New statistical method could improve search for genes involved in common diseases

May 17 2011, By Wileen Wong Kromhout

Recent breakthroughs in the analysis of genetic variation in large populations have led to the discovery of hundreds of genes involved in dozens of common diseases. Many of these discoveries were enabled by performing "meta-analysis," which combines information from multiple genetic studies in order to create even larger studies.

One of the difficulties in meta-analysis of genetic studies is "heterogeneity," or differences in the strength of genetic variants on the disease across the different studies. Previous methods for handling heterogeneity have performed very poorly compared with traditional approaches, even when heterogeneity is known to be present among the studies.

Now, Eleazar Eskin, an associate professor of computer science at the UCLA Henry Samueli School of Engineering and Applied Science, and recent Ph.D. Buhm Han have developed a new statistical method for combining association studies which performs well in the presence of heterogeneity.

This method should lead to the discovery of many more genes involved in diseases when applied to combine the results of existing genetic association studies.

More information: The research was recently published in the peer-reviewed *American Journal of Human Genetics* and is available online at www.cell.com/AJHG/abstract/S0002-9297(11)00155-8

Provided by University of California Los Angeles

Citation: New statistical method could improve search for genes involved in common diseases (2011, May 17) retrieved 19 April 2024 from https://medicalxpress.com/news/2011-05-statistical-method-genes-involved-common.html