# Writing Assignment #4

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The largest factor attributing to atrial fibrillation is a person's age. There are algorithms available for predicting a person's age based on the epigenetic changes to their DNA. There are cases where the algorithm may miscalculate a person's age due to what is known as epigenetic age acceleration. EAA may be a marker for faster than normal biological aging. Epigenetic aging can be affected by several factors such as genetic disorders, environmental influences, and other genome affecting materials. People with an EAA that exceeds their chronological age are designated to have a positive EAA. Those whose chronological age exceeds their epigenetic age are designated with a negative EAA.

Four epigenetic clocks were evaluated to associate epigenetic age with atrial fibrillation. These clocks were DNA methylation PhenoAge, Horvath, Hannum, and DNAm GrimAge. These algorithms were chosen due to their accuracy in calculating epigenetic age. While Epigenetic age has been correlated with other diseases, it has yet to be linked to Atrial Fibrillation.

The Horvath and Hannum clocks have been associated with the most incidents of clinical complications. While the PhenoAge clock was more useful for calculating chronological age. The GrimAge clock, as the name implies, was a tool used for predicting the mortality of an individual. The GrimAge clock had multiple variable inputs such as a methylation counter for the amount of cigarette packs smoked while taking into account the time of chronological age of the individual.

In all groups, a higher chronological age was associated with AF which is expected. For every additional 5 years to a person's chronological age, a 1.44-fold increase in AF incident. When positive EAA was investigated it was accompanied by a higher BMI and higher blood pressure, indicating decreased cardiac health. After analysis of incident AF and which clocks were associated with its prediction, it was found that PhenoAge and GrimAge were the two clocks bringing results of consistent AF predictions. This points to a clinical significance in using these clocks when evaluating risk of Atrial Fibrillation.

There was a sum of 2362 people in this study that did not have a history of AF. All participants were Caucasian. Of the participants, 55.6% were female and 44.4% were male. The mean epigenetic ages of the group was 58.6 with a margin of 10.2 years.

## References

Roberts, J. D. et al. Epigenetic age and the risk of incident atrial fibrillation. Circulation 144, 1899–1911 (2021).