INTRODUCTION TO ARBOR
What's new and demonstration

July 27, 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

CSCS
Centro Svizzero di Calcolo Scientifico
Swiss National Supercomputing Centre

JÜLICH Forschungszentrum | JÜLICH SUPERCOMPUTING CENTRE

Website: `arbor-sim.org`

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

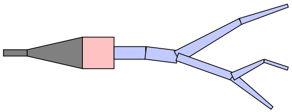
Ongoing collaborations:

- 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

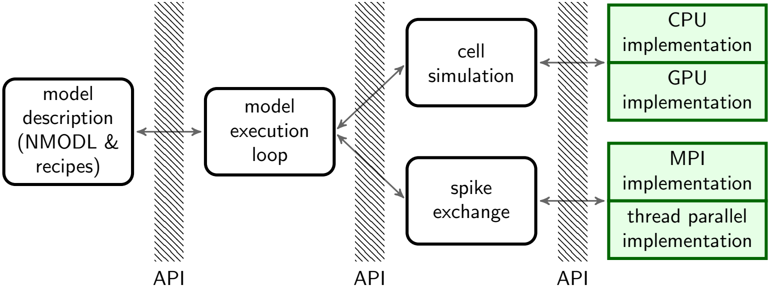
Mechanisms

- 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

Questions?

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

Acknowledgements: This research has received funding from the European Unions Horizon 2020 Framework Programme for Research and Innovation under the Specific Grant Agreement No. 720270 (Human Brain Project SGA1), Specific Grant Agreement No. 785907 (Human Brain Project SGA2), and Specific Grant Agreement No. 945539 (Human Brain Project SGA3).

EBRAINS Human Brain Project

DEMO TIME!

- We'll be doing the network ring tutorial:

  `docs.arbor-sim.org/en/latest/tutorial/network_ring.html`

- Connect at `https://lab.ebrains.eu`
- `pip install arbor`
- `wget https://github.com/arbor-sim/arbor/raw/v0.5.2/python/example/network_ring.py`

STEP 0

- Documentation at `docs.arbor-sim.org`
  - 'Concepts' for conceptual explanation
  - Python and C++ sections detail the matching conceptual pages
- Today's plan
  - Make a cell
  - Make a recipe
  - Run
  - Visualize results

STEP 1

Make a cell

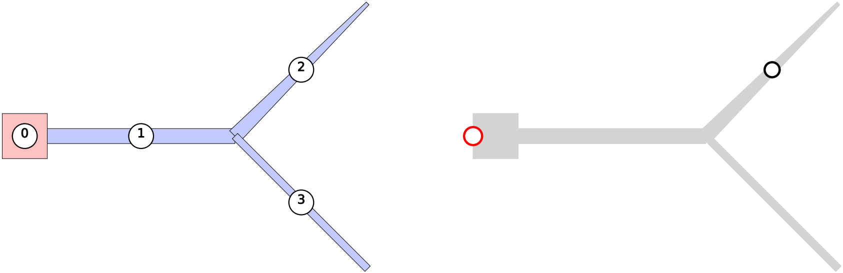


Figure: Left: Make a morphology of 4 segments: a soma (pink) and a branched dendrite (light blue). Right: We'll create labels for the root (red) and a synapse_site (black).

STEP 2

Make a network

- Cells are the basic building blocks in Arbor
- Recipes tie them together
- You'll make your own recipe by inheriting from `arbor.recipe`
- Some member functions need to be overridden

STEP 3

Make a simulation

- Describe
  1. context (what hardware do you have?)
  2. domain decomposition (how to use the hardware)
  3. simulation
- Start with an `arbor.simulation` object, and see what you need for it.
- (defaults are OK)
- We need to store handles to the samplers, because later we'll use `arbor.simulation.samples()` to retrieve results.

STEP 4

Show your results!

- We can extract results from
  - `arbor.simulation.spikes`
  - `arbor.simulation.samples`
- Print or plot
  - Suggestion: Pandas and Seaborn
  - `pip install pandas seaborn`

THE END
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