Discrete-event Simulation of Self-assembly Systems

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1 Motivation.

Self-assembly is the spontaneous and autonomous organization of components into patterns or structures. Self-assembly processes are common throughout nature and technology [8]. Naturally occurring self-assembly systems include viral protein shells, cellular cytoskeletons, and bacterial flagella and pili. Self-assembly has also emerged as a promising technology for nanometer-scale fabrication. The mathematical principles behind self-assembly have thus attracted considerable recent attention. Yet the kinetics of non-trivial self-assembly systems — the progress of the systems over time — remain extremely difficult to analyze due to the many physical details that are difficult to capture in abstract theoretical models and the propensity of these systems to exhibit "emergent" behaviors that are not easily predictable solely from a knowledge of low-level binding interactions. Without a firmer understanding of these kinetic properties, we cannot hope to design novel systems to have both rapid growth and high fidelity. Nor can we hope to understand biological self-assembly systems, which rarely exist at thermodynamic equilibrium. Simulation methods are therefore likely to be vital in understanding emergent properties of naturally occurring self-assembly systems, performing rapid *in silico* experimentation with possible interventions into those systems, and screening hypothetical novel systems for unforeseen difficulties prior to fabrication.

There have been many past approaches to simulating self-assembly, but there remain significant obstacles to the development of general, quantitative simulation tools. Differential equation models have provided quantitative simulations of large numbers of subunits [9, 4] but require substantial simplifications to be computationally tractable and cannot generally easily be adapted from one system to another. Simplified discrete-event models [1, 2] can provide efficient simulation and easy adaptability to new systems but have generally lacked quantitative accuracy and realistic models of binding kinetics. Highly detailed models that attempt to capture the physical forces underlying self-assembly phenomena can resolve many of these problems [6, 7, 5], but are difficult to parameterize and computationally intractable for all but very small systems. Our goal is to fill in important gaps in the range of systems these various approaches can model through the development of a quantitative simulation tool for generic self-assembly systems that is robust, efficient, and platform-independent.

2 Overview.

We have developed algorithms and data structures for fast, quantitatively accurate self-assembly simulation on biologically-relevant scales and incorporated them into a prototype simulation tool. We adapted the calendar queue [3] data structure to properties of a discrete event model of generic chemical assembly events to allow expected linear-time event processing across a broad range of self-assembly systems. This method further allows us to maintain realistic quantitative reaction rates even at very small system scales.

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Figure 1: Example specification of a subunit type for the simulator

We have combined these techniques with a generic representation of self-assembly subunits in an extensible Java object model. This approach allows us to model a broad range of system types using a single code base. Figure 1 shows how a specific type of assembly subunit can be specified for this model. Furthermore, work is currently underway on a versatile 3-D graphical interface to allow fine control over simulation specification and progress. This prototype simulation tool will provide a first step toward the availability of an efficient, generic, quantitative platform for *in silico* experimentation with self-assembly systems.

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