

NAME OF PRESENTING AUTHOR: Yuanxiang Zhang

EMAIL ADDRESS OF PRESENTING AUTHOR: yuanxiang.zhang@uq.edu.au

## Detection of assortative mating in the absence of spousal information

Yuanxiang Zhang<sup>1</sup>, Allan F McRae<sup>1</sup>, Peter M Visscher<sup>1</sup>, Loic Yengo<sup>1</sup>

<sup>1</sup> Institute for Molecular Bioscience, The University of Queensland, Brisbane, Australia

KEYWORDS: Assortative mating, GREML

### ABSTRACT:

Assortative mating, i.e., mate choice based on phenotypic similarity, increases the prevalence of extreme phenotypes in the population. To date, only a few methods can detect AM in the absence of spousal information, which is scarce. Here, we introduce the between-chromosome Genome-based Maximum Likelihood (GREML-BC), a new method, which can detect AM by quantifying how much cross-chromosomal genetic relatedness contributes to phenotypic resemblance in the population. In simulations, GREML-BC is statistically well powered to distinguish AM from random mating and statistical power increases monotonically with sample size and the degree of phenotypic resemblance between mates. We applied GREML-BC to 52 phenotypes measured on 347,819 unrelated European ancestry participants of the UK Biobank. We found significant evidence of AM for 15 complex traits, including fluid intelligence, smoking status, overall health rating, average household income and time spent watching TV. We show that AM on these traits is correlated with that on educational attainment, previously reported. In conclusion, GREML-BC is able to detect signal of AM using only genotypes and phenotypes of unrelated individuals, which makes it applicable to large biobank data where spousal information is absent.

GRANT SUPPORT: This research was supported by the Australian Research Council (Grant number: DE200100425).