**Supplementary Online Materials**

Heritability Estimation of Dichotomous Phenotypes Using a Liability Threshold Model on Ascertained Family-based Samples

- Wrote by Wonji Kim

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**About the work**

Numerous methods for estimating heritability have been proposed; however, unlike quantitative phenotypes, heritability estimation for dichotomous phenotypes is computationally and statistically complex, and the use of heritability is infrequent. In this study, we developed a statistical method to estimate heritability of dichotomous phenotypes using a Liability Threshold Model in the context of ascertained family-based samples. The Liability Threshold Model assumes dichotomous phenotypes are determined by unobserved latent variables that are normally distributed, and this model can be applied to general pedigree data. The proposed methods were applied to simulated data and Korean type-2 diabetes family-based samples, and the accuracy of estimates provided by the experimental methods was compared with that of established methods.

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Wrote and maintained by Wonji Kim. Please contact me. Any comments will be welcome.

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Manuscript The initial version of the manuscript including detailed methods

gen\_simuldata R function for generating family-based simulation data (첨부파일 gen\_simuldata.r)

LTMH\_Sourcecode R function for LTMH method and score test (LTMH\_Sourcecode.R)

Manual for R code A description for R function and example code

example data file An example fam file

**Citation:**

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