



## 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 2024 (flexible)

**Duration:** 6 months (M2)

**Scientific Tutor:** Mirko Francesconi, CRCN, Inserm  
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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<sup>1</sup>. 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?

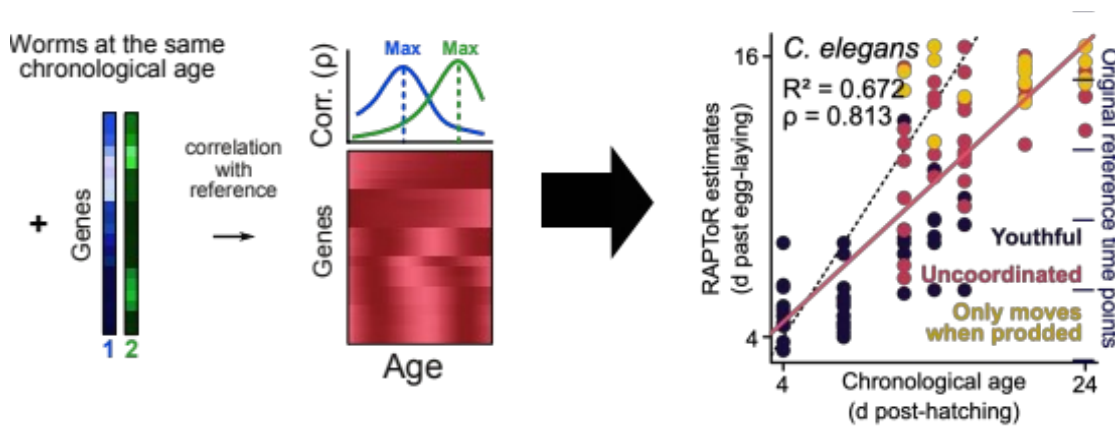
In my team, we address these fundamental questions using a genomic approach. We develop and use computational methods to extract from genomic data hidden information about the dynamical processes occurring in a cell or in an animal. For example we have recently developed RAPToR, a computational method to estimate the precise (and tissue-specific) biological age of an animal from its gene expression<sup>2</sup>. We (you) now will apply this method to analyse both published<sup>3</sup> an unpublished large scale bulk and single-individual transcriptomic dataset of ageing *C. elegans*.

You will learn how to manage, integrate and analyse big genomic 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](mailto:mirko.francesconi@ens-lyon.fr)



## References

1. Kirkwood, T. B. *et al.* What accounts for the wide variation in life span of genetically identical organisms reared in a constant environment? *Mech Ageing Dev* **126**, 439–43 (2005).
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. Golden, T. R., Hubbard, A., Dando, C., Herren, M. A. & Melov, S. Age-related behaviors have distinct transcriptional profiles in *Caenorhabditis elegans*. *Aging Cell* **7**, 850–865 (2008).