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## Review

(of Ph.D. thesis elaborated by Ms. Helena Skutkova, M.Sc., under supervision of Prof. Ivo Provaznik, Ph.D. entitled:  
"Evaluation of Organisms Relationship by Genomic Signal Processing")

### **Introduction**

Last decade can be characterized, from the certain point of view, by the rapid growing of processing of different kinds of data. Among many kinds of data, there is significant part, which belong to biological/biomedical data. It is relatively easy to find out the reason of the mentioned above fact. With no doubts, the reason is in enormous development of both software and hardware applications in bioinformatics.

Taking into account mentioned above, it is necessary to clearly emphasize, that subject of the presented to review Ph.D. thesis is far more than just actual. It appears that it will have a lasting effect on the evolution of the art such as bioinformatics.

### **Statistics**

The submitted to review and estimation thesis has 118 pages divided into 5 chapters and is ended up with conclusions. Except that, the part including bibliography is added and it counts 185 positions, which can be treated as very extensive elaboration. The other features of the nicely elaborated thesis are satisfied as well, i.e. the thesis is equipped with lists of abbreviations, figures and tables. Therefore, from the pure editorial point of view, I have no doubts that presented elaboration has been performed by well qualified scientific worker with high capabilities giving to the reader very clear impression. The first chapter is devoted to the presentation of phylogenetic analysis of DNA sequences and can be considered as a retrospective part shortly describing the well-known and widely applied methods such as distance methods, dynamic programming and multiple alignments of sequences. Chapter two presents a set of methods for numeric representation of DNA sequences and is ended with subchapter comparing presented approaches. The goals of the estimated dissertation have been defined inside the chapter three. The chapter four can be considered as a main part of thesis as presents methods for processing

of the created previously genomic signals. Finally the chapter five is devoted to analysis and presentation of phylogenetic analysis of both gene and whole genome signals representations.

### **Substantive part of thesis**

The presented dissertation consists of two part – theoretical and experimental and generally deals with many alternative techniques design and elaborated for analysis of genetic information of different organisms. The theoretical part is devoted to elaboration and presentation of two different approaches, both necessary to evaluate the relationship between organisms based on mutual similarity of genetic information contained in their DNA sequences. The first one is a phylogenetic analysis of character based records of DNA sequences. It is well known that such approach is computationally expensive due to the need of multiple sequence alignment, however it allows evaluation of both global and local similarity of DNA sequences. On the other hand, the second approach is represented by techniques for classification of DNA sequences in a form of numerical vectors representing characteristic features of their genetic information. The disadvantage of the second approach is that a group of so called “alignment-free” methods allow for fast evaluation of global similarity but unfortunately cannot evaluate local changes. The lasting contribution of the presented dissertation is in perfect agreement with current trends concerning computational intelligence methods applications i.e. an attempt to combine positive features of different methods to create a new one, which is the best from the particular task solution findings point of view. The elaborated approach applies numerical representation similar to 1D digital signal, i.e. representation that contains specific trend along x-axis. The second, experimental part of the presented thesis deals with design of a set of appropriate tools for genomic signal processing to allow evaluation mutual similarity of taxonomically specific trends. With the application of the mutual similarity of genomic signals, the classification in the form of dendrogram is applied. It perfectly corresponds to phylogenetic trees applied in standard phylogenetics.

### **Conclusions**

Taking into account previously mentioned facts, it has to be clearly and emphatically said that both the main objective as well as all the five sub-goals have been reached producing satisfactory results.

Therefore my final conclusion is that Ms. Helena Skutkova fulfilled with oversize usual requirements concerning the quality of elaborated Ph.D. dissertation. Unfortunately, the reviewer has not been equipped with information concerning the list of dissertation author's publications but fortunately currently it is relatively easy to perform suitable check-up having access to Web of Science database. This check-up looks as follows: there are 23 publications, published in most cases in the journals from so called Thomson-Reuters list with impact factors, these publications have been 219 times cited and finally the parameters like H-index = 7 and Total Impact Points = 40,17. At the level of application to obtain a Ph.D. degree the scientific achievements of Ms. Helena Skutkova are outstanding.

The only possible conclusion, in the light of all the above mentioned facts is to vote "for" granting to Ms. Skutkova the Ph.D. degree and this is my recommendation. Additionally, the board responsible for Ph.D. granting procedure may consider to grant mentioned Ph.D. degree with distinction.

A handwritten signature in blue ink, appearing to read "John".