## Non-additive genetic effects in academic performance

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### Introduction

GWAS leveraging measures collected at multiple time points have found novel genetic associations. We hypothesize that a subset of these variants may be involved in gene-by-gene (GxG) or gene-byenvironment (GxE) interaction. We propose an analytic approach that concurrently models SNPs' phenotype level and heteroskedastic effect longitudinally.

### Methods

Population and within-family longitudinal (and delta) GWAS in the form of a 3-level hierarchical generalized linear mixed effects model (HGLM) (Cao, Maxwell, and Wei 2015; Rönnegård, Shen, and Alam 2010):

$$Y_{ijk} = \mathbf{X}_{ijk}eta + G_{1ijk}\gamma_1 + G_{2ijk}\gamma_2 + \mu_{ijk} + \delta_{ij} + \epsilon_i,$$

where **X** is a matrix of covariates (i.e., time, sex, batch, 10 PCs) including the intercept with  $\beta$  as their respective effect size,  $G_1/G_2$  are the copies of the effect allele (expressed as deviation from the family mean) with  $\gamma_1/\gamma_2$  as their effect on phenotype mean,  $\mu_{ijk}$  is the random intercept of individual,  $\delta_{ij}$  is the genetic relatedness matrix (GRM) and

$$\epsilon_i \sim N(0, G_{0i}\sigma_0^2 + G_{1i}\sigma_1^2 + G_{2i}\sigma_2^2)$$

We assume uncorrelated variance components:  $\mu_{ijk} \sim N(0, \sigma_{\mu}^2), \quad \delta_{ij} \sim N(0, \sigma_F^2 \Phi), \text{ and } \epsilon_i \sim N(0, \mathbf{V_E})$ where  $\mathbf{V_E}$  is an  $n \times n$  matrix with the  $i^{th}$  diagonal equal to  $G_{0i}\sigma_0^2 + G_{1i}\sigma_1^2 + G_{2i}\sigma_2^2$  and  $\Phi$  is  $2 \times$  the kinship matrix.

# SNPs with heteroskedastic effect are indicative of GxG and GxE.

# We employ longitudinal (delta) GWAS and vQTL to detect them.





### Simulation Results

SNP mean vs. heteroskedastic effect visualized affecting phenotype variance and kurtosis.



Mean and variance effects are inherently correlated.



This mean-variance relationship must be decorrelated **(Young, Wauthier, and Donnelly 2018)**:  $d_l = \alpha_{vl} - r_{av}\alpha_{vl}$ .

Non-additive effects are more difficult to detect.



#### References

Cao, Ying, Taylor J. Maxwell, and Peng Wei. 2015. "A Family-Based Joint Test for Mean and Variance Heterogeneity for Quantitative Traits: Family-Based vQTL Test." *Annals of Human Genetics* 79 (1): 46–56. https://doi.org/10.1111/ahg.12089. Rönnegård, Lars, Xia Shen, and Moudud Alam. 2010. "Hglm: A Package for Fitting Hierarchical Generalized Linear Models." *The R Journal* 2 (2): 20. https://doi.org/10.32614/RJ-2010-009. Young, Alexander I., Fabian L. Wauthier, and Peter Donnelly. 2018. "Identifying Loci Affecting Trait Variability and Detecting Interactions in Genome-Wide Association Studies." *Nature Genetics* 50 (11): 1608–14. https://doi.org/10.1038/s41588-018-0225-6.