



Computing the survival probability density function in jump-diffusion models: A new approach based on radial basis functions

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ABSTRACT

We propose a numerical method to compute the survival (first-passage) probability density function in jump-diffusion models. This function is obtained by numerical approximation of the associated Fokker–Planck partial integro-differential equation, with suitable boundary conditions and delta initial condition. In order to obtain an accurate numerical solution, the singularity of the Dirac delta function is removed using a change of variables based on the fundamental solution of the pure diffusion model. This approach allows to transform the original problem to a regular problem, which is solved using a radial basis functions (RBFs) meshless collocation method. In particular the RBFs approximation is carried out in conjunction with a suitable change of variables, which allows to use radial basis functions with equally spaced centers and at the same time to obtain a sharp resolution of the gradients of the survival probability density function near the barrier. Numerical experiments are presented in which several different kinds of radial basis functions are employed. The results obtained reveal that the numerical method proposed is extremely accurate and fast, and performs significantly better than a conventional finite difference approach.

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1. Introduction

In this paper we propose an efficient numerical method to compute the survival (first-passage) probability density function in jump-diffusion models. Jump-diffusion models are extremely popular in mathematical finance, where they are used, for example, to describe the evolution of asset prices (see [17] and references therein), or the dynamics of firms subject to default [36,61]. The survival probability density function of a jump-diffusion process is a quantity of interest in financial risk management. For instance, it allows to efficiently value portfolios of barrier options [55]; moreover, it can be employed for pricing corporate bonds and credit derivatives in first-passage models of default risk [61]; in addition, as shown in [1], it can be used to estimate the distance to default of a firm.

In this paper we will focus our attention on computing the survival probability density function for the popular Merton's model [51], that is a geometric Brownian motion with log-normally distributed jumps. However, other types of jump probability distributions can be handled as well. Furthermore our approach could be easily extended to other diffusion models

employed in finance, among which we mention the CEV model [13], stochastic volatility models [29,39], credit risk models [1,12], Brownian motions with time-dependent coefficients [2], or two-dimensional log-normal diffusions [60].

We also observe that in [40–42] Hurn and coauthors have shown how the parameters of stochastic models used in financial risk management can be conveniently estimated by numerical approximation of the associated Fokker–Planck equations. Then the approach developed in the present paper, which is focused on the numerical approximation of a Fokker–Planck equation, is also suitable for model calibration purposes.

Finally the numerical techniques developed in this paper have a broad range of applications not only in finance. In fact the problem of computing the survival probability density function is important also in other areas of science and engineering, such as, for example, mechanics [5,11,25,59], biology [43,49,52,54], and optics [8].

The survival probability density function of a jump-diffusion process satisfies a Fokker–Planck partial integro-differential equation, with suitable boundary conditions and Dirac initial condition. This problem requires numerical approximation, which must be performed with special care. In fact, first of all, the integral operator is a non-local operator and, for the sake of computational efficiency, must be handled appropriately. In particular, when finite difference/finite element methods are employed, the integral term is often evaluated using a fast convolution

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