echo PROJECT

LECTURES SERIES

"Epigenetic-based age acceleration in a representative sample: utero stressors timing"

December 14 2023, 15:00-17:00

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Biomarkers developed from DNA methylation (DNAm) data are of growing interest as predictors of health outcomes. However, it is still unclear how epigenetic aging relates to inutero stressors, such as housing insecurity and accelerated biological aging. Epigenetic processes, such as DNA methylation, play a vital role in fetal growth and development (Agha et al. 2016; Schmitz and Duque 2022), and a harmful prenatal environment can impact epigenetic patterns and fetal development. Studies have shown that exposures during the in-utero period, such as maternal smoking, diet, and famine, can affect DNA methylation patterns (Agha et al. 2016; Auclair and Weber 2012; Hyun and Jung 2020; Spano et al. 2022). Their small sample size has limited previous studies on the association between birth weight and DNA methylation. They also mainly focus on specific genomic regions and have limited accounting for gestational age.

This study uses data from the Future Families and Child Wellbeing Study (FFCWS), based on a stratified, multistage probability sample of children born in large U.S. cities between 1998 and 2000, with around 75% of the births being to unmarried mothers.