Fast sparse canonical correlation with flashpca — Supplementary Material

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1 Reproducibility

Code to reproduce these experiments is at `https://github.com/gabraham/scca-paper`.

2 HapMap data preprocessing and quality control

The HapMap3 phase III [1] genotypes were obtained from `ftp://ftp.ncbi.nlm.nih.gov/hapmap/genotypes/2009-01_phaseIII/plink_format/`. Gene expression levels were obtained from `http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-264`.

We excluded individuals who were non-founders, had genotyping missingness >1%, or did not have matching gene expression data, resulting in 601 individuals. We excluded non-autosomal SNPs, SNPs with MAF <5%, missingness >1%, and deviation from Hardy-Weinberg equilibrium $P<5 \times 10^{-6}$ using PLINK 1.9 [2, 3], leaving 1,125,747 SNPs (see below). Missing genotypes were randomly imputed according to the frequencies of the non-missing observations.

For the gene expression data, we used a subset consisting of the 21,800 probes that were analysed by [4], utilising the original authors' normalised data. Following [4], we performed PCA on the genotypes within each population, and for the GIH, MEX, MKK, and LWK regressed out 10 PCs of the genotypes (as well as intercept) from the corresponding gene expression levels, in order to adjust for the higher levels of admixture within these populations. We further filtered probes with low variance (std. dev. <0.1), leaving 18,193 probes. Both the gene expression levels and the genotypes were standardised to zero-mean and unit-variance.

3 Timing experiments

For timing of `flashpcaR::scca` and `PMA::CCA`, we used contiguous subsets of chromosome 1 (1000, 5000, 10,000, 20,000, and 50,000 SNPs, out of 18,193 SNPs in total) and contigous subsets of the 18,193 gene expression probes (1000, 10,000, and all 18,193 probes).

We used the R package `microbenchmark` [5] to run 30 replications of each timing experiment. For all experiments we estimated one pair of canonical vectors (u_1, v_1). For both `PMA::CCA` and `flashpcaR::scca`, we initialised v_1 by using `flashpcaR::flashpca` to precompute the rank-1 singular value decomposition of $\mathbf{X}^T\mathbf{Y}$ (that is, $\mathbf{X}^T\mathbf{Y} \approx u_1 d_1 v_1^T$). For `PMA::CCA`, we increased the maximum number of iterations to match that used by `flashpcaR::scca` (default=1000), in order to prevent early termination of the algorithm before adequate numerical convergence was achieved. The command-line version of `flashpca` initialised v_1 using normally-distributed variates.

All experiments were run in R 3.2.2 [6] on 64-bit Ubuntu Linux 12.04 on an Intel Xeon CPU E7-4830 v2 @ 2.20GHz. Time for the commandline `flashpca` include loading of data into RAM. We used flashpca v1.2.6 (`https://github.com/gabraham/flashpca`) and PMA v1.0.9 [7].

4 Comparison of predictive power

Utilising the chromosome 1 genotypes (89,603 SNPs) and all 18,193 gene expression levels, we used 5-fold cross-validation to compare `flashpcaR::scca` and `PMA::CCA`, over a 2D grid of 30×25 penalties, estimating one pair of canonical vectors. The final predictive power was computed as the average Pearson correlation $\bar{\rho}$ in the $k = 1, \ldots, 5$ test folds:

$$\bar{\rho} = \frac{1}{5} \sum_{k=1}^{5} \mathrm{Cor}(\mathbf{X}_{test}^k u^k, \mathbf{Y}_{test}^k v^k).$$

References

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