CERNopenlab

The BioDynaMo Project

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What is BioDynaMo?

- ► Large scale platform for biological simulations
- ► Provides access to growing computational resources
- ► Hides complexity of distributed computing
- ► Promotes reproducibility of results
- ► Flexible system that supports different specialities

Software Development Practices

- ▶ C++ style guide with code formatter and cpplint
- ▶ BioDynaMo Developers Guide
- ▶ Github code repository
- ▶ Automated tests
- ▶ Valgrind memory leak checks
- ▶ Continues integration using Travis-CI
- ▶ Code coverage reports
- ▶ Documentation (doxygen, github wiki)
- ▶ CMake build system
- ▶ Communication: mailing list, slack and skype
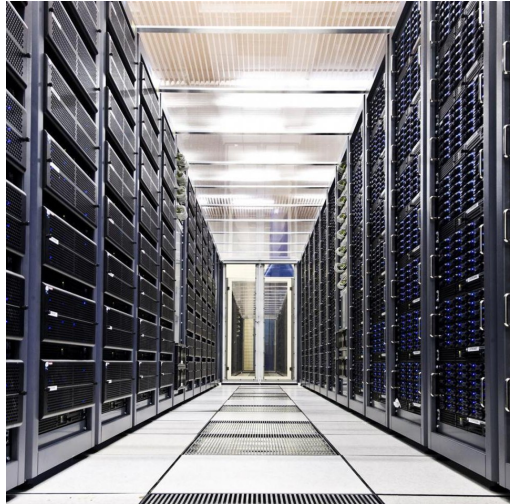
Travis CI

BioDynaMo
The Biology Dynamic Modeller

CMake
Cross-platform Make

slack

Intel Modern Code Developer Challenge

- Gamification approach
- Over 1,000 participating students
- Winner achieved speedup of 320x
  - Memory layout transformations (AOS to SOA)
  - OpenMP
  - Custom memory allocator
  - Intel cilk plus arrays

Porting from Java to C++

Step 5
Run automated tests

Step 1
Pick a Java class with few dependencies
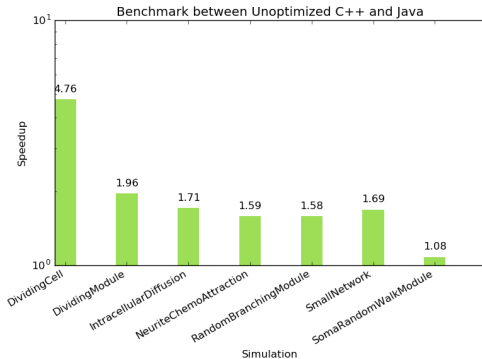
Step 2
Refactor remaining Java application

Step 3
Translate Java code into C++

Step 4
Write code to enable communication between Java and C++

Benchmark between Unoptimized C++ and Java

Speedup vs Simulation:
- DividingCell: 4.76
- DividingModule: 1.96
- IntracellularDiffusion: 1.71
- NeuriteChemoAttraction: 1.59
- RandomBranchingModule: 1.58
- SmallNetwork: 1.69
- SomaRandomWalkModule: 1.08

- ▶ Improve development process
  - ▶ Static code checkers
  - ▶ Git commit hooks
  - ▶ Publish doxygen and coverage reports to website
- ▶ Continue architecture redesign
- ▶ Verification
- ▶ HPC on Cloud

Thank you!