Research Stage

Title: Regulation of gene expression dynamics in space and time

Where: Quantitative regulatory genomics team, LBMC http://www.ens-lyon.fr/LBMC
ENS de Lyon, 46, allée d'Italie, 69364 LYON CEDEX 07, France

When: Beginning of 2019 (flexible)

Duration: 6 months

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Keywords: Big data, integrative genomics, machine learning, gene regulation, gene expression dynamics.

Description of the project:
Gene expression is a highly dynamical process, yet the majority of the genome-wide studies focus on static pictures of gene expression. But genome wide expression data are highly multidimensional and contain a lot of hidden information what is going on in a cell or in an animal. In my lab and develop and use computational methods to extract this hidden information. This for example allow to reconstruct gene expression dynamics from static gene expression data. The big aim is to understand how gene expression is regulated in space and time in animals both by genetic and non-genetic factors, both at single animal and single cell level[1-4].

You will learn how to manage, integrate and analyse big gene expression and genomic data using state-of-the-art machine learning tools, to address fundamental biological questions.

A good level of English is absolutely required, such as good computational skills. Scripting skills in a programming language among R, Matlab or Python and good statistical skills are highly desirable. Database management is also desirable.

In short, if you have good computational and data analysis skills and you want to crack the secrets of the regulation of gene expression dynamics, join the "Quantitative Regulatory Genomics" team at the LBMC!

For further information contact Mirko.francesconi@ens-lyon.fr

References

1   Francesconi, M. & Lehner, B. The effects of genetic variation on gene expression dynamics during development. *Nature* **505**, 208-211, doi:10.1038/nature12772. Epub 2013 Nov 24. (2013).
2   Perez, M. F., Francesconi, M., Hidalgo-Carcedo, C. & Lehner, B. Maternal age generates phenotypic variation in Caenorhabditis elegans. *Nature* **552**, 106-109, doi:10.1038/nature25012 (2017).
3   Francesconi, M. *et al.* Single cell expression analysis uncouples transdifferentiation and reprogramming. *bioRxiv* (2018).
4   Francesconi, M. & Lehner, B. Reconstructing and analysing cellular states, space and time from gene expression profiles of many cells and single cells. *Mol Biosyst* **11**, 2690-2698, doi:10.1039/c5mb00339c (2015).