

Smoldyn: Spatial Cell Biology Simulation

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SMOLDYN is a simulator that helps researchers model cell biology with nanometer scale resolution. It represents proteins or other molecules as individual spherical particles. It represents membranes as thin surfaces, assembled from triangles, spheres, or other primitives. The particles diffuse, react, and interact with membranes in 1, 2, or 3-dimensional continuous space, much as they would in real systems. Smoldyn is exceptionally accurate, having rate errors that are always below 2.5% (for isolated processes). Users typically use Smoldyn by writing text input files and running the software from a command line shell (Mac, Windows, or Linux). They can also use it within the Virtual Cell software, or by interfacing to the Libsmoldyn code library from their own code or other software. I am currently adding support for biological filaments.

Smoldyn is one of the more popular spatial cell biology simulators. It is typically used for modeling cell systems, such as *E. coli* chemotaxis, or for biophysics investigations, such as the effects of diffusion barriers in membranes. It can also be used to analyze FRAP, single-particle tracking, and other imaging experiments. See <http://www.smoldyn.org>.

In this tutorial, I will summarize the tools that are available for spatially accurate cell biology modeling. Then, I will briefly explain how Smoldyn works. Afterwards, I will explain how to use Smoldyn, and how to find additional information about it. Finally, I will guide interested participants through the development of a simple simulation.