

The human gene connectome server - An online tool for prioritizing disease-causing gene variants by biological distance

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To determine the disease-causing allele(s) underlying human disease, high-throughput genomic methods are applied and provide thousands of gene variants per patient. We recently developed a novel approach, the “human gene connectome” (HGC) – a concept, method and database that describes the set of all in silico-predicted biologically plausible routes and distances between all pairs of human genes. With the HGC, we generated a “gene-specific connectome” for each human gene – the set of all human genes ranked by their predicted biological proximity to the core gene of interest, available at: <http://lab.rockefeller.edu/casanova/HGC/>. We demonstrated that the HGC is the most powerful approach for prioritizing high-throughput genetic variants in Mendelian disease studies. However, there is currently no effective gene-centric online interface for ranking genes by biological distance. We describe here the human gene connectome server (HGCS): a powerful, easy-to-use interactive online tool that enables researchers to prioritize any list of genes according to their biological proximity to core genes (i.e. genes that are known to be associated with the phenotype), and to predict novel gene pathways. We demonstrated the effectiveness of the HGCS for detecting herpes simplex encephalitis genes in patients’ whole exome sequencing data. The HGCS is freely available to use for non-commercial users at: <http://hgc.rockefeller.edu/>.

Biography

Yuval Itan holds a Ph.D. and M.Res. in Modeling Biological Complexity from University College London, the CoMPLEX program, and a B.Sc. in Computational Biology from Bar Ilan University, Israel. Since 2010 he is performing *in-silico* cutting edge research to identify variants that confer susceptibility to infectious diseases in high-throughput genomic and proteomic data, including the development of novel state-of-the-art methods for this purpose.

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