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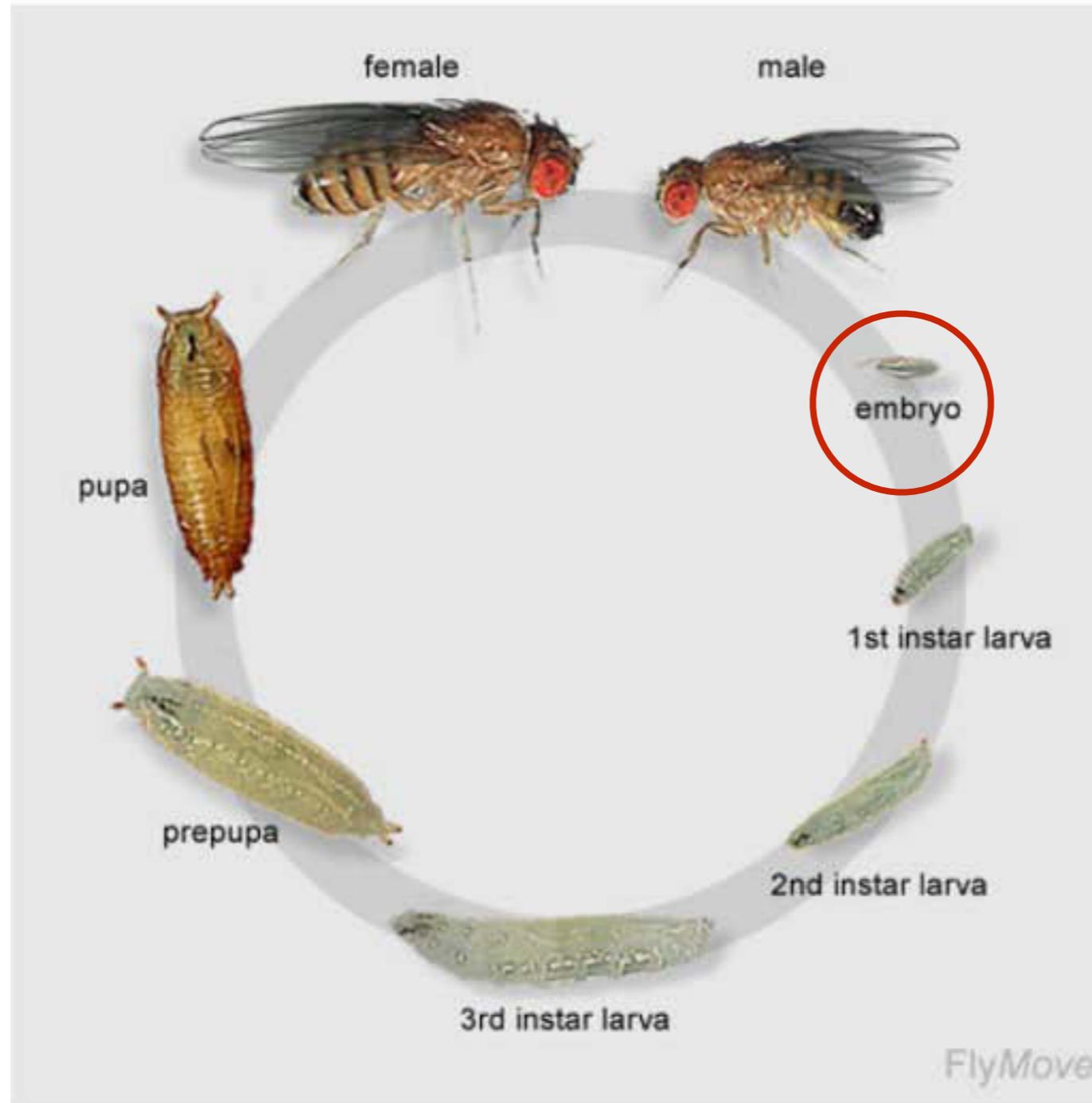
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# **Diffusion-reaction in developing early embryos to measure length**

# *Drosophila melanogaster* (fruit fly) developmental cycle

9 days



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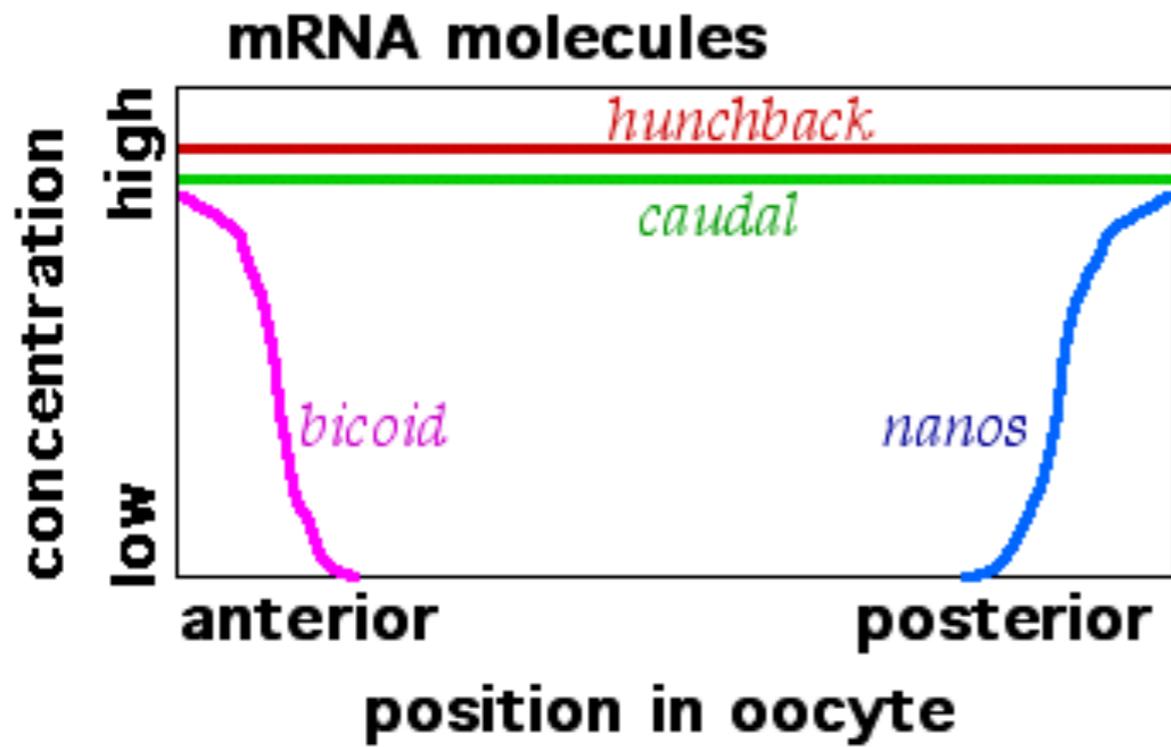
Screenshot of Edward B. Lewis, Christiane Nüsslein-Volhard, Eric F. Wieschaus, [The Nobel Prize in Physiology or Medicine 1995 winners](#) removed due to copyright restrictions.

# make a super simple fruit fly trap



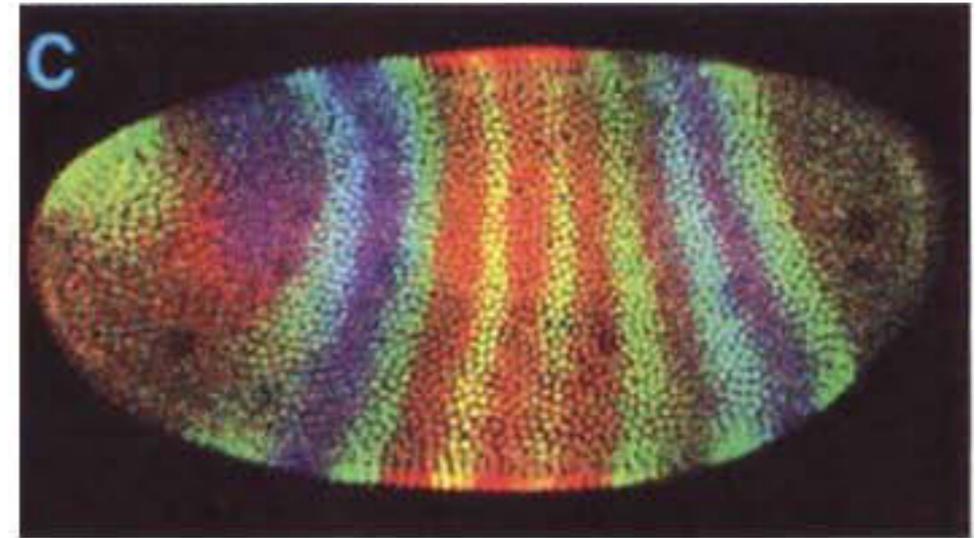
## Materials:

- small glass bowl
- wine or juice
- dish soap
- plastic wrap
- bamboo skewer



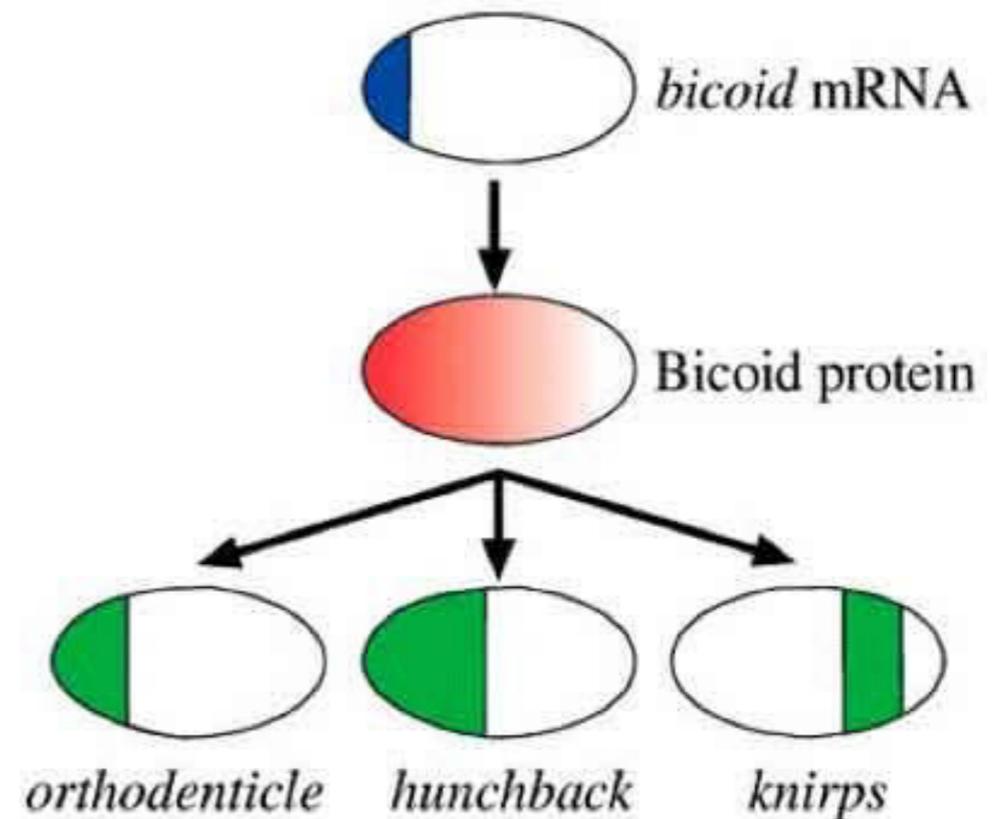
Courtesy of [Fred the Oyster](#); figure in the public domain.

Figure of *Drosophila* early embryo protein gradients removed due to copyright restrictions.



Hughes & Krause, *Methods Mol Biol*, 2008

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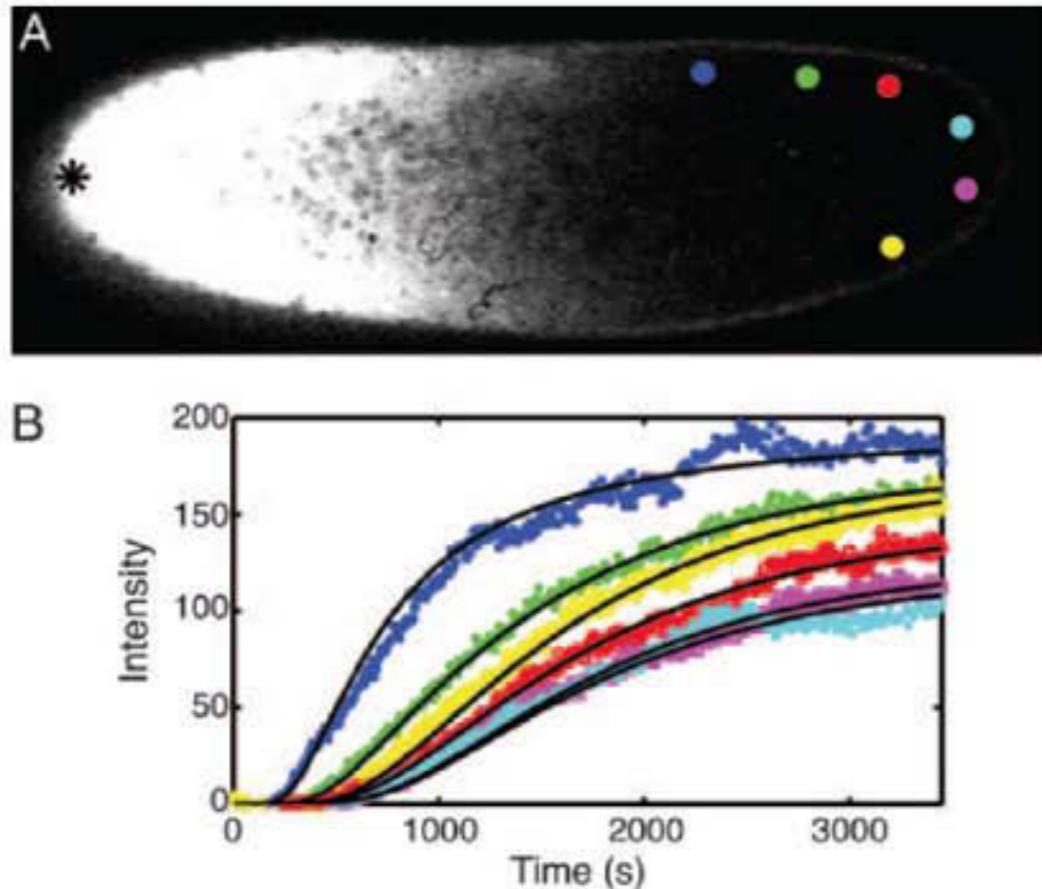
# Diffusion and scaling during early embryonic pattern formation

Thomas Gregor<sup>1,2,3,4</sup>, William Blalek<sup>1,2</sup>, Rob R. de Ruyter van Steveninck<sup>1</sup>, David W. Tank<sup>1,2</sup>, and Eric F. Wieschaus<sup>1,3,4</sup>

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Contributed by Eric F. Wieschaus, November 1, 2005

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**Fig. 1.** Diffusion of inert molecules in the *Drosophila* embryo. (A) Two-photon image of a wild-type *D. melanogaster* embryo 8 min after injection of fluorescently labeled dextran molecules at the mid-plane of the embryo. The tip of the glass micropipette used for the injection is located at the anterior pole (black asterisk on the left side of the image). Colored discs show areas where fluorescence intensity was analyzed. (B) Changes in the fluorescence intensity with time for the six color-corresponding discs in A, extracted from a time series of images taken with a frame rate of 8 s. Solid lines represent the time courses computed from the best fit of a numerical 3D diffusion model. Note that 18 curves (6 per focal plane) are fit by the solutions of the same diffusion equation, with only a single free parameter, the diffusion constant  $D$ . (C) Diffusion coefficients of dextran molecules of different hydrodynamic radii (red dots). The solid line represents diffusion coefficients expected from the modified Stokes-Einstein relation (10),  $D = k_B T / (6\pi\eta R) + b$ , with a viscosity  $\eta = 4.1 \pm 0.4$  cP and  $b = 6.2 \pm 1.0$   $\mu\text{m}^2/\text{s}$ ; dashed line is at the value of  $b$ .

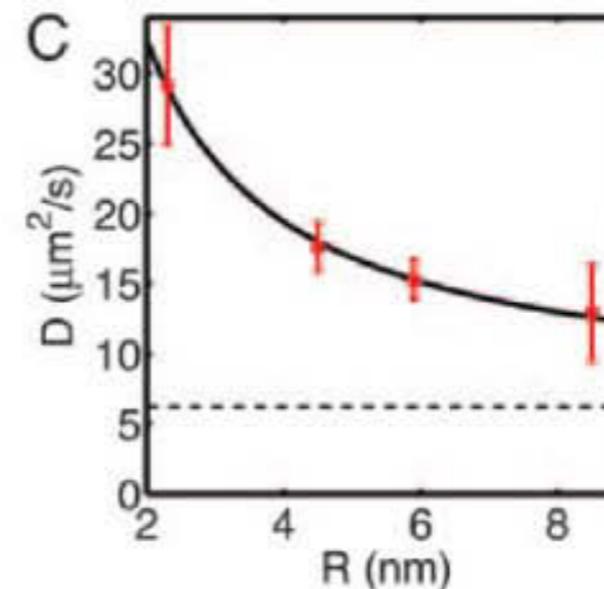
In the simplest model (14), Bcd protein diffuses through the embryo and decays with a lifetime  $\tau$ . The spatiotemporal dynamics of the concentration profile are determined by

$$\frac{\partial c(\vec{r}, t)}{\partial t} = D\nabla^2 c(\vec{r}, t) - \frac{1}{\tau} c(\vec{r}, t), \quad [1]$$

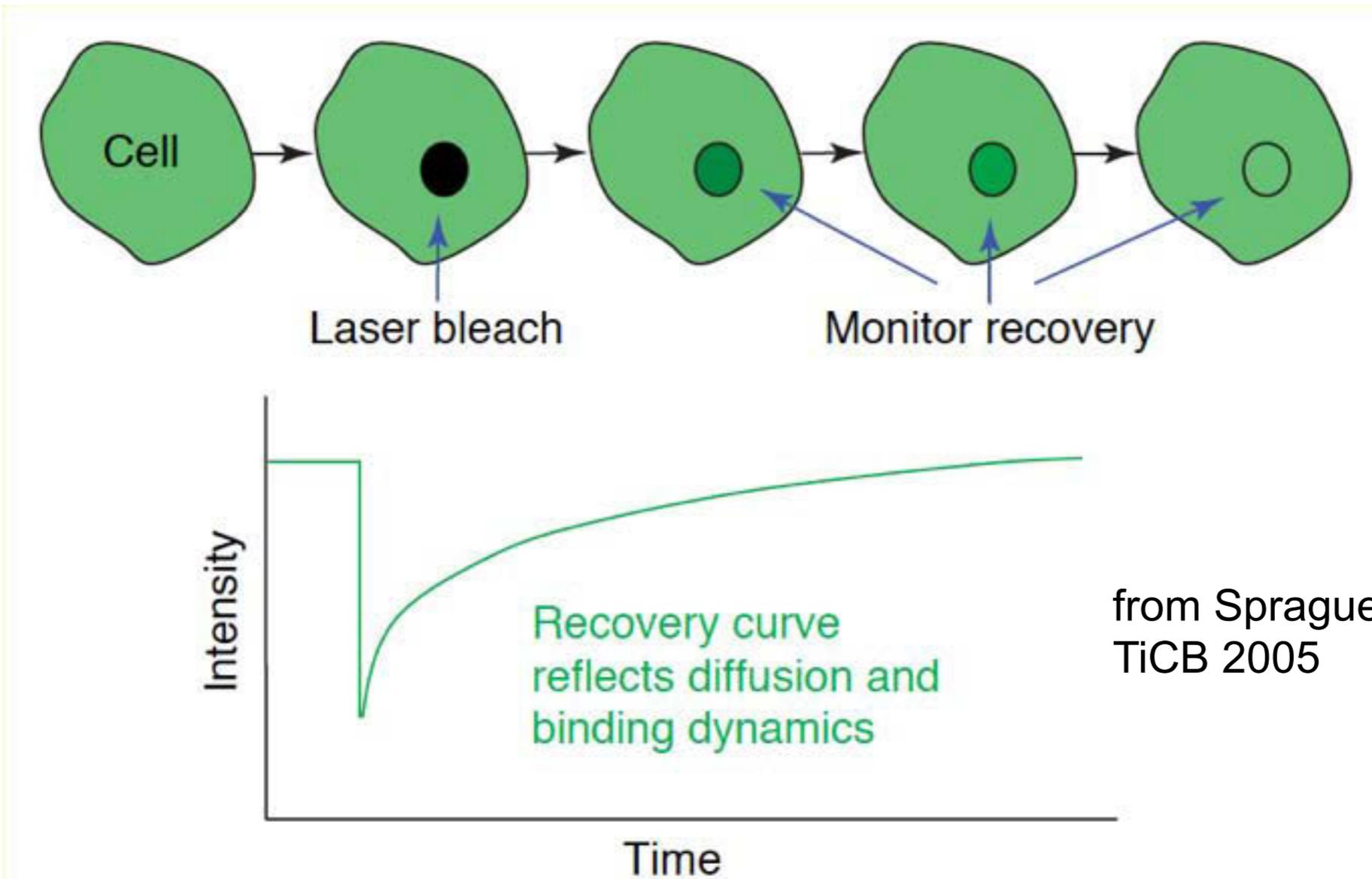
where  $D$  is the diffusion constant. The steady state therefore is determined by

$$D\nabla^2 c_{ss}(\vec{r}) = -\frac{1}{\tau} c_{ss}(\vec{r}). \quad [2]$$

If there is a source (translation of maternal RNA) at  $x = 0$  and no variations along the dorsal-ventral direction, then the solution, projected along the anteroposterior axis, is  $c_{ss}(x) = A \exp(-x/\lambda)$ , where  $\lambda = \sqrt{D\tau}$ , and the constant  $A$  is set to match the diffusive flux to the translation rate at  $x = 0$ ; this solution is valid if  $L/\lambda \gg 1$ , as observed. Identifying staining intensity as proportional to concentration, and allowing for background fluorescence  $B$ , the raw data of Bcd immunofluorescence intensities were fitted by  $I = A \exp(-x/\lambda) + B$  for abscissae  $x \in 15\text{--}85\%$  egg length. A nonlinear Nelder-Mead fitting procedure was used to estimate the parameters  $A$ ,  $B$ , and  $\lambda$  for each embryo (13).



# **Fluorescence Recovery After Photobleaching (FRAP) to measure diffusion and reaction in situ**



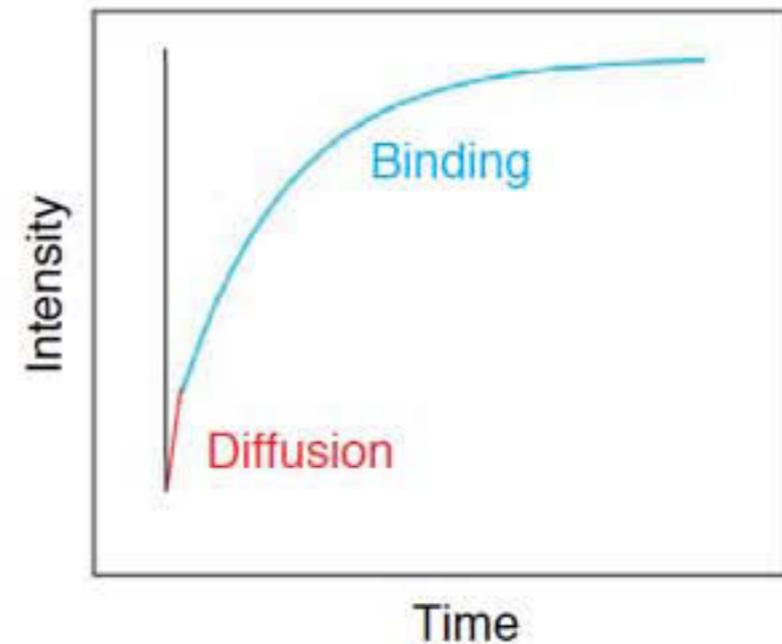
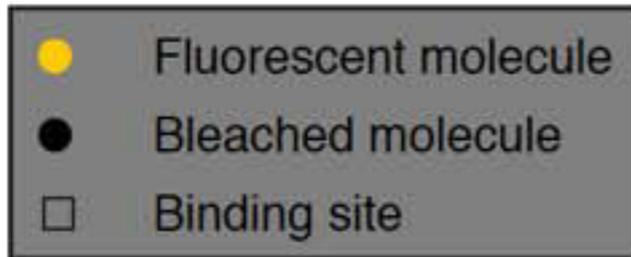
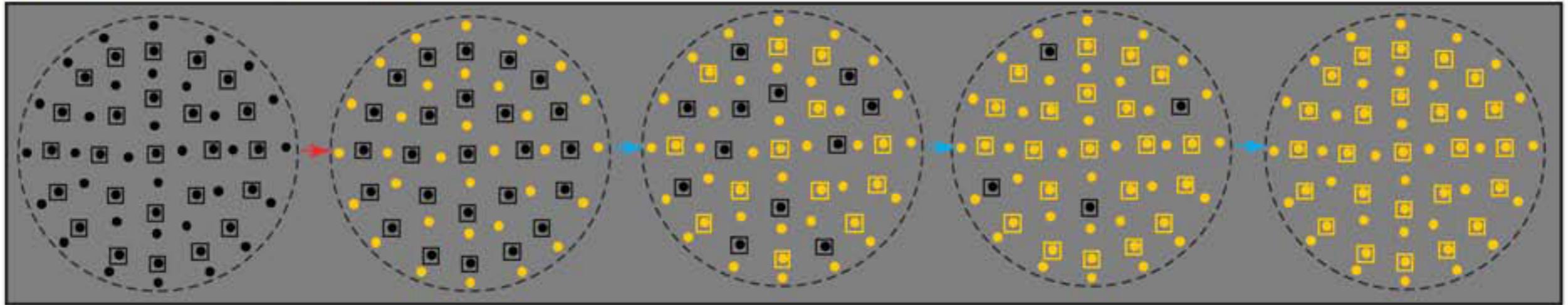
from Sprague & McNally  
TiCB 2005

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Source: Sprague, Brian L. and James G. McNally. "FRAP analysis of binding: proper and fitting." Trends in Cell Biology 15, no. 2 (2005): 84-91.

diffusion-dominated  
recovery:

$$\frac{\partial f}{\partial t} = D_f \nabla^2 f \quad \text{frap}(t) = f(t) = e^{-\frac{\tau_D}{2t}} \left[ I_0 \left( \frac{\tau_D}{2t} \right) + I_1 \left( \frac{\tau_D}{2t} \right) \right]$$

(a) Diffusion-uncoupled FRAP

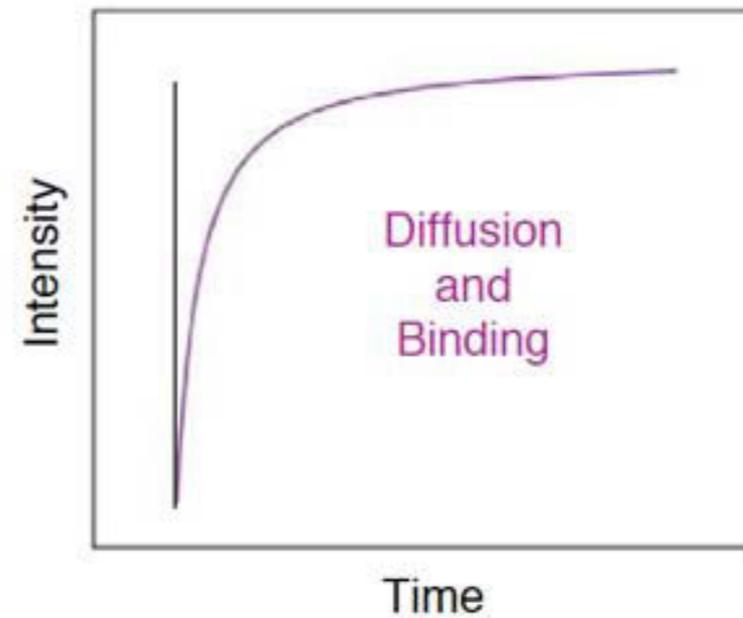
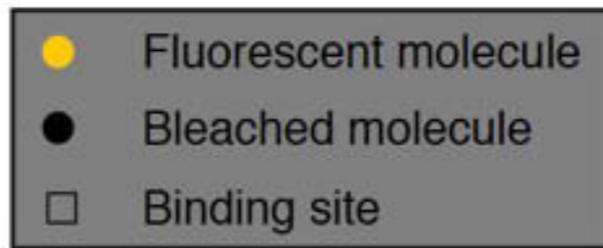
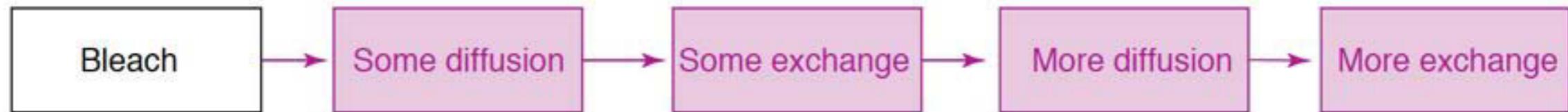
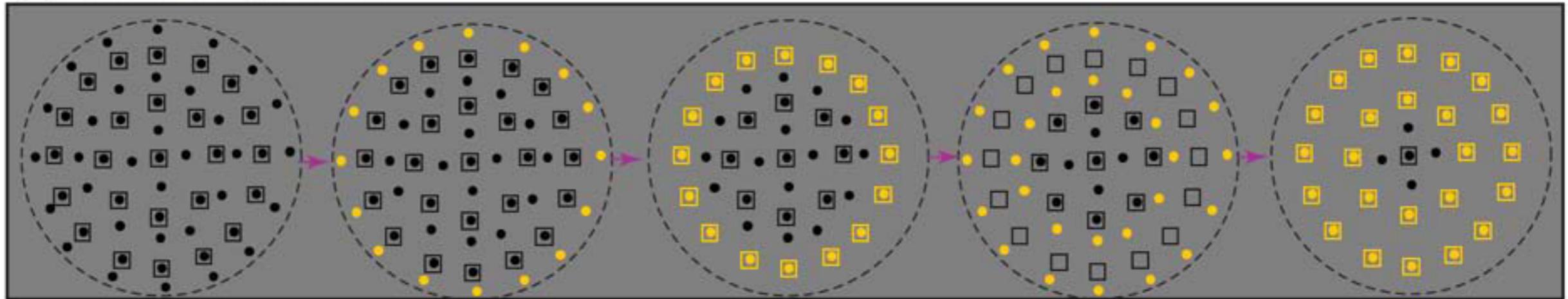


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 Source: Sprague, Brian L. and James G. McNally. "FRAP analysis of binding: proper and fitting." Trends in Cell Biology 15, no. 2 (2005): 84-91.

reaction-dominated  
(off-rate) recovery:

$$frap(t) = 1 - C_{eq} e^{-k_{off}t}$$

(b) Diffusion-coupled FRAP



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effective diffusion  
recovery:

$$\frac{\partial f}{\partial t} = D_f \nabla^2 f - k_{\text{on}}^* f + k_{\text{off}} c \quad D_{\text{eff}} = \frac{D_f}{(1 + (k_{\text{on}}^*/k_{\text{off}}))}$$

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