On the binomial method for the generation of stochastic trajectories

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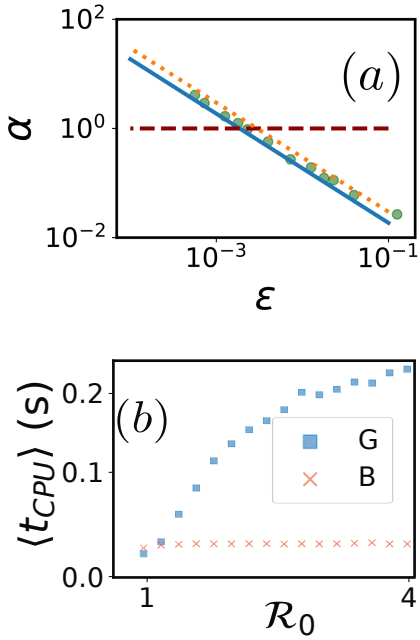
Stochastic processes are one of the main pillars of complexity science [1]. Indeed, the list of fruitful applications is endless and we can name some paradigmatic examples like the study of population dynamics in ecology, gene expression, metabolism in cells, finances and market crashes, epidemiology, telecommunications, chemical reactions, quantum physics and active matter, to name a few [2]. As models become more intricate, there arises a technical challenge of producing numerically stochastic trajectories in feasible computation times, since unbiased methods that generate unbiased realizations of stochastic trajectories may become unpractical due to lengthy computations. Alternatively, approximate numerical methods are one of the most used strategies to extract information from many-interacting-agents systems. In particular, the binomial method is of extended use to deal with epidemic, ecological and biological models, when unbiased methods like the Gillespie algorithm can become unpractical due to high CPU time usage required. However, some authors have criticized the use of this approximation and there is no clear consensus about whether unbiased methods or the binomial approach is the best option [3, 4].

In this work, we analyze the issue on whether the binomial method is competitive compared to unbiased methods [5]. We proof, through both numerical and analytical evidence, that the systematic errors of the binomial method scale linearly with the discretization time. Using this result, we can establish a rule for selecting the optimal discretization time and number of simulations required to estimate averages with a fixed precision while minimizing CPU time consumption. Furthermore, we derive a rule of simple and practical use that can tell us in which cases the binomial method is superior to unbiased algorithms. In general, the advantage of using the binomial method depends on the target precision: the use of unbiased methods becomes more optimal as the target precision increases. We quantify the relative efficiency of the binomial versus the unbiased method as the ratio α of CPU times taken by each method to achieve a desired precision ϵ. In particular, values of $\alpha < 1$ indicate that the unbiased method is more effective than the binomial. We plot in panel (a) of the figure the ratio α as a function of the precision ϵ in the case of a simulation of an all-to-all connected Susceptible-Infected-Susceptible model. The dots are the results of the numerical simulations using the binomial method with the obtained optimal values for the discretization step and number of realizations, while the solid and dotted lines are theoretical result obtained from our scaling analysis. In panel (b) of the same figure we fix the precision $\epsilon = 0.01$, and plot the CPU-time to generate the ensemble of trajectories for different values of the basic reproductive number $\mathcal{R}_0$ for both the binomial (B) and the Gillespie (G) methods. Except for $\mathcal{R}_0 \approx 1$, where they perform similarly, the binomial method takes always less time than the Gillespie algorithm.

In summary, this work provides a solution for the existing debate regarding the use of the binomial approximation to sample stochastic trajectories. The discretization time of the binomial method needs to be chosen carefully since large values can result in errors beyond the desired precision, while low values can produce extremely inefficient simulations. A proper balance between precision and CPU time consumption is necessary to fully exploit the potential of this approximation and make it useful. The efficiency of the binomial method is superior to the unbiased approaches only when the target precision is above a certain threshold value.



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