Master thesis project – Leveraging AI and big data to build a state-of-the-art transcriptomics-based aging clock

Background

Big datasets are increasingly becoming available in biology, enabling the development of predictive models of unprecedented accuracy. In the field of aging, this has led to the emergence of "aging clocks" which can predict individuals' ages using various types of omics data. Transcriptomics-based aging clocks hold great potential due to the large number of transcriptomic datasets. However, the lack of robust and accurate models has so far hindered their widespread applications. Our laboratory has developed a state-of-the-art transcriptomics-based aging clock, demonstrating its ability to predict cellular age across different datasets. Nonetheless, further improvements can be made by gathering more training data and testing additional modeling strategies.

Project aims and description

First the student will gather and preprocess relevant datasets to expand our existing transcriptomic database. Second, he will test and compare different modeling strategies, benchmarking them with published models. Third, and only if time permits, the student will apply his new state-of-the-art model to large scale Perturb-Seq datasets to map the genetic landscape of cellular age.

Contact

If this sounds of interest to you, don't hesitate to contact:

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