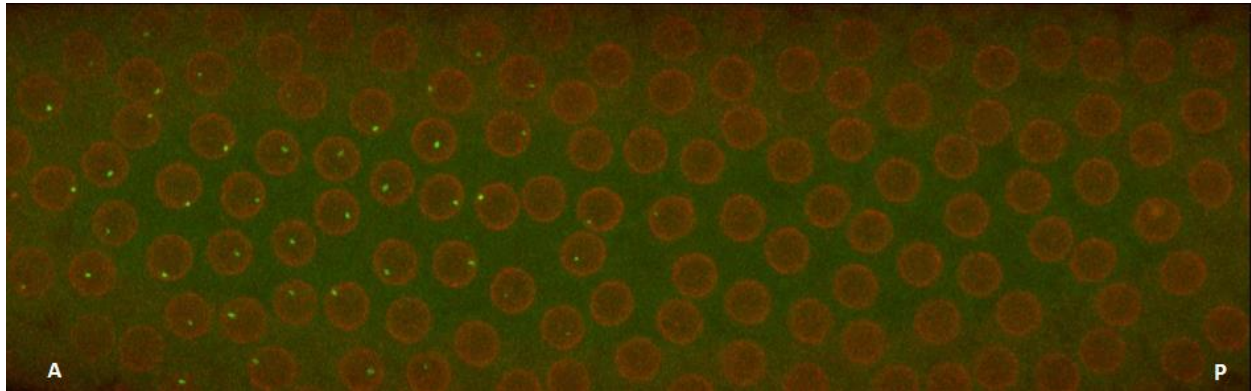


Live fluorescence microscopy as a tool to study morphogen dynamics during *Drosophila melanogaster* embryonic development

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In embryos, cell differentiation occurs via the formation of spatial gradients of molecules called morphogens, which control the expression of a number of target genes determining cell identity. A common model system to study morphogens is the Bicoid gradient, which determines antero-posterior (AP) patterning in *Drosophila melanogaster*, or fruit fly. We are especially interested in understanding how a noisy morphogen input can give a precise output of its target, and accomplish robustness during embryonic development. Here, we aim to apply novel methods in both fly genetics (to label the nascent mRNA of target genes) and fluorescence imaging (to detect the fluctuations in signal caused by the periodic creation of new mRNA at transcription sites) in order to measure the rate of transcription of the Bicoid target gene, hunchback, in each nucleus along the AP axis (see Figure).



Systematic measurements will allow us to determine which factors influence this transcription rate (e.g. morphogen diffusion rate, morphogen/target concentration, and polymerase activity at the target promoter), especially in the border region where there is a switch between expression and no expression. Given the rapidity of establishment of a precise transcriptional response, our hypothesis is that this response at the border relies on a memorization process, allowing nuclei to recall Bicoid concentration from one cycle to the next, by keeping track of the Hunchback promoter transcriptional status across mitosis. Future experiments aiming to challenge this hypothesis, using novel methods in live embryonic imaging are discussed.

Despods, J., Tran, H., Ferraro, T., Lucas, T., Perez Romero, C., Guillou, A., ... Walczak, A. M. (2016). Precision of readout at the hunchback gene. *PLoS Computational Biology*, in revisio(October), 1–35. <http://doi.org/10.1101/063784>