SUMMARY OF Ph.D. DISSERTATION

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Title		
A Study on Biological Dat	a Modelling	

Abstract

Biological data modelling is somewhat specific because the variability of data remains significant even if the experiment were carefully designed. It is nothing more than the sign of alive that homeostasis or constancy is maintained in any of biological phenomena. It is also often the case when biological data is obtained only once as a function of time. The aim of this thesis to seek for possible ways to a good biological data modelling, which will be suggested by three case studies.

The first case study is on modelling five bird count series observed monthly. Each of the series was decomposed into three components: long trend, short trend and irregular by two step smoothing. It was clearly shown that a simple linear transformation of the long trends as a whole is a good modelling for capturing relationships between bird count series and environmental changes. It turned out that there are two bird groups, one of which increases in number as an increase of resident area and the other decreases as a decrease of farmland area. Each short trend also allows us to understand the seasonality of the behaviour of each bird.

The second case study is on modelling swimmers' speeds over the course of a male 200 m freestyle race. The model is based on a dynamical model reflecting the trade-off between drag and propulsion in swimming. It does not only fit well the data but also provide a good description of the swimming strategies of each swimmer from phase to phase in the race. An individual factor measuring how much faster or slower the individual swims relative to the average swimming speed is estimated. This factor is, as expected, closely related to the final outcome of the race.

The third case study is on modelling membrane potential of a neuron. A simple but powerful input and output system has been created by noting that each nerve cell system has two different type of synapses; chemical and electrical ones. Three phase model has been introduced for the input as well as for the spikes, which is a simplified Hodgkin-Huxley model but with an extra phase, pre-activation phase. Spike occurrences are modelled by a point process with the intensity proportional to the derivative of the input. The model would be applicable for any other membrane potential changes of a neuron as an integrated model.

An important implication of these case studies is that the models created are not on a simple extension of existing theories or models. Such models could not be obtained without careful analysis of the given data. Honest approach to the data was a key to success. As a summary, it is shown that data-driven approach is likely to open a new horizon particularly in biological data modelling because an innovative modelling is always necessary to cope with the large variability of the data.