



INTRODUCTION TO ARBOR

What's new and demonstration

June 29, 2021 | Brent F. B. Huisman | Jülich Supercomputing Centre

WHAT IS ARBOR?

Arbor is a library for implementing performance portable network simulations of multi-compartment neuron models.

- Simulate large networks of morphologically-detailed, spiking neurons
- Library: you control your program/workflow. Interoperable.
- Portable: scientific description is separate from execution instructions. E.g. run one scientific description on laptop CPU, GPU cluster or future hardware.
- *Performance* portable: add optimized backends for new computer architectures. Currently supported:
 - Distributed parallelism using MPI
 - CUDA backend for NVIDIA and AMD GPUs
 - Vectorized backends for x86-64 (KNL, AVX, AVX2) and Arm64 (NEON, SVE) intrinsics
- Executes on all HPC systems in the HBP (and outside).

WHO IS ARBOR?

Open development style through Github

- Issues, PR workflow, Discussions, Slack/Gitter
- Code quality: PR review, unit testing, CI at Github and CSCS

Core contributors

- Ben Cumming
- Nora Abi Akar
- Stuart Yates
- Anne Küsters
- Thorsten Hater
- Brent Huisman

Website: arbor-sim.org



CSCS

Centro Svizzero di Calcolo Scientifico
Swiss National Supercomputing Centre



JÜLICH
Forschungszentrum

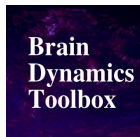
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INCF/OCNS Software Working Group



NeuroFedora



nest-initiative.org



A Python simulation framework for
easy whole-brain neural mass modeling



PyNN



Ankur Sinha, Shailesh Appukuttan, Stewart Heitmann, Caglar Cakan, Nikola Jajcay, Christoph Metzner, Felix B. Kern, Zohreh Vaziri, Amelie Aussel, Brent Huisman, Malin Sandström, Daniele Avitabile, Thomas Nowotny, James Knight, Charl Linssen, Andrew P. Davison, Shavika Rastogi, Marcel Stimberg, Joe Graham



GitHub: <https://ocns.github.io/SoftwareWG/> & <https://github.com/OCNS/SoftwareWG/discussions>

Neurostars: <https://neurostars.org/t/ocns-infrastructure-software-tools-sig-meet-and-greet-initial-discussions>

ARBOR STATUS

- Latest release: v0.5.2
- 42 Github forks
- 1300+ commits to main branch
- loc: C++ header: 68k, C++: 68k, Python: 16k, reStructuredText: 8k
- 24 contributors, from 9+ institutions

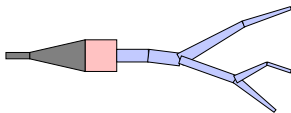
Ongoing collaborations:

- FIPPA - extend Arbor by key plasticity processes to simulate and analyze the long-term adaptive dynamics of large-scale, morphologically-detailed neuronal networks
- Arborio - large-scale model of the inferior olive of the cerebellar complex as a case study
- LFPy - investigating Arbor as possible backend
- Co-simulation - Nest, Elephant, TVB

BUILDING ARBOR

begins with the computational model of neurons

- Arbor simulates networks of multi-compartment neurons
- Neurons: approximated by axonal delay, synaptic functions and a set of cables connected in a tree.
- Cables: characterized as electrical compartments (frustums) composed of ion channels, cable resistance and capacitance.
- Neurons represented as sparse, close-to-band matrices to be solved (e.g. by Hines solver) against known current states due to synaptic conductance.
- Network and spike exchange between neurons at synapses are represented by concatenations of matrices.



USER DESIGN

Describe the neuroscience first ...

Cells

- Cells represent the smallest model to be simulated
- Cells are the smallest unit of work distributed across processes
- Types:
 - Cable cells
 - Leaky integrate-and-fire cells
 - Spiking cells
 - (Benchmark cells)

Recipes

- Recipes describes models in a cell-oriented manner and supplies methods to:
 - Map global cell identifier gid to cell type
 - Describe cells (Cable cell 123, what is it's morphology?)
 - List all connections from other cells that terminate on a cell
- Advantage: parallel instantiation of cell data

USER DESIGN

... then translate it into execution.

Cell groups

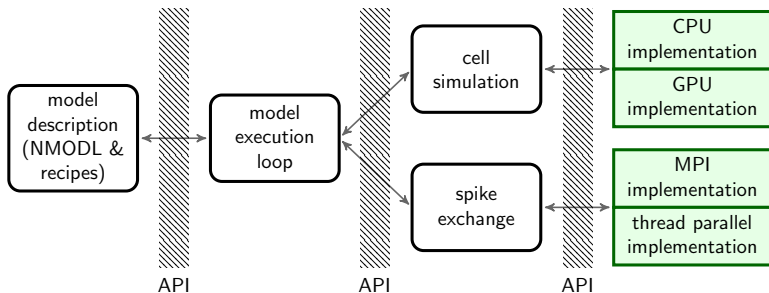
- Cell groups represent a collection of cells of the same type together with implementation of their simulation
- Partitioning into cell groups provided by decomposition
- A **simulation** manages instantiation of model and scheduling of spike exchange as well as integration for each cell group

Mechanisms

- In a recipe, mechanisms are specifications of ion channel and synapse dynamics. Advantage: parallel instantiation of cell data.
Implementations of mechanisms:
- Hand-coded for CPU/GPU execution
- A translator (modcc) compiles a subset of NMODL to architecture-optimized vectorized C++ or CUDA
- Soon: Arblang

INTERNAL DESIGN

Programming interface ensures extensibility



- Components can be substituted according to the internal API.

DESIGN

Summary

Arbor internal model:

- Internal API decouples model description, execution, spike exchange and cell simulation
- Computational work is hidden in pluggable backends, allowing automatic generation for different architectures

User models are composed of:

- Cells representing the smallest unit of computation
- Recipes representing a parallelizable set of neuron construction and connections
- Mechanisms representing ion channel and synapse dynamics

INTEROPERABILITY, PORTABILITY AND EXTENSIBILITY

Why are they relevant to a computational neuroscientist?

- Why a library?
 - Makes Arbor interoperable with other tools and your way of working.
- What is portability?
 - Write your science and let Arbor worry about how to efficiently execute it.
- What is performance portability?
 - You can extend Arbor to take advantage of new hardware without having to modify your scientific description. Your scientific description will continue to work.

WHAT'S NEW?

- Expanded set of tutorials
- CI significantly expanded
 - Automated building of Python and Spack packages
 - Soon: Ebrains CD
- File format compatibility: cell morphologies
 - SWC
 - NeuroML
 - Neurolucida ASCII
 - Arbor Cable Cell
- Arbor GUI
 - Focussed on cell design, decoration
 - Can run single cell model simulations

WHAT'S COOKING?

- Arbor mechanism description language (codename ARBLANG)
 - Declarative
 - Simple, extendable and maintainable
 - Capable of performing powerful optimizations on the source code
 - Make support in other simulators easy, make Arblang translatable to/from similar DSLs (eg: NEUROML/LEMS, NMODL, SBML)
- Crack the nut of distributed gap junctions
 - MSc will study Wave Relaxation method this summer
 - Arborio is investigating *multi*-GPU cell groups
- Implement synaptic plasticity, synaptic scaling, and structural plasticity
 - FIPPA
- LFP estimation
 - Arborio

WRAP UP

- Web: arbor-sim.org
- Docs: docs.arbor-sim.org
- Community: github.com/arbor-sim/arbor/discussions

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EBRAINS



Human Brain Project

TO THE DEMO!

- To the demo!
- `docs.arbor-sim.org/en/latest/tutorial/network_ring.html`

A BRIEF HISTORY OF ARBOR

- CSCS were working with EPFL on HPC-ification Neuron, Moose, Brian
- Ben Cumming pitched the idea of a clean break to FZJ, where Alex Peyser picked it up
 - Fundamental to Arbor and the investment of CSCS and FZJ in it: better use of computational resources
 - To our knowledge, Arbor is one of the few HBP-grown projects!
- Nest-MC (multi-compartment Nest) is born, unrelated to Nest however
 - initial commit: december 3, 2015
- September 28, 2017: renamed to Arbor
- October 12, 2018: first formal release, v0.1
- April 1, 2020: v0.3 release with Python wrapper
- July 15, 2020: Brent Huisman hired as Product Owner
- May 15, 2021: arbor-sim.org acquired