SUBJECT: Bioinformatics methods in analysis of medical databases

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SCIENTIFIC DISCIPLINE: biomedical engineering

DESCRIPTION: Nowadays, there is a very rapid increase in medical data worldwide. Patients are described by several hundreds, or in the case of genetic data - thousands/millions of numbers. In practice, however, individual measurements (features) are often evaluated and dependencies between them are overlooked. Selection of features associated with a specific clinical outcome is an important problem. The aim of the planned PhD thesis is to use a variety of bioinformatics and statistical methods to analyze large and complex medical databases.

Anthropometric, demographic data, biomarkers derived from blood, results of therapeutic interventions, genetic and other data will be analyzed in patients with various diseases. In addition to the typical statistical analysis, it is planned to use bioinformatics methods (as *lasso* - least absolute shrinkage selection operator, *SVM* - support vector machine and others) in order to select a set of features related to a specific clinical problem and to perform patients classification. Interaction of features will be investigated. The selection of appropriate method to analyze the medical database is a key priority. *Machine learning* type of method can be beneficial for some datasets, whereas *linear regression* or *analysis of correlation* will be the most suitable for others [1-2].

Systematic and comprehensive approach to medical databases, appropriate visualization, contribute to proper clinical interpretation, help to diagnose and optimize therapy of a single patient.

The project will be carried out at IBBE PAS, in the international cooperation with Karolinska Institute (Stockholm).

BIBLIOGRAPHY:

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