Introduction

Heritability (the proportion of variability attributable to genetic sources) is a vital quantitative genetic measure. Non-zero heritability is needed to certify a trait as a “phenotype”. Heritability can also be used as a general measure of biological validity, e.g. ranking different pre-processing techniques by heritability of the resulting phenotype. While such comparisons can be done element-wise over the phenotypes (e.g. by voxels or surface elements), a whole-brain summary of heritability can simplify the comparisons.

We propose a simple measure of aggregate heritability that is easy to compute and involves no ACE model fitting. We derive analytical results that show this aggregate measure is closely related to the average of element-wise heritability. We validate the analytical results with simulations and illustrate the method on 22 different phenotypes based on the data of 196 subjects from the publicly released Human Connectome Project (HCP) [1], comparing the ranking of this fast aggregate method to the slower traditional ACE-based estimates of average heritability (see also applications in [2][3]).

Methods

We arrange data from an imaging twin study into a subject-by-element data matrix, with one row for each subject and one column for each data element (e.g. voxel, surface element, etc). Conventional heritability analyses work on a single univariate phenotype, here a single column. Our method proceeds by computing the correlation coefficient between rows, over phenotypic elements. That is, each subject pair generates one correlation coefficient between rows, over phenotypic elements. For each subject and one column for each data element (e.g. voxel, surface element, etc), we arrange data from an imaging twin study into a subject-by-element data matrix, with one row for each subject and one column for each data element (e.g. voxel, surface element, etc). Conventional heritability analyses work on a single univariate phenotype, here a single column. Our method proceeds by computing the correlation coefficient between rows, over phenotypic elements. That is, each subject pair generates one correlation coefficient between rows, over phenotypic elements. For each subject and one column for each data element (e.g. voxel, surface element, etc).

Results

Fig. 1 shows simulation results, plotting bias of AggHe relative to the variance-weighted (top) and unweighted (middle) mean summaries, and the standard deviation for AggHe (bottom). While demeaning-only experiences some bias, the results of original data and demeaning & variance-normalisation have comparatively good bias with small variance.

In Fig. 2, real data results show AggHe compared to summary measures of heritability using 22 phenotypes. There is a monotonic relationship found between AggHe and these summaries for both estimates (top) and p-values (bottom). As expected we found a closer relationship between AggHe and the variance-weighted mean than with the un-weighted mean.

Conclusions

Our simulations indicate that the analytical results were relatively accurate for aggregate heritability with original data and after demeaning & variance-normalisation. Using real data, the extremely fast aggregate heritability is highly similar to the traditional (more computationally intensive) mean heritability summaries obtained by fitting an ACE model.

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References