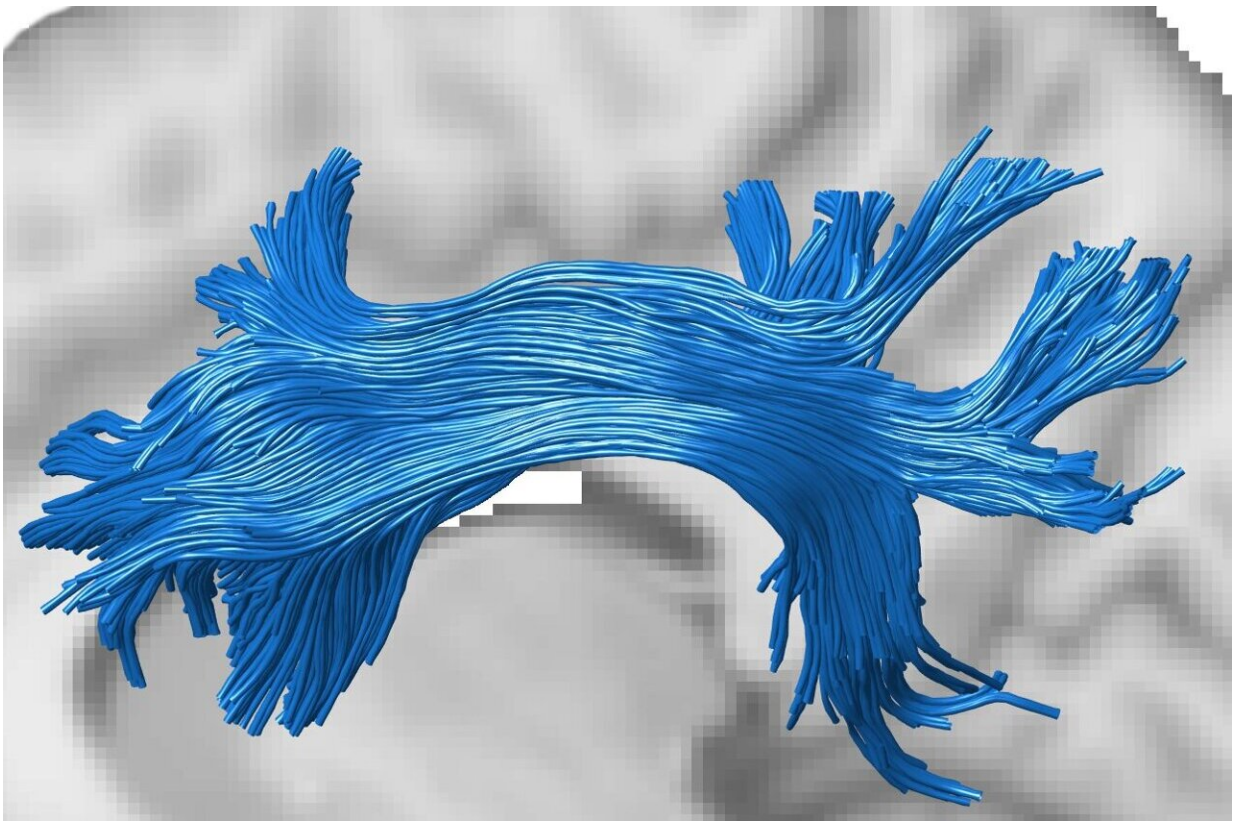# Researchers use GPUs to evaluate human brain connectivity

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The image shows the superior longitudinal fasciculus (SLF), a white matter tract that connects the prefrontal and parietal cortex, two attention-related brain regions. The tract was estimated with diffusion MRI and tractography in the living human brain. Credit: Varsha Sreenivasan and Devarajan Sridharan

A new GPU-based machine learning algorithm developed by researchers

at the Indian Institute of Science (IISc) can help scientists better understand and predict connectivity between different regions of the brain.

The algorithm, called Regularized, Accelerated, Linear Fascicle Evaluation, or ReAl-LiFE, can rapidly analyze the enormous amounts of data generated from diffusion Magnetic Resonance Imaging (dMRI) scans of the human brain. Using ReAL-LiFE, the team was able to evaluate dMRI data over 150 times faster than existing state-of-the-art algorithms.

"Tasks that previously took hours to days can be completed within seconds to minutes," says Devarajan Sridharan, Associate Professor at the Centre for Neuroscience (CNS), IISc, and corresponding author of the study published in the journal *Nature Computational Science*.

Millions of neurons fire in the brain every second, generating electrical pulses that travel across neuronal networks from one point in the brain to another through connecting cables or "axons." These connections are essential for computations that the brain performs. "Understanding brain connectivity is critical for uncovering brain-behavior relationships at scale," says Varsha Sreenivasan, Ph.D. student at CNS and first author of the study. However, conventional approaches to study brain connectivity typically use animal models, and are invasive. On the other hand, dMRI scans provide a non-invasive method to study brain connectivity in humans.

The cables (axons) that connect different areas of the brain are its information highways. Because bundles of axons are shaped like tubes, water molecules move through them, along their length, in a directed manner. dMRI allows scientists to track this movement in order to create a comprehensive map of the network of fibers across the brain, called a connectome.
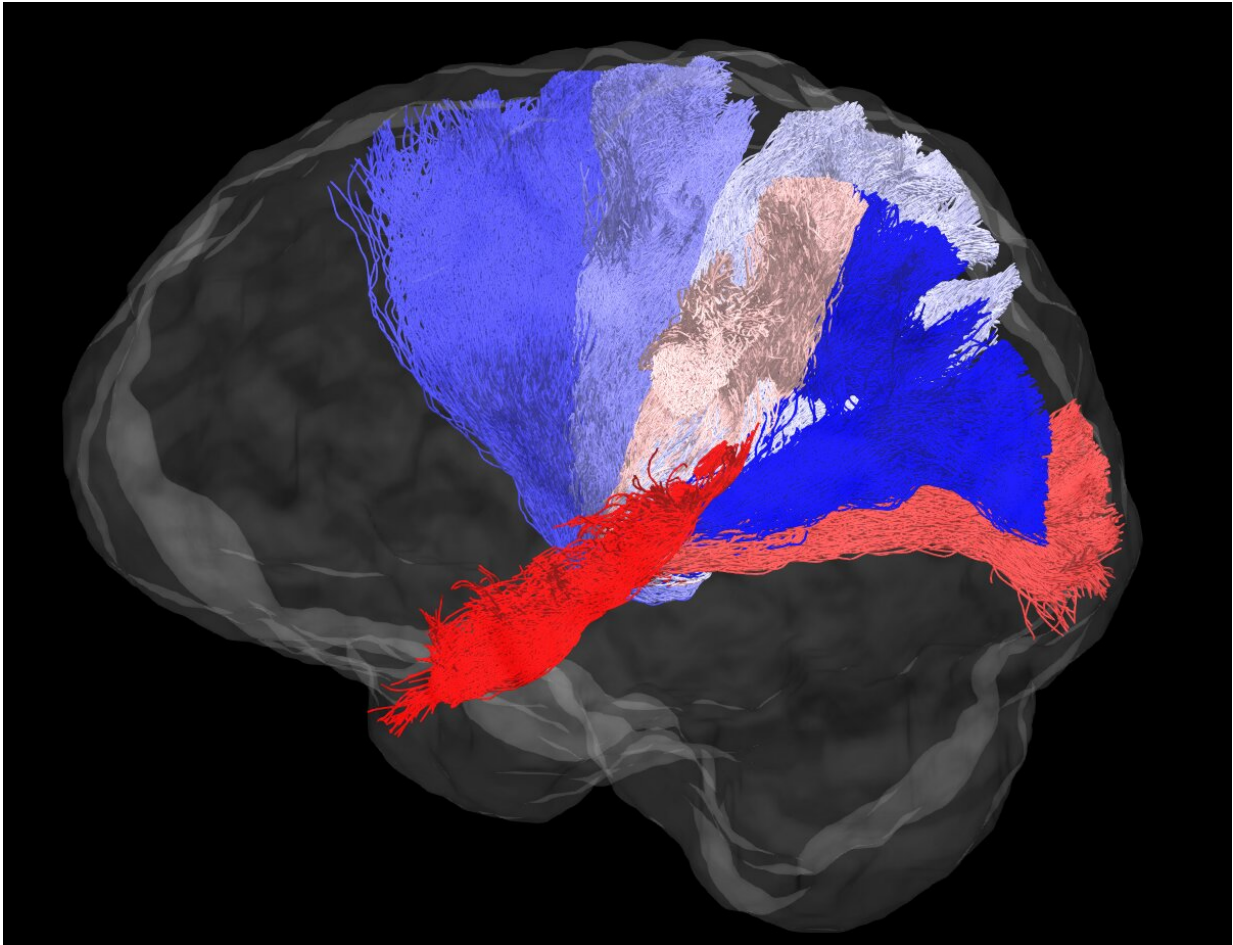
The image shows connections between the midbrain and various regions of the neocortex. Connections to each region are shown in a different color, and were all estimated with diffusion MRI and tractography in the living human brain. Credit: Varsha Sreenivasan and Devarajan Sridharan

Unfortunately, it is not straightforward to pinpoint these connectomes. The data obtained from the scans only provide the net flow of water molecules at each point in the brain. "Imagine that the water molecules are cars. The obtained information is the direction and speed of the vehicles at each point in space and time with no information about the

roads. Our task is similar to inferring the networks of roads by observing these traffic patterns," explains Sridharan.

To identify these networks accurately, conventional algorithms closely match the predicted dMRI signal from the inferred connectome with the observed dMRI signal. Scientists had previously developed an algorithm called LiFE (Linear Fascicle Evaluation) to carry out this optimization, but one of its challenges was that it worked on traditional Central Processing Units (CPUs), which made the computation time-consuming.

In the new study, Sridharan's team tweaked their algorithm to cut down the computational effort involved in several ways, including removing redundant connections, thereby improving upon LiFE's performance significantly. To speed up the algorithm further, the team also redesigned it to work on specialized electronic chips—the kind found in high-end gaming computers—called Graphics Processing Units (GPUs), which helped them analyze data at speeds 100-150 times faster than previous approaches.

This improved algorithm, ReAl-LiFE, was also able to predict how a human test subject would behave or carry out a specific task. In other words, using the connection strengths estimated by the algorithm for each individual, the team was able to explain variations in behavioral and cognitive test scores across a group of 200 participants.

Such analysis can have medical applications too. "Data processing on large scales is becoming increasingly necessary for big-data neuroscience applications, especially for understanding healthy brain function and brain pathology," says Sreenivasan.

For example, using the obtained connectomes, the team hopes to be able to identify early signs of aging or deterioration of brain function before they manifest behaviorally in Alzheimer's patients. "In another study, we

found that a previous version of ReAL-LiFE could do better than other competing algorithms for distinguishing patients with Alzheimer's disease from healthy controls," says Sridharan. He adds that their GPU-based implementation is very general, and can be used to tackle optimization problems in many other fields as well.

  More information: Varsha Sreenivasan et al, GPU-accelerated connectome discovery at scale, *Nature Computational Science* (2022). DOI: 10.1038/s43588-022-00250-z

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