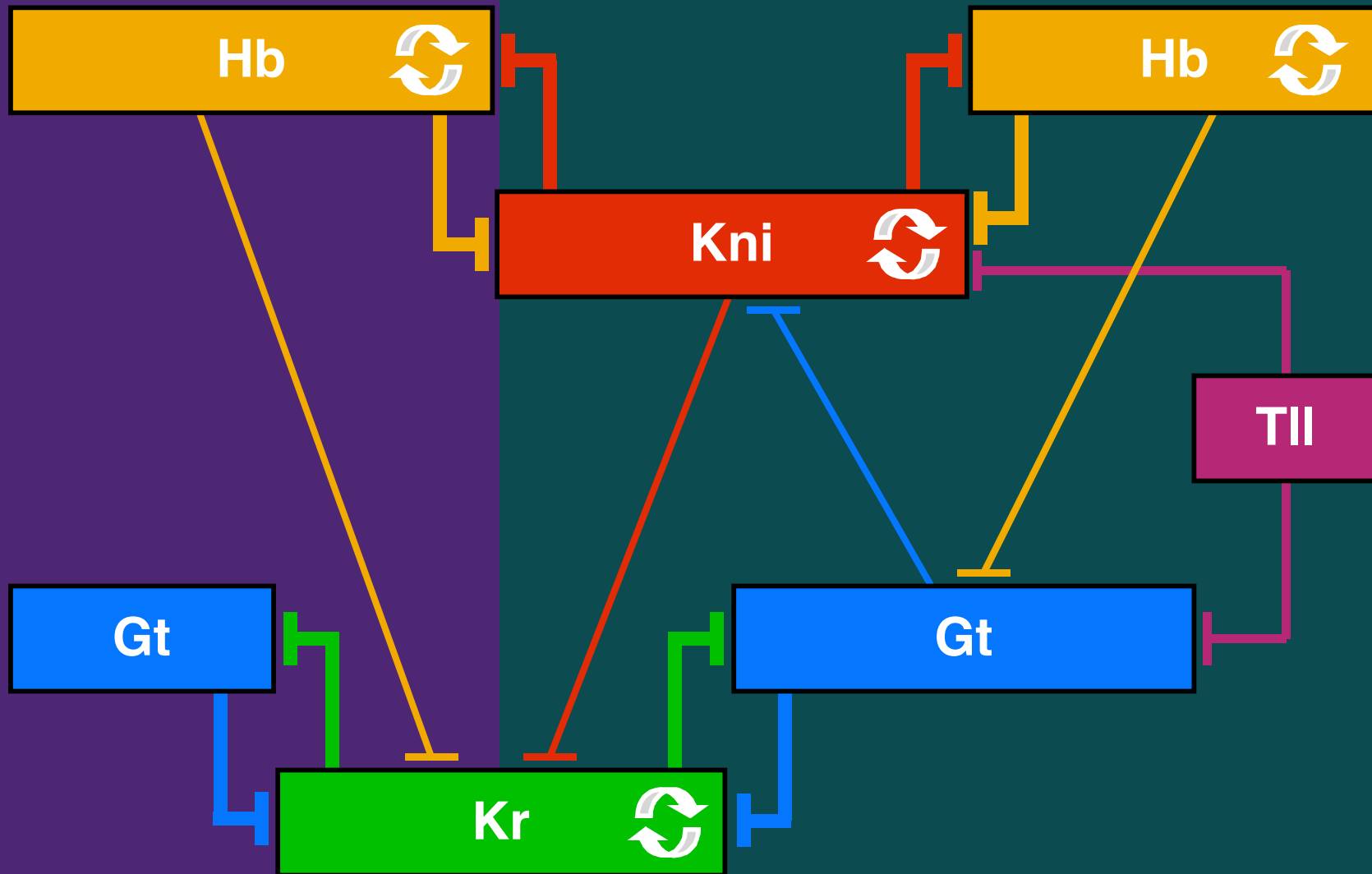


Weak Constraint

N = 10

## Gt and hb repression



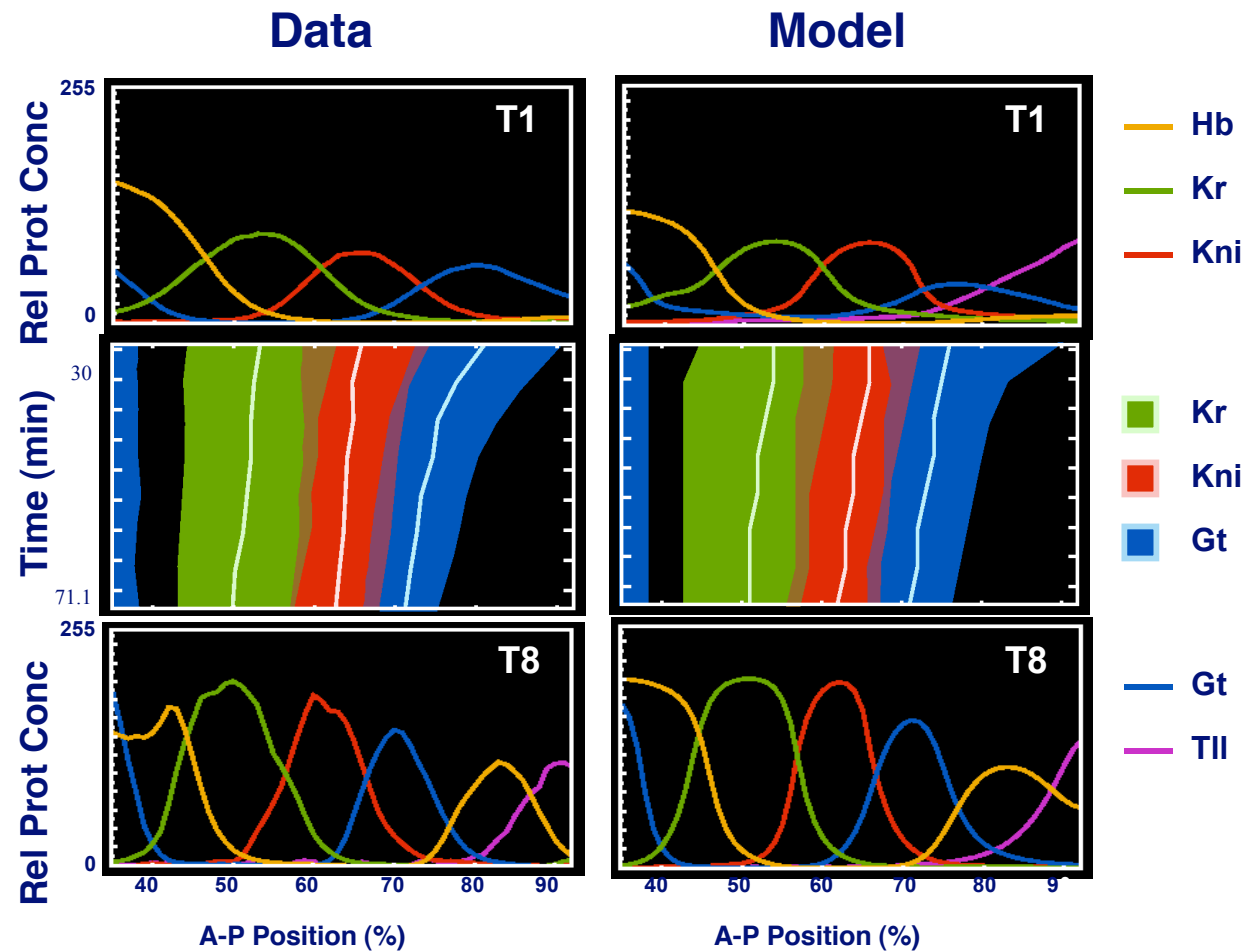


Bcd

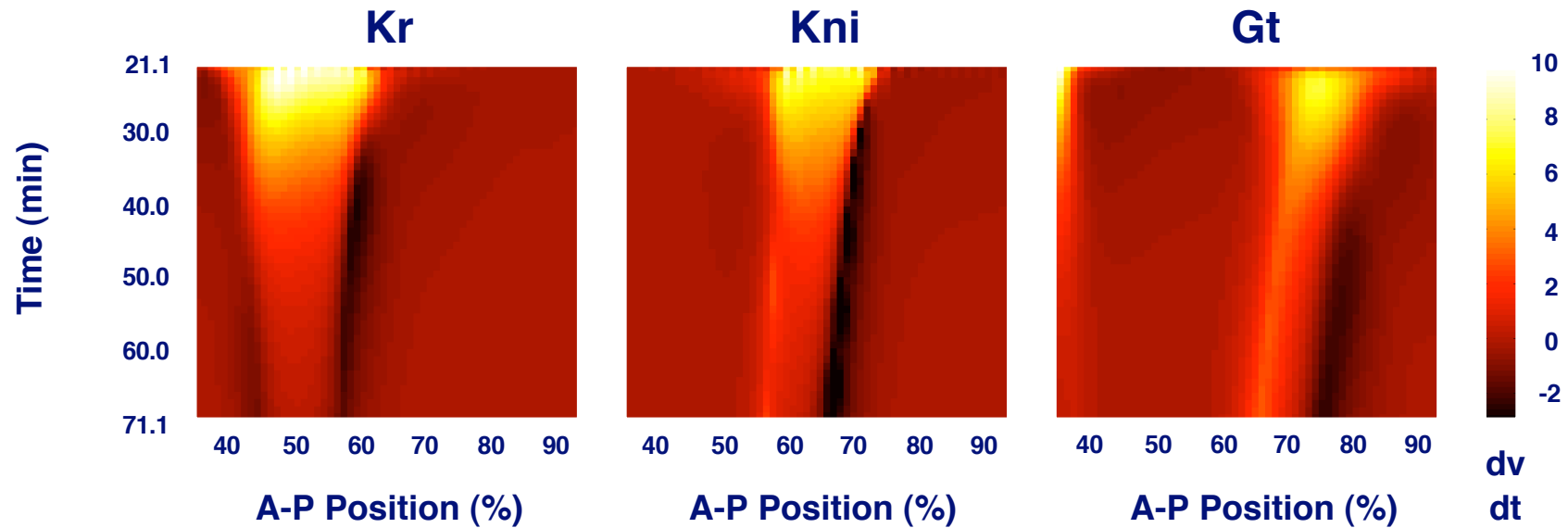
Cad

Jaeger, Samsonova, Reinitz et al. (2004) Genetics, in press.

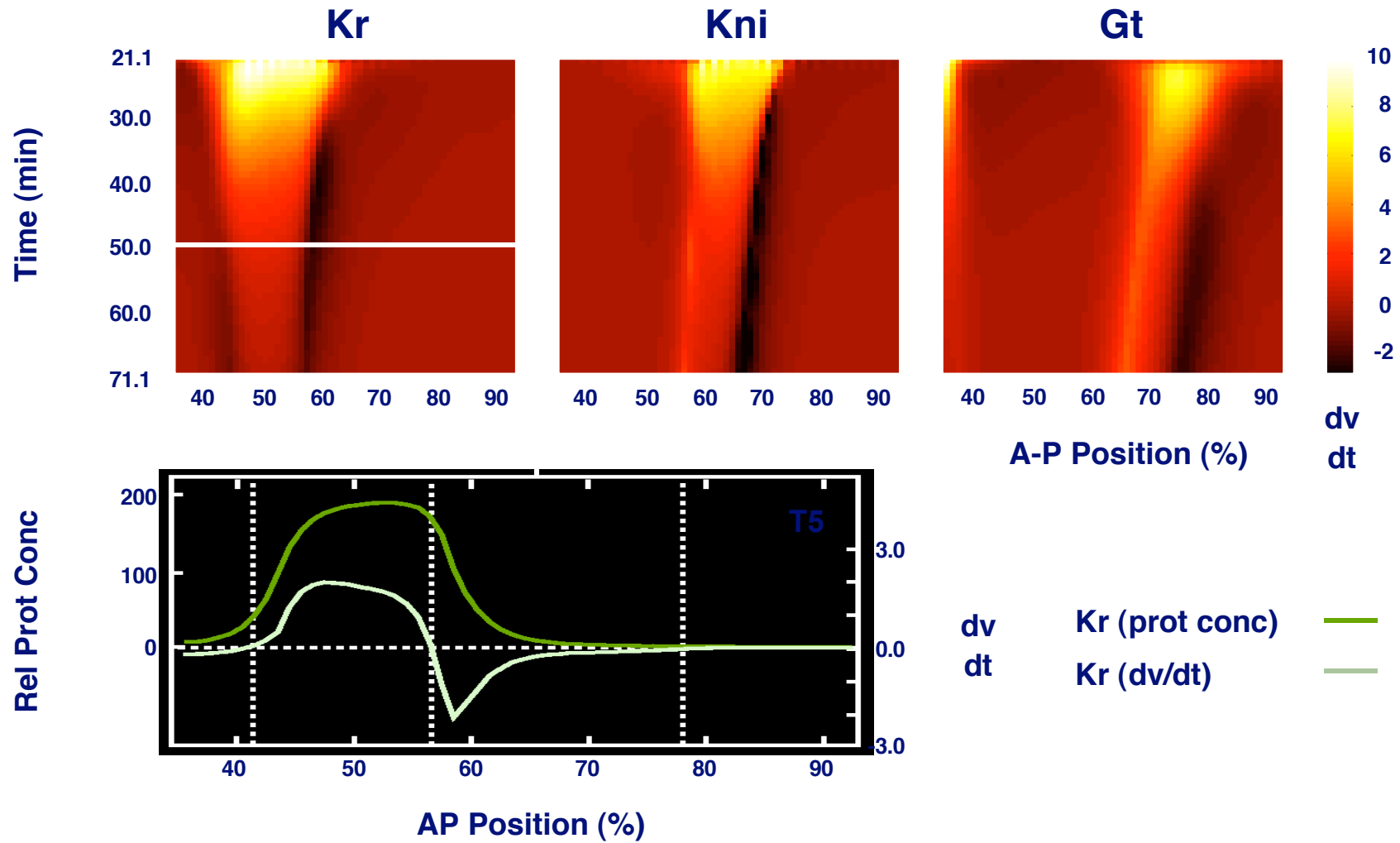
# Gap Gene Expression



# Domain Shifts: Mechanism



## Spatial Dynamics: Domains of Synthesis and Decay

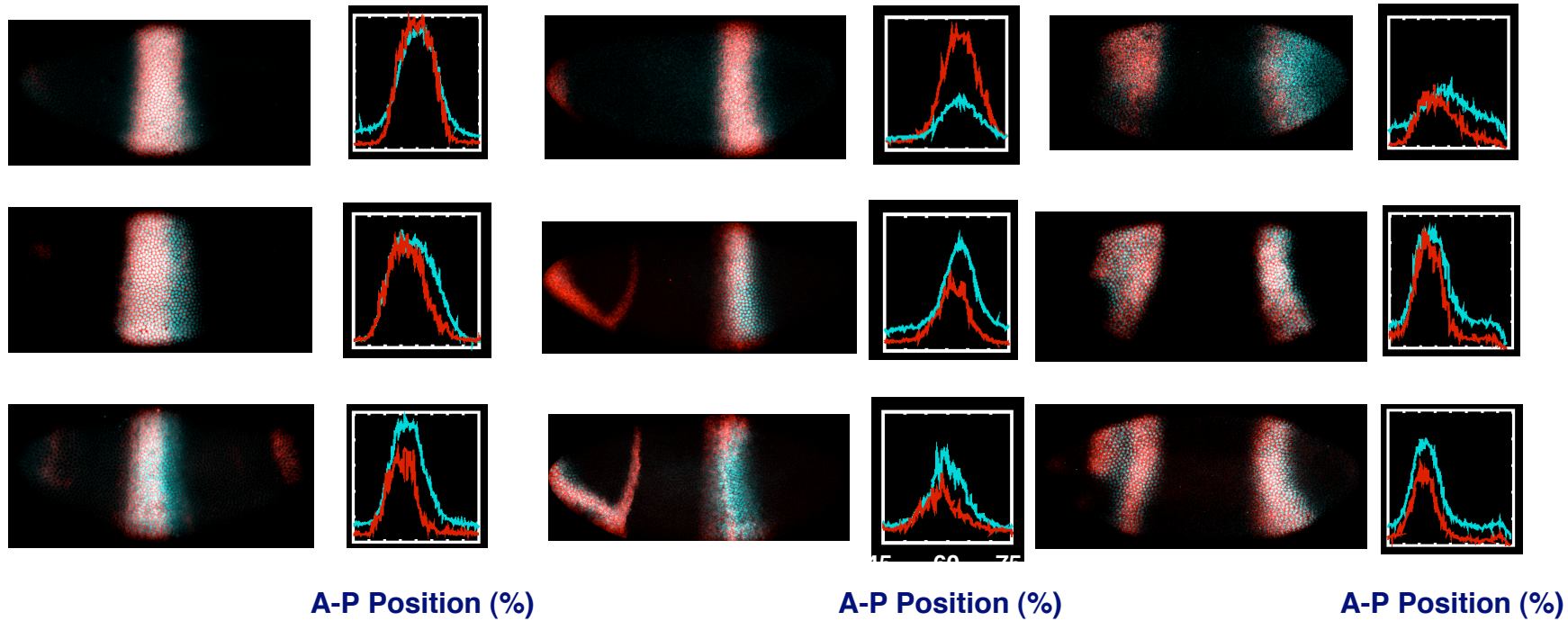


# Gap Domains: RNA vs Protein

*Kr*

*kni*

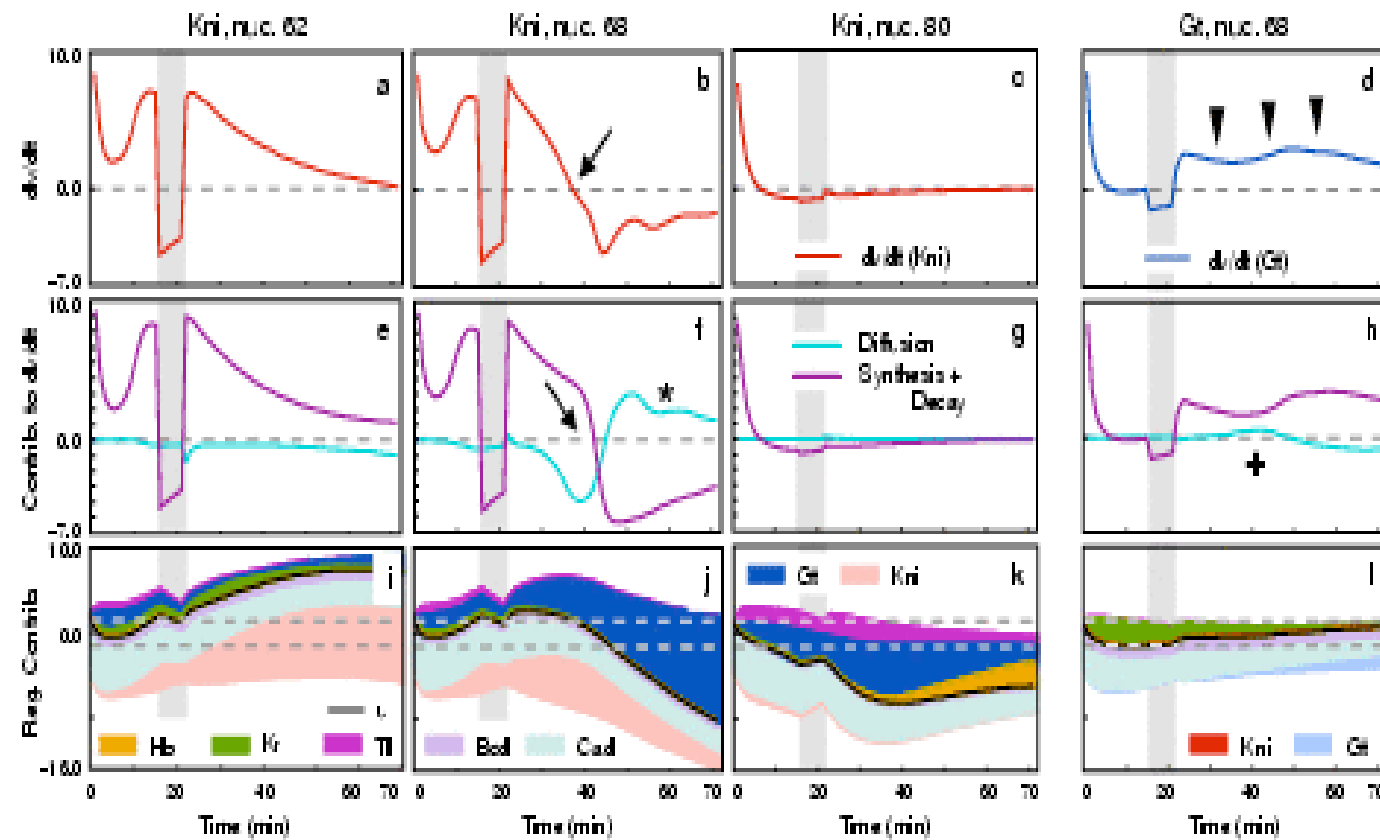
*gt*



RNA  
Protein

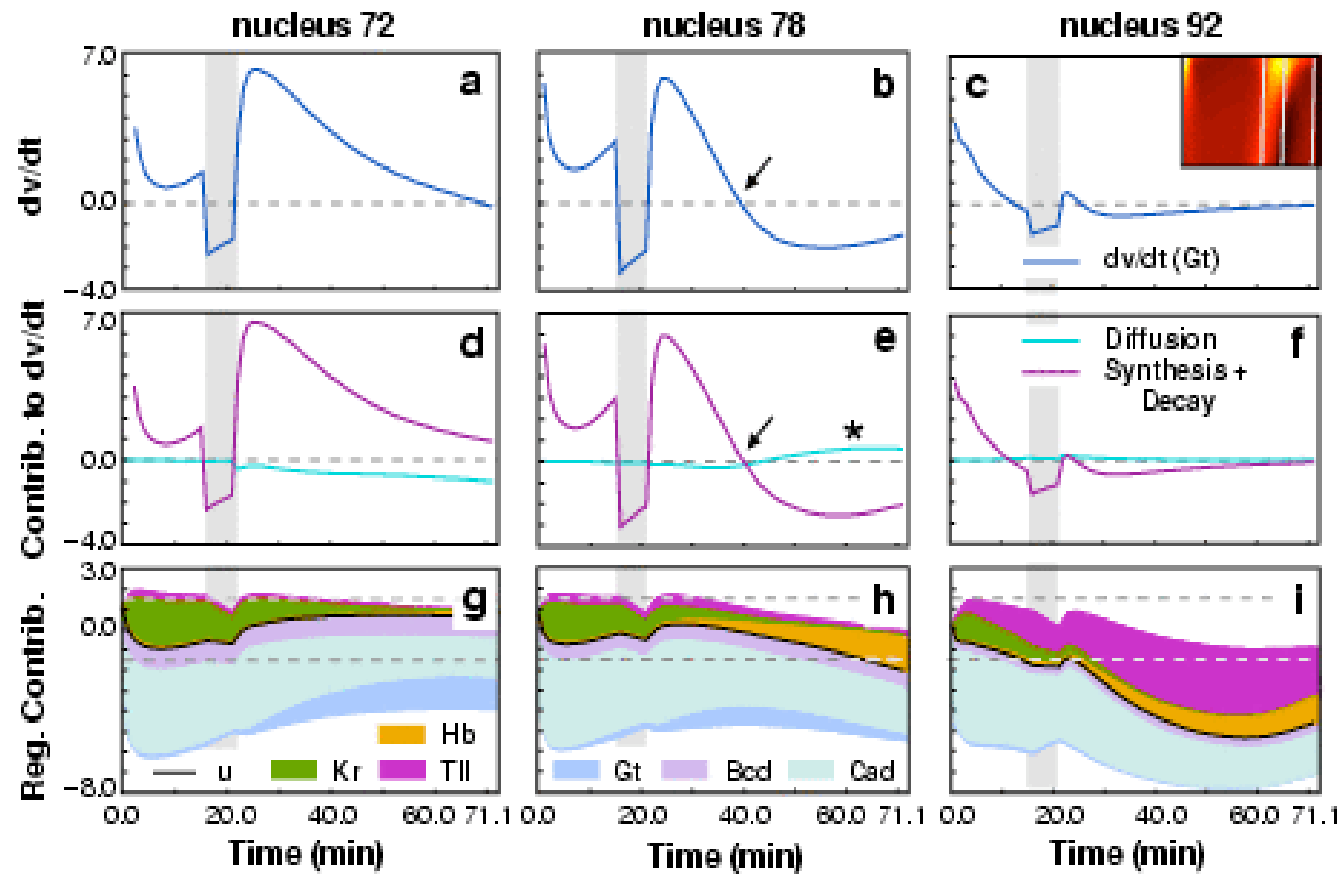
RNA  
Protein

# Shift in the posterior *kni* boundary





# Shift in the posterior boundary of the posterior *gt* domain



# Constraints on the T Matrix

	<i>bcd</i>	<i>cad</i>	<i>hb</i>	<i>Kr</i>	<i>gt</i>	<i>kni</i>	<i>tll</i>
<i>hb</i>	0/1/9	3/1/6	2/2/6	4/6/0	2/4/4	10/0/0	3/5/2
<i>Kr</i>	0/0/10	0/1/9	7/3/0	1/2/7	10/0/0	10/0/0	10/0/0
<i>gt</i>	1/0/9	2/1/7	8/2/0	10/0/0	2/6/2	3/7/0	10/0/0
<i>kni</i>	1/1/8	1/1/8	9/1/0	6/4/0	10/0/0	0/2/8	8/2/0



Activation



No Interaction  
(cutoff = 0.01)



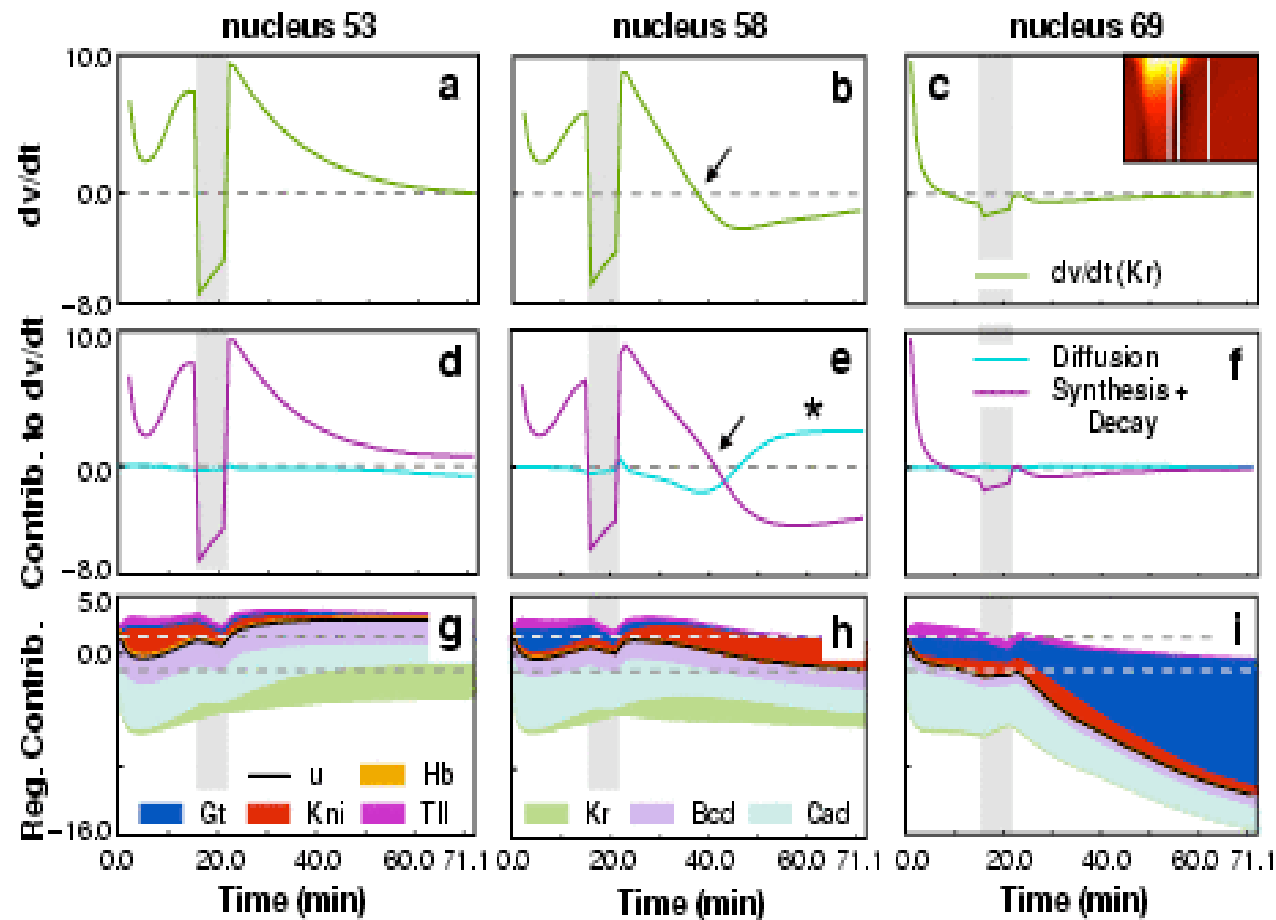
Repression



Weak Constraint

N = 10

# Shift in the posterior Kr boundary



# Constraints on the T Matrix

	<i>bcd</i>	<i>cad</i>	<i>hb</i>	<i>Kr</i>	<i>gt</i>	<i>kni</i>	<i>tll</i>
<i>hb</i>	0/1/9	3/1/6	2/2/6	4/6/0	2/4/4	10/0/0	3/5/2
<i>Kr</i>	0/0/10	0/1/9	7/3/0	1/2/7	10/0/0	10/0/0	10/0/0
<i>gt</i>	1/0/9	2/1/7	8/2/0	10/0/0	2/6/2	3/7/0	10/0/0
<i>kni</i>	1/1/8	1/1/8	9/1/0	6/4/0	10/0/0	0/2/8	8/2/0



Activation



No Interaction  
(cutoff = 0.01)



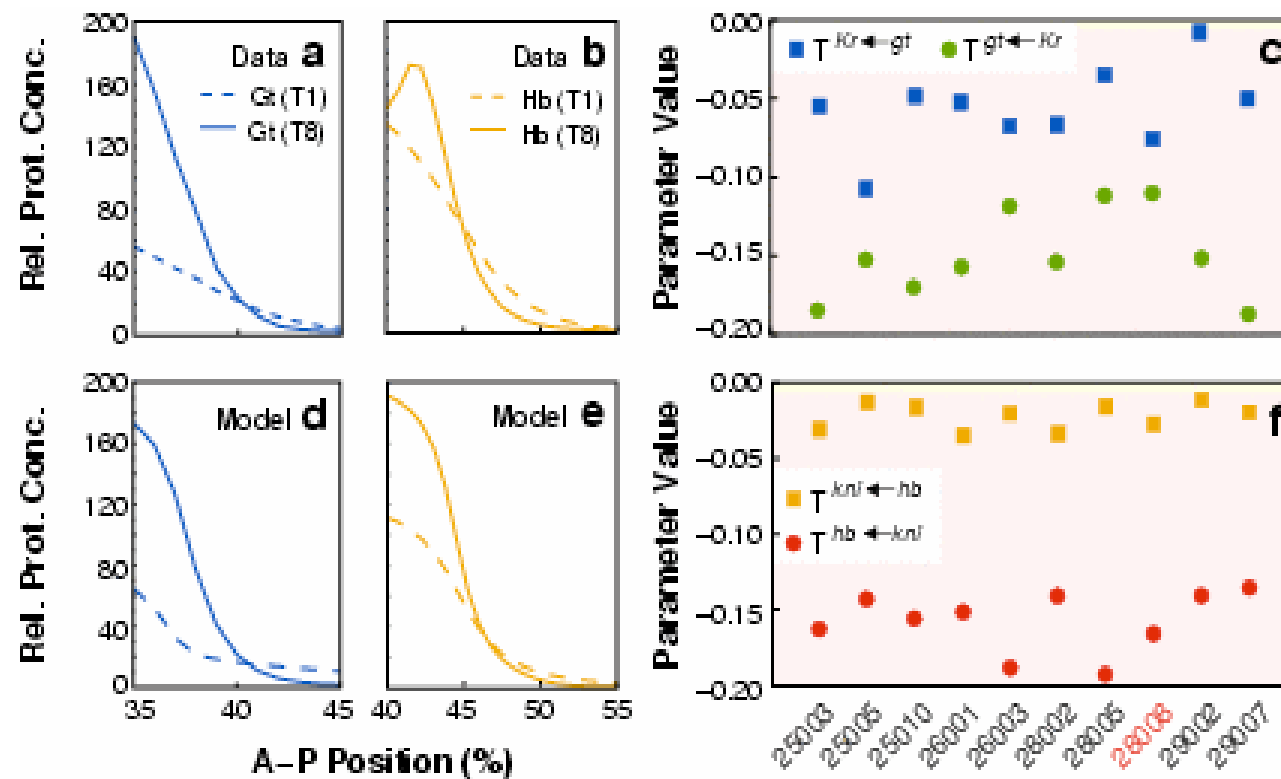
Repression



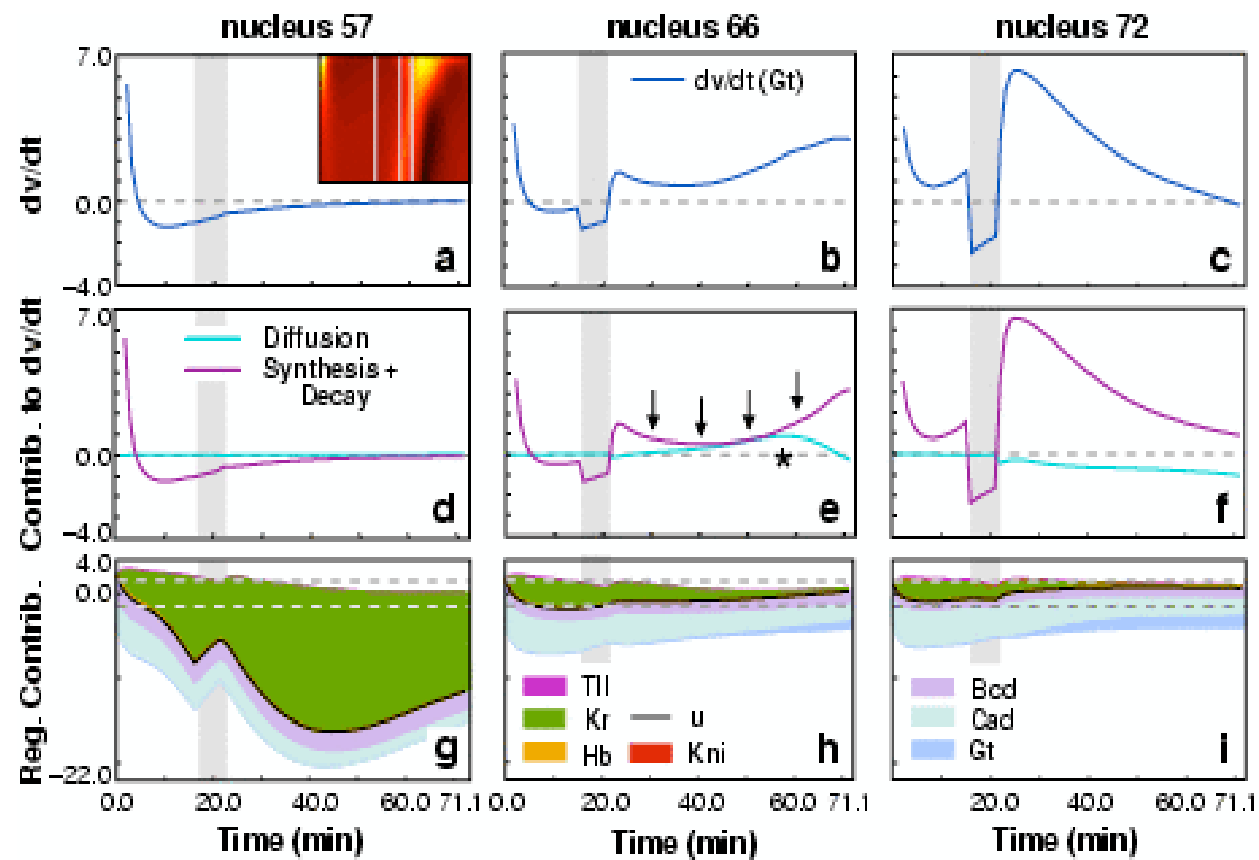
Weak Constraint

N = 10

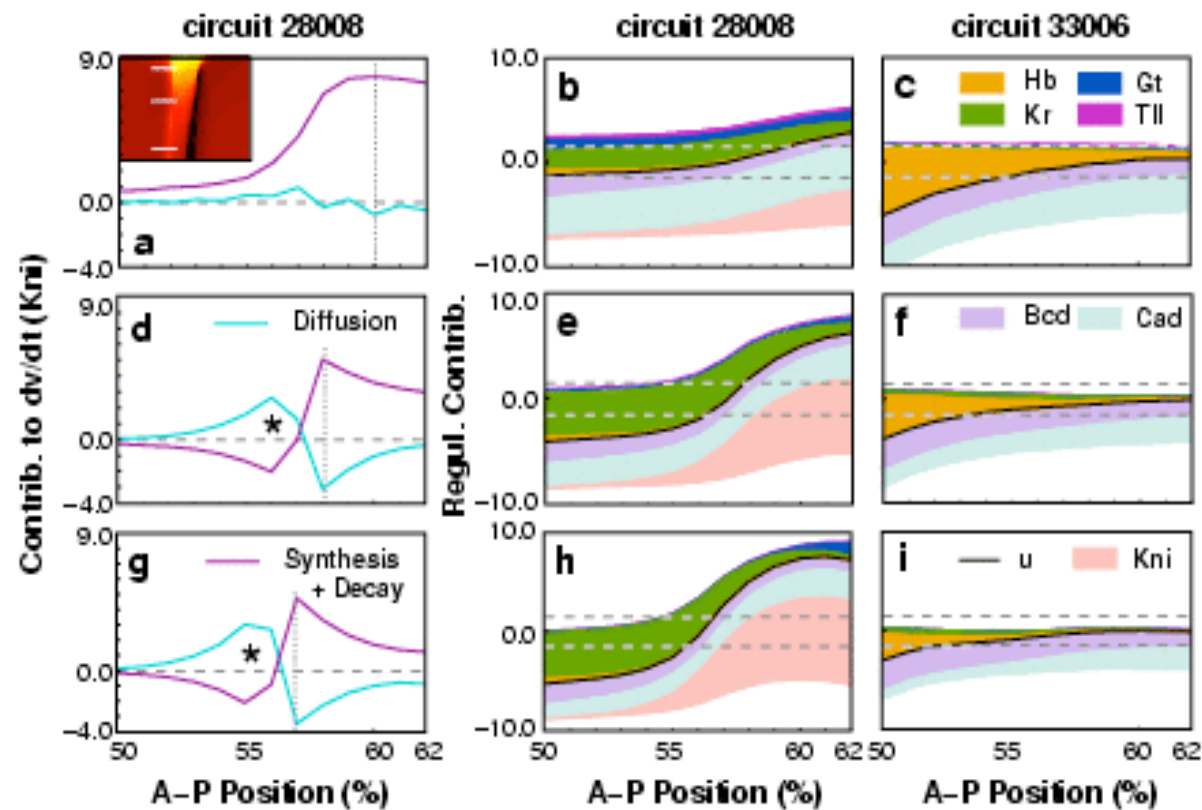
No shifts for the posterior boundaries  
of *gt* and *hb* anterior domains



# Shift in the anterior boundary of the posterior *gt* domain



# Shift in the anterior boundary of the posterior *kni* domain



# Posterior Boundaries

central *Kr* domain

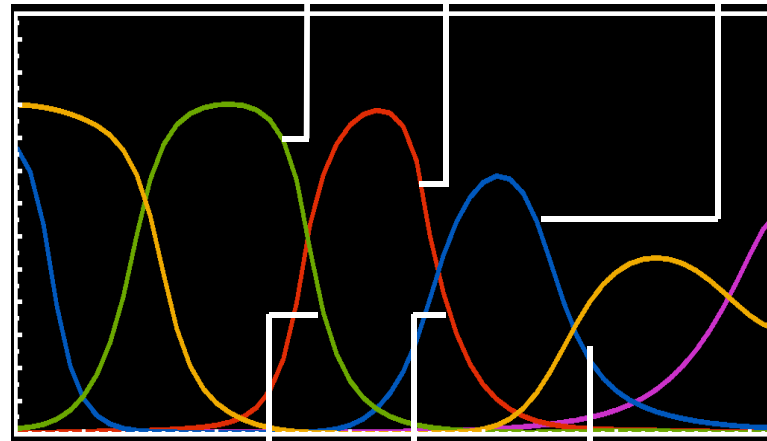
asymmetric repression by *Kni*

posterior *kni* domain

asymmetric repression by *Gt*

posterior *gt* domain

asymmetric repression by *Hb*



posterior *kni* domain

follows sharpening of

posterior boundary of anterior *hb*

posterior boundary of posterior *kni*

posterior *gt* domain

follows shift of

posterior boundary of central *Kr*

posterior *hb* domain

follows shift of

# Anterior Boundaries



# Posterior Boundaries

anterior *hb* domain

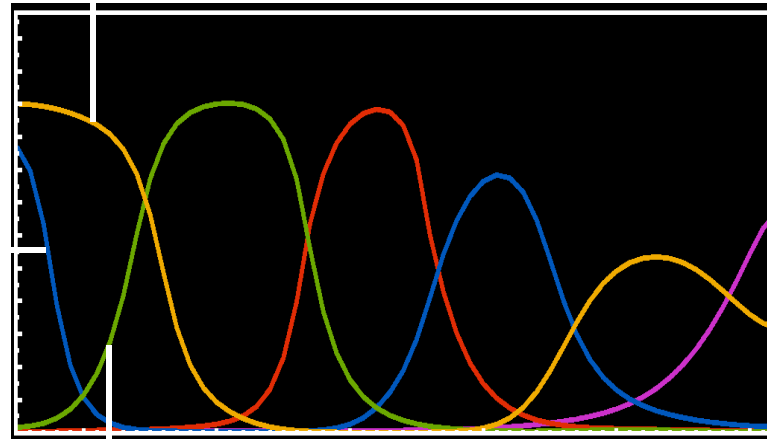
no shift

strong repression by **Kni**

anterior *gt* domain

no shift

strong repression by **Kr**



central *Kr* domain

very small shift

diffusion

early insufficient repression by *Gt*

# Anterior Boundaries

# Conclusions

- ❑ Proper positioning of gap gene domains requires specific regulatory interactions between gap genes.
- ❑ Positional information in early embryo is dynamic and can no longer be seen as a static coordinate system imposed on embryo by maternal genes.
- ❑ Posterior domains shift because of regulative cross-interactions. Anterior domains form in place under the control of maternal positional information. Thus, a mosaic mode of development prevails in the anterior and a regulative mode in the posterior of an embryo.
- ❑ Bcd is a Turing morphogen, not a modern morphogen, since it does not determine different territories of gene expression directly.

# Acknowledgments

## St. Petersburg

Alexander Samsonov

Maxim Blagov

Vitaly Gursky

Konstantin Kozlov

Dimitry Malashonok

Ekaterina Myasnikova

Andrei Pisarev

Ekaterina Poustelnikova

Anastassia Samsonova

Svetlana Surkova

<http://urchin.spbcas.ru/flyex>

<http://flyex.ams.sunysb.edu/flyex>

## Stony Brook

Carlos Alonso

Jean Cadet

Lucas Carey

King-Wai Chu

Yuefan Deng

Lorraine Greenwald

Hilde Janssens

Johannes Jaeger

Dave Kosman

Manu

Alexander Spirov

## Los Alamos

Shuling Hou