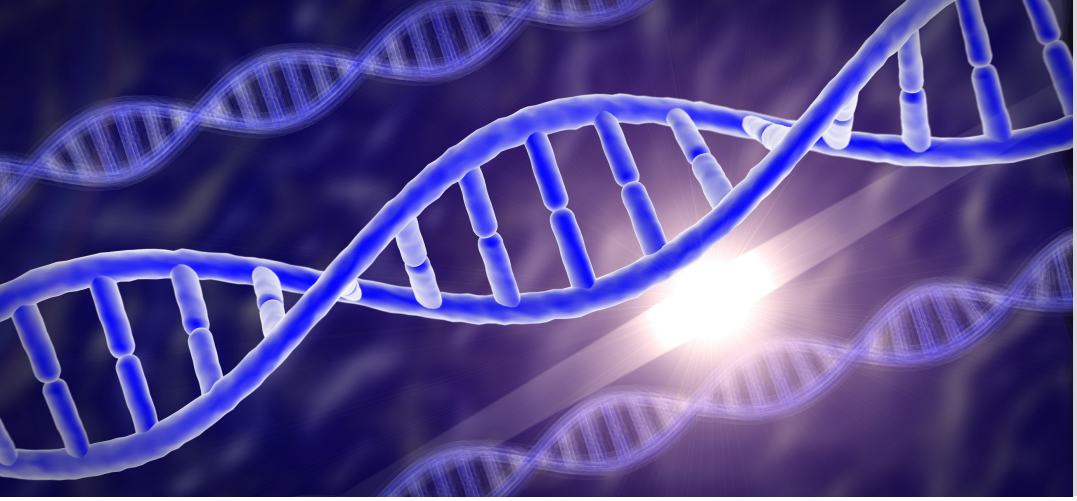

Andrea Allegrini

MULTIVARIATE GENETIC ANALYSES OF COGNITIVE AND PSYCHOPATHOLOGY RELATED TRAITS: 4 STUDIES

Throughout my PhD work I employed different multivariate genetic and genomic approaches (i.e. simultaneous analysis of more than one outcome variable) applied to the prediction of cognitive related traits and to investigate the co-occurrence of various dimensions of child psychopathology dimensions across development.

In a first study I investigated the role of multivariate genetic approaches to improve polygenic (i.e. involving variation across the genome) prediction of cognitive and educationally relevant traits across childhood (https://www.nature.com/articles/s41380-019-0394-4). Comparing different methods, I showed that polygenic prediction of general intelligence and educational achievement is substantial. For example, it rivals the prediction that can be derived from parental educational level and socioeconomic status. Furthermore, highlighting the importance of multivariate approaches, I showed that the predictive power of polygenic scores can be improved by including information about genetically correlated traits.

As polygenic scores become more powerful, they can be employed to investigate questions regarding the interplay between genetics and the environment. Within a multivariable (i.e. involving multiple predictors) prediction framework, in a second study, I found evidence for widespread gene-environment correlation underlying educational achievement in childhood. I showed that genetic and environmental predictors of educational achievement overlap substantially:

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the predictive power of genetic predictors is partly derived from the environment and vice versa. In turn, I did not find evidence that gene – environment interactions play an important role in the prediction of educational achievement. (https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1009153)

In a third study, I systematically investigated the manifestation of a common dimension of psychopathology (the so-called 'p factor') across development. I found that diverse forms of child psychopathology generally load on a common p factor - which is highly heritable - and that there are substantial genetic influences on the stability of p across childhood. Furthermore, I found evidence for genetic overlap between general risk for psychiatric disorders in adulthood and p in childhood, even as early as the age of 7 (https://acamh.onlinelibrary.wiley.com/doi/full/10.1111/jcpp.13113).

Lastly, I extended this research on the developmental co-occurrence of child psychopathologies, via a collaboration between the Twin Early Development Study and the Netherlands Twin Registry. In this work (https://psyarxiv.com/t486z/) I demonstrate that direct relationships between psychopathology dimensions within individuals, and between siblings within a family, partly explain the co-occurrence of psychopathologies in childhood; suggesting that these should be taken into account in developmental models of comorbidity.