Precision Genetic Neurodepidemiology: from risk factors to statistical prediction, prevention and clinical translation

Natàlia Vilor Tejedor[1]

[1]Genetic Neuroepidemiology and Biostatistics group, BarcelonaBeta Brain Research Center, Barcelona, Spain; Deparment of Human Genetics, Radboud University Medical Center, Nijmegen, Netherlands; Computational Biology and Health Genomics group, Center for Genomic Regulation, Barcelona, Spain, Spain

This talk will delve into biostatistical strategies advancing the field of genetic neuropidemiology. Recent advancements have enabled more precise identification of genetic and environmental factors, significantly enhancing brain health, risk stratification, disease prediction, and prevention strategies. Key highlights include applying multivariate models to extensive genomic, environmental, and brain imaging datasets, and the assessment and implementation of statistical tools designed for data integration. These methods further emphasize incorporating diversity and sex-specific mechanisms into study populations, bolstering the applicability and accuracy of our findings. The implications of these advances extend beyond improved diagnostic accuracy, paving the way for potential biological pathways that support personalized medicine, prevention, and targeted therapeutic interventions.

Keywords: Genetic neuroepidemiology; multivariate models; data integration; personalized medicine; disease prediction