



08
NOV.
2022

🕒 de 13h à 14h

📍 Salle de formation du PRABI

SÉMINAIRE

Methodological pitfalls in the construction of epigenetic clock models

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Presentation of the nature of DNA methylation data captured from Illumina Methylation Assays (Homo sapiens). Evaluation of the impact of cofactors (sex, cell composition, latent factors) on the performance of the machine learning model (elastic-net + bootstrap). Illustration: the impact of tobacco consumption on blood's epigenetic age.