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Multiple omics ageing clocks

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Biological age, a measure of deterioration and ageing that is distinct from chronological age has been found to predict disease and mortality [1]. The first published measure of biological age was Hannum's epigenetic clock. Hannum's clock took the form of an elastic net regression model predicting age, built from whole blood CpG methylation data, the ratio of this predicted age to chronological age was used to measure apparent methylomic ageing rate (AMAR) [2]. Hannum's work was extended by Horvath using the same methodology, but a larger number of: CpG markers, individuals and tissue types [3].

Since the publication of these landmark epigenetic clocks, ageing clocks have been built using telomere length [4], facial morphology [5], metabolomics [1], glycomics [6] and proteomics [7]. Each of these ageing clocks have shown that chronological age compared to biological age can be used as an indicator of health outlook. These models have the potential to inform health and lifestyle advice in order to improve individuals' health [7]. Here we test replication of published ageing clocks using approximately 1,000 individuals from the cross-sectional population cohort ORCADES, that are highly annotated with 877 phenotypes spanning glycomics, lipidomics, metabolomics and proteomics.

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