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# Incorporating postleap checks in tau-leaping

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By explicitly representing the reaction times of discrete chemical systems as the firing times of independent, unit rate Poisson processes, we develop a new adaptive tau-leaping procedure. The procedure developed is novel in that accuracy is guaranteed by performing postleap checks. Because the representation we use separates the randomness of the model from the state of the system, we are able to perform the postleap checks in such a way that the statistics of the sample paths generated will not be biased by the rejections of leaps. Further, since any leap condition is ensured with a probability of one, the simulation method naturally avoids negative population values.

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## I. INTRODUCTION

The procedure developed in this paper is a tau-leaping method for simulating the evolution of discrete stochastic chemical systems. The novelty of the procedure is that a postleap check is performed after each step in order to guarantee accuracy. Postleap checks have been avoided in the past because of the worry that rejecting leaps will bias the statistics of the sample paths. This problem is bypassed in our method by storing all the information gained during each leap for future use. By performing a postleap check to ensure accuracy, the method developed in this paper naturally avoids negative population values without the need for any extra effort in either a programming or numerical sense.

Consider a chemically reacting system consisting of  $N \geq 1$  chemical species,  $\{X_1, \dots, X_N\}$ , undergoing  $M \geq 1$  chemical reactions, each of which is equipped with a propensity function (or intensity function in the mathematics literature)  $a_k(X(t))$ , which is a function of the state of the system at time  $t$ ,  $X(t) \in \mathbb{Z}_{\geq 0}^N$ . Let  $\nu_k, \nu'_k \in \mathbb{Z}_{\geq 0}^N$  be the vectors representing the number of molecules of each species consumed and created in the  $k$ th reaction, respectively. If  $R_k(t)$  is the number of times that the  $k$ th reaction has taken place up to time  $t$ , then the state of the system at time  $t$  is given by

$$X(t) = X(0) + \sum_{k=1}^M R_k(t)(\nu'_k - \nu_k).$$

The fundamental assumption of stochastic chemical kinetics states that the probability that reaction  $k$  takes place in the infinitesimal amount of time  $(t, t+\Delta t)$  is given by  $a_k(X(t))\Delta t + O(\Delta t^2)$ , and that the probability that more than one reaction takes place is  $O(\Delta t^2)$ .<sup>1,2</sup> That is, given  $X(s)$  for  $s \leq t$ ,  $P(R_k(t+\Delta t) - R_k(t) = 1) = a_k(X(t))\Delta t + O(\Delta t^2)$ , and  $P(R_k(t+\Delta t) - R_k(t) \geq 2) = P(R_k(t+\Delta t) - R_k(t) \geq 1, R_j(t+\Delta t) - R_j(t) \geq 1) = O(\Delta t^2)$ , for  $j \neq k$ . For each  $k \leq M$ , let  $Y_k(\cdot)$  be an independent, unit rate Poisson process. Then for any  $T > 0$  and small  $\Delta T > 0$ ,  $P(Y_k(T+\Delta T) - Y_k(T) = 1) = \Delta T + O(\Delta T^2)$ , and  $P(Y_k(T+\Delta T) - Y_k(T) \geq 2) = O(\Delta T^2)$ .

$\geq 1, Y_j(T+\Delta T) - Y_j(T) \geq 1) = O(\Delta T^2)$ , for  $j \neq k$ . Because the propensity function of reaction  $k$  is  $a_k(X(t))$ , and hence constant until the next reaction takes place, we see that given  $X(s)$  for  $s \leq t$ ,

$$\begin{aligned} P\left(Y_k\left(\int_0^{t+\Delta t} a_k(X(s))ds\right) - Y_k\left(\int_0^t a_k(X(s))ds\right) = 1\right) \\ = a_k(X(t))\Delta t + O(\Delta t^2), \end{aligned}$$

and the probability of more than one reaction is  $O(\Delta t^2)$ . Thus,  $R_k(t)$  can be written as

$$R_k(t) = Y_k\left(\int_0^t a_k(X(s))ds\right). \quad (1)$$

The state of the system at time  $t$  can, therefore, be represented as the solution to the following stochastic equation:

$$X(t) = X(0) + \sum_{k=1}^M Y_k\left(\int_0^t a_k(X(s))ds\right)(\nu'_k - \nu_k). \quad (2)$$

We note that even though the processes  $Y_k$  are independent, the processes  $Y_k(\int_0^t a_k(X(s))ds)$  are dependent because they depend on  $X(s)$ , for  $s \leq t$ .<sup>3</sup> Equation (2) is typically called a random time change representation in the mathematics literature.<sup>4-7</sup>

Note that there are  $M+1$  distinct time frames in Eq. (2). The first time frame is the actual, or absolute time  $t$ . However, each Poisson process  $Y_k$  brings its own “internal” time frame. Equation (1) shows that at absolute time  $t$ , the amount of “internal time” that has passed for the process  $Y_k$  is  $T_k(t) = \int_0^t a_k(X(s))ds$ . This observation leads us to the following definition.

**Definition 1.1.** For each  $k \leq M$ ,  $T_k(t) = \int_0^t a_k(X(s))ds$  is the *internal time* of the Poisson process  $Y_k$  at absolute time  $t$ .

We note that the values  $T_k(t)$  defined above do not actually have units of time. In fact, they are unitless. However, they serve the purpose of allowing us to know where we are on the “time frames” of the Poisson processes  $Y_k$  at absolute time  $t$ .

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*Remark.* It is important to recognize that for any  $T_2 \geq T_1 \geq T_k(t)$ , the increment  $Y_k(T_2) - Y_k(T_1)$  is independent of the state of the system  $X(t)$ . This independence follows from the usual properties of the Poisson process and will eventually allow us to reject leaps without adding any bias to the system.

The outline of the paper is as follows. In Sec. II, we will briefly introduce several exact simulation methods for chemical systems and a widely used approximate method known as tau-leaping. While all of the methods presented in Sec. II are well known, we will consider each through the perspective of Eqs. (1) and (2), which we believe lends insight. In Sec. III, we present our new adaptive tau-leaping procedure that incorporates a postleap check. In Sec. IV, we compare the efficiency of our new algorithm to the current adaptive tau-leaping procedures on a model of a decaying dimer.

## II. BACKGROUND

### A. Exact simulation methods

In order to generate sample paths for a given system, all exact simulation methods attempt to answer each of the following two questions at a given moment of time  $t$ :

- (1a) When does the next reaction take place?
- (2a) Which reaction takes place at that future time?

By answering both questions repeatedly, a sample path is constructed. We see from Eq. (1) that the above questions are equivalent to:

- (1b) What will be the absolute time of the next firing of the processes  $Y_k(\int_0^t a_k(X(s))ds)$ ?
- (2b) Which process will fire at that time?

Note that neither the state of the system  $X(t)$  nor the propensity functions  $a_k(X(t))$  change between reactions. Therefore, assuming that no other reaction fires first, the next firing time of the process  $Y_k(\int_0^t a_k(X(s))ds)$  will be exponentially distributed with parameter  $a_k(X(t))$ . Of course, the logic used in the previous sentence is only valid until the time of the first firing of the various processes, for at that time the state of the system, and hence the propensity functions, will change. Therefore, we may only conclude that the next firing time of the processes  $Y_k(\int_0^t a_k(X(s))ds)$  will occur at the minimum time of the exponentially distributed random variables, and the reaction that takes place is simply the one associated with the realized minimum value. Repeated application of the above idea is the first reaction method.<sup>1</sup> The next reaction method<sup>8</sup> and modified next reaction method<sup>4</sup> use the same principles as the first reaction method except that by efficient use of information, both need to only generate one exponential random variable per iteration as opposed to the  $M$  needed in the first reaction method. See Ref. 4 for full details on how the next reaction method and modified next reaction method achieve this efficiency. The Gillespie algorithm,<sup>1,2</sup> or stochastic simulation algorithm (SSA), answers the first question by using the fact that the minimum of  $M$  exponentially distributed random variables with parameters  $a_k$  is exponentially distributed with parameter  $\sum_{k=1}^M a_k$ . To answer the second question, the Gillespie algorithm uses the fact that the probability that the  $j$ th expo-

nential random variable achieves the minimum is  $a_j / \sum_{k=1}^M a_k$ . Therefore, for every iteration of the Gillespie algorithm one random number is needed to find when the next reaction occurs, and one random number is needed to determine which reaction occurs at that later time.

We note that the algorithms described above are considered exact simulation methods because they generate *statistically* exact sample paths for the system (2). Typically, one wishes to use such methods to generate many sample paths in order to approximate the underlying probability distributions of the system of interest.<sup>9-12</sup> However, there are instances when the exactness of the methods makes them ineffectual and approximate techniques are needed.

### B. An approximate method: Tau-leaping

Because they simulate every reaction that takes place, statistically exact methods are slow for systems in which many reactions take place over short amounts of time. As the algorithms described in this paper are typically used for Monte Carlo simulations in which thousands, tens of thousands, or even hundreds of thousands of sample paths are needed to get an accurate picture of the underlying probability distributions, it is clear why simulation speed is critical. Therefore, approximate techniques have been developed that will generate sample paths significantly faster than the exact methods and will do so with an acceptable amount of error. One such method is tau-leaping.<sup>13</sup>

Consider Eqs. (1) and (2). We make the observation that there are two natural places where we can approximate the system: the Poisson processes  $Y_k$  and the propensity functions  $a_k$ . In standard tau-leaping, only the propensity functions are approximated. More specifically, if one assumes that  $a_k(X(t))$  is relatively constant in the time interval  $(t, t + \tau)$  (this assumption is typically called the *leap condition*), then, conditioned on  $X(s)$  for  $s \leq t$ , the number of times the  $k$ th reaction fires in the time interval  $(t, t + \tau)$  can be approximated by

$$\begin{aligned} \text{No. of firings} &= R_k(t + \tau) - R_k(t) \\ &= Y_k\left(\int_0^{t+\tau} a_k(x(s))ds\right) \\ &\quad - Y_k\left(\int_0^t a_k(x(s))ds\right) \\ &\approx Y_k\left(a_k(x(t))\tau + \int_0^t a_k(x(s))ds\right) \\ &\quad - Y_k\left(\int_0^t a_k(x(s))ds\right). \end{aligned} \quad (3)$$

Each  $Y_k$  is a unit rate Poisson process and so, conditioned on  $X(s)$  for  $s \leq t$ ,

$$Y_k \left( a_k(x(t))\tau + \int_0^t a_k(x(s))ds \right) - Y_k \left( \int_0^t a_k(x(s))ds \right) \stackrel{d}{=} \text{Poisson}(a_k(x(t))\tau), \quad (4)$$

where the equality is in distribution. Therefore, we use Poisson random variables to approximate how many times each reaction has fired from time  $t$  to  $t+\tau$ , and we update the system via

$$x(t+\tau) = x(t) + \sum_{k=1}^M N_k(\nu'_k - \nu_k), \quad (5)$$

where  $N_k$  is a Poisson random variable with parameter  $a_k(x(t))\tau$ . We note that based upon the approximation used in Eq. (3), tau-leaping is similar to an Euler method.

The subtlety of tau-leaping is in selecting a  $\tau$  before each step so that the leap condition holds over the time interval  $(t, t+\tau)$ . A typical way to make this explicit is to search for a  $\tau$  so that for some small  $\epsilon > 0$

$$|a_k(X(t+\tau)) - a_k(X(t))| \leq \max\{\epsilon a_k(X(t)), c_k\}, \quad (6)$$

where  $c_k$  is the rate constant for reaction  $k$ , which is the smallest amount that a propensity function can change. The question now becomes how to go about selecting the largest  $\tau$  for which we will be reasonably sure that the condition (6) will be satisfied.

The tau-leaping method proposed by Cao *et al.*<sup>14</sup> chooses  $\tau$  before each step to be the largest value for which both the estimated mean and the estimated standard deviation of the random variable on the left side of Eq. (6) satisfies that condition. It is shown in Ref. 14 that a computationally efficient way to do this is to compute the  $2N$  quantities

$$\hat{\mu}_i(X(t)) = \sum_{j=1}^M (\nu'_j - \nu_j) a_j(X(t)), \quad i = 1, \dots, N,$$

$$\hat{\sigma}_i^2(X(t)) = \sum_{j=1}^M (\nu'_j - \nu_j)^2 a_j(X(t)), \quad i = 1, \dots, N,$$

and then take  $\tau$  to be the value given by

$$\tau = \min_{i \in [1, N]} \left\{ \frac{\max\{\epsilon X_i(t)/g_i, 1\}}{|\hat{\mu}_i(X(t))|}, \frac{(\max\{\epsilon X_i(t)/g_i, 1\})^2}{\hat{\sigma}_i^2(X(t))} \right\}, \quad (7)$$

where  $g_i$  for each species  $X_i$  is a simple prescribed function of  $X_i(t)$  whose form is fixed at the beginning of the simulation and is given in Appendix A. In computing  $\tau$  with the above method, the leap condition that is actually being satisfied is

$$|X_i(t+\tau) - X_i(t)| \leq \max\{\epsilon X_i(t)/g_i, 1\}, \quad (8)$$

which then approximately satisfies the leap condition (6). See Ref. 14 for full details. The tau-leaping algorithm presented below chooses tau by a preleap computation using Eq. (7).

**Algorithm 1.** (Cao *et al.*<sup>14</sup> preleap computation tau-leaping)

- (1) Initialize. Set the initial number of molecules of each species  $x \in \mathbb{Z}_{\geq 0}^N$  and set  $t=0$ .
- (2) Calculate the propensity function  $a_k$  for each reaction.
- (3) Calculate  $\tau$  according to Eq. (7).
- (4) For each  $k \leq M$ , let  $N_k = \text{Poisson}(a_k\tau)$ .
- (5) Set  $x = x + \sum_{k=1}^M N_k(\nu'_k - \nu_k)$  and  $t = t + \tau$ .
- (6) Return to step 2 or quit.

There are two technical features of standard tau-leaping that remain to be discussed. The first feature is that during each iteration the algorithm should compute  $a_0 = \sum_{k=1}^M a_k$  and then do the tau leap only if the  $\tau$  calculated via Eq. (7) is larger than some small multiple of  $1/a_0$ , but do one or more time steps with an exact simulation method otherwise. Switching between tau-leaping and an exact method is reasonable because the benefits of tau-leaping as compared with exact methods evaporate, and become negative, as  $\tau \rightarrow 1/a_0$ , which is the expected amount of time until the next reaction.

The second feature is more subtle. For each leap, it is possible that the leap condition will be violated so badly that some population values will become negative. In fact, negative population values have been found to occur in simulations using tau-leaping on systems of interest.<sup>15,16</sup> As negative population values are physically unreasonable, this constitutes a problem, and a number of solutions have been proposed. Tian and Burrage<sup>16</sup> and Chatterjee and Vlachos<sup>17</sup> independently developed a method in which binomial random variables, as opposed to Poisson random variables, are used to perform the leap. Because binomial random variables have bounded support, the parameters of the binomial random variable can be chosen in a way that guarantees no molecular species will become negative in the course of a leap. Cao *et al.*<sup>15</sup> then developed a method to handle the potential of negative population values in which the reactions are partitioned into two sets before the calculation of  $\tau$ : critical reactions and noncritical reactions. For some predetermined integer  $n_c$  between 2 and 20, the set of critical reactions is defined to consist of those reactions with a positive propensity function that is within  $n_c$  firings of exhausting one of its reactants. Having split the reactions in such a way before a leap, the algorithm performs a standard tau leap for the noncritical reactions concurrent with a standard Gillespie algorithm step for the critical reactions. It is guaranteed that among all the critical reactions there will be at most one firing during the leap, thereby significantly reducing, but not completely doing away with, the chance of achieving a negative population value. If a negative population value is still achieved, the tau is shortened and the leap is repeated. See Ref. 15 for the full details of this method.

While both the binomial tau-leaping method and the “critical reaction method” guarantee negative population values will be avoided, neither addresses the underlying problem of what is driving population values negative: that the leap condition is badly violated at times. Instead of handling this larger problem, both the binomial tau-leaping method and the partitioning method of Cao *et al.* only handle it when species numbers are low (although this is admittedly the most important time to handle this problem). Also, the fact that population values can become negative in the absence of



specific machinery designed to keep them positive points out that other such large violations of the leap condition are most likely occurring elsewhere in the simulation, yet are going unnoticed.

### III. A NEW TAU-LEAPING PROCEDURE

Through a postleap check the procedure developed in this section will only accept leaps that demonstrably satisfy a leap condition. A consequence of such enforcement will be that achieving negative population values will be impossible, and so the partitioning machinery of Cao *et al.* will no longer be necessary. Further, as the method proposed will adaptively choose tau based upon the success or failure of the previous leap, there will be no need to calculate tau before each leap via Eq. (7).

#### A. Conceptual framework

The method proposed in this section relies heavily on the following two facts: (1) the internal time frames of the Poisson processes are distinct from each other and from the absolute time frame and (2) for  $T_2 \geq T_1 \geq T_k(t)$ , the value  $Y_k(T_2) - Y_k(T_1)$  is independent from the state of the system  $X(t)$ . Consider Eqs. (1) and (2). Suppose that at time  $t$  we have knowledge of the state of the system,  $X(t)$ , the propensity functions,  $a_k = a_k(X(t))$ , the various internal times  $T_k = T_k(t) = \int_0^t a_k(X(s)) ds$ , and the number of firings of each Poisson process up to time  $t$ ,  $C_k \doteq Y_k(T_k(t))$ . However, we suppose we have no information about the values  $Y_k(T) - Y_k(T_k)$  for  $T > T_k$ . At this time we attempt to perform a leap with some predetermined  $\tau$ . By Eq. (4), the number of jumps of  $Y_k$  over the internal time period  $(T_k, T_k + a_k\tau)$  has a Poisson distribution with parameter  $a_k\tau$ . We therefore generate  $M$  Poisson random variables and denote them by  $N_k$ . Note that we have now fixed the value  $Y_k(T_k + a_k\tau) = N_k + C_k$  for the course of the simulation. We next approximate the state of the system at time  $t + \tau$  via Eq. (5) and check the leap condition. If we verify that the leap condition has been satisfied, we may accept the updated system and attempt another leap.

If the leap condition is not satisfied, we do not accept the leap and we do not update the system. Instead, we decrease the tau value by choosing some  $\tau^* < \tau$  and attempt another leap over this shorter time period. However, we still know that  $Y_k(T_k + a_k\tau) = C_k + N_k$ , for each  $k$ , and should condition upon this knowledge when calculating  $Y_k(T_k + a_k\tau^*)$ . Note that knowing  $Y_k(T_k + a_k\tau) = C_k + N_k$  is not the same as claiming to know that reaction  $k$  fired  $C_k + N_k$  times by time  $t + \tau$ . The former equation is simply a statement about the values of the Poisson process  $Y_k(\cdot)$ , while the latter is a statement about the actual firings of the system by a certain time. We prove the following theorem in the appendix.

**Theorem 3.1.** Let  $Y(t)$  be a Poisson process with intensity  $\lambda$ , and let  $0 \leq s < u < t$ . Then, conditioned on  $Y(s)$  and  $Y(t)$ ,  $Y(u) - Y(s)$  has a binomial  $(Y(t) - Y(s), r)$  distribution, where  $r = (u - s)/(t - s)$ .

By Theorem 3.1, the distribution of  $Y_k(T_k + a_k\tau^*) - Y_k(T_k)$ , conditioned on  $Y_k(T_k) = C_k$  and  $Y_k(T_k + a_k\tau) = C_k + N_k$ , has a binomial  $(N_k, p_k)$  distribution, where  $p_k = \tau^* / \tau$ . After choosing the number of times  $Y_k$  jumps in the internal

time period  $(T_k, T_k + a_k\tau^*)$  according to the binomial distribution just calculated, we repeat the process of attempting an update of the state of the system and of checking the leap condition. If this leap is also rejected, we simply store the information on how many times  $Y_k$  jumped by internal time  $T_k + a_k\tau^*$ , shorten tau, and try again. For the next attempted leap, we only need to condition on  $Y_k(T_k)$  and  $Y_k(T_k + a_k\tau^*)$  because of the independence of intervals of Poisson processes. Eventually, a leap will be accepted and we may move forward in both absolute and internal time.

We note that when we accept a leap and are ready to attempt another one we may have stored the value of  $Y_k(T)$  for many different internal times,  $T \geq T_k$ . When we attempt another leap, the next proposed internal time will either fall between two internal times we have stored, or will fall beyond our last stored internal time. In the former case, Theorem 3.1 may be applied because of the independence of intervals of Poisson processes. In the latter case, the number of firings will be given as the number of firings up to the last stored internal time, plus a Poisson random variable accounting for the extra internal time.

The above description is the backbone of our new method. At each absolute time  $t$  we will attempt a leap of size  $\tau$ . Supposing that we have stored the information  $T^1, \dots, T^d$  and  $Y_k(T^1), \dots, Y_k(T^d)$ , with  $T^1, \dots, T^d > T_k$ ,  $T_k + a_k\tau$  will either fall between two of the stored internal times or fall beyond  $T^d$ . As above, in the case when  $T^i \leq T_k + a_k\tau < T^{i+1}$  for some  $i$ , we apply Theorem 3.1 by conditioning upon  $Y_k(T^i)$  and  $Y_k(T^{i+1})$  and choosing from the appropriate binomial distribution. Finally, we add the random variable chosen to  $Y_k(T^i) - C_k$  to find how many times  $Y_k$  jumped between the internal times  $T_k$  and  $T_k + a_k\tau$ . In the case when  $T_k + a_k\tau \geq T^d$  we generate a Poisson random variable with parameter  $T_k + a_k\tau - T^d$  and add it to  $Y_k(T^d) - C_k$  to find the number of jumps. Acceptance or rejection of the leap then depends on checking the leap condition. If we do reject the leap, we would then store the information just learned about each  $Y_k$ , shorten  $\tau$ , and try again. By storing the information gained about the processes  $Y_k$  after each attempted leap we see that no information about the processes  $Y_k$  will be lost in the course of a simulation. Because all of the randomness in the system resides in the processes  $Y_k$ , we conclude that the rejection of leaps will not bias the statistics of the sample paths.

We have not yet described how to update  $\tau$  after each failed or accepted leap and will do so now. In the following tau updating procedure, we suppose that we have already fixed the  $\epsilon$  of the leap condition (8) as  $\bar{\epsilon}$ :

- (1) If a leap is rejected because it fails the leap condition for  $\epsilon = \bar{\epsilon}$ , then decrease  $\tau$  by multiplying it by some  $p < 1$ .
- (2) If a leap is accepted because it satisfied the leap condition for  $\epsilon = \bar{\epsilon}$ , but would have failed the leap condition if  $\epsilon = 3\bar{\epsilon}/4$ , then decrease  $\tau$  by multiplying it by some  $p^*$  that satisfies  $p < p^* < 1$ .
- (3) If a leap is accepted because it satisfied the leap condition for  $\epsilon = \bar{\epsilon}$ , and would have satisfied the leap condi-

tion if  $\epsilon = 3\bar{\epsilon}/4$ , then increase  $\tau$  by raising it to the power  $q$  for some  $0 < q < 1$ .

Unlike the method of Cao *et al.*, we are not making an effort to select the largest possible  $\tau$  for which the leap condition will hold. However, based upon the tau updating procedure given above, it should be clear that we are attempting to select a tau that is at least near such a maximal value. However, as the value of  $\epsilon$  itself is rather arbitrary, it does not seem critical to select such a “largest” tau.

We point out that step 2 in our tau updating procedure is useful to keep the number of rejected leaps down. In essence, step 2 forces the algorithm to always attempt to satisfy the leap condition for a smaller value of epsilon than what was originally chosen, but does not reject the leap if such a restrictive condition is not met. Because the generation of Poisson and binomial random variables are computationally intensive procedures, attempting to limit the number of failed leaps, and hence the number of random variables generated, seems reasonable.

## B. The new algorithm

The logic of the previous section gives us a new adaptive tau-leaping procedure that incorporates postleap checks without biasing the sample paths. Before presenting the algorithm, however, some notation is needed. Each Poisson process  $Y_k$  will have an associated matrix  $S_k$  that will serve to store the information gained from leaps that fail the postleap check. Each  $S_k$  has two columns. The first column will store internal times (as opposed to absolute times). The second column will store the number of firings of  $Y_k$  up to the internal time in the first column. That is, the elements of row  $i$  satisfy  $Y_k(S_k(i, 1)) = S_k(i, 2)$ . The first row of  $S_k$  will always contain the present internal time and the number of times  $Y_k$  has fired up to that time. Also,  $T_k = T_k(t)$  will always denote the current internal time of  $Y_k$  and  $Y_k(T_k)$  will be denoted by  $C_k$ . Combining the above gives that at each step we have  $T_k = S_k(1, 1)$  and  $C_k = S_k(1, 2)$ . Finally, the values  $row_k$  will be used to update the rows of the matrices  $S_k$  after every step.

*Algorithm 2.* (Postleap check tau-leaping)

- (1) Initialize. Set the initial number of molecules of each species  $x \in \mathbb{Z}_{\geq 0}^N$  and calculate the propensity functions  $a_k$ . Set  $t=0$  and for each  $k$  set  $T_k = C_k = 0$ , and  $S_k = [0, 0]$ . Calculate  $\tau$  via Eq. (7). Set  $0 < p < p^* < 1$  and  $0 < q < 1$ .
- (2) For each  $k$ , do the following:
  - (a) Let  $B_k$  = the number of rows of  $S_k$ .
  - (b) If  $a_k\tau + T_k \geq S_k(B_k, 1)$ ,
    - Set  $N_k = \text{Poisson}(T_k + a_k\tau - S_k(B_k, 1)) + S_k(B_k, 2) - C_k$ .
    - Set  $row_k = B_k$ .
  - (c) else
    - Find the index  $I_k$  such that

$$S_k(I_k - 1, 1) \leq T_k + a_k\tau < S_k(I_k, 1).$$

- Set  $r = (T_k + a_k\tau - S_k(I_k - 1, 1)) / (S_k(I_k, 1) - S_k(I_k - 1, 1))$ .
  - Set  $N_k = \text{binomial}(S_k(I_k, 2) - S_k(I_k - 1, 2), r) + S_k(I_k - 1, 2) - C_k$ .
  - Set  $row_k = I_k - 1$ .
- (3) Check whether the leap condition holds with the selected  $N_k$ .
  - (4) If yes, accept leap:
    - (a) Update each  $S_k$ .
      - Delete all rows less than or equal to  $row_k$  and shift all other rows down. Add a new first row of  $[T_k + a_k\tau, C_k + N_k]$ .
    - (b) Set  $t = t + \tau$ .
    - (c) For each  $k$ , set  $T_k = T_k + a_k\tau$  and  $C_k = C_k + N_k$ .
    - (d) Update  $\tau$  according to the tau updating procedure of the previous section.
    - (e) Set  $x = x + \sum_{k=1}^M N_k(\nu'_k - \nu_k)$  and recalculate the propensity functions.
    - (f) Return to step 2 or quit.
  - (5) Else, reject leap:
    - (a) Update each  $S_k$ .
      - Add the row  $[T_k + a_k\tau, C_k + N_k]$  between rows  $row_k$  and  $row_k + 1$  (if  $row_k + 1 > B_k$ , just add a last row to  $S_k$ ).
    - (b) Decrease  $\tau$  by setting  $\tau = p\tau$ .
    - (c) Return to step 2 or quit.

*Remark.* In the above algorithm, no population value can become negative after an accepted leap. Unlike the binomial tau-leaping method or the splitting of the reactions into critical and noncritical subsets, however, Algorithm 2 handles the underlying problem that could cause negative population values. That is, the leap condition will never be violated.

We note that the manner in which we choose our  $\tau$  will generally lead to smaller  $\tau$  values than the preleap computation method for a given value of  $\epsilon$  and for a given state of the system  $X(t)$ . Therefore, for a given  $\epsilon$  we expect that our method will need more simulation time than Algorithm 1, but will produce more accurate results. Thus, in order to find which algorithm is more efficient we will need to compare them with different  $\epsilon$  values. Also, we note that Algorithm 1 chooses its tau values based upon the current state of the system, whereas Algorithm 2 chooses its tau values based upon the success or failure of the previously attempted leap. While it is true that each method will (at least statistically) produce the same leap for a given state of the system and a given  $\tau$ , we note that over the course of an entire simulation the difference in how each algorithm selects their tau values will cause the statistics of the sample paths to diverge. Therefore, it is entirely plausible that one method will achieve higher accuracy than the other through fewer steps. This is demonstrated in Sec. IV.

### C. Switching to an exact algorithm

As noted in the paragraph following Algorithm 1, it is sometimes advantageous to switch between a tau-leaping method and an exact method. Doing so for Algorithm 2 is nontrivial as there could be stored information in the matrices  $S_k$ . If any of the  $S_k$  matrices have stored information, then the distributions of the future states of the system do not solely depend on the current state of the system. One could discard all stored information (that is, delete the information in the matrices  $S_k$ ) and switch to an exact method. In this case, it is important to recognize that by discarding the stored information, we have, in effect, changed the Poisson processes  $Y_k$ , and such a change adds a potential bias to the choice of sample paths. For example, it is possible that the algorithm needed to switch to an exact method because one or more of the processes  $Y_k$  had significantly more firings than was expected over a short period of internal time. By discarding this stored information, we may be inadvertently biasing the system away from such instances. Typically, however, there are not many switches made from tau-leaping to an exact method in the course of a simulation, and so the bias that is added may be negligible. Further, simply deleting the rows of the  $S_k$  matrices would be simple to implement.

Another option is to keep all of the stored information contained in the  $S_k$  matrices and switch to an exact method. In this case, we preserve the fact that we are not approximating the processes  $Y_k$  in our simulation. The exact method to which we will switch is similar to the modified next reaction method. See Ref. 4 for a detailed explanation of the modified next reaction method.

We begin by letting  $P_k$  denote the internal time of the next firing of the Poisson process  $Y_k$ . That is, for each  $k$  we let  $P_k = \min\{T > T_k \mid Y_k(T) > Y_k(T_k)\}$ . We will then find the amount of absolute time that passes until the next reaction takes place, and the reaction that happens at that time, by minimizing over  $(P_k - T_k)/a_k$ . There are two cases to consider in the calculation of  $P_k$ :

*Case 1:* If there is no stored information for the  $k$ th reaction we may use the fact that the  $Y_k$ 's are independent, unit rate Poisson processes and set  $P_k = T_k + \ln(1/r_k)$ , where  $r_k$  is uniform (0,1).

*Case 2:* If there is stored information for the  $k$ th reaction channel we must condition upon that information in order to calculate the distribution of the next firing time. In the Appendix we show the following.

**Lemma 3.2.** Let  $Y(t)$  be a Poisson process with intensity  $\lambda$ . Let  $t > 0$  and  $0 = Y(0) < Y(t) = N$ . Let  $P^1 = \min\{s \mid Y(s) > 0\}$ . Then, for  $0 \leq r \leq t$ ,  $P(P^1 > r \mid Y(t) = N) = (1 - r/t)^N$ .

We let  $B_k$ ,  $C_k$ , and  $T_k$  be as in Algorithm 2. By Lemma 3.2, we may calculate  $P_k$  in the following manner. First, find the index  $j$  such that  $C_k = S_k(j, 2)$  and  $C_k < S_k(j+1, 2)$ . Thus, the next firing of  $Y_k$  happens in the internal time interval  $[S_k(j, 1), S_k(j+1, 1)]$ . If no such  $j$  exists, set  $P_k = S_k(B_k, 1) + \ln(1/r_k)$ , where  $r_k$  is uniform(0,1). If such a  $j$  does exist, let  $t_k = S_k(j+1, 1) - S_k(j, 1)$  and let  $N_k = S_k(j+1, 2) - S_k(j, 2)$ .  $N_k$  gives the number of firings of the Poisson process  $Y_k$  in the internal time period  $[S_k(j, 1), S_k(j+1, 1)]$ , which is of length

$t_k$ . By Lemma 3.2,  $P_k - S_k(j, 1)$  has distribution function  $(1 - r/t_k)^{N_k}$  and so we may set  $P_k = S_k(j, 1) + t_k(1 - r_k^{1/N_k})$ , where  $r_k$  is uniform (0,1).

**Algorithm 3.** An exact stochastic simulation algorithm given stored information.

- (1) Input: the number of molecules of each species,  $t$ , and for each  $k$ , the following from Algorithm 2:  $a_k$ ,  $S_k$ ,  $T_k$ , and  $C_k$ .
- (2) For each  $k$ , find  $P_k$  as described in the previous paragraph.
- (3) Set  $\Delta_k = (P_k - T_k)/a_k$ .
- (4) Set  $\Delta = \min\{\Delta_k\}$  and let  $\Delta_\mu$  be the value at which the minimum is realized.
- (5) Set  $t = t + \Delta$  and update the number of each molecular species according to reaction  $\mu$ .
- (6) For each  $k$ , set  $T_k = T_k + a_k \Delta$ .
- (7) Set  $C_\mu = C_\mu + 1$ .
- (8) Find  $P_\mu$  as described in the previous paragraph.
- (9) Recalculate the propensity functions.
- (10) Update each  $S_k$  by deleting all rows with internal times less than or equal to  $T_k$  and adding a new first row of  $[T_k, C_k]$ .
- (11) Return to step 3 or return to tau-leaping or quit.

*Remark.* After the first time step, the above algorithm uses only one random variable per time step. Also, Algorithm 3 becomes the modified next reaction method if all of the information in each  $S_k$  is exhausted before the switch back to tau-leaping is made.

We have shown how to switch successfully from tau-leaping with Algorithm 2 to the exact method in Algorithm 3. However, we now have to consider how to switch back. It is not instantly clear that we can simply discard the information contained in the unused  $P_k$  values without adding bias to our system. We also note that we can not simply incorporate the  $P_k$  values into the  $S_k$  matrices because each  $S_k$  contains information about how many jumps of  $Y_k$  have taken place up to different internal times and not information about the exact jump times. However, the following theorem allows us to discard the information stored in the  $P_k$  values when we switch from Algorithm 3 back to Algorithm 2. The proof can be found in the Appendix.

**Theorem 3.3.** The statistics of the firing times of each reaction channel are unaffected by discarding the  $P_k$  values when we switch from the exact method of Algorithm 3 to tau-leaping in Algorithm 2.

### IV. A NUMERICAL EXAMPLE

We compare the different tau-leaping methods on a model of an unstable dimer that has been used in a number of earlier papers.<sup>13,14,18</sup> The model consists of four reactions and three species. The reactions are





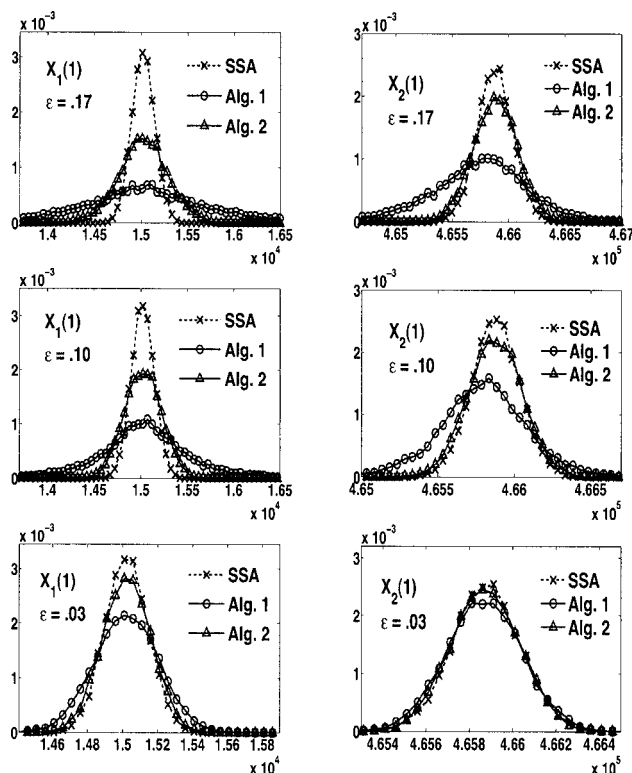


FIG. 1. Histogram plots of  $X_1(1)$  and  $X_2(1)$  for  $\epsilon=0.03, 0.10, 0.17$ . Each plot was generated by simulating the system (9)  $10^4$  times using the SSA (dashed curve with “x”), Algorithm 1 (solid curve with “o”), and Algorithm 2 (solid curve with “ $\Delta$ ”). Algorithm 2 is consistently more accurate than Algorithm 1, as was expected.

with rate constant  $c_1=1$ ,  $c_2=0.002$ ,  $c_3=0.5$ , and  $c_4=0.04$ . The propensity functions are  $a_1(X)=X_1$ ,  $a_2(X)=(0.002/2)X_1(X_1-1)$ ,  $a_3(X)=0.5X_2$ , and  $a_4(X)=0.04X_2$ . We chose initial conditions of  $X_1(0)=10^6$ ,  $X_2(0)=10^3$ , and  $X_3(0)=0$ . We imposed the leap condition (8) in Algorithm 1 by calculating tau before each leap according to Eq. (7) and imposed the leap condition in Algorithm 2 by checking that the condition was satisfied after every leap. For Algorithm 2 we chose  $p=0.75$ ,  $p^*=0.9$ , and  $q=0.98$  as the values for our tau updating procedure described at the end of Sec. III A.

For  $\epsilon=0.17$ ,  $\epsilon=0.1$ , and  $\epsilon=0.03$  as the  $\epsilon$  values of the leap condition (8), we simulated the above system  $10^4$  times using Gillespie’s original algorithm (SSA), Algorithm 1, and Algorithm 2. The simulations were performed using MATLAB on a 2 GHz processor running on the Debian operating system. To generate Poisson and binomial random variables, we used the MATLAB Poisson and binomial random number generators. Each simulation began at time  $t=0$  and ended at time  $t=1$ . In Fig. 1, we show the histograms of  $X_1(1)$  and  $X_2(1)$  for the different values of  $\epsilon$ . We see that for each  $\epsilon$  Algorithm 2 is significantly more accurate than Algorithm 1. As was pointed out at the end of Sec. III B, however, the tau selection strategy for Algorithm 2 will naturally choose smaller values of  $\tau$  for a given value of  $\epsilon$ . Therefore, it is not surprising that Algorithm 2 is significantly more accurate for each  $\epsilon$ . The CPU times for the different methods and different  $\epsilon$  values are given in Table I. As was predicted in Sec. III B, the increased accuracy of Algorithm 2 for each  $\epsilon$  came at the price of longer CPU times.

TABLE I. CPU times needed for Algorithms 1 and 2 to complete  $10^4$  simulations of system (9) for different  $\epsilon$  values.

CPU times	$\epsilon=0.17$	$\epsilon=0.10$	$\epsilon=0.03$
Algorithm 1	31 CPU min	46 CPU min	120 CPU min
Algorithm 2	60 CPU min	82 CPU min	226 CPU min

In Fig. 2, we plot the histograms of  $X_1(1)$  and  $X_2(1)$  generated by the Gillespie algorithm (SSA), Algorithm 1 with  $\epsilon=0.03$ , and Algorithm 2 with  $\epsilon=0.1$ . We see that the histograms of the different tau-leaping methods with their respective  $\epsilon$  values are now nearly equivalent in their accuracy. However, based upon the CPU times in Table I, in order to get such accuracy Algorithm 1 required 46% more CPU time than Algorithm 2. We therefore see that, at least for this model, our new postleap check method is more efficient than the preleap computation method.

We next simulated the system 100 times using Algorithm 1 with  $\epsilon=0.03$  and Algorithm 2 with  $\epsilon=0.1$ , except this time we added machinery to keep track of how many leaps were needed in each algorithm to complete the simulation. We found that Algorithm 2 took an average of 203.4 successful leaps per simulation and rejected an average of 37.8 leaps. We found that Algorithm 1 took an average of 466.8 leaps. Therefore, Algorithm 2 needed 56% fewer successful leaps than Algorithm 1, which implies that the average size of tau for the successful leaps of Algorithm 2 was approximately double that of Algorithm 1. The reason Algorithm 2 can achieve similar accuracy to Algorithm 1 with larger average tau values was explained at the end of Sec. III B.

## V. DISCUSSION

By explicitly representing the reaction times of discrete stochastic chemical systems as the firing times of independent, unit rate Poisson processes, we have developed an accurate and efficient adaptive tau-leaping procedure. The main difference between the method developed in this paper and the current adaptive tau-leaping methods is that we enforce our leap conditions via a postleap check. Also, we have demonstrated how to reject leaps without biasing the sample paths. Further, as a consequence of always satisfying a given leap condition, our procedure is guaranteed to never produce negative population values, which is in contrast to current

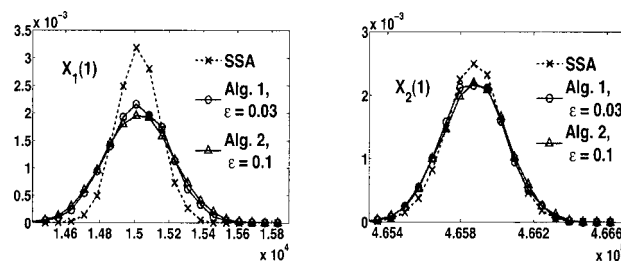


FIG. 2. Histogram plots of  $X_1(1)$  and  $X_2(1)$  found from  $10^4$  simulations of system (9). We show the SSA (dashed curve with x), Algorithm 1 with  $\epsilon=0.03$  (solid curve with o), and Algorithm 2 with  $\epsilon=0.1$  (solid curve with  $\Delta$ ). The distributions of the sample paths generated by Algorithms 1 and 2 with these  $\epsilon$  values have similar accuracies and can therefore be used as a fair test for efficiency.



methods in which extra machinery is needed to guarantee that population values remain non-negative. Finally, through an example of an unstable dimer, we have demonstrated that the method proposed in this paper is not only accurate, but also efficient.

Algorithm 2 will surely not be more efficient than Algorithm 1 for all chemical reaction systems. However, by enforcing a postleap check in such a way that the statistics of the sample paths are not biased by the rejection of a leap, we are confident that Algorithm 2 will be more accurate and will have better stability properties for all chemical reaction systems. We also note that the method we have developed is easily adaptable to any leap conditions, not just those given by Eqs. (6) and (8). Such adaptability is in contrast to methods that compute  $\tau$  before each leap, which need a new tau computation procedure for every new leap condition.

This paper represents a first step in developing and analyzing tau-leaping methods through an understanding of the random time change representation given in Eq. (2). Future work will focus on error analysis, the development of high order methods, and the incorporation of delays in tau-leaping.

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## APPENDIX A: DEFINITION OF FUNCTIONS

The functions  $g_i = g_i(X(t))$  used in Eq. (7) are defined as follows. Let  $\text{HOR}(i)$  denote the highest order of reaction in which species  $X_i$  appears as a reactant.

- (i) If  $\text{HOR}(i) = 1$ , take  $g_i = 1$ .
- (ii) If  $\text{HOR}(i) = 2$ , take  $g_i = 2$ , except if any second-order reaction requires two  $X_i$  molecules in which case take  $g_i = 2 + 1/(X_i(t) - 1)$ .
- (iii) If  $\text{HOR}(i) = 3$ , take  $g_i = 3$ , except if some third-order reaction requires two  $X_i$  molecules in which case take

$$g_i = \frac{3}{2} \left( 2 + \frac{1}{X_i(t) - 1} \right),$$

except if some third-order reaction requires three  $X_i$  molecules in which case take

$$g_i = 3 + \frac{1}{X_i(t) - 1} + \frac{2}{X_i(t) - 2}.$$

## APPENDIX B: PROOFS

*Proof of Theorem 3.1:* Without loss of generality, we suppose that  $s=0$  and  $Y(0)=0$ . Let  $Y(t)=N$  and  $0 < u < t$ . Then

$$\begin{aligned} P(Y(u) = j | Y(t) = N) &= P(Y(u) = j, Y(t) = N) / P(Y(t) = N) \\ &= P(Y(t) - Y(u) = N - j) P(Y(u) = j) / P(Y(t) = N) \\ &= \frac{e^{-\lambda(t-u)} (\lambda(t-u))^{N-j}}{(N-j)!} \frac{e^{-\lambda u} (\lambda u)^j}{j!} \frac{N!}{e^{-\lambda t} (\lambda t)^N} \\ &= \binom{N}{j} \left( \frac{u}{t} \right)^j \left( 1 - \frac{u}{t} \right)^{N-j}. \end{aligned}$$

□

*Proof of Lemma 3.2:*

$$\begin{aligned} P(P^1 > r | Y(t) = N) &= P(Y(r) = 0 | Y(t) = N) \\ &= P(Y(r) = 0, Y(t) = N) / P(Y(t) = N) \\ &= P(Y(t) - Y(r) = N) P(Y(r) = 0) / P(Y(t) = N) \\ &= \frac{e^{-\lambda(t-r)} (\lambda(t-r))^N}{N!} \frac{e^{-\lambda r}}{e^{-\lambda t} (\lambda t)^N} = (1 - r/t)^N. \end{aligned}$$

□

*Proof of Theorem 3.3:* If there are no stored reaction times for reaction channel  $k$ , then discarding the extra information contained in  $P_k$  is done by invoking the loss of memory property. Now suppose that there is stored information for reaction  $k$ . The firing times less than  $T > 0$  of a Poisson process  $Y$ , conditioned on  $Y(T)$ , are uniform(0,  $T$ ) random variables. Therefore, it is sufficient to show that for a uniform( $a, b$ ) random number  $U$ ,  $P(U > s+x | U > x) = (b - (s+x)) / (b - x)$ , thus showing that the conditional statistics are uniform( $x, b$ ). The calculation is simple and is omitted. □

<sup>1</sup>D. T. Gillespie, J. Comput. Phys. **22**, 403 (1976).

<sup>2</sup>D. T. Gillespie, J. Phys. Chem. **81**, 2340 (1977).

<sup>3</sup>H. Andersson and T. Britton, *Stochastic Epidemic Models and Their Statistical Analysis* (Springer, New York, NY, 2000).

<sup>4</sup>D. F. Anderson, J. Chem. Phys. **127**, 214107 (2007).

<sup>5</sup>K. Ball, T. G. Kurtz, L. Popovic, and G. Rempala, Ann. Appl. Probab. **16**, 1925 (2006).

<sup>6</sup>S. N. Ethier and T. G. Kurtz, *Markov Processes: Characterization and Convergence* (Wiley, New York, 1986).

<sup>7</sup>T. G. Kurtz, Stochastic Proc. Appl. **6**, 223 (1978).

<sup>8</sup>M. Gibson and J. Bruck, J. Phys. Chem. A **105**, 1876 (2000).

<sup>9</sup>A. Arkin, J. Ross, and H. H. McAdams, Genetics **149**, 1633 (1998).

<sup>10</sup>H. H. McAdams and A. Arkin, Proc. Natl. Acad. Sci. U.S.A. **94**, 814 (1997).

<sup>11</sup>E. M. Ozbudak, M. Thattai, I. Kurtser, A. D. Grossman, and A. van Oudenaarden, Nat. Genet. **31**, 69 (2002).

<sup>12</sup>H. E. Samad, M. Khammash, L. Petzold, and D. Gillespie, Int. J. Robust Nonlinear Control **15**, 691 (2005).

<sup>13</sup>D. T. Gillespie, J. Chem. Phys. **115**, 1716 (2001).

<sup>14</sup>Y. Cao, D. T. Gillespie, and L. R. Petzold, J. Chem. Phys. **124**, 044109 (2006).

<sup>15</sup>Y. Cao, D. T. Gillespie, and L. R. Petzold, J. Chem. Phys. **123**, 054104 (2005).

<sup>16</sup>T. Tian and K. Burrage, J. Chem. Phys. **121**, 10356 (2004).

<sup>17</sup>A. Chatterjee and D. G. Vlachos, J. Chem. Phys. **122**, 024112 (2005).

<sup>18</sup>D. T. Gillespie and L. R. Petzold, J. Chem. Phys. **119**, 8229 (2003).