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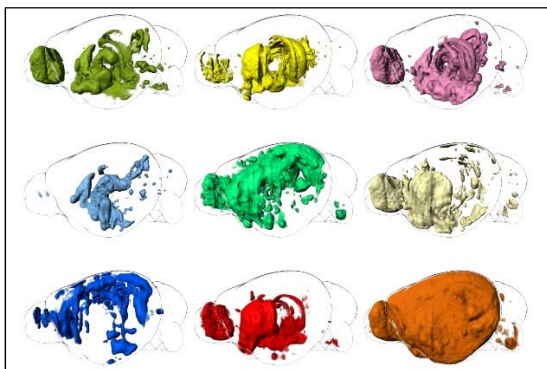
Big data in neuroscience: new method links genome data with brain functions

Scientists in Vienna created a bridge between neuronal circuits and genomes: a multidisciplinary team of researchers from the Centre for Virtual Reality and Visualisation (VRVIS) and the Research Institute of Molecular Pathology (IMP) in Vienna found a method that links big data on brains and genomes to explore functional ties. The method could open a new angle on the characterisation of psychiatric diseases.

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In silico prediction of brain functional neuroanatomy by genetically weighted connectivity analysis (GWCA). Functional maps were generated from weighting brain networks with functional genetic meta data associated with central amygdala circuitry, dopaminergic signalling, feeding, hypothalamic circuitry, fear memory consolidation, panic disorder, learning in a stressful context, social bonding and synaptic plasticity (left to right, top to bottom). © IMP/VRVis

A key objective in neuroscience and psychiatry is to understand how genes influence structure, function and development of brains. Behavioural traits related, for example, to fear or the perception of pain can depend on the interaction of multiple genes. Characterising precisely those genes that contribute to the formation and function of specific neuronal networks is one of the big challenges in modern neurobiology. Until now, work in this field required tremendous efforts and yielded only incomplete answers.

A new method, first presented last year and now published in a special issue of the journal *Neuroimage*, shows an innovative way to bridge readily available data sets on genomes and neuronal networks: using the vast amount of information that both genomics and neuronal mapping gathered in recent years, the scientists generated functional, neuroanatomical maps. These maps tie in genes responsible for neuronal circuits that underlie certain behavioural traits. All of this was done on a computer, using genome and connectome data from publicly accessible sources.

The scientists then tested the reliability of their method: using gene data, they correctly simulated neuronal circuits that are known to contribute to specific traits of psychiatric diseases. Moreover, it was possible to identify previously unknown neuronal connections by combining genetic and network data, thereby improving the quality of existing neuroanatomic maps.

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Improved ways to study psychiatric diseases

Wulf Haubensak of the IMP, who contributed to the study, elaborates possible applications: “In the future, we could use the method to investigate links between genetic variation and changes in behaviour, for example in psychiatric patients. We could explore the neuronal basis of different forms of autism or anxiety disorders in more detail.” This method might lead to a more complete understanding of the interplay between genes and complex behavioural disorders.

At the heart of the study lies an algorithm that links gene expression data to data on neuronal connectivity, allowing the computation of synergic effects of relevant genes on the neuronal networks. “The visualisation of neuronal connections starts with the raw data”, says Florian Ganglberger, PhD student at the VRVis and first author of the study. “This is why we focussed on the development of a mathematical method.”

“Our approach allows us to use readily available ‘big data’ sources, that are generated world-wide by the big brain research initiatives,” says Katja Bühler, head of the Biomedical Image Informatics Group of VRVIS. “This data allows neuroscientists to investigate the links between genes, brain structures and functions in silico, and therefore more rapidly, more cheaply and in more targeted ways.”

Outlook on future work

Basic research can use the method to generate more detailed neuroanatomical maps, including genetic information. Scientists can do computer simulations of experiments to reduce the need for follow-up experiments that would involve people or animals. Medical research could use the method to explore a new angle on the links between genome and brain in the study of psychiatric diseases.

Original publication

Ganglberger F, Kaczanowska J, Penninger JM, Hess A, Bühler K, Haubensak W (2017). Predicting functional neuroanatomical maps from fusing brain networks with genetic information. *Neuroimage*. 2017 Sep 3. pii: S1053-8119(17)30712-7.
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About the IMP

The Research Institute of Molecular Pathology (IMP) in Vienna pursues world-class research in basic molecular biology. It is located at the Vienna BioCenter and largely sponsored by Boehringer Ingelheim. With over 200 scientists from 40 countries, the IMP is committed to scientific discovery of fundamental molecular and cellular mechanisms underlying complex biological phenomena. www.imp.ac.at

About VRVis

The Research Center for Virtual Reality and Visualization (VRVis) is Austria's leading research center for visual computing and conducts with more than 70 employees innovative research and development projects in cooperation with industry and universities. www.vrvis.at