Title: Differences in ageing-associated DNA methylation changes at different ages

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Abstract
Ageing can be defined as time-dependent changes in the functionality and integrity of cells and tissues, that decrease the fitness of an organism. The ageing process starts early in life, and the ageing-associated changes can be quantified from the 3rd decade of life. However, the changes do not occur at uniform pace through life. Changes in DNA methylation have been very convincingly associated with ageing, but research has focused on changes that occur linearly with increasing age throughout the lifespan.
Here, we are utilizing the Young Finns Study (YFS), a population cohort consisting of three generations, to identify ageing-associated DNA methylation changes in young adulthood (18-36 years, n=830), in mid-life (41-56 years, n=1309) and in later life (59-92 years, n=1342). We aim to identify ageing patterns that are shared by all three age groups, but more importantly those that are specific to one.
With our first analyses, we have observed more ageing-associated methylation sites in the youngest age group as compared to the oldest. Of individual methylation sites identified in all age groups, many show differences in magnitude of ageing-associated change. One example of this is ELOVL2, the most often reported ageing-associated locus, where the yearly change in methylation was observed to be largest for the youngest age group.
One interpretation of our findings is that the results in the younger individuals reflect intrinsic ageing processes, not yet confounded by diverging lifestyles or diseases. The described research is still ongoing, and thus suggestions for additional analysis strategies are most welcome.