

# Resource Summary Report

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## SimTKCore

RRID:SCR\_008268

Type: Tool

### Proper Citation

SimTKCore (RRID:SCR\_008268)

### Resource Information

**URL:** <https://simtk.org/home/simtkcore>

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**Description:** SimTK Core is one of the two packages that together constitute SimTK, the biosimulation toolkit from the Simbios Center. The other major component of SimTK is OpenMM which is packaged separately. This SimTK Core project collects together all the binaries needed for the various SimTK Core subprojects. These include Simbody, Molmodel, Simmath (including Ipopt), Simmatrix, CPodes, SimTKcommon, and Lapack. See the individual projects for descriptions. SimTK brings together in a robust, convenient, open source form the collection of highly-specialized technologies necessary to building successful physics-based simulations of biological structures. These include: strict adherence to an important set of abstractions and guiding principles, robust, high-performance numerical methods, support for developing and sharing physics-based models, and careful software engineering. Accessible High Performance Computing We believe that a primary concern of simulation scientists is performance, that is, speed of computation. We seek to build valid, approximate models using classical physics in order to achieve reasonable run times for our computational studies, so that we can hope to learn something interesting before retirement. In the choice of SimTK technologies, we are focused on achieving the best possible performance on hardware that most researchers actually have. In today's practice, that means commodity multiprocessors and small clusters. The difference in performance between the best methods and the do-it-yourself techniques most people use can be astounding easily an order of magnitude or more. The growing set of SimTK Core libraries seeks to provide the best implementation of the best-known methods for widely used computations such as: Linear algebra, numerical integration and Monte Carlo sampling, multibody (internal coordinate) dynamics, molecular force field evaluation, nonlinear root finding and optimization. All SimTK Core software is in the form of C++ APIs, is thread-safe, and quietly exploits multiple CPUs when they are present. The resulting pre-built binaries are available for download and immediate use. Audience: Biosimulation application programmers interested in including robust, high-performance physics-based simulation in their domain-specific applications.

**Abbreviations:** SimTKCore

**Resource Type:** software application, simulation software, software resource

**Defining Citation:** [PMID:20107615](#)

**Keywords:** computational algorithm, high-performance, linear algebra, numerical integration, numerical method, optimization, monte carlo sampling, multibody dynamics, molecular force field evaluation, nonlinear root finding, optimizing, cpodes, simbody, ipopt, molmodel, mit license, linux, mac os x, windows

**Funding:** NIGMS U54 GM072970

**Resource Name:** SimTKCore

**Resource ID:** SCR\_008268

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**Record Last Update:** 20260728T043302+0000

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## Ratings and Alerts

No rating or validation information has been found for SimTKCore.

No alerts have been found for SimTKCore.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.