

CLSA Approved Project

Applicant

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Project Title

Exploring epigenetic age and its role on age-related changes in phenotypes

Project Summary

DNA methylation is an epigenetic modification to DNA in which methyl molecules are added to cytosines, one of the four bases that compose the genetic code. Methylation is an important way of turning DNA on and off, allowing the same DNA to operate differently in the various types of cells in the body. Methylation can change upon exposure to smoking, diseases, treatments, and with age. The changes in methylation with age are very consistent across healthy individuals. Therefore, models have been built using methylation data that estimate "epigenetic age", that is, estimating whether an individual is aging faster or slower than what would be expected based on calendar time. Our goal in this project is to see how DNA methylation is associated with traits such as type 2 diabetes and heart disease, and how these relationships are modified by or interact with epigenetic age.

Keywords

Aging, DNA methylation, High dimensional modelling