

Genetic influences on brain functional and structural connectivity

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The project consisted in studying the genetic influence on brain connectivity using Magnetic Resonance Imaging (MRI), using a special protocol (diffusion imaging or DWI).

Kaikai has been working on the validation of using a new model (Fibre Orientation Distribution, FOD) based on measurements data from 37 individuals that were scanned twice over a short period of time (days). No change in the brain was expected to occur in this short period of time and therefore any variation was assumed to be an estimation of the measurement variability and noise. This experiment was conducted and a map estimating the reliable areas and connections has been established.

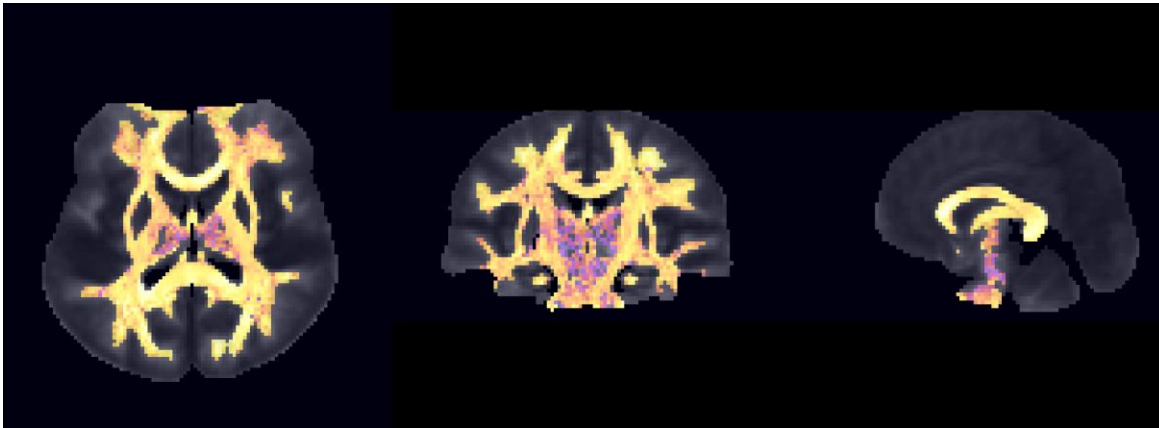


Figure 1 shows the areas of the brain connectivity that have reliability greater than 0.6 in our experiments. Only those areas will be considered in the subsequent analysis.

Second, Kaikai has established a processing pipeline to analyse all the imaging data (100+ twins). This includes methods to perform the statistical analysis on how to study the effect of gene in the connection strength. It is highly novel and requires days of processing using super computer available at Monash University and the CSIRO. The software for image processing and statistical analysis are developed under the cluster environment and shared with the research collaborators at Queensland Institute of Medical Research (QIMR). Positive feedbacks with regard to the data processing and experimental results are received.

Finally, the experiments have been carried out using the image processing and analysis pipeline previously developed and validated on the test-retest data. Novel findings will be reported in a journal publication in preparation. For the first time, the results suggest that inter-hemispheric connections are more genetically driven than the connectivity associated with the somatosensory network. The figure below shows those very novel results.

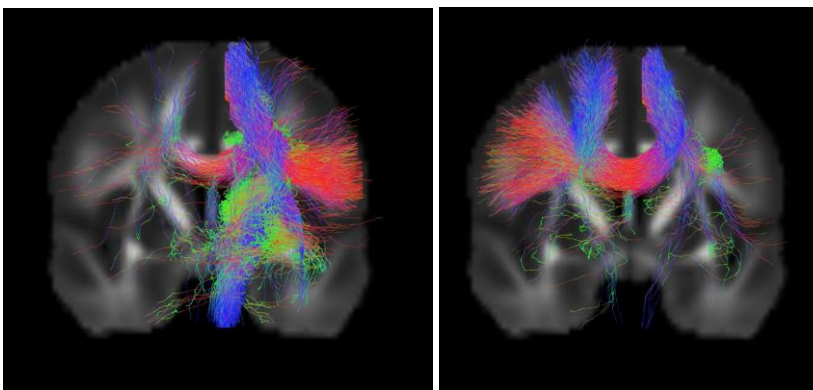


Figure 2. The left panel shows the connections from a patch on the brain surface corresponding to the somatosensory areas which have low heritability, whereas the right panel shows the connection from the same brain areas which have a high heritability. This is the first time that such findings can be shown thanks to a novel statistical and image analysis methods.