

THEORETICAL BASIS OF NEW METHODOLOGY OF MATHEMATICAL-STATISTICAL DECISION MAKING WITH THE HELP OF BIOMARKERS FROM MASS SPECTRA

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There are at disposal N_S mass spectra for the group of N_S provably *sick* patients, N_H mass spectra for the group of N_H provably *healthy* patients and finally N_E mass spectra for patient whose state of health is being *examined*. With this quite general data a doctor in clinic should make decision about null hypothesis

H_0 : patient is healthy

(against *alternative* that *patient is not healthy*) as correctly as possible. In addition this doctor should make decision about miscellaneous null hypotheses

H_0 : patient is healthy in

$$\langle x_{j_1}; x_{j_2} \rangle \cup \langle x_{j_3}; x_{j_4} \rangle \cup \dots \cup \langle x_{j_{2m-1}}; x_{j_{2m}} \rangle$$

where $\langle x_{j_1}; x_{j_2} \rangle \cup \langle x_{j_3}; x_{j_4} \rangle \cup \dots \cup \langle x_{j_{2m-1}}; x_{j_{2m}} \rangle$ is unified set of m intervals on the whole spectral range respecting single biomarkers, or respecting (certain biologically autonomous) groups of biomarkers. The proposed *Theoretical basis of new methodology of mathematical-statistical decision making with the help of biomarkers from mass spectra* enables to solve these thorny problems. The *new methodology*, as opposed to the methods (1,2) used so far, solves the problems universally.

Nowadays this proposal is discussed in detail through e-mail with firms Geneva Bioinformatics S.A. (Prof. Ron D. Appel, Ph.D. and Dr. Frdrique Lisacek, Ph.D.) and Bruker Daltonik GmbH in Bremen (Dr. Wolfgang Pusch, Ph.D.).

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