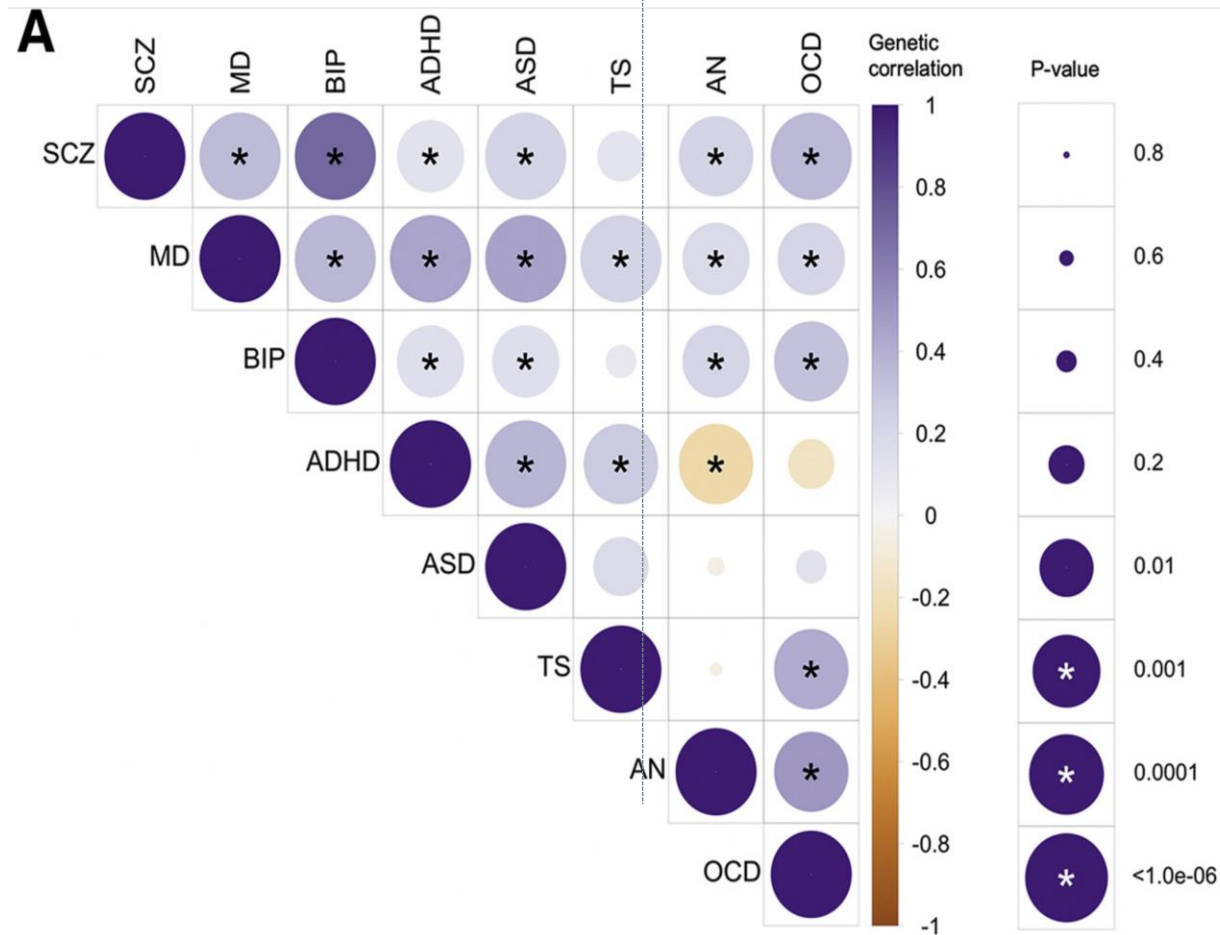


Step 3: Running usermodel

Pervasive Genetic Overlap Necessitates Multivariate Methods



Genomic structural equation modelling provides insights into the multivariate genetic architecture of complex traits

Andrew D. Grotzinger , Mijke Rhemtulla, Ronald de Vlaming, Stuart J. Ritchie, Travis T. Mallard, W. David Hill, Hill F. Ip, Riccardo E. Marioni, Andrew M. McIntosh, Ian J. Deary, Philipp D. Koellinger, K. Paige Harden, Michel G. Nivard & Elliot M. Tucker-Drob

Framework for modeling patterns of genetic associations across broad constellations of traits

How to specify a model in lavaan

We use the lavaan formula language, slightly extended:

Regression:

$$A \sim B$$

(Co)variance:

$$A \sim\sim A; A \sim\sim B$$

Factor:

$$F1 =\sim A + B + C + D$$

Fix a parameter:

$$A \sim\sim 1*B \text{ (the covariance between A and B is 1)}$$

Name a parameter:

$$A \sim\sim a*B \text{ (the covariance between A and B = parameter label a)}$$

Allows you to use model constraints for this parameter:

$$a > .001$$

usermodel takes 2 required arguments:

1. covstruc: The output from LDSC.

2. model: The model that is being estimated (written in lavaan syntax)

Other optional arguments include:

- **std.lv:** whether to use unit variance identification (fixing factor variances to 1) for model identification (TRUE/FALSE)
- **imp_cov:** whether function should return the model implied and residual matrices. This can (sometimes) be useful for troubleshooting model fit issues