An agent-based simulation framework for complex systems

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In this abstract we present a new approach to the simulation of complex systems as biological interaction networks, chemical reactions, ecosystems, etc. It aims at overcoming previously proposed analytical approaches that, because of several computational challenges, could not handle systems of realistic complexity.

The proposed model is based on a set of agents interacting through a shared environment. Each agent functions independently from the others, and its behavior is driven only by its current status and the "content" of the surrounding environment.

The environment is the only "data repository" and does not store the value of variables, but only their presence and concentration.

Each agent performs 3 main functions:

1. it samples the environment at random locations
2. based on the distribution of the sampled data and a proper Transfer Function, it computes the rate at which the output values are generated
3. it writes the output "products" at random locations.

The environment is modeled as a Really Random Access Memory (R2AM). Data is written and sampled at random memory locations. Each memory location represent an atomic sample (a molecule, a chemical compound, a protein, an ion, ...). Presence and concentration of these samples are what constitutes the environment data set. The environment can be sensitive to external stimuli (e.g., pH, Temperature, ...) and can include topological information to allow its partitioning (e.g. between nucleus and cytoplasm in a cell) and the modeling of sample "movements" within the environment.

The proposed approach is easily scalable in both complexity and computational costs. Each module could implement a very simple object as a single chemical reaction or a very complex process as a gene translation into a protein. At the same time, from the hardware point of view, the complexity of the objects implementing a single agent can range from a single software process to a dedicated computer or hardware platform.