

Arbor

A morphologically detailed neural network library for modern high performance computer architectures

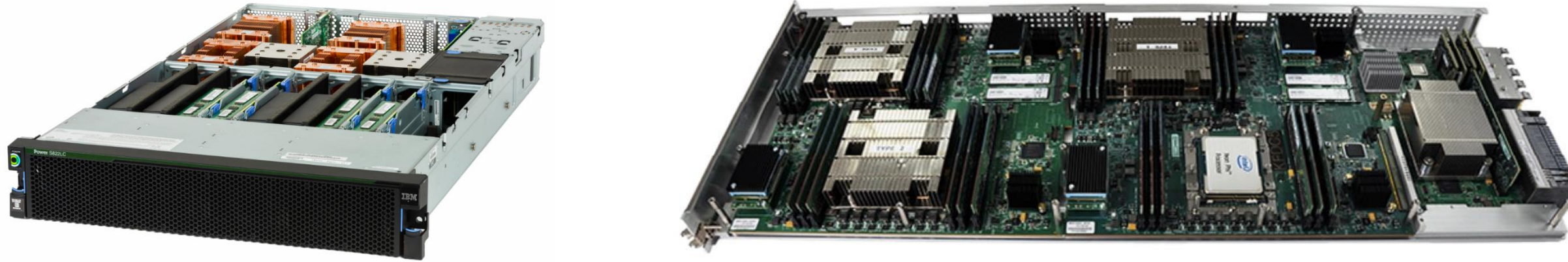
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Why Arbor?

Many core HPC architectures are becoming the norm



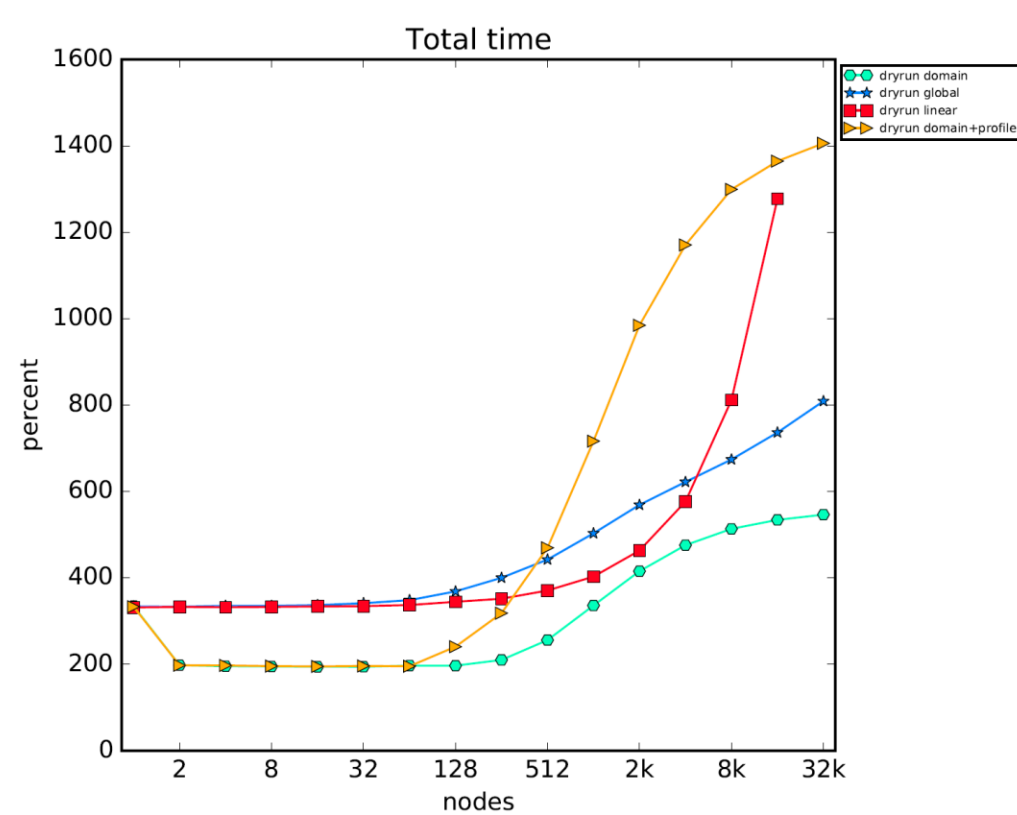
The HBP PCP prototype systems at Jülich. Both are a radical departure from current technology.

left: Juron, IBM "fat node" with Power8 CPUs and 4 GPUs. right: Julia, Cray XC "blade" with 4 Intel KNL nodes.

We need to develop simulators designed to exploit these architectures *now*. Arbor aims to meet this need, alongside other efforts to add many core support to existing software.

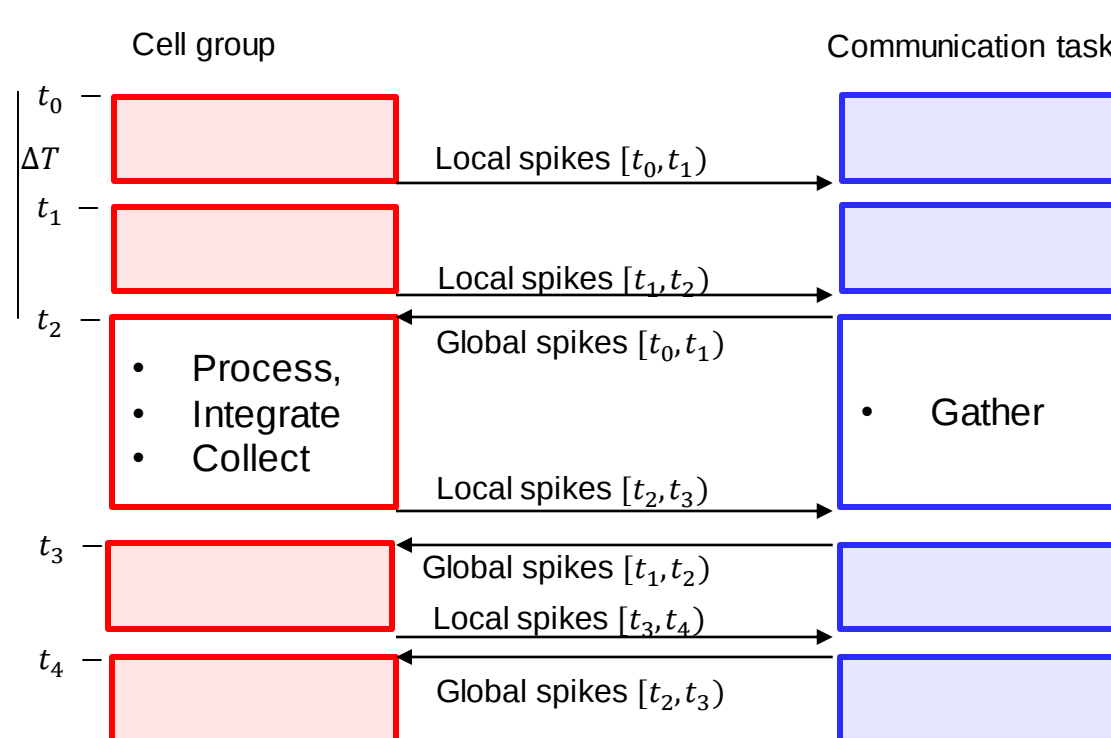
Designing software for the *many core* environment from the *ground-up* will pay off.

Preparing for communication at exascale



Performance modelling is required to predict and understand scaling issues ahead of time.

Naïve linear spike exchange (red) grows exponentially with large node numbers. The improved implementation (green) does not show this problem.



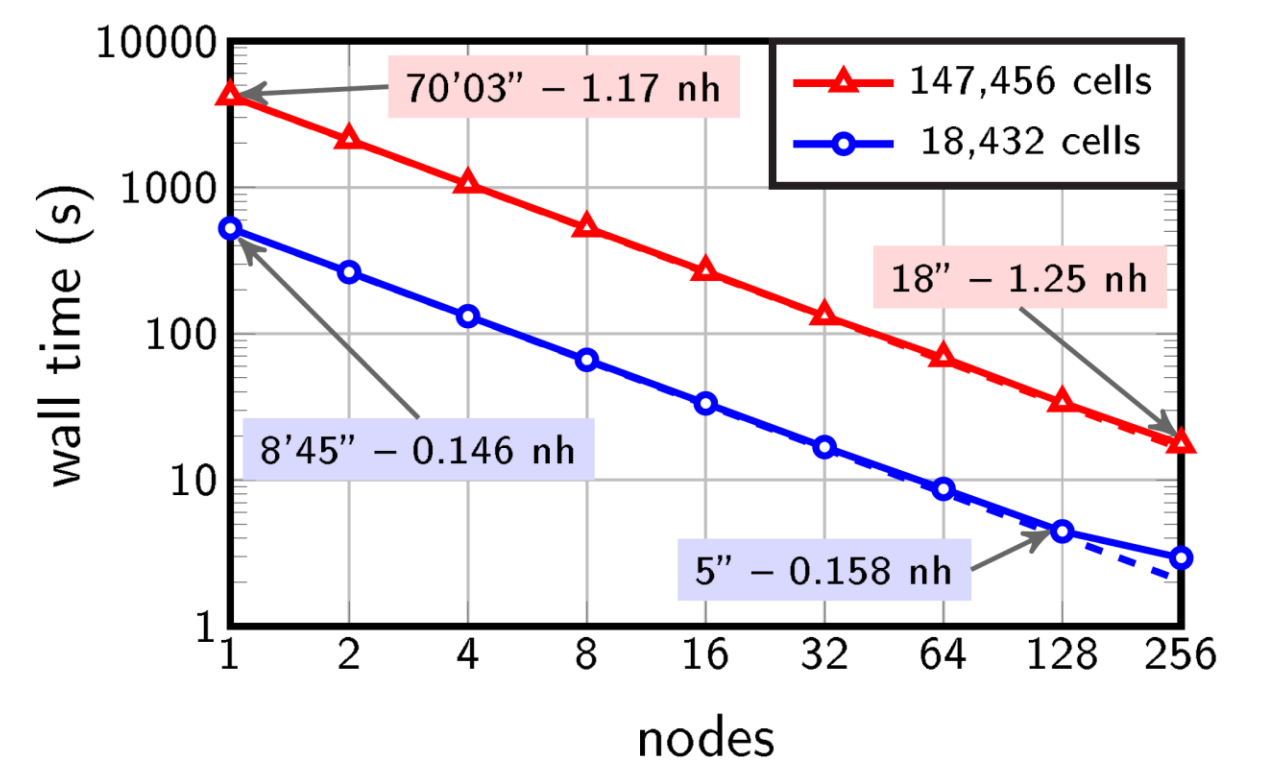
Overlap of spike communication and processing at the single cell group / task level.

During the gathering of the global spikes $[t_1, t_2]$ by the communication task, the cell group can: process the local spikes for $[t_0, t_1]$, integrate the state to t_3 and collect the global spikes for $[t_2, t_3]$.

Performance of the prototype

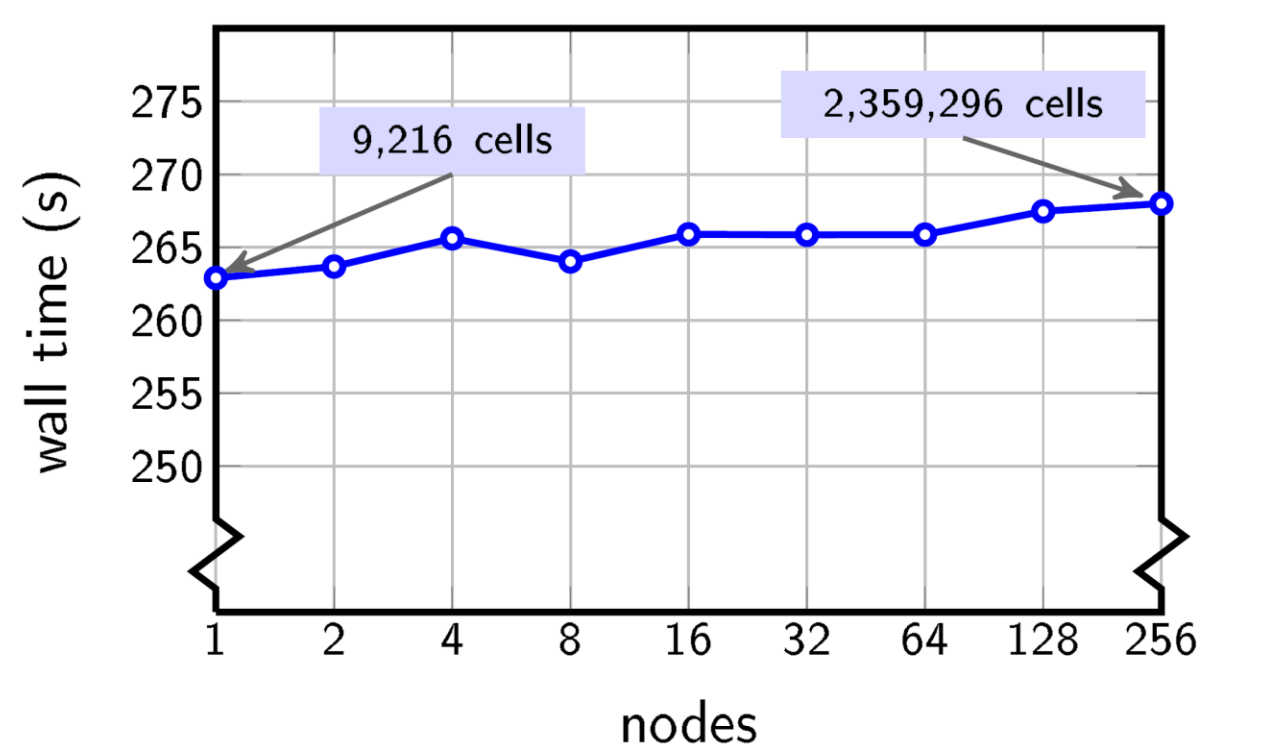
cluster	Cray XC40: 36 cores & 64GB per node
Cell model	300 compartments & 2000 synapses each, Passive dendrites, Hodgkin Huxley soma
duration	500 ms

Add nodes for a faster simulation



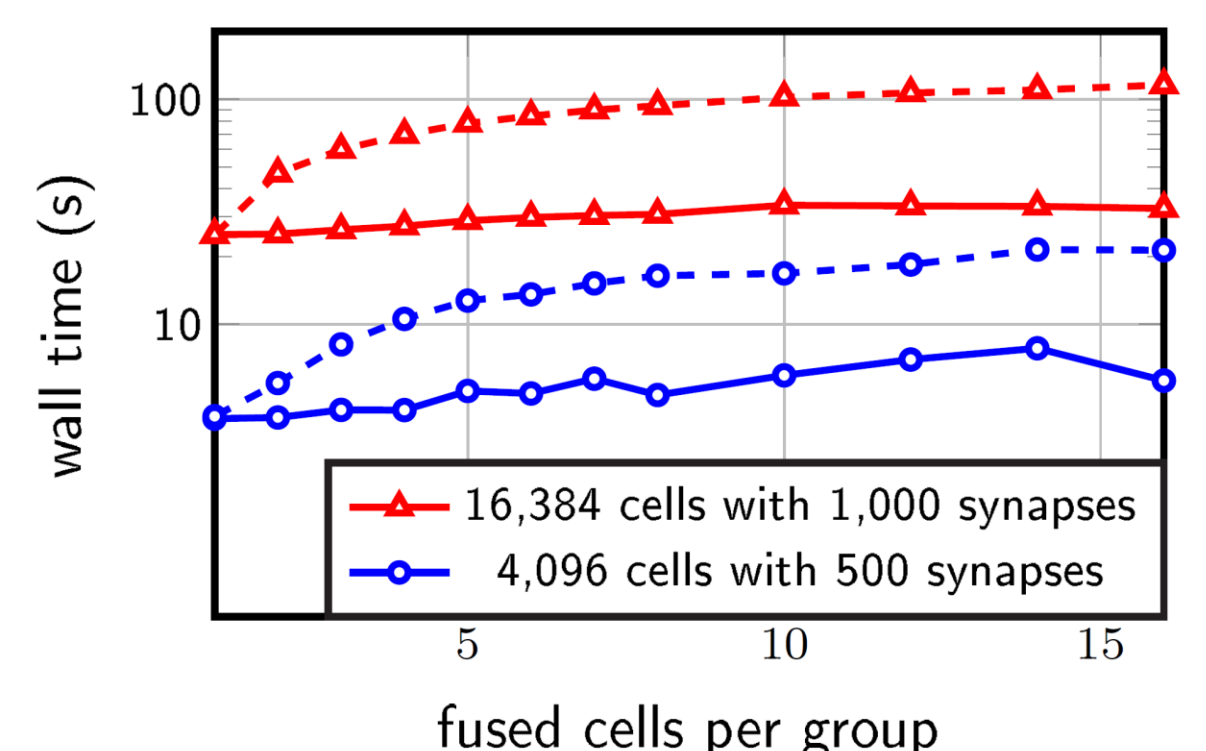
The simulation runtime of a model with fixed size as a function of the number of compute nodes. The runtime is greatly decreased by adding nodes.

Add nodes for a bigger simulation



The simulation runtime of a model with 256 cells per core as a function of the number of nodes. The increase in runtime of a model 256 times larger is only a couple of percent.

Use the advanced features



Two models are run on the Inter KNL with and without the advanced high-speed memory (solid and dashed lines respectively). The bundling of work items allows for important optimization for some models and architectures.

Who

Developed by a team from three HPC Centers: Jülich, CSCS and BSC

- Part of HPC infrastructure work package in the HBP
- Part of the NEST family
- The team provides know-how in computer science, math, neuroscience and software development

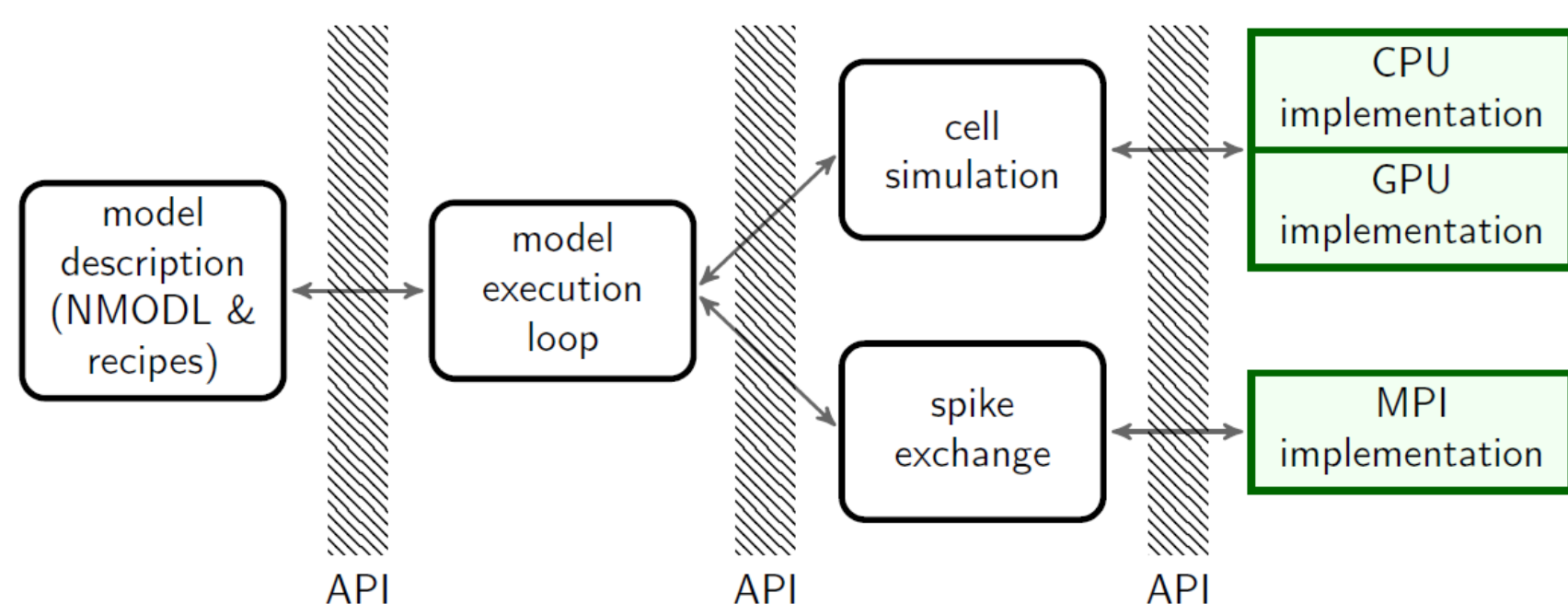
How

Arbor is designed from the ground up for *many core* architectures.

- Written in modern C++, CUDA, Intel TBB and HPX.
- Uses sound development practices including unit testing, continuous Integration, and validation
- Open source and community-driven

Prototype

- Supports NMODL for ion channels and synapses
- Distributed building of networks with millions of cells
- Finite volume discretization of the cable equation
- Validated against Neuron
- Kinetic schemes for detailed biological models
- Unit and performance tests



The prototype is designed to be modular. This allows plug-in of different simulation and communication implementations.

Do you want to know more?

The source code of the prototype is in an open repository on GitHub. It is not ready for general release, but we want to share our work with the community. *If you would like to know more, contribute or collaborate, please contact us!*

web	eth-cscs.github.io/nestmc
source	github.com/eth-cscs/nestmc-proto
email	bcumming@cscs.ch a.peyser@fz-juelich.de

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