NAME OF PRESENTING AUTHOR: Fartein Ask Torvik

EMAIL ADDRESS OF PRESENTING AUTHOR: fato@fhi.no

LOCATION OF PRESENTING AUTHOR: Europe

TIME ZONE OF PRESENTING AUTHOR: GMT+2 Central European Summer Time

TYPE OF SUBMISSION: Oral paper/ Poster

MEMBER STATUS: Non-member

ELIGIBLE FOR THOMPSON AWARD: No
ELIGIBLE FOR ROWEWARD: No

TITLE: Assortative mating and the usefulness of polygenic scores in extended pedigrees

FULL AUTHOR LIST: Fartein Ask Torvik (1,2), Espen Moen Eilertsen (3), Laurie Hannigan (4), Alexandra Havdahl (3,4,5), Eivind Ystrom (3,5)

AFFILIATIONS:
1. Centre for Fertility and Health, Norwegian Institute of Public Health, Oslo, Norway
2. Department of Psychology, University of Oslo, Oslo, Norway
3. PROMENTA Research Center, Department of Psychology, University of Oslo, Oslo, Norway
4. Nic Waals Institute, Lovisenberg Diaconal Hospital, Oslo, Norway
5. Department of Mental Disorders, Norwegian Institute of Public Health, Oslo, Norway

KEYWORDS: Assortative mating, polygenic scores, structural equation modelling

ABSTRACT:

Partners resemble each other in many traits, including educational attainment, psycho-pathology, and height. Mating is often assumed to be random in genetic studies and the results can be biased when it is not. Polygenic scores offer a straightforward means of assessing the genetic similarity of partners that arises from assortative mating. However, estimating the correlation between partners' polygenic scores is likely to provide an under-estimate of the actual genetic correlation because polygenic scores are imperfect measures of the genetic factors that give rise to a phenotype. Structural equation modelling (SEM), which is commonly used with data from twins and other kinds of relatives, provides a flexible way to incorporate polygenic scores with phenotypic data from multiple individuals. Incorporating polygenic scores in an SEM framework allows an estimation of the relationship between latent variables (genetic factors) that are the topic of the research, rather than the observed indicators of these (polygenic scores). We use pheno-

typic data on educational attainment, height, and symptoms of major depressive disorder from 70107 mother-father dyads and polygenic scores on 13096 mother-father dyads participating in the Norwegian Mother, Father, and Child Cohort Study. We present a novel structural equation model which uses data on phenotypes and polygenic scores for unrelated individuals to estimate heritability and genetic correlations – in this case, genetic correlations between partners – including results for educational attainment, psychopathology, and height.