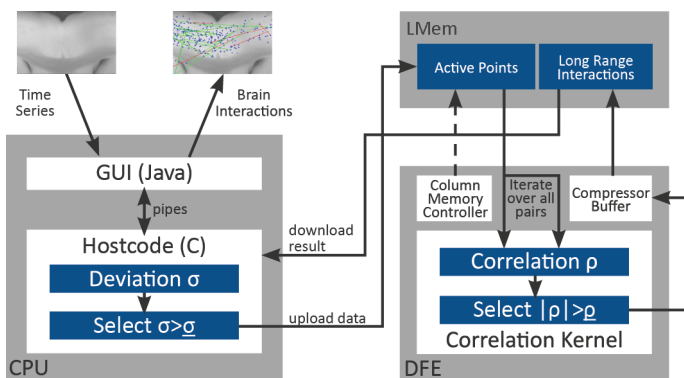


Brain Network Demo

Real-Time Computational Biology

At a Glance

- Correlation analysis of a brain network, showing correlations suggesting long-range interaction between neurons in an experiment.
- Real time 348x260 images from an experiment on brain tissue with analysis window of 30 frames per second
- Real time computation allows scientists to actively modify the ongoing experiment and improve the quality of scientific results
- Dataflow Engine code written in MaxCompiler, CPU code written in C, GUI in Java. C and Java code communicate over Unix pipes.



Accelerated application architecture

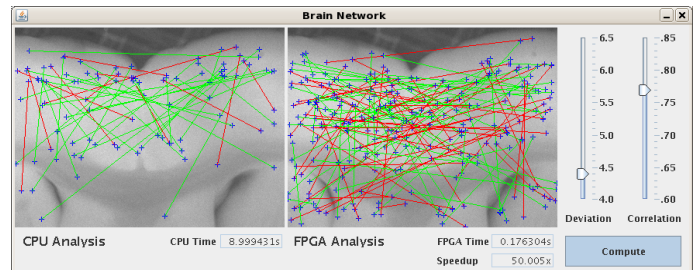
The Maxeler Brain Network demo shows how Maxeler Dataflow Engine (DFE) technology can be applied to computational biology, a field with several compute-intensive problems related with the exponential explosion of available biological data.

The overall Brain Network application is based on the reasonable assumption that the brain can be view as a network of interacting neurons. Thus, classical network algorithm such as linear correlation analysis may be useful to infer long-range interactions during particular brain activities. Brain data are collected at runtime as a time series of CCD images of rodent brain tissue. The underlying “wet” experiment detects brain activity as changes in luminosity due to a fluorescent protein (Liano et al, 2009).

Maxeler Brain Network demo implements linear correlation analysis over a loop of brain images. The CPU selects active points over a time windows by calculating their standard deviations. Then, these active points are transferred to the onboard LMem in order to perform an all-to-all correlation analysis on DFE. This latter step has quadratic complexity $O(n^2)$ and is the target of the acceleration. Finally, edges that exceed a given correlation threshold are copied back to CPU as result. The demo shows both CPU & DFE computations.

Maxeler DFEs provide a massive level of parallelism for Brain Network analysis,

both as super-pipelined architecture and as multiple computing units (e.g. 8 or more pipelines on MAX3 DFEs). The achieved speedup over a single-core Intel Xeon is around 50 fold. This speed meets real-time deadlines up to 46,000 active points, a sufficient amount to deal with every biologically significant case. The DFE also offers power efficiency since its kernels run at 150 MHz, a lower frequency compared to state-of-the-art CPUs.



Application GUI

How to Run the Demo

- Run `./run.sh` in the demo directory to launch the GUI.
- Click 'Compute' to start correlation analysis on a predefined loop of brain images.
- Two different windows show CPU and DFE calculations in parallel. The GUI reports their comparative running times in terms of speedup.
- Positive correlations are drawn as green lines, negative correlations are drawn as red lines.
- The left slider modifies the deviation threshold. You can analyze a larger set of points (with an increased computational effort) by lowering its value.
- The right slider modifies the correlation threshold. This affects the amount of correlations edges that are selected and drawn at runtime.

Further Reading

For more information on the experimental technique used to collect the brain data:

D. A. Liano et al. *Rapid and Sensitive Mapping of Long-Range Connections In Vitro Using Flavoprotein Autofluorescence Imaging Combined With Laser Photostimulation*. Journal of Neurophysiology, vol 101, pp 3325-3340, June 2009.

Maxeler Advantage

- Desktop MaxWorkstation with single MAX3 DFE is capable of processing brain data in real time during the “wet” experiment, with equivalent performance to 4 high-end Intel data center compute nodes.
- For data center processing, a MaxNode with 4 MAX3 DFEs is equivalent to 17 high-end Intel nodes.