МОДЕЛИРОВАНИЕ В НАУЧНЫХ ИССЛЕДОВАНИЯХ

CHOICE OF THE PARAMETERS OF THE CUSUM ALGORITHMS FOR PARAMETER ESTIMATION IN THE MARKOV MODULATED POISSON PROCESS

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Abstract: CUSUM algorithm for controlling chain state switching in the Markov modulated Poisson process was investigated via simulation. Recommendations concerning the parameter choice were given subject to characteristics of the process. Procedure of the process parameter estimation was described.

Keywords: Markov modulated Poisson process, parameter estimation, sequential change point detection, CUSUM algorithm.

Introduction. Markovian arrival processes (MAP) form a powerful class of stochastic processes introduced in [1] and [2] and thereafter they are widely used now as models for input flows to queueing systems where the rate of the arrival of customers depends on some external factors.

We consider the Markov-modulated Poisson process (MMPP) where the intensity of the flow of events is controlled by the continuous time Markovian chain with two states. Transitions between states happen at random instants. The sojourn time in the *i*-th state is exponentially distributed with the parameter α_i, where $i = 1, 2$.

The flow of events has the exponential distribution with the intensity parameter λ_1 or λ_2 subject to the state of the Markovian chain. We also suppose that $\alpha_i << \lambda_i$. Both all the parameters and the moments of switching of the controlling chain state are supposed to be unknown.

Our paper [3] develops the sequential analysis approach to the MMPP parameter estimation. The cumulative sum control chart (CUSUM) approach is used to detect the switching instants of the controlling chain state.

In this paper, we study quality characteristics of our algorithm subject to the choice of the CUSUM algorithm parameters. Due to correlation between the observation and non-stationary structure of the process its theoretical investigation is hardly ever possible. So, the characteristics are studied via simulation as at the paper mentioned above.

Algorithm and Simulation Procedure.

Consider the process $\{\tau_i\}_{i\geq 1}$, where $\tau_i = t_i - t_{i-1}$ is the length of the *i*-th interval between arriving events in the observed flow. If the controlling chain is in the *i*-th state then the mean length between events is equal to $1/\lambda_i$. So at the first stage of our procedure we try to detect the instants of the chain transition from one state to another as the instants of change in the mean of the process τ_i using CUSUM procedures.

Let the parameters λ_1, λ_2 satisfy the condition

$$0 < \lambda_2 < \lambda_1,\ 1/\lambda_2 - 1/\lambda_1 \geq \Delta \qquad (1)$$

where Δ is a certain known positive parameter. Choose then an integer parameter k describing the memory depth. If there are no changes of the controlling chain state within the interval $[t_{i-k-1}, t_i]$ then the values τ_i and τ_{i-k} have the identical exponential distribution with the mean $1/\lambda_1$ or $1/\lambda_2$. If the chain state changes within the interval $[t_{i-k-1}, t_i]$ then the expectations of the values τ_i and τ_{i-k} are different.

As the initial state of the chain is unknown, we shall consider two CUSUM procedures simultaneously. The first procedure is set up to detect increase in the mean of the process and hence, decrease of the intensity, and the second procedure is set up to detect decrease in the mean and hence, increase of the intensity. For the first procedure we introduce the sequence of the statistics

$$z_i^{(1)} = \tau_i - \tau_{i-k} - \Delta, \quad i > k. \tag{2}$$

For the second procedure we introduce the sequence of the statistics

$$z_i^{(2)} = \tau_{i-k} - \tau_i - \Delta, \quad i > k. \tag{3}$$

So the expectations of statistics (2), (3) change from negative values to positive when the intensity of the process changes. We introduce positive values $h^{(1)}$ and $h^{(2)}$ as the procedures thresholds and construct the cumulative sums $S_i^{(1)}$ and $S_i^{(2)}$ which are recalculated at the instants t_i. The sums are defined as follows

$$S_0^{(l)} = \Delta; \quad l = 1,2, S_i^{(l)} = \max\{0, S_{i-1}^{(l)} + z_i^{(l)}\}, i > k; \; S_i^{(l)} = 0, \quad if \quad S_i^{(l)} \geq h_l.$$

Reaching the threshold h_l by the sum $S_i^{(l)}$ results in a decision considering the parameters changes.

As our two procedures are identical, we supposed that initially the controlling chain was at the first state and investigated the first procedure.

The proposed algorithm has the following parameters: the memory depth k, the parameter Δ, which provides the change in the mean of the statistics $z_i^{(l)}$ from negative to positive after the change point, and the thresholds h_l. Their influence on delay and false alarm characteristics was studied via simulation. It was performed in R-project software.

Recommendations on the Parameter Choice. Analysing the simulation results we can give some recommendation on the parameter choice.

The CUSUM algorithm for MMPP parameter estimation can be used in the following conditions:

- the intensity of the controlling chain state switchings is significantly less then the intencity of the input flow of events, i.e., $\lambda_i > r\alpha_i$, $r \geq 30$;
- the difference of the mean lengths of the interval between the input flow events in different states of the controlling chain $\delta = 1/\lambda_2 - 1/\lambda_1$ is not less than 0,5;
- the threshold parameters $h^{(l)} \approx 20/\lambda_l$;
- the memory depth parameter *k* belongs to the interval [15,25];
- the parameter Δ is less than $\delta/2$.

If these conditions do not hold true then we can not guarantee the correct change point detection because either false alarms or skips of the change could appear rather often.

As the algorithm is applied a posteriory to a fixed volume sample, one has a possibility to implement it several times for different sets of parameters until the conditions above are fulfilled.

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MODELLING OF CELLULAR STRUCTURES OBTAINED BY X-RAY PHASE CONTRAST IMAGING

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Nowadays computed tomography provides the possibility to image internal cellular structures of embryos. A major challenge is a high accuracy image segmentation of tissues and individual cells. The process of manual image segmentation is time consuming and error prone. It can be partially replaced or augmented by cell modelling techniques developed by computer scientists based on biological, physiological and statistical properties of real embryos.

Key words: imaging methods, microscopy, X-ray phase contrast, image segmentation, modelling of cellular structures.

Introduction. At the recent times, embryogenesis became one of the promising areas in cell biology, developmental biology, genetics and toxicology. Despite the fact that the processes of embryogenesis have been studied since the last century, latest methods of computed tomography allow to obtain new knowledge about the processes of embryo development and allow to create detailed three-dimensional models of its internal structure.

Xenopus Laevis embryos are often used as model organisms for tracking ontogenesis stages. Ease of maintenance and manipulations made this organism an important object of embryology and developmental biology. Using Xenopus Laevis embryos, scientists can clearly trace the processes of displacement and differentiation of cells, forming tissues and individual organs [1].

Images, used for a detailed study of the embryo cellular structure, were obtained at European Synchrotron Research Facility (ESRF) and the Advanced Photon Source (APS) using X-Ray phase contrast [2] techniques.

After tomographic reconstruction was completed, three-dimensional image has to be processed to remove noise and artifacts to reach a result that allows distinguishing the cells and cellular structures (Fig. 1).

However, manual processing of the acquired images to obtain detailed three-dimensional model is a time-consuming task and, therefore, may be replaced or supplemented by the modelling techniques.

At the initial stage of cell modelling, cell data are collected: shape, size and location, then the segmentation of individual cell types is performed. The next step is the generating cellular structures based on the analysed statistics and geometric models of the segmented cells. Final stage is a visualization of a three-dimensional model. The paper pays special attention to methods of imaging and cell segmentation.

Review on imaging techniques. Obtaining images of the cell structures can be performed using the opportunities of microscopy and computer tomography. Application of these imaging techniques depends on the size of the studied structures, their physical and optical properties.

For getting the information about the cell structure and intracellular processes, the following methods can be clarified: elemental, chemical, molecular and morphological analysis [3].

For imaging cells on the basis of their molecular properties, ultraviolet-visible confocal fluorescence imaging [4] and multiphoton fluorescence imaging [5] are used.