A new method to identify mutated genes in human diseases

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Researchers from the University of Turin, Italy and the University of Nijmegen, The Netherlands, have devised a new method that may help the medical community to determine the genetic basis of many common diseases. Their findings are described in an article published March 21st in the open-access journal *PLoS Computational Biology*.

Thousands of human diseases originate from mutations in one or more genes. Identification of mutated genes is a crucial first step towards understanding the molecular mechanisms at the origin of diseases and devising a treatment. In many cases, we do not know the identity of the affected gene, only a chromosomal region (typically containing hundred of genes) in which the mutation is located.

The research group, led by Ferdinando Di Cunto and Paolo Provero, analyzed gene expression data (patterns of gene activity in tissues and cell lines) from thousands of published experiments to identify genes showing patterns comparable to the ones of mutated genes in similar diseases. The study identified candidate genes for 81 diseases, including various forms of epilepsy and muscular dystrophy.

As in all such analyses, the results must be verified experimentally. However, the task of understanding the molecular basis of many diseases could be significantly simplified by the results of this work.

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