Open position for a PhD in gene regulation

to work in a multidisciplinary environment: molecular and cellular biology, imaging, applied mathematics

Project: Visualization of cell fate determination by real time imaging of transcription

Cells adopt different fates and single cell RNA sequencing revealed that this occurs via 'cell trajectories', in which the transcriptome of a cell evolves from a one epigenetic state to another, and this in a cell-defined manner. This dynamic view is reconstructed *a posteriori* from snapshots of multiple cells located at different points along the trajectories. How a single cell makes choices and moves in real time along such trajectories is therefore not known. **Here, the PhD candidate will address this key issue by developing novel methods enabling the visualization of gene transcription in single cells and real time.** Mouse Embryonic Stem cells (mES) differentiating in neurons will be used as a model. The project will be done in close collaboration with an applied mathematics team, where another PhD student will model the gene regulatory networks involved.

Requirements: Master in life science (molecular biology, cellular biology or biophysics), preferably in the gene expression field. Competence in cellular imaging will be a plus. Interest to work within an inter-disciplinary collaborations and to work autonomously while integrated in a team.

Where: team of Edouard Bertrand at the IGH/CNRS in Montpellier (https://www.igh.cnrs.fr/en/).

When: November 1st, 2024; fully funded PhD position (3 years).

Application: Please provide: a motivation letter; a CV; contact details of previous supervisor. Application should be sent to Dr. Edouard Bertrand (edouard.bertrand@cnrs.fr). **Deadline: October 7th, 2024.**

Some recent publications

- Cell cycle-dependent mRNA localization in P-bodies. Safieddine, A., Benassy, MN.,..., Bertrand, E., Bénard, M., Weil. D. **Mol. Cell**, in press.
- BurstDECONV: a signal deconvolution method to uncover mechanisms of transcriptional bursting in live cells. Douathy, M., Topno, R., Lagha, M., Bertrand, E.*, Radulescu, O.* ***Nucl. Acids Res***. (2023), 51:e88.
- Stochastic pausing at latent HIV-1 promoters generates transcriptional bursting. Tantale, K., Garcia-Oliver, E., L'Hostis, A., Yang, Y., Robert, MC., Gostan, T., Basu, M., Kozulic-Pirher, A., Andrau, JC., Muller, F., Basyuk, E.*, Radulescu, O.*, and E. Bertrand*. ***Nat. Comm*** (2021), 12:4503.
- RNA labeling technology grants access to live plant single cell transcriptional dynamics: application to phosphate repression signaling cascade. Hani, S., Laura Cuyas, L., David, P., Secco, D., Whelan, J., Thibaud, MC., Müller, F., Pochon, N., Javot, H., Merret, R., Faklaris, O., Maréchal, E., Bertrand, E.*, and L. Nussaume*. ***Nature Plants*** (2021), 7, 1750-64.
- A conserved choreography of mRNAs at centrosomes reveals a localization mechanism involving active polysome transport. Safieddine, A., Coleno, E., Salloum, S., Traboulsi, A., Kwon OS., Lionneton, F., Georget, V., Robert, MC., Gostan, T., Lecellier, C., Chouaib, R., Pichon, X., Le Hir, H. , Zibara, K., Peter, M., and E. Bertrand. ***Nat. Comm*** (2021), 12:1352.
- A growing toolbox to image gene expression in single cells: sensitive approaches for demanding challenges. Pichon, X., Lagha, M., Mueller, F. and Bertrand, E. ***Mol. Cell***, 2018, 71:468-480.