Anterior-Posterior Development in Flies

How does a growing embryo form into a complex organism? This is a complicated question, but one place to start is to just ask – how does the embryo pick a front side and a back side? We will consider a simple scenario believed to be true in, at the very least, some species of flies.

A simple mechanism to do this is as follows: imagine placing a source of a protein somewhere in the embryo. This protein diffuses and decays around in the cell, and where this protein is present, the embryo develops its back side. Where it isn't present, the cell develops its front side. In flies, this protein is called "bicoid". Now, let us model the bicoid as a diffusive protein with diffusion constant D, and a decay time τ. For simplicity, we will assume that the bicoid is constrained to the outer shell of the embryo, which we model as a cylinder of radius R and length $L \gg R$. If the bicoid only effectively moves along the length of the embryo (remember, we're only trying to distinguish between front and back), we can model the bicoid as obeying the 1D diffusion equation

$$\frac{\partial c}{\partial t} = D\frac{\partial^2 c}{\partial x^2} - \frac{c}{\tau}.$$

Here $c(x,t)$ is the concentration of the bicoid protein.

(a) Suppose we have a source of bicoid at one end of the embryo, at $x = 0$, and that the other end is at $x = L > 0$. If L is "large", argue that c essentially exponentially decays for $x > 0$. What is the length scale λ of this exponential decay, and what does it mean for L to be large?

(b) Reasonable values for bicoid are $\tau \approx 10^3$ s and $D \approx 5\ \mu\text{m}^2/\text{s}$. The typical length scale of an embryo is $L \approx 0.5$ mm. Compute λ. Is L "large"? Can bicoid effectively be used to distinguish between the front and back of the embryo?

Unfortunately, our model has a fatal flaw. Different fly species have different sized embryos, and our model has a fixed length scale λ. Each fly embryo roughly speaking has a same sized "front" and "back". Now, you might say that each fly species has a different bicoid protein with a different value of λ. Thus, just because each species is different, we can arrange $\lambda \sim L$, so each species has a front half and a back half. The issue is that the bicoid proteins are morally the same in each embryo. Thus, another mechanism is required to increase λ so that it can scale as L.

Here is a proposed mechanism which is very elegant. Let us suppose that the surface of the embryo is dotted with nuclei, and that the bicoid can only decay inside the nuclei. Now, suppose that each nucleus has a fixed surface area a, and there are a fixed number N of these nuclei, which is the same for all fly embryos. Suppose that these nuclei are uniformly spaced out along the surface of the embryo. Furthermore, let us suppose that for each embryo, we approximately have $R = \alpha L$.

(c) Assuming that c does not vary substantially on the length scale of the nuclei, explain why we can model the presence of these nuclei by replacing τ with τ_{eff}, where

$$\tau_{\text{eff}} = \frac{2\pi L^2 \tau}{Na}.$$

(d) Verify that now $\lambda \sim L$. Thus this simple mechanism solves our problem!