

Recent Progress and Future Work Towards Reproducible Stochastic Biological Simulation

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Stochastic simulations are commonly used to quantitatively or semi-quantitatively describe the dynamics of biological systems. At various scales and in multiple applications, stochastic simulation better reflects observed biological processes and robustness. Various methods are widely used to incorporate stochasticity into biological simulation, such as the Gillespie stochastic simulation algorithm for systems biology modeling, stochastic Boolean networks for network modeling, and the Cellular Potts model methodology for multicellular modeling. Proving reproducibility of simulation results is critical to establishing the credibility of a model. To this end, BioModels, the largest repository of curated mathematical models, tests and reports the reproducibility of simulation results for all submitted models when possible. A recent study showed that about 50% of the deterministic ordinary differential equation models on BioModels could not be reproduced when applying criteria for reproducibility to the information provided in their associated publication, reflecting a current crisis of reproducibility. Furthermore, there are no well-accepted metrics or standards for reproducing stochastic simulation results, thus perpetuating the crisis of reproducibility for a broad class of biological models. This breakout session aims to establish an accepted framework for testing the reproducibility of stochastic simulations in biological modeling. The session will provide an overview of recent progress towards defining quantitative measures to determine whether stochastic simulation results can be reproduced, and when results have been reproduced. Attendees will discuss current issues to address towards consensus and broad adoption in relevant modeling communities, as well as future work towards reproducibility of stochastic simulation results using multiscale and complex models.