# Epigenetic Age Predictor for Mice

## Understanding of aging in mice

Mice are often used as a model system to elucidate how aging is affected by genetic factors, diet, knockout of specific genes, or other interventions. Such research provides insight into how aging can be modulated. To this end, it is important to have a reliable and quantitative measure for the state of aging.

## Epigenetic age-predictions in mice

Aging is associated with highly reproducible DNA-methylation changes at specific sites in the genome (so called CpG sites). Such age-associated epigenetic modifications were first described in humans and they occur also in other mammals. We designed and validated an epigenetic age predictor for blood samples of mice. It is based on three relevant CpG sites in the genes *Prima1*, *Hsf4*, and *Kcns1*. For C57BL6 mice the correlation of these age-predictions with real chronological age was $R^2 = 0.93$ with a mean absolute error of less than 5 weeks (Figure 1). For DBA mice, which have a shorter life-expectancy, the model can be adjusted. Our three-CpG-predictor provides a simple and cost-effective biomarker to determine biological age in large intervention studies with mice.

## Comparison with other assays

In comparison to analysis of life-length the results of epigenetic age predictions are rapidly available. Other epigenetic clocks were generated based on deep-sequencing data of the entire genome. In contrast, our method uses targeted pyrosequencing of three CpGs. This approach is much faster, more cost-effective, and it provides a similar precision as whole genome sequencing based age-predictors.

## What do I need?

Only small blood volumes are required that can be taken from living mice. As DNA is relatively stable, it can be shipped at room temperature. The DNA-methylation levels at the three relevant CpGs are then measured by pyrosequencing and are then integrated into the linear regression model for prediction of biological age. In comparison to the "real" chronological age it is then possible to identify parameters that accelerate or decelerate the aging process.

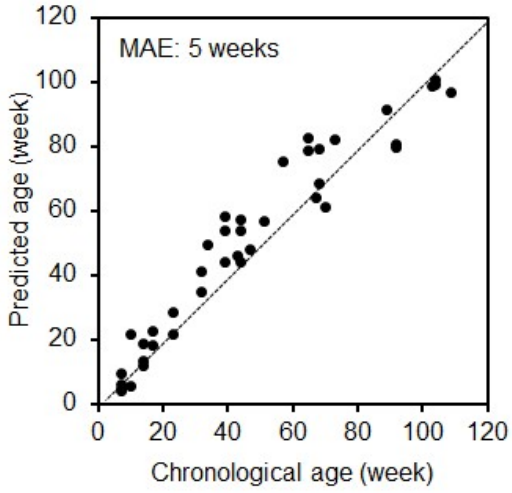


***Figure 1: Age-estimation of murine blood samples.*** *Blood samples were analyzed by pyrosequencing of the three specific CpG sites (data of two independent validation sets from different labs). Our three-CpG model facilitates age-estimation with a mean absolute error (MAE) from chronological age of about 5 weeks.*

## Our service for you:

- You provide either 50 - 100 µL of frozen blood (taken by submandibular bleeding, tail vein puncture, or post mortem) or 200 ng of genomic DNA from blood.
- We perform DNA isolation (optionally) and bisulfite conversion.
- We amplify the relevant regions and analyze the DNA-methylation at three relevant CpG sites by pyrosequencing.
- We predict the biological age of your samples.
- Results - including pyrograms, raw data, and graphical presentation - are provided by Email.

## Publication:


- Yang H et al., *eLife*, ***7***:*e37462 (2018) doi: 10.7554/eLife.37462*


## Further Information

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