Open position for a post-doc in computer vision

to work in a multidisciplinary environment:

computer vision, biophysics and biology

Project: Systematic analysis of gene expression in single cells by high throughput detection of single mRNAs
Characterizing gene expression at the level of single cells and in the context of the cellular space is a difficult challenge that is driving important conceptual breakthroughs. Messenger RNAs are synthesized at a gene in the nucleoplasm and translated into proteins at specific cytoplasmic locations. Single molecule FISH (smFISH) identifies and localizes all mRNA molecules produced by a given gene, in every cell of large populations. SmFISH thus possesses unique advantages to study gene expression, mRNA localization and local translation. In this project, the candidate will use and further develop algorithms in image analysis and computer vision to process large scale smFISH screens. Computer vision tasks include challenging segmentation and point cloud classification tasks, some of which have to be addressed with novel state-of-the-art methods in order to answer important biological questions related to RNA localization and local translation in neurons. The candidate will quantify RNA localization in neuronal processes and determine how localization patterns are altered in neurodegenerative diseases. The candidate will relate live and fixed cell data and develop novel methods to predict cell fate.

Requirements: PhD. Competence and/or familiarity in Python scripting, image analysis concepts and tools. Interest to work within an inter-disciplinary collaborations and to work autonomously while integrated in a team.

Where: Thomas Walter lab at the Ecole des Mines in Paris (https://thomaswalter.github.io); Florian Müller in Pasteur (https://research.pasteur.fr/fr/member/florian-muller/); Edouard Bertrand lab at IGH/CNRS in Montpellier (https://www.igh.cnrs.fr/en/).

When: September 1st; 2 year contract with possibilities for extension.

Application: Please provide: a motivation letter; a CV; contact details of previous supervisor. Application should be sent to Dr. Thomas Walter (thomas.walter@mines-paristech.fr); or Dr. Edouard Bertrand (edouard.bertrand@igh.cnrs.fr). **Deadline: July 15th.**

Recent publications

- A computational framework to study sub-cellular mRNA localization. **Nat. Comm**, 2018, 9:4584. Samacoits, A., Chouaib, R., Safieddine, A., Traboulsi, A., Ouyang, W., Zimmer, C., Peter, M., **Bertrand, E.***, Walter, T.*, Mueller, F.*
- FISH-quant v2: a scalable and modular tool for smFISH image analysis. **Imbert A**, Ouyang W, Safieddine A, Coleno E, Zimmer C, Bertrand E, Walter T, Mueller F. RNA. 2022; 28:786-795.
- 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.** A conserved choreography of mRNAs at centrosomes reveals a localization mechanism involving active polysome transport. ***Nat. Comm*** (2021), 12:1352.
- Chouaib, R., Safieddine, A., Pichon, X., Kwon, OS., Samacoits, A., Traboulsi, AM., Tsanov, N., Robert, MC., Coleno, E., Poser, I., Zimmer, C., Hyman, A. A., Le Hir, H., Zibara, K., Peter, M., Mueller, F.*, Walter, T.*, and **E. Bertrand*.** A localization screen reveals translation factories and widespread co-translational protein targeting. ***Developmental Cell***, 2020, 54:773-791. *See commentary in Dev. Cell doi:10.1016/j.devcel.2020.09.006*