**Stochastic binding of $Ca^{2+}$ in the dyadic cleft: continuous vs. random-walk description of diffusion.**

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**Abstract:**
It is a common understanding that diffusion in signaling micro domains cannot be described properly by a deterministic and continuous model. Several recent publications claim that as the number of participating particles in these volumes goes down, the deterministic description becomes invalid or does not make sense and Random walk (RW) methods have to be employed. We simulate the Ca2+ dynamics in a small volume in a myocyte continuously and deterministically by a coupled system of reaction-diffusion equations, and also with a fully stochastic RW model and we stochastically simulate the event of a single Ca2+ ions binding to single receptors in both models. The distributions of the bind events from the RW model are used to test the goodness-of-fit of the equivalent distributions predicted by the continuous model, using Kolmogorov-Smirnov tests. We find that the bind distributions from the continuous model fit the collected bind events from the RW simulations. Our results show that if a stochastic model is used for single Ca2+ ions binding to receptors in small sub-cellular volumes, a deterministic and continuous model of the reaction-diffusion dynamics in the actual volume can be used. In our study we also present a novel model for evaluating the stochastic event of a diffusing molecule binding to a stationary or mobile receptor based on a macroscopic rate law. The model is analytical and the accuracy is therefore not dependent on the time step.