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Circadian rhythms' modeling using artificial intelligence methods

Abstract

Paper presents a RBF and Takagi-Sugeno model for a circadian rhythm example. The data was obtained from Circadian Rhythm Laboratory at the University of South Carolina. Other aspect of this article is to show that artificial intelligence methods can find a use also in biology - in this case namely in the chronobiology which is one of the newest areas of interest in natural sciences.

Keywords: circadian rhythm, RBF networks, Takagi-Sugeno, modeling

1. Introduction

A circadian rhythm (see [1] and [5]) is a roughly-24-hour cycle in the biochemical, physiological or behavioural processes of living entities. The term „circadian" comes from the Latin *circa*, „around", and *diem*, „day". It means literally „approximately one day". The formal study of biological temporal rhythms such as daily, weekly, seasonal is called chronobiology.

Circadian rhythms allow organisms to anticipate and prepare for precise and regular environmental changes.

The earliest known account of a circadian rhythm dates from the 4th century BC in descriptions of the marches of Alexander the Great. Currently one of the most important circadian rhythms laboratories is placed in the University of South Carolina. It's director is Dr. Roberto Refinetti.

To differentiate genuinely endogenous circiadian rhythms from coincidental or or apparent ones, three general criteria must be met:

- the rhythm persist in the abscence of cues
- they persist equally precisely over a range of temperatures
- the rhythms can be adjusted to match the local time

Circadian rhythms are important in determining the sleeping and feeding patterns of all animals, including human beings. There are clear patterns of core body temperature, brain wave activity, hormone production, cell regeneration and other biological activities linked to this daily cycle.

2. Data description

The data for experiments was taken from the Circadian Rhythm Laboratory data repository at http://www.circadian.org. The files contain data on the body temperature (in [C]), metabolic heat production (in [W]) and dry heat loss (in [W]) of two rats (*Rattus norvegicus*) maintained in constant darkness at 24 [C] for a period of 4 days. Data resolution is 6 minutes, so the file contains the total number of 960 samples.

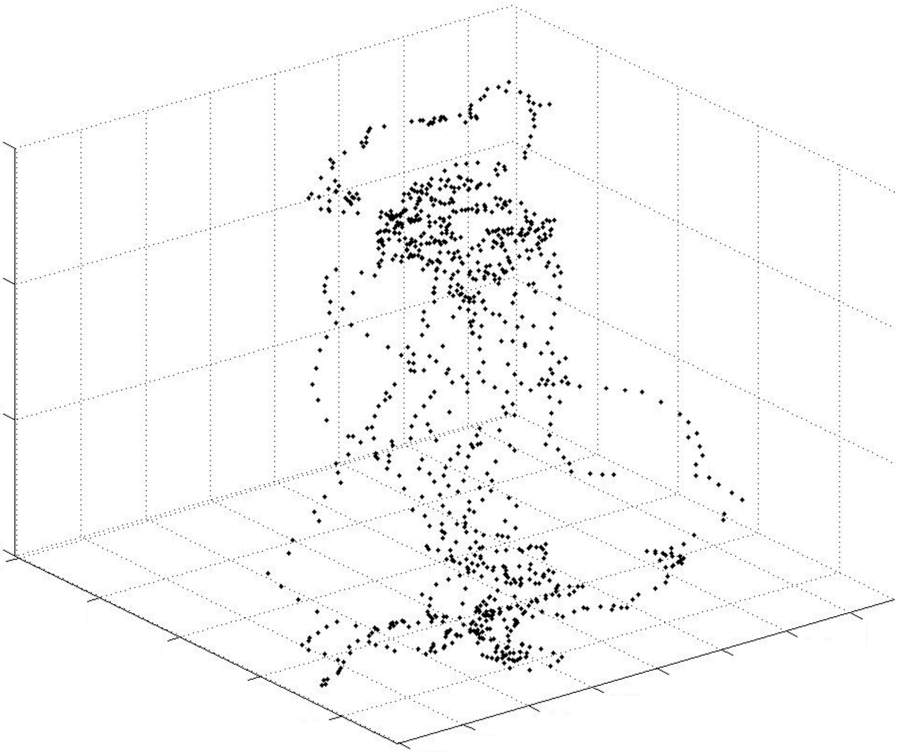

Fig. 1 Illustration of the data

The two outputs for this system of course are metabolic heat production and dry heat loss. The output is a body temperature of the rat. At Fig.1 the surface of the system is illustrated.

3. The way of build a model

Because the dimensionality is not big, there was no need to research dependencies between variables (significance indices). Besides this was not an aim of this article.

Two models using artificial intelligence methods, was built. The first is a RBF network [2] and the second one is Takagi-Sugeno model [4]. In both cases the way of processing is similar. The most important difference is that in RBF models we use Gauss functions and in the second case - a set of rules.

First step in building both models was a clusterization which was carried out using a simple method of k-means. As a result of clusterization 4 data clusters were obtained. Then it's centres were used as a centres of Gauss function and as a rules in Takagi-Sugeno model.

The use of RBF network and Takagi-Sugeno model is dictated by one of very interesting features in each method. Depending on the total number of Gauss functions (or rules) we can treat a global model as a set of local models. In particular case, when the total number of Gauss functions (or rules) is equal to the number of samples, a global model should be the same as a set of small local models for each sample (of course if we don't talk about the surface of the system, but only about the average error of the model).

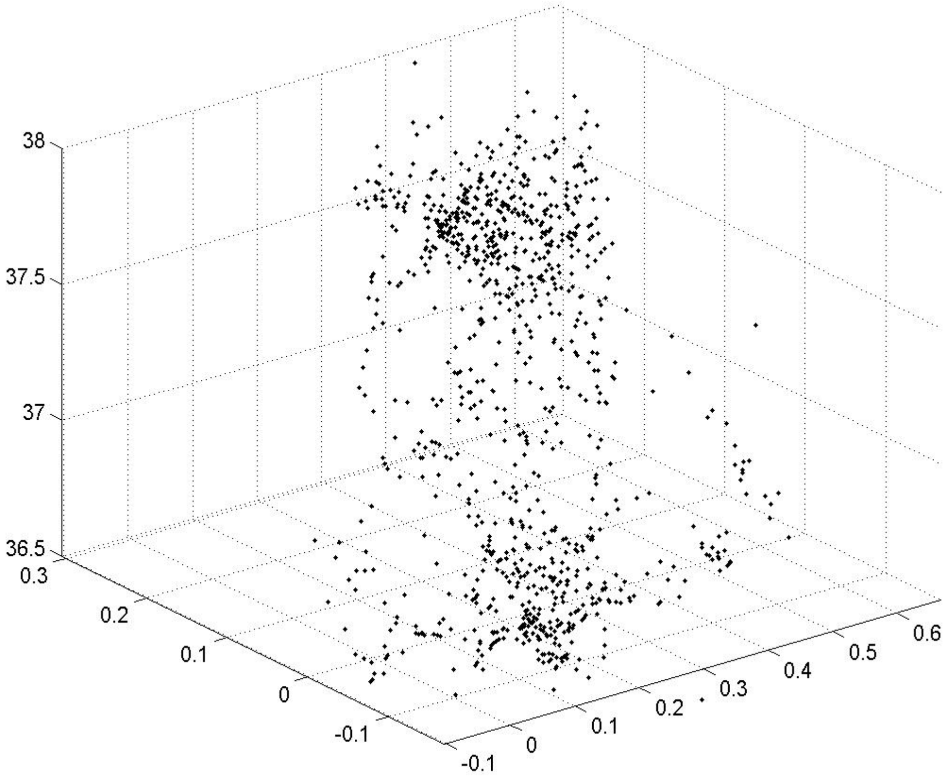

Fig. 2 Illustration of the RBF model

At the Fig.2 the result RBF model is shown. At the Fig.3 a comparison between the system and a model is illustrated.

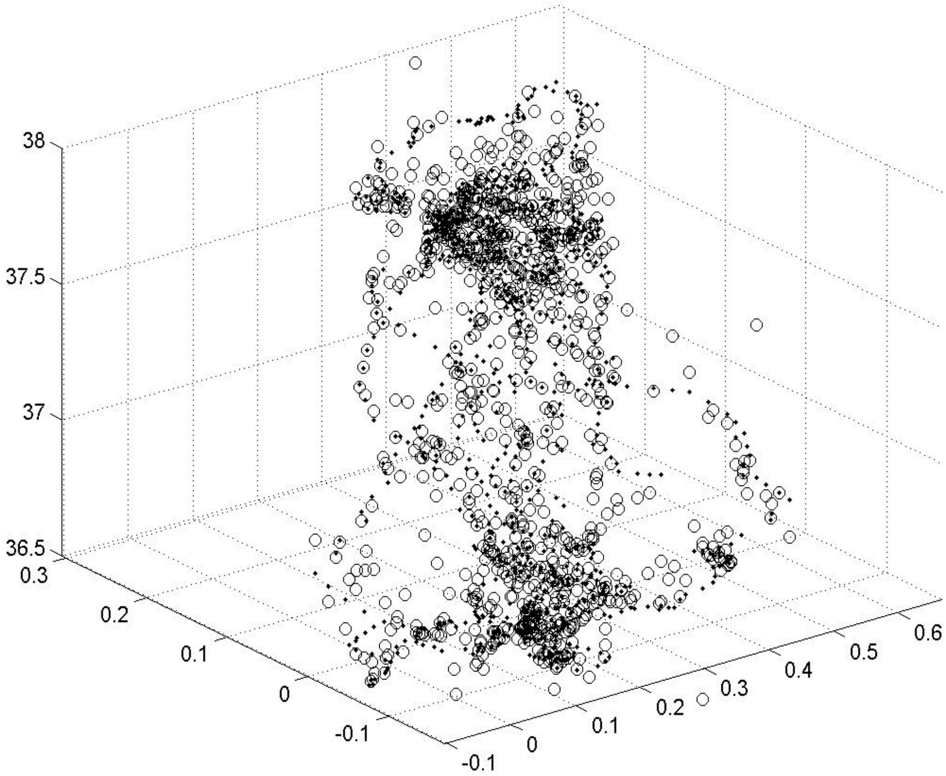

Fig. 3 A comparison between the RBF model and the system

The average error for the RBF model was at the level of 9.272% which is quite good result (we have only four clusters). The Takagi-Sugeno model was very similar and because of the publication limits the figures are not shown. The average error for the Takagi-Sugeno model was at 10.967%.

4. A comparison with other methods

To compare artificial methods with other well known methods of modelling other experiments were carried out too. Here are the results:

- Least Squares Method - average error 10.198%
- k-nn search methods (MCS, TIEC) - average error from 8.329% to 10.301%
- NCN method (described in [3]) - average error from 7.766% to 9.863%

The Least Squares Method gave a simple linear global model with similar value of the average error, but the reliability of this model is debatable.

In the case of k-nn search methods, the first step was to eliminate some excessive data and then build a local model for each data sample. It resulted with a better model with smaller average error and bigger reliability.

The last method is to build a simple local linear model for each sample. So, the reliability of this model should be statistically better. And the best results were obtained.

5. Conclusions

In this paper the ability to use artificial intelligence method in chronobiology was discussed. The total number over 1000 experiments were carried out. As a result it can be said, that artificial intelligence methods can be a usable tool also in modelling of circadian rhythms. These methods are as good as other well known methods. Of course they don't guarantee the best results - it's easy to understand why. The quality of a model is often dependent from the characteristics of a data and of course from the way of the modeling. There is no one universal method which can be used in all areas of science, life etc. This paper proves it very clearly.

References

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