First Pass Monte Carlo Simulation of Basic Eukaryotic Cell Cycle Regulation Mechanism

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The regulation of the cell cycle inspires much interest in the scientific community due to its critical role in areas of concern such as cellular differentiation, the healing process, and cancer. This essential mechanism exceeds in complexity, and thus “quantitative tools are necessary to probe reliably into the details of cell cycle control (Tyson and Novak, 2001)”. With the surmounting experimental data and detailed mathematical models available, we have started building a spatially realistic, stochastic model that takes advantage of recent functional improvements to the MCell/DReAMM simulation and visualization environment to provide the sought after quantitative, detailed view of cell cycle control. Our model expands mathematical models by incorporating local chemical dynamics, cellular compartmentalization, and important physical interactions that all intimately impact the quantitative and qualitative properties of the cell cycle and are not explicitly addressed in a biologically meaningful way by current mathematical models.