Problems for fly morphogenesis project

Problem 1 (prelab). Under the French flag model, we assume that the position of the cephalic furrow is the point where the Bcd protein concentration passes a threshold. We define this threshold concentration to be $[Bcd]^*$. Let $[Bcd]_{0,\mathrm{wt}}$ be the anterior Bcd concentration for $2\times$ *bcd* dosage (wild type). Let x_{wt} be the position of the cephalic furrow when $[Bcd]_0 = [Bcd]_{0,\mathrm{wt}}$. Finally, let x_α be the position of the cephalic furrow when $[Bcd]_0 = \alpha[Bcd]_{0,\mathrm{wt}}$. Here, α is the gene dosage factor. E.g., if we have $1\times$ dosage, this is half of wild type, so $\alpha = 1/2$.

Derive an expression for x_α as a function of λ, α, $[Bcd]_{0,\mathrm{wt}}$, and $[Bcd]^*$. Write down an expression for $x_\alpha - x_{\mathrm{wt}}$, the shift in furrow positioning due to dosage. This should be a function only of λ and α.

Problem 2 (prelab). To check the validity of the French flag model, we need to know the value of the Bcd concentration profile decay length λ. Driever and Nüsslein-Volhard measured the concentration profile of Bcd and fit an exponential curve, but did not report the value of λ. We will calculate λ from their data so we have it in hand going into our furrow measurements.

Use the digitized wild type Bcd immunostain data from Figure 3A of the Driever and Nüsslein-Volhard paper (in the file `wt_bcd_driever_fig_3A.csv`) and perform a curve fit to determine λ. The value of λ should be in units of fraction of the total embryo length. *Hint:* The Driever and Nüsslein-Volhard data have a background signal. Therefore, the function you should use to fit the data is

$$[Bcd] = b + [Bcd]_0 \mathrm{e}^{-x/\lambda},$$

where b is the background signal. Your three fit parameters are then b, $[Bcd]_0$, and λ. You can modify the Matlab tutorial on nonlinear regression to fit this function.

Problem 3. We produced flies with the genotype $bcd/+$ on the third chromosome. We did this by mating

$$♀\ \frac{+}{+} \times ♂\ \frac{bcd}{bcd},$$

so all offspring are $bcd/+$. Say instead we crossed

$$♀\ \frac{+}{+} \times ♂\ \frac{bcd}{TM3,\ Sb^1}.$$

What would the genotypes of the female offspring be? (Think about the contents of the "urns" from the handout we gave you about fly crosses.) How could we pick the ones that are $bcd/+$?

Problem 4. Discuss how you process the images to determine the cephalic furrow position. Justify your choice on how the furrow position is defined.

Problem 5. In our experiment, $\alpha = 1/2$ for the mutant flies. In problems 1 and 2, you generated a prediction on how the position of the cephalic furrow should change. Do your experimental results agree with this prediction?

Problem 6. In lab, we only looked at two dosage levels of *bcd*. Driever and Nüsslein-Volhard looked at four dosage levels. Plot the your predictive expression from problems 1 and 2 for $x_\alpha - x_{\text{wt}}$ versus α on the same plot as Driever and Nüsslein-Volhard's measurements of the furrow position. For convenience, here are the values for the position of the furrow (in units of fractional embryo length) measured in their paper:

1× dosage	0.27
2× dosage	0.35
3× dosage	0.41
4× dosage	0.44