Simulation Modelling Practice and Theory 72 (2017) 150–167

Contents lists available at ScienceDirect

Simulation Modelling Practice and Theory

journal homepage: www.elsevier.com/locate/simpat

Multilevel branching and splitting algorithm for estimating rare event probabilities

Agnès Lagnoux[a,*], Pascal Lezaud[b]

[a] Institut de Mathématiques de Toulouse, Université Toulouse 2 Jean Jaurès, France
[b] ENAC - Ecole Nationale de l'Aviation Civile, Université de Toulouse, France

ARTICLE INFO

Article history:
Received 5 February 2016
Revised 14 December 2016
Accepted 15 December 2016

Keywords:
Splitting
Rare event probability estimation
Monte Carlo
Branching process
Simulation
Variance reduction
First crossing time density
Conformal maps

ABSTRACT

We analyze the splitting algorithm performance in the estimation of rare event probabilities in a discrete multidimensional framework. For this we assume that each threshold is partitioned into disjoint subsets and the probability for a particle to reach the next threshold will depend on the starting subset. A straightforward estimator of the rare event probability is given by the proportion of simulated particles for which the rare event occurs. The variance of this estimator is the sum of two parts: with one part resuming the variability due to each threshold, and the second part resuming the variability due to the number of thresholds. This decomposition is analogous to that of the continuous case. The optimal algorithm is then derived by cancelling the first term leading to optimal thresholds. Then we compare this variance with that of the algorithm in which one of the threshold has been deleted. Finally, we investigate the sensitivity of the variance of the estimator with respect to a shape deformation of an optimal threshold. As an example, we consider a two-dimensional Ornstein–Uhlenbeck process with conformal maps for shape deformation.

1. Introduction

The risk modeling approach consists of, first, formalizing the system under consideration, and second, using mathematical or simulation tools to obtain some estimates [2,29]. Analytical and numerical approaches are useful, but may require many simplifying assumptions. On the other hand, a Monte Carlo simulation is a practical alternative when the analysis requires fewer simplifying assumptions. Nevertheless, obtaining accurate estimates of rare event probabilities, say about 10^{-9} to 10^{-12}, using traditional techniques requires an extremely large amount of computing time.

Many techniques for reducing the number of trials in a Monte Carlo simulation have been proposed, such as importance sampling or trajectory splitting ([24]). In the splitting technique, we suppose that there exists some well-identifiable intermediate states that are visited more frequently than the target states themselves, and behave as gateways to reach the rare event. Thus, we consider a decreasing sequence of events B_i leading to the rare event B:

$$B := B_{M+1} \subset B_M \subset \ldots \subset B_1 \,. \tag{1}$$

* Corresponding author.
E-mail address: lagnoux@univ-tlse2.fr (A. Lagnoux).

http://dx.doi.org/10.1016/j.simpat.2016.12.009
1569-190X/

Then $p := \mathbb{P}(B) = \mathbb{P}(B|B_M)\mathbb{P}(B_M|B_{M-1})\dots\mathbb{P}(B_2|B_1)\mathbb{P}(B_1)$, where on the right-hand side, each conditioning event is "not rare". These conditional probabilities are, in general, not available explicitly. Instead, we know how to make the particles evolve from level B_i to the next level B_{i+1} (e.g. Markovian behavior).

The principle of the algorithm is first to simultaneously run several particles starting from level B_i. After a period of time, some have evolved "badly", while others have evolved "well", that is, they have succeeded in reaching the threshold B_{i+1}. Then the "bad" particles are moved to the position of the "good" ones, and so on, until B is reached. In such a way, the more promising particles are favoured. Examples of this class of algorithms can be found in [3], with their "go with the winners" scheme, in [20] and [13] with approximate counting, and in a more general setting in [9,11,12,14,26].

The difficulty comes from the complexity of the dynamics of the particles. A simpler analysis can be completed by focusing only on the underlying Markov chain that represents the changes of thresholds. In this technique, we make a Bernoulli trial to check whether or not the set event B_1 has occurred. In that case, we split this trial into R_1 Bernoulli subtrials, and for each of them we again check whether or not the event B_2 has occurred. This procedure is repeated at each level, until B is reached. If an event level is not reached, then neither is B, and we stop the current retrial. Using N independent replications of this procedure, we have considered $NR_1\dots R_M$ trials, taking into account, for example, that if we have failed to reach a level B_i at the ith step, the potential $R_i\dots R_M$ retrials have failed. Clearly the particles reproduce and evolve independently.

An unbiased estimator of p is given by the quantity:

$$\widehat{p}_{M+1} = \frac{N_B}{N\prod_{i=1}^{M} R_i},$$

where N_B is the total number of trajectories having reached the set B. Considering that this algorithm is represented by N independent Galton–Watson branching processes, as seen in [22], the variance of $\widehat{p}_{M+1}$ can then be derived, and depends on the probability transitions and the mean numbers of particles' successes at each level. Leading by the heuristic presented in [31,32], an optimal algorithm is derived by minimising the variance of the estimator for a given budget (or computational cost). This cost is defined as the expected number of trials generated during the simulation, with each trial weighted by a cost function.

The optimisation of the algorithm suggests that all transition probabilities be taken as equal to a constant, and the numbers of splitting be equal to the inverse of this constant [22]. Then we deduce the number of thresholds M, and finally the number N of replications. In fact, optimal values are chosen in such a way so as to balance between the increase of the variance when the number splitting is small and the exponential growth in computational effort when too much splitting is used.

In the higher dimension, the engineering community has proposed algorithms to estimate rare event probabilities. Subset simulation, which is also based on a partitioning of the space into nested subsets, uses the Markov Chain simulation (in particular, the Metropolis Hastings scheme), see [7]. Importance sampling techniques have also been developed in that framework. When the failure region is not too complex to describe, schemes to construct importance sampling algorithms have been introduced that are based on design points (see e.g., [6], and [21], and the references therein), or adaptive presamples (see e.g., [5] and the references therein). When the complexity of the rare event increases, it appears to be difficult to construct an efficient importance sampling scheme [30].

In this paper, we continue the multidimensional approach and theoretically study the algorithm introduced in [17] and [15], particularly in order to obtain a new expression of the variance of the estimator analogous to that of the continuous case [24]. Thus, we assume that each threshold is partitioned into s disjoint subsets and the probability for a particle starting from a threshold to reach the next threshold will depend on the starting subset. Unlike the unidimensional case, the difficulty of reaching the next threshold differs according to the starting subset; it may be that the threshold is no longer an iso-probability level. In this context, the variance of the estimator $\widehat{p}_{M+1}$ is the sum of two parts: with one part resuming the variability due to each threshold and the second part resuming the variability due to the thresholds' number (see Proposition 3.1). For the unidimensional case, only the second term remains. The optimal algorithm is then derived by cancelling the first term of the variance leading to iso-probability levels and by optimising the other parameters as in the unidimensional case.

Furthermore, by introducing new operators, we obtain an alternative expression of the variance which is more tractable when we wish to compare the variance of the estimators in an algorithm with M thresholds with the variance in an algorithm in which one of the threshold has been deleted. More precisely, we study the need for an intermediate threshold and derive a procedure to detect whether or not to keep it. In order to obtain a simple criteria, we assume the optimal shape of the thresholds of the optimal algorithm. Finally, we investigate the sensitivity of the variance of $\widehat{p}_{M+1}$ with respect to a shape deformation of the threshold, relative to the optimal shape.

The remainder of this paper is divided into five sections. In Sections 2–4, we present, theoretically analyze and optimise the splitting algorithm in the multidimensional case. Next, Sections 5 and 6 deal with the sensitivity analysis of the variance as previously presented. In particular, in Section 6, we illustrate a way by which to deform the shape of the thresholds in order to get uniform occupation densities with a 2D Ornstein–Uhlenbeck process. Finally, we complete the paper with a conclusion and some perspectives. More details and all proofs are in the Appendices.