

Statistical test increases power of genetic studies of complex disease

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The power of genome-wide association studies (GWAS) to detect genetic influences on human disease can be substantially increased using a statistical testing framework reported in the May issue of the journal *Genetics*.

Despite the proliferation of GWAS, the associations found so far have largely failed to account for the known effects of genes on complex disease—the problem of "missing heritability." Standard approaches also struggle to find combinations of multiple genes that affect disease risk in complex ways (known as genetic interactions).

The new framework enhances the ability to detect genetic associations and interactions by taking advantage of data from other genomic studies of the same population. Such information is increasingly abundant for many human populations.

The authors demonstrated that their method improves performance over standard approaches. They also re-examined real GWAS data to find promising new candidates for genetic interactions that affect bipolar disorder, [coronary artery disease](#), Crohn's disease, and rheumatoid arthritis.

"We think practically everyone who's ever done a case-control GWAS could benefit from reanalyzing their data in this way," said author Saharon Rosset, associate professor of statistics at Tel Aviv University.

"This paper offers a significant advance in mapping genes involved in disease. The approach makes use of available data to substantially improve the ability to identify genetic components of disease," said Mark Johnston, Editor-in-Chief of the journal *Genetics*.

More information: S. Kaufman and S. Rosset. Exploiting Population Samples to Enhance Genome-Wide Association Studies of Disease. *Genetics* May 2014 197:337-349 DOI: [10.1534/genetics.114.162511](https://doi.org/10.1534/genetics.114.162511) Available online May 7, 2014. www.genetics.org/content/197/1/337

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