



Chaotic time series prediction with employment of ant colony optimization

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ABSTRACT

In this study, the novel method to predict chaotic time series is proposed. The method employs the ant colony optimization paradigm to analyze topological structure of the attractor behind the given time series and to single out the typical sequences corresponding to the different part of the attractor. The typical sequences are used to predict the time series values. The method was applied to time series generated by the Lorenz system, the Mackey–Glass equation, and weather time series as well. The method is able to provide robust prognosis to the periods comparable with the horizon of prediction.

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1. Introduction

Broad range of chaotic processes that one can meet in the real life and technical systems inspires a great interest to chaotic models and particularly, to chaotic series prediction. Meanwhile, predictive models and routines used to be applied to forecast stationary time series (such as ARIMA-models and others) are failed to cope with chaotic series prediction problem. It could be explained by essential non-linearity of systems that generates chaotic series and complex geometrical structure of the systems' attractors. The complex dynamics manifests itself in various ways like rapid changes of the time series, positive Lyapunov exponents, fractal dimensions of attractors and others (Strogatz, 2001). Recently, a plenty of biologically inspired models have been proposed to derive the structure of the strange attractor out of a series and predict the series. One could divide them into three main groups in accordance with the artificial intelligence theories they used to reconstruct the state space (Wang, Chi, Wu, & Lu, 2011) and to analyze time series. The first group is the neural networks that able to employ their approximative capability in order to single out different local trends occurred in a series and predict them with simple linear models installed in them (Gan, Peng, Peng, Chen, & Inoussa, 2010; Wong, Xia, & Chu, 2010). One should mention here singular spectrum analysis method used to analyze singular values of covariance matrix of the series and extract information about the local trends (Elsner & Tsonis, 1996). The second group is fuzzy and neuro-fuzzy models used to create robust and transparent predictive systems (Fu, Wub, Jeng, & Ko, 2010; Gu & Wang, 2007). The third one is the systems based on different distributed artificial

intelligence approaches such as genetic algorithms (Mirzaee, 2009), particle swarm optimization (Zhao & Yang, 2009), ant colony optimization (Niu, Wang, & Wu, 2010; Toskari, 2009), and others. They could be used to adjust parameters of other models (Pan, Jiang, Wang, & Jiang, 2011), but also they possess their own predictive capabilities. One could mention a number of works, where ant colony optimization applied to forecast different chaotic series (power supply demand (Ünler, 2008), electric load (Hong, 2010), traffic flow (Hong, Dong, Zheng, & Lai, 2011), financial series (Weng & Liu, 2006).

This paper employs ACO in order to extract information about strange attractor topological structure out of a given time series and to predict it using information being extracted. We assume that all transient processes in the system behind the chaotic time series at hand have been completed and the time series reflects the movement in the neighborhood of strange attractor however complex it is. The second assumption is that the series meets Takens theorem conditions and respectively one could analyze the attractor structure using its elements. Consequently, trajectory of the system should move along the same part of the attractor frequently and one could meet analogous (similar) sequences in the time series.

The rest of the paper is organized as follows. Section 2 outlines general notions of ant colony optimization and describes state space used to represent inner structure of the attractor underlying the time series. Section 3 presents a complete description of prediction routine. Section 4 provides the results of prediction for the series generated by the Lorenz system, the Mackey–Glass equations, and for weather time series for Kiev city. Section 5 provides the conclusions.

2. Ant colony optimization

2.1. General description of ant colony optimization

Ant colony optimization (ACO) is metaheuristics used to find paths in a graph best with respect to the predefined functional

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(Dorigo, 1992; Dorigo & Gambardella, 1997) ACO has been inspired by real ants search for food and retains some biological terms. For instance, the term ant stands for the simplest search agent moving along the graph, a pheromone stands for the weight of a graph edge; pheromone evaporation means that pheromone for each edge is diminished for a small predefined quantity every iteration. The basic idea of ACO-type algorithms consists of two interweaved rules. Ants constantly move along the graph and an outer observer appreciates the path of each ant according to a certain quality functional. After that pheromone of each edge belonged to the path is updated with respect to the calculated quality functional value. On the other hand, each ant chooses the edge of the graph taking into account the amount of pheromone corresponding to this edge. It allows ACO to combine the ability of DAI methods to find the globally best solution with a high speed of convergence pertain to gradient algorithms. Pheromone is evaporated after each iteration. It leads to that after some iterations all ants is inclined to move in the vicinity of the best solutions. Mathematically the rules are expressed by the following formulas:

$$P_{ij}(t) = \frac{\tau_{ij}(t)^\alpha \left(\frac{1}{d_{ij}}\right)^\beta}{\sum_{k \in \text{all allowed vertices}} \tau_{ik}(t)^\alpha \left(\frac{1}{d_{ik}}\right)^\beta}, \quad (2.1)$$

$$\tau_{ij}(t+1) = (1-p)\tau_{ij}(t) + \sum_{k \in \text{ant, that chose edge } (i,j)} \frac{Q}{L_k}, \quad (2.2)$$

where $P_{ij}(t)$ – the probability of the ant transition along the edge (i,j) , $\tau_{ij}(t)$ – the amount of pheromone, corresponding to the edge (i,j) , d_{ij} – the distance between node i and node j , α, β – parameters to control the influence of $\tau_{ij}(t)$ and d_{ij} , p – the pheromone evaporation coefficient, L_k – the cost of the k th ant’s path, Q is a constant.

2.2. Graph creation

The necessary precondition to apply ACO to any problem is to reformulate the problem in the terms of nodes and edges and to provide oneself with reasonable quality functional (Niu et al., 2010). One could find examples of the graphs and functionals for data mining problems in Abraham, Grosan, and Ramos (2006). For the chaotic series prediction problem the graph should represent inner structure of the attractor behind the series and be able to collect information about typical sequences pertaining to different parts of the attractor. Firstly, the analyzed series is normalized for all its elements to be in the range $[0, 1]$. Secondly, one should quantize the interval $[0, 1]$ into subintervals $[\bar{y}_i, \bar{y}_{i+1}]$, $i = \bar{1}, \bar{M}$, where $M = 1/\varepsilon$, ε describes the necessary exactitude of prognosis. Another parameter to be introduced is a maximal possible distance between two adjacent numbers of series’ elements belonged to the same sequence. Thirdly, one could formulate the search graph of the series as complete multigraph $(G = \langle V, E \rangle, |V| = M, |E| = D)$ with the number of vertices equal to the necessary number of the subintervals (M), and with each pair of vertices to be linked by D edges. A movement from i th vertex to j th one through k th edge corresponds to the fact that two elements of the time series belong to i th and j th subintervals respectively and the difference between their positions in the series is equal to k .

A set of the typical sequences is an auxiliary structure need to be introduced in order to launch the algorithm. The typical sequence $L(d_1(\delta_1), d_2(\delta_2), \dots, d_{n-1}(\delta_{n-1}), d_n)$ is characterized by subintervals’ numbers d_1, d_2, \dots, d_n and differences $\delta_1, \delta_2, \dots, \delta_{n-1}$ between positions of the sequence elements in the series.

The graph and the set of typical sequences allow one to represent correctly typical sequences frequented in the series, e.g. belonged to different parts of a strange attractor. We assume that the sequence $L(d_1(\delta_1), d_2(\delta_2), \dots, d_{n-1}(\delta_{n-1}), d_n)$ describes the part

of the series starting from observation $y[n]$ if it meets the following inequality:

$$\left| y \left[n + \sum_{j=1}^i \delta_j \right] - \frac{d_{i+1}}{N} \right| < \varepsilon, \quad \forall i = 0 \dots k, \quad (2.3)$$

3. Algorithms for series analysis and prediction

The above mentioned considerations allow ones to formulate following algorithms to encode the information about attractor behind the time series structure and its typical sequences and to predict the time series.

The algorithm for series analysis.

- Step 0: Construct the search multigraph for given values of algorithm parameters. Initialize all multigraph edges by initial equal quantity of pheromone. Create the empty set of typical sequences.
- Step 1: Place ants by random to elements of given time series and start new iteration.
- Step 2: Each ant moves to the new element of the time series and, in doing so, adds new part to its current sequence. The probability of its transition to the new time series element is equal to pheromone quantity for the respective multigraph edge.
- Step 3: Calculate the number of entries of the sequence in the time series – C_L^k .
- Step 4: Add new sequence to the set of typical sequences, if $\frac{C_L^k}{C_L^{k-1}} \geq C_{min}$, where C_{min} is the algorithm parameter. Delete the respective ant. Add pheromone to the edges of the multigraph corresponding to the newly added sequence.
- Step 5: Delete the respective ant, if $C_L^k < C_{max}$, where C_{max} is the algorithm parameter.
- Step 6: Go to the step 2, if there are any ants in the population. Go to the step 8, otherwise.
- Step 7: Evaporate pheromone for all edges of the multigraph. Go to the step 1.

The algorithm terminates, if the quantity of pheromone is not changed more than p_ε during last k iterations.

The algorithm for series prediction.

For each time moment to be prognosed $x_t, t \in (t_o; t_o + N)$, where t_o is the number of last known observation, N is the maximum possible length of the time series part occupied by the sequence.

- Step 1. Find all sequences from the set of typical sequences that correspond to known either already prognosed part of the time series and include the x_t element.
- Step 2. Single out the sequences from the set of sequences created at the step 1, if: $\forall i : 0 < i < L : |x_{t+i}^{old} - x_{t+i}^{new}| < D_{max}$, Where L is the length of time series part, occupied by the sequence, $x_{t+i}^{new}, x_{t+i}^{old}$ – the starting number of current and previous sequence entrance in the time series.
- Step 3. Clusterize the sequences from the set created at the step 2 with respect to their prognosis for x_t .
- Step 4. Single out the cluster for which standard deviation of the cluster sequences’ values and known either already prognosed part of the time series is minimal.
- Step 5. Calculate prognosed value as average value for the x_t for the sequences of the cluster.

The sequences collect information about the attractor and average, in a sense, sequences of the time series. It makes the prediction routine robust and allows one to use the predicted values as initial ones for further predictions.

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