

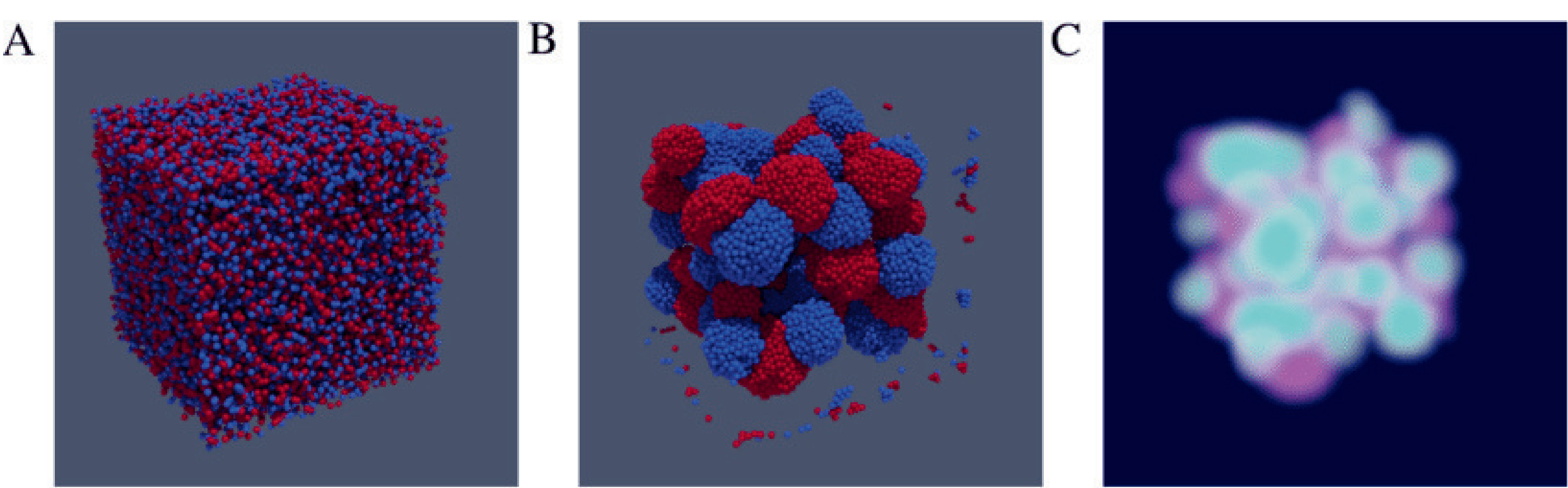
IMPROVING BIODYNAMO'S PERFORMANCE USING ROOT C++ MODULES



ISAAC MORALES, VASSIL VASSILEV, LUKAS BREITWEISER, TOBIAS DUSWALD AND FONS RADEMAKERS

INTRODUCTION

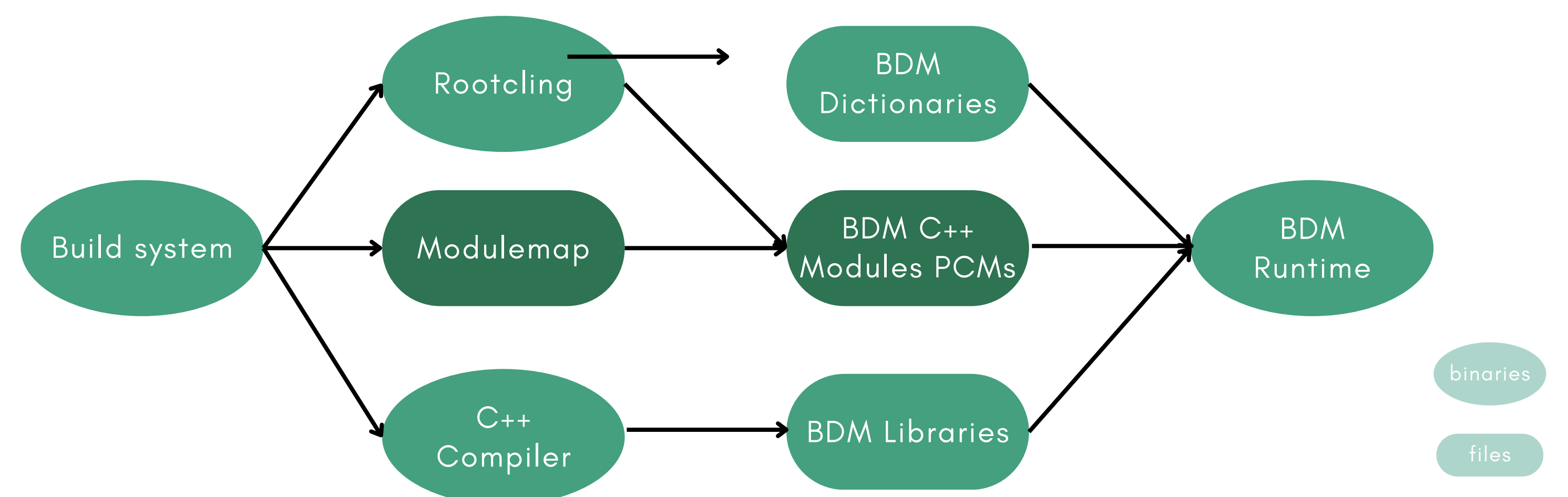
- **BioDynaMo:** An agent-based simulation platform used for complex simulations in areas like cancer research, epidemiology, and social sciences.
- **ROOT Integration:** BioDynaMo uses ROOT for statistical analysis, random number generation, C++-based Jupyter notebooks, and I/O operations.
- **Project Aim:** Enhance BioDynaMo's performance by improving its reflection system using C++ Modules from ROOT.



Lukas Breitwieser et al (2020). BioDynaMo: an agent-based simulation platform for scalable computational biology research.

BACKGROUND

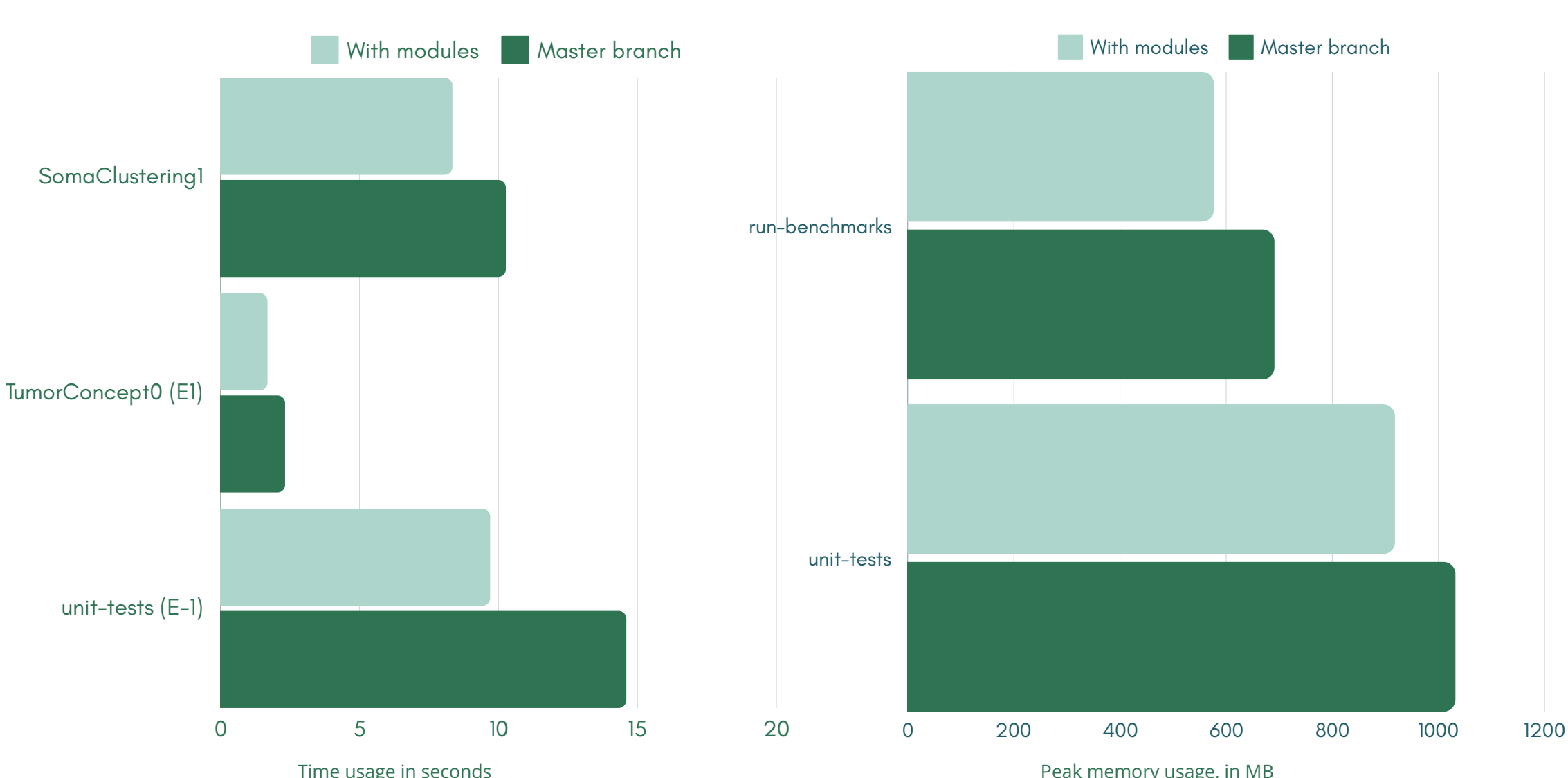
- **Current Challenges:**
 - BioDynaMo's reflection system relies on cling, which suffers from **runtime performance and memory usage** issues due to **repeated parsing** of library descriptors.
- **C++ Modules in ROOT:**
 - Developed by the LLVM community, C++ Modules offer an I/O-efficient, on-disk representation of C++ code.
 - Promises to optimize both runtime memory usage and performance by **avoiding repeated parsing** of invariant code.



PRELIMINARY RESULTS

Still pending many tests, the initial results meet our expectations.

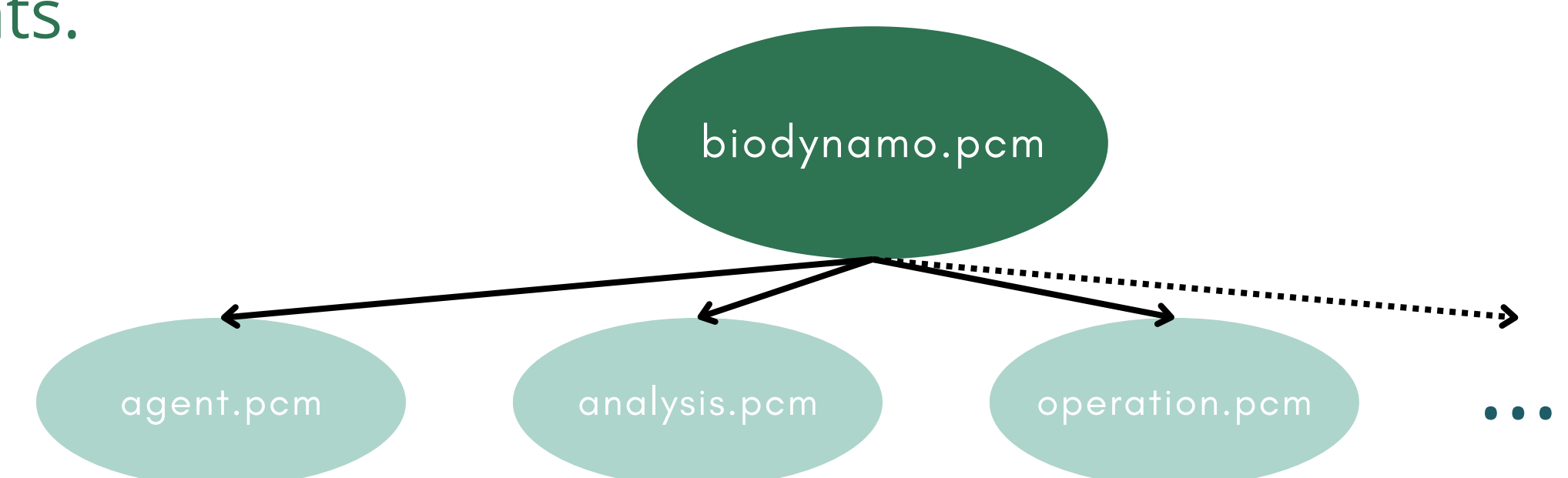
- **Benchmarks:** Between **18%-27%** improvement in time and **16.5%** in peak memory usage.
- **Unit tests:** **33.6%** improvement in time and **11%** in peak memory usage.



Many tests still need to be conducted, including more rigorous evaluations. These forthcoming tests will be essential to ensure the robustness and reliability of the results and to further validate the improvements observed in the initial assessments.

CONCLUSION AND FUTURE WORK

- Integrating C++ Modules for BioDynaMo libraries is expected to provide significant performance enhancements.
- **Future Work:**
 - Complete the integration and optimization.
 - Conduct detailed benchmarking to quantify performance gains.
 - Explore further module-based optimizations for BioDynaMo's core components.



REFERENCES AND ACKNOWLEDGMENTS

- Breitwieser, L. et al (2020). BioDynaMo: an agent-based simulation platform for scalable computational biology research.
- Vassilev, V. (2016). Optimizing ROOT's Performance Using C++ Modules. Journal of Physics Conference Series.
- Vassilev, V., Lange, D., Muzaffar, M. S., Rodozov, M., Shadura, O., & Penev, A. (2020). C++ Modules in ROOT and Beyond. In EPJ Web of Conferences (Vol. 245, p. 05011). EDP Sciences.

Special thanks to the Compiler Research Group, Vassil Vassilev and the BioDynaMo and ROOT communities



UNIVERSIDAD DE GRANADA