

# **Brownian Motion in Cellular Membrane Receptors**

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Background: Membrane bound receptors are important in cell signaling. Malfunctions in cell signaling are involved in many forms of cancer, immune diseases, and diabetes. The role of receptors is to initiate the signaling process by binding the signaling molecule, and then forming small aggregates (dimers or oligomers) with other receptors. This process involves the random movement of receptors, which in turn is impacted by the presence of various obstacles that form the “membrane landscape”.

Goals: In this project we develop a simulation framework to study the random movement of receptors in the presence of linear obstacles. The immediate goal is to characterize the resulting motion patterns and explore the mechanism of clustering / confinement; the longer term goal is to develop algorithms that would reconstruct the underlying landscape based primarily on the observable movement patterns.

Results: We developed a simulator that generates Brownian motion trajectories in a rectangular simulation space. A landscape of partially blocking obstacles is specified as a set of line segments. The resulting trajectories are output into files and also summarized in a localization density map. The analysis module extracts displacements over an arbitrary number of time steps. Based on the latter, the mean square displacement is estimated. For a more sophisticated analysis, we calculate the Kolmogorov-Smirnov statistic and use it to derive an effective diffusion coefficient for a given number of time steps. This approach can be easily extended to fit more complicated distribution functions.