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Multi-omics prediction of complex traits and exposers: polygenic and DNA methylation scores

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ABSTRACT:

DNA-based predictors of complex traits and exposures can serve to improve prediction of health and behavioral outcomes, to optimize risk stratification, and are increasingly considered for application in social sciences and education. Whereas DNA-based predictors are static, other predictors such as those based on epigenome data are dynamic and may capture both genetic and environmental information. We will discuss prediction by polygenic scores and DNA methylation scores created using weights derived from summary statistics of large genome- and epigenome-wide studies, for several traits (birth weight, BMI, left-handedness, and aggression) and exposures (prenatal maternal smoking and smoking). Predictive ability of the scores in multi-omics prediction models was evaluated on the Netherlands Twin Register cohorts of adults and children with DNA methylation in blood and buccal cells. We examined if the DNA methylation scores add predictive value above the polygenic scores for DNA methylation data obtained from different tissues and ages. Our studies illustrate the value of combining polygenic scores with information from methylation data for complex traits and exposure prediction.

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