

Biological Neural Network Simulation on Supercomputers using NEST

What is NEST?

NEST is a simulator for spiking neural network models that focuses on the dynamics, size and structure of neural systems rather than on the exact morphology of individual neurons.

NEST is ideal for networks of spiking neurons of any size, for example:

- Models of information processing e.g. in the visual or auditory cortex of mammals,
- Models of network activity dynamics, e.g. laminar cortical networks or balanced random networks,
- Models of learning and plasticity.

Why supercomputers for Neural Network Simulation?

The human brain exhibits a sparse, recurrently, and specifically connected network of about 10^{11} neurons, each having of the order of 10^4 synapses to other neurons; its simulation is challenging due to the required memory to represent the structure and the simulation time to solve the dynamics. Such simulations naturally call for the use of supercomputers; machines at the current frontier of processing capability. The neuroinformatics tools employed in this endeavor must be adapted to the computer platforms, even though these systems have typically not been designed with the specific requirements of neuroinformatics applications in mind. The primary objective driving the development of the majority of supercomputer architectures is maximizing floating point performance, rather than providing the large amounts of working memory and high memory bandwidth required by neuronal network simulations. Moreover, the data transfer to and from these machines is often problematic, although specialized parallel I/O solutions do exist (Frings et al., 2009). However, tools cannot be developed solely to capitalize on the properties of supercomputer architectures – first and foremost they must serve the demands generated by the neuroscientific domain.

Running large Neural Network Simulations on Supercomputers: (<http://journal.frontiersin.org/Journal/10.3389/fninf.2012.00026/full>)

Specification of Employed Computer Architectures

The K computer, located at the Advanced Institute for Computational Science in Kobe, Japan, is a distributed-memory supercomputer system that includes 88,128 CPUs (705,024 cores) and 1.4 PB RAM (Yonezawa et al., 2011). The theoretical performance of the system is 11.28 PFlops. A compute node in the K system is mainly composed of a CPU, memory modules of 16 GB, and a chip for the interconnect of nodes. The CPU architecture is a SPARC64 VIIIfx developed by Fujitsu, Ltd., which has 8 cores with 32 kB data cache each and 6 MB shared L2 cache, operating at a clock frequency of 2 GHz. Theoretical performance per chip is 128 GFlops. Each core has two SIMD units that concurrently execute four double precision floating point multiply and add operations. The compute nodes are connected with the “Tofu” (*torus connected full connection*) interconnect network, a six-dimensional mesh/torus network (Ajima et al., 2009). The bandwidth per link is 5 GB/s. A three-level parallel programming model is available on the K computer: (1) SIMD processing in the core, (2) thread programming in a compute node using OpenMP directives, (3) distributed-memory parallel programming with MPI.

The JUGENE computer was in operation at the Jülich Research Centre, Germany from 2008 to 2012. It is a BlueGene/P distributed-memory supercomputer system developed by IBM that included 73,728 compute nodes (294,912 cores) and 144 TB RAM. Its theoretical performance was 1 PFlops. In the BlueGene/P architecture, each compute node has a 32 bit Power PC 450 CPU, which has 4 cores running at 850 MHz, a shared 4-way SMP L3 cache of 8 MB, and 2 GB of RAM. Each core has a dual floating point unit. The theoretical performance per chip is 13.6 GFlops. The compute nodes are connected with a three-dimensional torus network with a bandwidth per link of 425 MB/s.

Results

The paper is reliably able to predict the number of nodes and wall time needed for a simulation using their memory abstraction and analysis technique.

The research work made it to the headlines in multiple science magazines in mid-2013.

(<http://eandt.theiet.org/news/2013/aug/nest-neural-network.cfm>)

“

A network consisting of 1.73 billion nerve cells connected by 10.4 trillion synapses has been created using the power of a Japanese supercomputer.

Despite being the biggest neuronal simulation to date, the process requiring 82,944 processors only represented about 1 per cent of the neuronal network of a human brain.

The supercomputer completed in 40 minutes the equivalent amount of activity that is observed to take place in the living brain within one second.

“

NEST 2.6.0 (Neural Simulation Tool) was released on 23 December 2014 as open source software. It implements the technology described in the article "Spiking network simulation code for petascale computers" by Susanne Kunkel et al. (doi:10.3389/fninf.2014.00078). NEST is the technological basis of the network simulator of the HBP(Human Brain Project). The article demonstrates that neuroscience can make full use of petascale supercomputers.