NPDR Supplementary Material

Trang T. Le¹, Bryan A. Dawkins² and Brett A. McKinney^{2,3*}

 ¹Department of Biostatistics, Epidemiology and Informatics, University of Pennsylvania, Philadelphia, PA 19104
²Department of Mathematics, University of Tulsa, Tulsa, OK 74104
³Tandy School of Computer Science, University of Tulsa, Tulsa, OK 74104

March 3, 2019

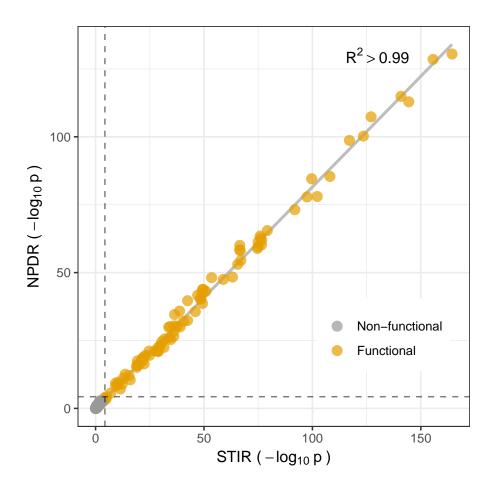


Figure S1: Similarity between NPDR and STIR for one simulation of m=200 samples and p=1000 attributes. In 100 replications, R^2 ranges from 0.9827 to 0.9994. STIR is based on a t-test of projected distances and NPDR is based on a logistic regression of projected distances.

References

[1] Trang T Le, Ryan J Urbanowicz, Jason H Moore, and Brett A McKinney. Statistical inference relief (stir) feature selection. *Bioinformatics*, page bty788, 2018.

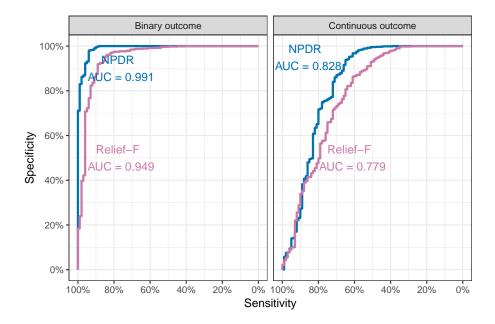


Figure S2: Precision-Recall Curves (PRC) for Relief-F and NPDR for simulated case-control data with interactions (left) and RRelief and NPDR for simulated continuous outcome data with main effects (right). Simulation uses m=200 samples and p=1000 attributes with 100 functional.

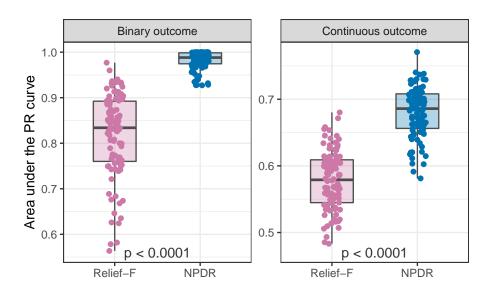


Figure S3: NPDR and Relief comparison of area under the PRC for 100 replicate simulations of case-control (left) and continuous (right) data. All simulations use m=200 samples and p=1000 attributes with 100 functional. NPDR yields significantly higher auPRC.

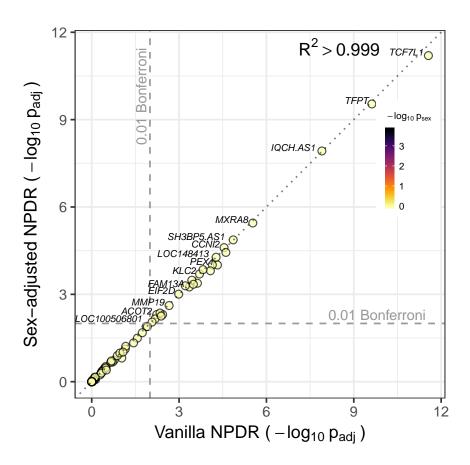


Figure S4: NPDR with and without sex adjustment for analysis of MDD-associated genes in Le et al.'s RNASeq dataset. Adjustment for the sex covariate has a negligible effect on the resulting P values for each important gene because of the balanced study design. Both methods yield consistent results with STIR from previous study (Fig. 4 of Ref. [1]), not shown.

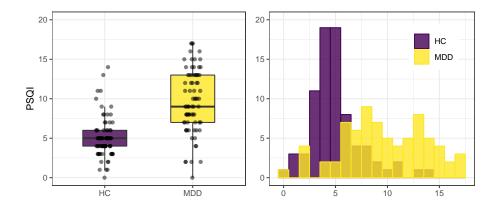


Figure S5: The distribution of the Pittsburgh Sleep Quality Index (PSQI) among individuals with and without MDD.