libRoadRunner: A High Performance SBML Simulation and Analysis Package

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(manuscript in submission)

libRoadRunner

Complex problems in computational biology **require highly efficient simulations, analyses or parameter optimizations** with thousands of cells and thousands of species and reactions in each cell.

- **Results**
  - Highly innovative cross-platform, open-source software library
    - easy integration with existing computational code
    - highly efficient
    - capable of handling very large and complex SBML models
  - Uses novel just in time (JIT) compiler to compile SBML based models to optimized native machine code at runtime using LLVM
  - Runs on x86 and ARM based processors
  - Comprehensive native Python bindings
  - Full suite of stoichiometric and metabolic control analysis routines
- **Availability & Implementation**
  - Self-contained library with native C, C++ & Python bindings for Linux, Mac Os & Windows
  - www.libroadrunner.org

LibRoadRunner Projects

- James A. Glazier, Biocomplexity Institute, Indiana University

  - Multi-cell simulation of tissue morphogenesis

  - **CompuCell3D**

- Jean-Marie Bouteiller, Biomedical Engineering Department, University of Southern California

  - Large scale modeling of synaptic, neuronal and neuron network dynamics (**MEMORY** platform)

- Matthias König, Computational Systems Biochemistry

  - Multi-scale modeling of liver metabolism in **Virtual Liver Network**