Research Internship (M2)

Title: Understanding inter-individual variation in ageing from single individual gene expression profiling

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

When: Beginning of 2025 (flexible)

Duration: 6 months (M2)

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Keywords: Aging, Interindividual-variation, big data, integrative genomics, machine learning, gene regulation, gene expression dynamics.

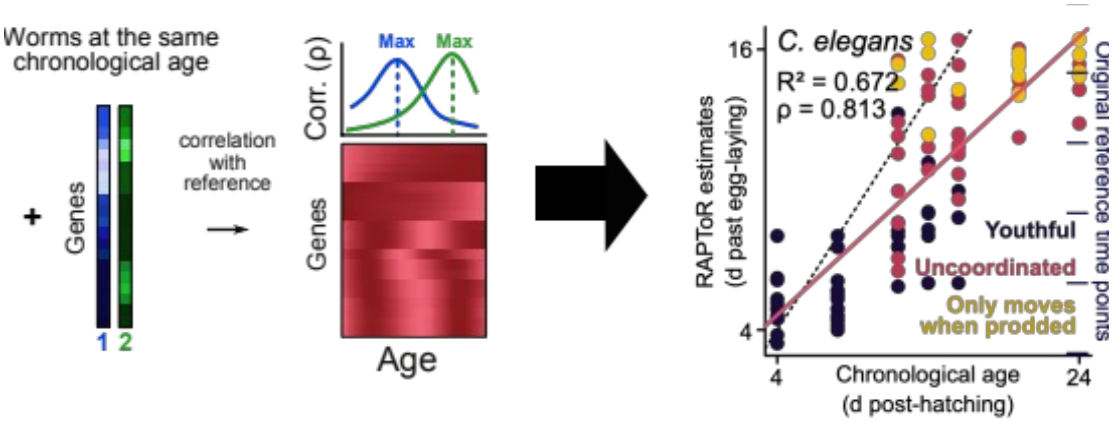
Background and description of the project:
C. elegans is a self-fertilizing nematode and all individuals are genetically identical, yet their lifespan is hugely variable even when they grow in the same controlled environment[1]. What are the sources of this inter-individual variation? Do all individuals age in the same manner but at different speed? Or are there different aging trajectories?
In my team, we address these fundamental questions using a genomic approach. We develop and use computational methods to extract from hidden information about the dynamical processes occurring in a cell or in an animal from transcriptomic data. We have recently developed RAPToR, a computational method to estimate the precise (and tissue-specific) biological age of an animal from its gene expression[2]. You will now apply this method and other machine learning techniques to analyse published large-scale single-individual[3] and single-cell transcriptomic[4,5] dataset of ageing *C. elegans* to understand the sources of interindividual variation in aging.

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

A good level of English is absolutely required, such as good computational skills. Programming skills in any language among R, Matlab or Python and good statistical skills are highly desirable.

In short, if you have good computational and data analysis skills and you want to understand interindividual variation in aging, join the "Quantitative Regulatory Genomics" team at the LBMC!

For further information and to apply contact mirko.francesconi@ens-lyon.fr



References

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2. Bulteau, R. & Francesconi, M. Real age prediction from the transcriptome with RAPToR. *Nat Methods* 1–7 (2022) doi:10.1038/s41592-022-01540-0.
3. Eder, M. *et al.* Systematic mapping of organism-scale gene-regulatory networks in aging using population asynchrony. *Cell* **0**, (2024).
4. Roux, A. E. *et al.* Individual cell types in C. elegans age differently and activate distinct cell-protective responses. *Cell Reports* **42**, 112902 (2023).
5. Gao, S. M. *et al.* Aging Atlas Reveals Cell-Type-Specific Regulation of Pro-longevity Strategies. 2023.02.28.530490 Preprint at https://doi.org/10.1101/2023.02.28.530490 (2023).