USEFUL VERSIONS OF LIMIT THEOREMS FOR CERTAIN NON-STATIONARY MARKOV-FELLER CHAINS

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ABSTRACT

The central limit theorem (CLT) and the law of the iterated logarithm (LIL) are the most common limit theorems. Although limit theorems for positive Harris recurrent Markov chains are already well-investigated (see e.g. [1]), they are still the subject of research for a wider class of Markov chains.

Together with D. Czapla and K. Horbacz we have proven certain criteria on the CLT and the LIL for a quite general class of Markov chains. Our aim was to provide useful assertions which may prove to be useful in studying, in terms of limit theorems, certain stochastic models developed in natural sciences (especially, molecular biology). Therefore we do not require any form of continuous dependence of the given Markov chain on the initial conditions (as is necessary to assume for the results in [2,3] to hold). We do not even directly require the exponential mixing property (see e.g. [4] for the precise formulation). Instead, we propose a set of relatively easily verifiable conditions, which yield the exponential ergodicity in the context of weak convergence of measures (according to [5, Theorem 2.1]), as well as the CLT [6, Theorem 3.2] and the LIL [7, Theorem 3.7].

The class of Markov-Feller chains for which we establish limit theorems may be characterized briefly by the following two properties. Firstly, the transition operator of the chain under consideration enjoys a non-linear Lyapunov-type condition. Secondly, there exists an appropriate Markovian coupling whose transition function can be decomposed into two parts, one of which is contractive and dominant in some sense. The construction of such a coupling is adapted from [5], which, in turn, is inspired by the prominent results of M. Hairer [4].

To justify the usefulness of stating such criteria, we decided to verify them for a particular discrete-time Markov system, for which we were not able to verify conditions proposed in [2] and [3]. The piecewise-deterministic Markov process defined via interpolation of the explored Markov chain can be used e.g. to describe a model for gene expression (cf. [8] and the references therein).

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