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Professor Paul Matthews is the Edmond and Lily Safra Chair in Translational Neuroscience and Therapeutics and Head of the Division of Brain Sciences at Imperial College London and a Visiting Professor in the LKC Medical School of Nanyang Technological University. He is an Honorary Consultant Neurologist within the Imperial College Healthcare Trust and at the Oxford Radcliffe Hospitals, as well as a Fellow by Special Election of St Edmund Hall, Oxford. He studied Chemistry and obtained a DPhil in Biochemistry from the University of Oxford, received his MD degree and house officer training at Stanford University and specialist training in Neurology at the Montreal Neurological Institute.

Professor Matthews' current research interests include development of novel imaging methods for studying human variation and in vivo molecular neuropathology with a specific focus on investigation of mechanisms linking neuroinflammation to late life neurodegeneration. He was awarded an OBE in 2008 for Services to Neuroscience, elected Fellow of the Academy of Medical Sciences in 2014 and Fellow of the Acadamea Europea in 2015.

Understanding individual variation through the brain functional connectome

Approaches relying on functional connectomic mapping and analyses of individual nodes or network activity are contributing to explanations of individual differences in cognitive stage. They also are providing new insights into more fundamental variations between individuals. For example, brain functional connectomic networks can show different topologies in different people, suggesting different cognitive (computational) strategies associated with different functional connectomic states. The functional anatomical organization of the brain can be explored with additional brain parcellation methods that provide complementary, locally based descriptors. Models relating functional connectomics or parcellations to clinically relevant variations in cognitive state or behavior both can be extended in other ways. For example, because variations in network metastability or synchrony provide optimal conditions for different aspects of information processing, dynamic network models should provide better discriminants of individual variation than do those based on those based on time averaged data.

These functional imaging measures provide endophenotypes reflecting quantiative traits. While the science still is immature, there is encouraging evidence that genetic variation in population behavioral traits or disease is reflected in differences in functional connectivity states or traits. For example, properties of resting state networks show some heritability apparently distinct from that for brain structure, although there is a substantial environmentally determined component and differences in network functional architecture also appear modestly heritable, consequences of which may relate to the heritability of intelligence.

With the mounting evidence that functional connectivities are meaningfully sensitive to environment and experience, as well as to genetic determinants, functional connectomics thus provides a tool for exploring interactions between nature and nurture. With the recent availability of large, consistently acquired imaging datasets with associated phenotypic data from sources such as the Human Connectome Project or UK Biobank, data-driven models that can account for generalizable aspects of this heterogeneity are being explored. These, in turn, should begin to allow determinants of variation to be defined. Some current approaches to the problem will be reviewed in the context of results recently emerging from studies enabled by the new population-based imaging resources.