MASTER 2 BMC
PARCOURS GENOPATH
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Titre : Understanding inter-individual variation in ageing from single individual gene expression

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Sujet de stage :
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.

Modèle et techniques utilisées :
C. elegans, single individual and single cell transcriptomic data, machine learning, R software.

Publications d'intérêt :

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. 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).