

Limit theorems for a class of piecewise-deterministic Markov processes with application to a model of gene expression

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Our main goal is to establish the strong law of large numbers (SLLN) (with the help of [7]) and the central limit theorem (CLT) for a subclass of piecewise-deterministic Markov processes (PDMPs) evolving in a Polish space (see [4]). On the way to these results, we provide sufficient conditions for the existence of an exponentially attractive invariant distribution for the Markov chain given by the post-jump locations of a PDMP belonging that subclass. The main tool for proving this result is [5, Theorem 2.1], which in turn is based on the asymptotic coupling methods introduced by Hairer [2]. Furthermore, we obtain a one-to-one correspondence between invariant measures of such a chain and the PDMP.

To be more precise, we investigate a PDMP arising from a dynamical system which evolves through random jumps in a closed subset, say Y , of a separable Banach space (Fig. 1). The jumps occur at random time points (for which we write $\tau_n : \Omega \rightarrow [0, \infty)$) according to a Poisson process. The evolution of such a system between jumps is deterministically governed by a finite collection of semiflows (say $S_i : \mathbb{R}_+ \times Y \rightarrow Y$, where $i \in \{1, \dots, N\}$), which are being switched between each other at the jump times (like e.g. in [1]). The location directly after the jump is determined by a randomly chosen (continuous) transformation ($w_\theta : Y \rightarrow Y$, where θ belongs to an arbitrary compact space) of the current position (cf. [3]), which is additionally perturbed by a random shift ($H_n : \Omega \rightarrow Y$) within an ε -neighbourhood. From this point onwards, until the next jump, the process is driven by a new, randomly selected semiflow, whose choice depends on the post-jump location and the precedingly running semiflow.

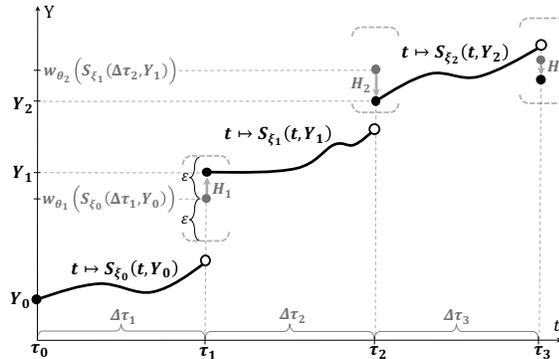


Figure 1: A trajectory of $(Y(t))_{t \geq 0}$.

The main object of our study is a time-homogeneous Markov process determined by the above-described dynamical system. It has the form $(Y(t), \xi(t))_{t \geq 0}$, wherein

$Y(t)$ stands for the position of the system at time t , and $\xi(t)$ is the index of the semiflow that defines the trajectory from t until the next jump. The post-jump locations of such a process are described by the Markov chain $(Y_n, \xi_n) := (Y(\tau_n), \xi(\tau_n))$, $n \in \mathbb{N}_0$. The phase space $X := Y \times \{1, \dots, N\}$ is considered with the metric defined by $d_c((i, u), (j, v)) := \|u - v\| + c\delta(i, j)$, where δ is the discrete distance in $\{1, \dots, N\}$, and c is a sufficiently large constant, which depends on certain parameters occurring in the model under consideration.

The main assumptions underlying our model are quite naturally met by a wide class of semiflows, determined by differential equations (in Banach spaces) involving dissipative operators. Consequently, the model can be motivated by various dynamical processes investigated within natural sciences. We shall demonstrate, for example, that the prokaryotic gene expression in the presence of transcriptional bursting (cf. [6]) can be modeled by a PDMP consistent with our framework. The consideration of switching semiflows enables us to take into account also the influence of bursts on the dynamics of the protein degradation process.

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