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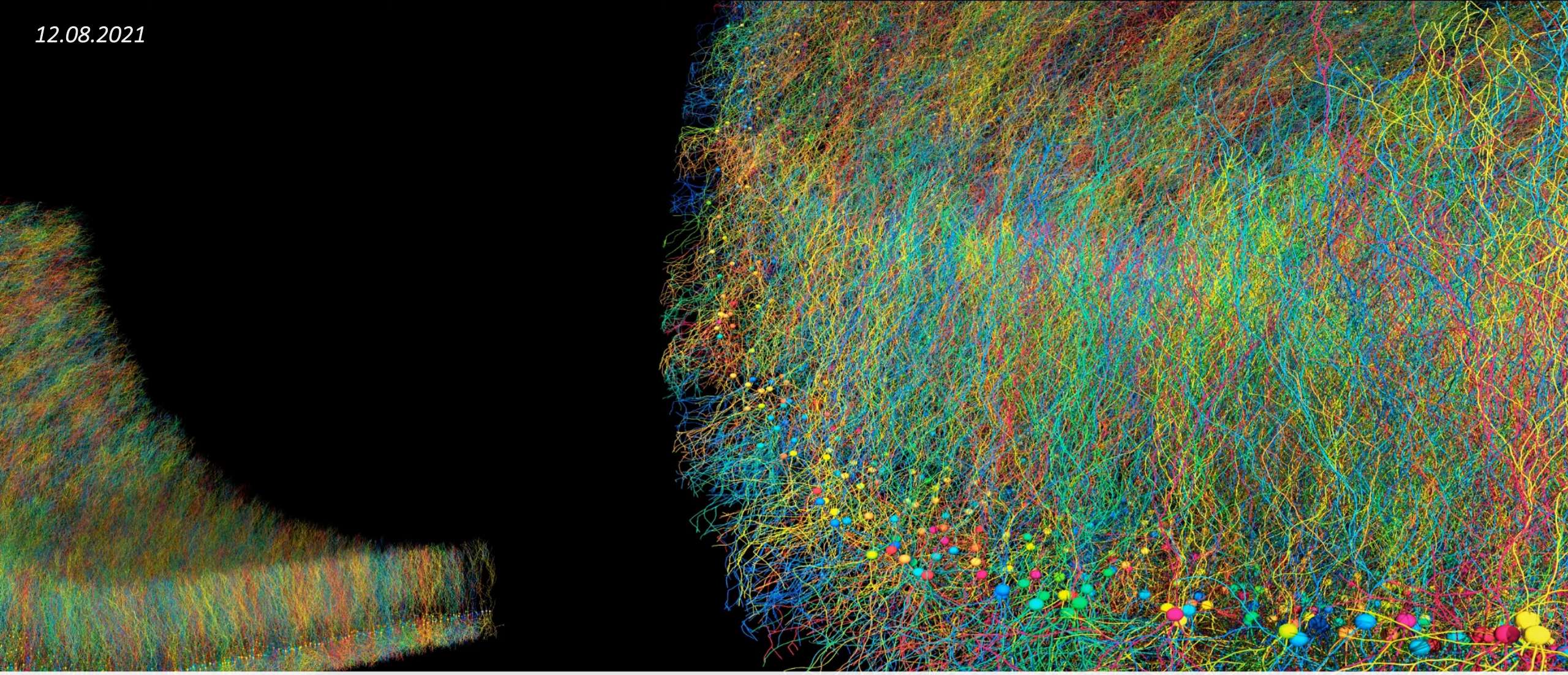

CERN openlab

BioDynaMo

CERN

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Supervisors: Fons Rademakers & Ahmad Hesam

What is BioDynaMo

- Open-source, high performance, general purpose, agent-based modeling for studying complex biological systems.

- Solves some of the problems *In silico simulations* have due to
  - Moore's law
  - Dennard Scaling
  - Developed for a specific use

- BioDynaMo system properties:
  - **Agent-based**
  - **General Purpose**
  - **Large Scale**
  - **Easily Programmable**
  - **Quality Assured**

- BioDynaMo Platform Use:
  1. **Formulate Problem**
  2. **Assemble Simulation**
  3. **Execute Simulation**
  4. **Analyze Results**
  5. **Publish and Contribute**
  6. **Add New Modules and Use**

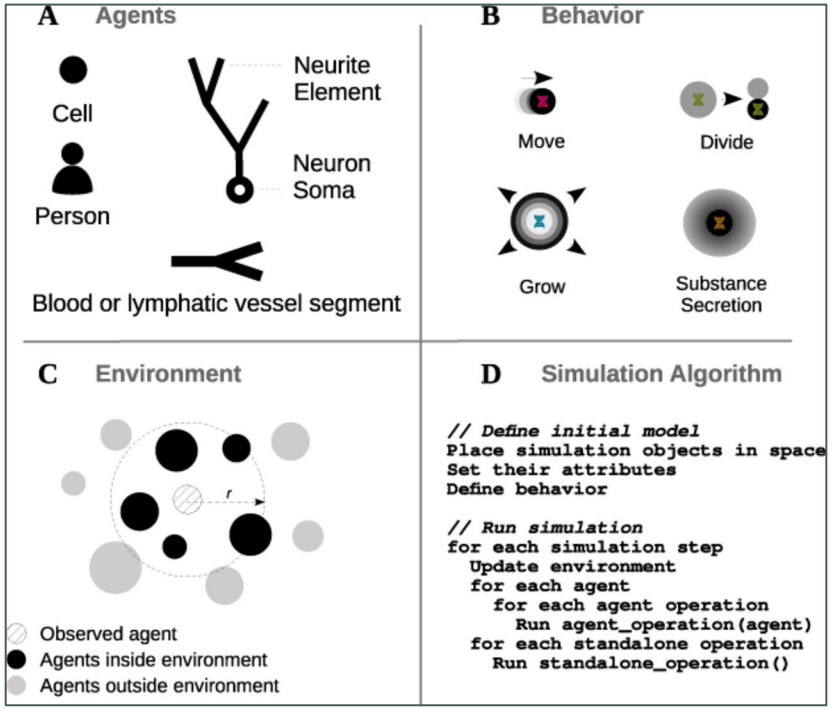


Figure 1: BioDynaMo core simulation concepts

What is BioDynaMo

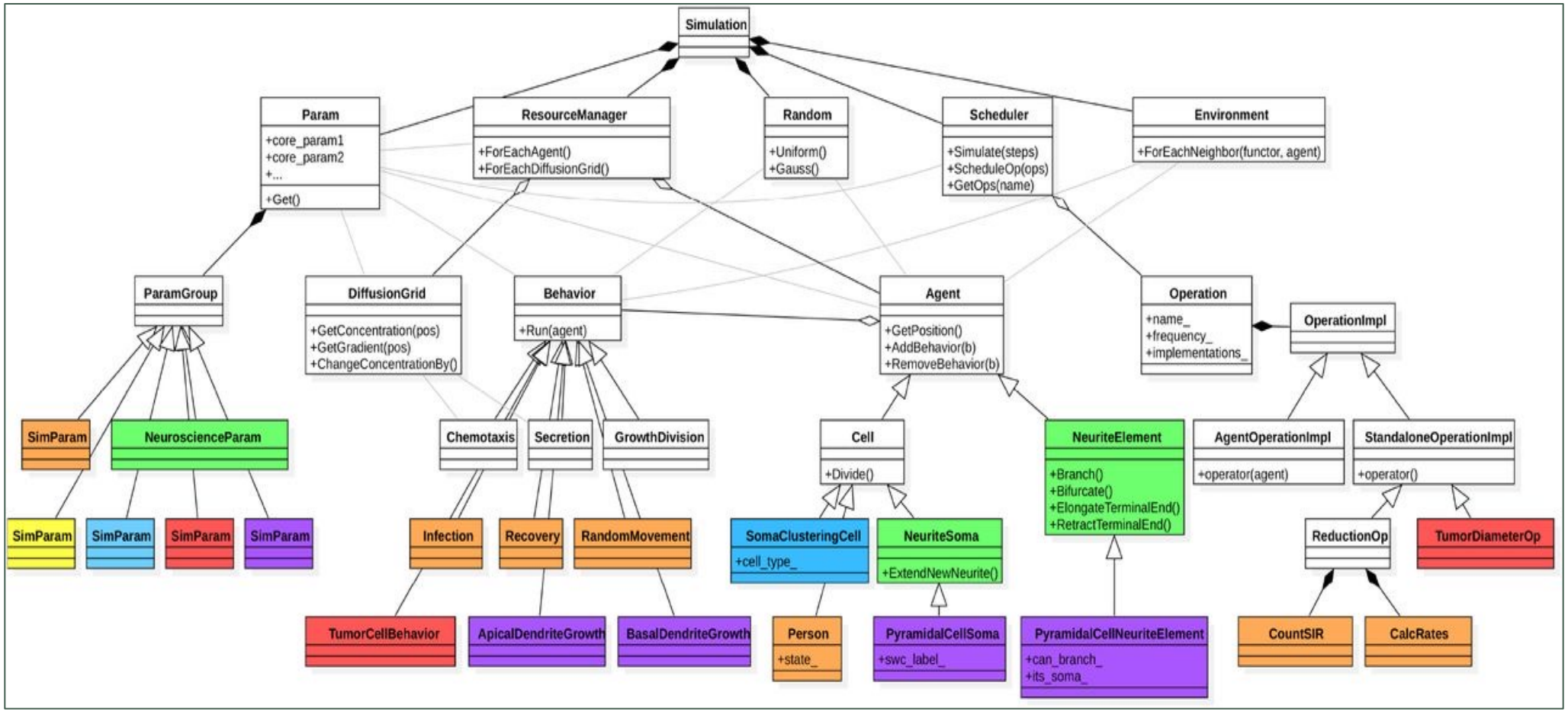


Figure 2: BioDynaMo software design and modularity

Use Cases

Neuroscience

Use of BioDynaMo to model neurite growth of pyramidal cells using chemical cues.

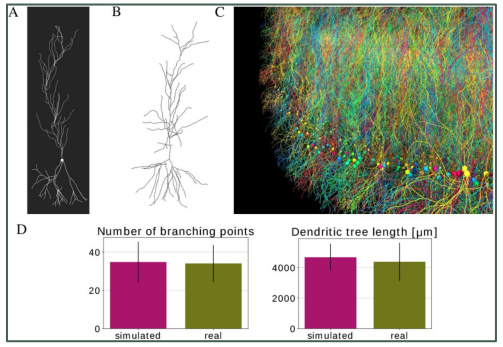
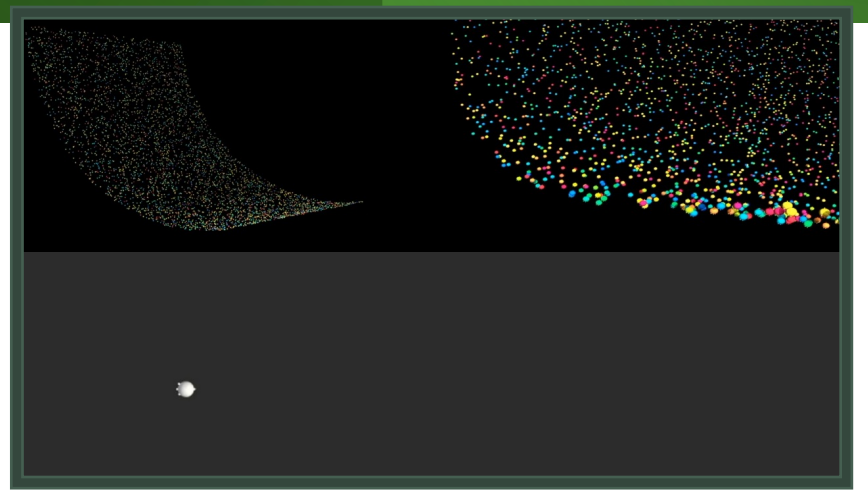


Figure 3: Pyramid cell simulation



Video Demo

Epidemiology

Use of BioDynaMo to model two behaviors of cell clustering.

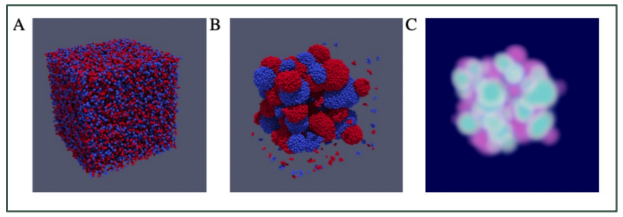


Figure 4: Soma clustering simulation

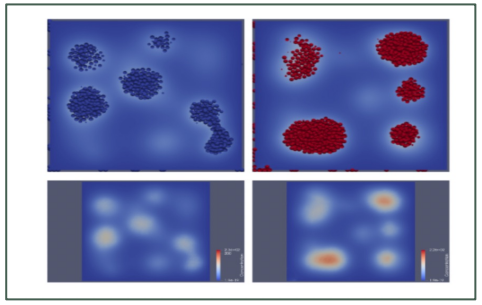
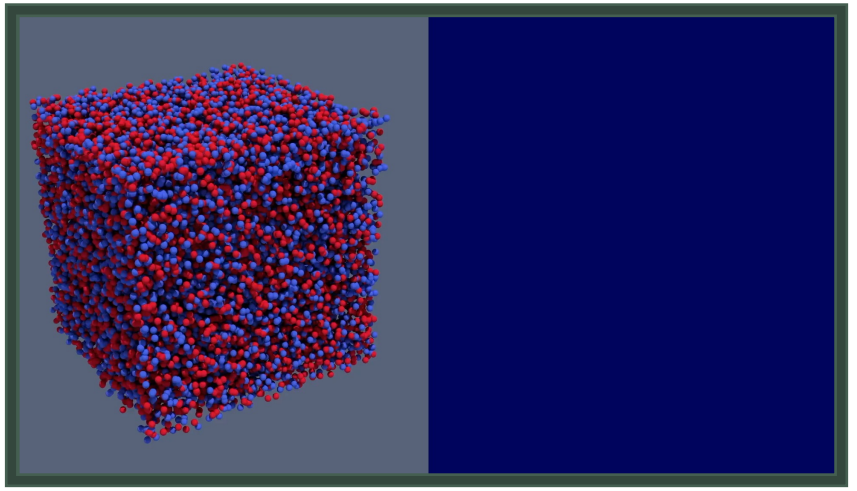


Figure 5: Soma clustering cross seciton



Performance Analysis

- **Performance improvements against established agent-based simulators(Cortex3D)**
  - BioDynaMo and Cortex3D use the same method to determine mechanical forces between agents and the same model to grow neural morphologies.
  - Significant speedup between 18 and 78× .
  - Runtime of 1 hour 37 minutes, 6 hours 49 minutes, and 3 hours 54 minutes with respect to neuroscience, oncology, and epidemiology use cases.
- **Scalability of BioDynaMo**
  - Increased the number of agents used in the comparison with Cortex3D and reduced the number of simulation timesteps to 10.
  - The maximum speedup ranged between 65× and 75×, which corresponds to a parallel efficiency of 0.90 and 1.04.
  - Performance improved even after all physical cores were utilized and hyper-threads were used.
- **Impact of calculating the mechanical forces on the GPU using soma clustering simulations.**
  - The benchmarks were executed on System C, comparing an NVidia Tesla V100 GPU with 32 CPU cores (64 threads).
  - We observed a speedup of 1.27 × for cell growth and division, and 5.04 × for soma clustering.

Results and Discussions

- BioDynaMo is more than three orders of magnitude faster than Cortex3D.
- With enough memory, BioDynaMo is capable of supporting hundreds of billions of agents.
- BioDynaMo allows researchers to:
  - Develop models in computational biology field in a modular architecture manner,
  - Collect results fast thanks to the parallelized execution engine,
  - Model billions of agents on a single server,
  - Produce results that correspond to validated experimental data.

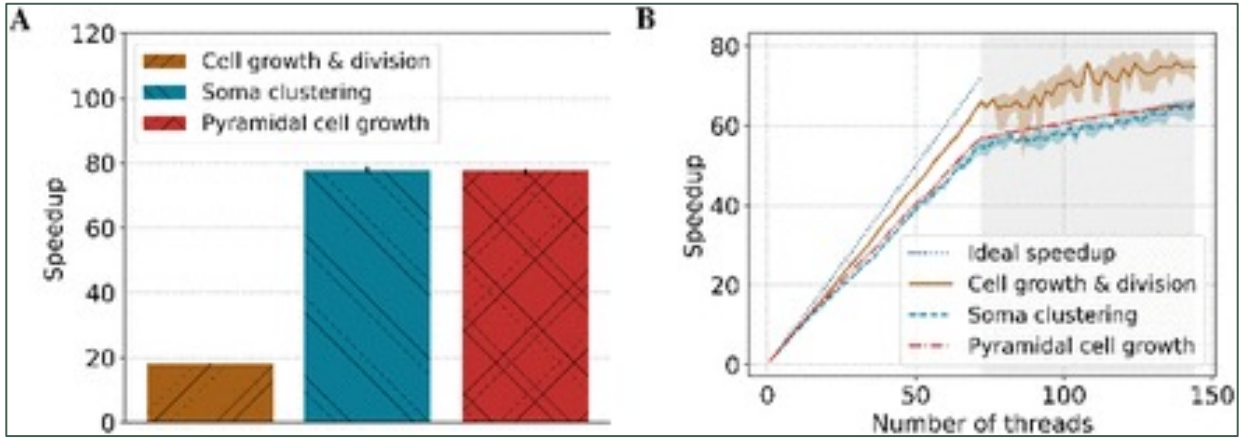
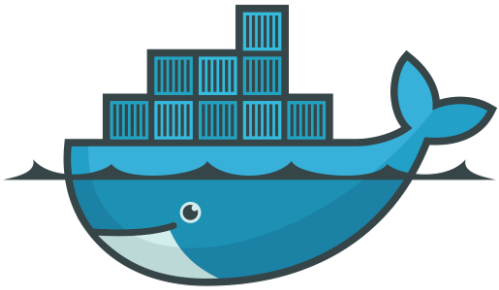
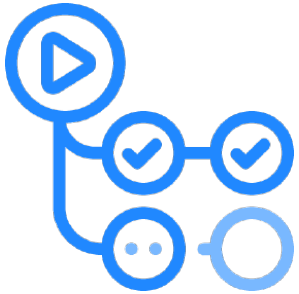


Figure 6: BioDynaMo performance analysis

Making BioDynaMo More Accessible

- BioDynamo Container Available on Docker-hub with all Prerequisites Installed .
- Easy To Run Jupyter Notebooks Available on BioDynamo Website.
- Notebooks can be executed in Browser using My-Binder.
- GitHub Actions build and push Latest BioDynamo Version to Docker-hub

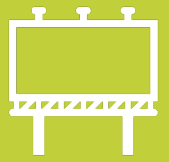




Thank You

Preprint of the BioDynaMo paper:

https://www.biorxiv.org/content/10.1101/2020.06.08.139949v2



Supplementary information:

https://doi.org/10.5281/zenodo.4501515

BioDynaMo webpage:

https://biodynamo.org