

Computational Method for Predicting Biological Aging

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BACKGROUND

Aging is a complex process that manifests different in different people. Chronological age does not accurately reflect the process of aging on a molecular level. Though fundamental processes underlying human aging are still not known, epigenetic changes such as nucleosome positioning, histone modifications, and genome wide DNA methylation patterns have been linked to the aging process. One of the challenges in studying these epigenetic effects is identifying biomarkers and precisely quantifying the actual rate of aging in an individual. There are reports available linking the methylation markers to the human aging, but no quantitative models have been established which can measure the actual rate of aging.

TECHNOLOGY DESCRIPTION

Scientists at UCSD have developed a unique computational method that measures and compares the human aging rate using DNA methylation markers. This is a quantitative model based on measuring CpG markers from the whole blood of human individuals ages 19 to 101. This measures the rate at which an individual's methylome ages, and is impacted by gender and genetic variants. The optimal version of the model incorporates 71 methylation markers that are highly predictive of age and are associated with genes associated with age-related conditions. Several markers are also implicated in obesity and metabolism. Although the original model was developed using markers found in whole blood, from an original cohort of more than 650 individuals, it has been tested with high predictability against secondary cohorts and other tissue sources. The computer software has many potential applications and is available for licensing.

APPLICATIONS

- Forensic diagnosis of human actual age from any tissue including blood and saliva.
- Prediction of human aging rate.
- Health assessment.
- Assessment of environmental factors and their effect on human aging.
- Biomarker to study age-related diseases.
- Biomarker tissue assay for drugs and chemical compounds that can retard or accelerate

human aging.

- Markers of cellular senescence.

RELATED MATERIALS

- [Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates](#); Gregory Hannum, Justin Guinney, Ling Zhao, Li Zhang, Guy Hughes, Srinivas Sadda, Brandy Klotzle, Marina Bibikova, Jian-Bing Fan, Yuan Gao, Rob Deconde, Menzies Chen, Indika Rajapakse, Stephen Friend, Trey Ideker - 01/24/2013

PATENT STATUS

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OTHER INFORMATION

KEYWORDS

Aging Rate, Methylome, Biomarkers

CATEGORIZED AS

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