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BIOINFORMATICS — FOREWORD

Bioinformatics is a relatively new scientific discipline on the borderline between biology, informatics, medicine, chemistry and physics. This term appeared in the scientific literature for the first time in 1993, and already in 2008 more than 1200 scientific biomedical publications (according to Medline database, www.ncbi.nlm.nih.gov) claimed bioinformatics applications.

Bioinformatics, identified with computational biology by some, can be defined as science that solves biological problems by computational means. This issue of "Kosmos" includes reviews from various fields of bioinformatics, a survey of these shall substitute for an in-depth definition of this novel branch of science.

Traditionally, since the 70-ties of the XXth century, computational biology dealt with analyses of protein and nucleotide sequences. In this issue, I. MAKAŁOWSKA presents the novel knowledge on gene structure and history that can be gained by whole genome bioinformatic analysis. M. KASPRZAK and A. ŚWIERCZ discuss computational methods used in data processing in order to assemble full genomic sequences. S. CEBRAT and co-workers present interesting conclusions on genome and its evolution obtained by simple modeling.

Another historical field is structural bioinformatics dealing with analysis and prediction of three-dimensional structures of biological macromolecules. W. Nowak discusses recent trends and successes of molecular dynamics methods used to simulate macromolecular motions. Articles by M. PASENKIEWICZ-GIERULA and S. FILIPEK cover structural analysis in the difficult but biologically essential cases of macromolecules within the cell membrane.

Computational methods are also applied to larger biological systems — metabolic pathways, networks of related genes, whole cells and groups of cells. Applications of this kind are addressed by papers from the borderline between bioinformatics and systems biology. M. DĄBROWSKI and B. KAMIŃSKA discuss studies of gene expression regulation mechanisms. J. BŁAŻEWICZ and co-workers describe applications of Petri nets to biological process modeling, and P. PAWŁOWSKI addresses purported scale-free properties of biological networks. Ł. GŁOWACKI writes on methods of assessing biological diversity in ecosystems.

Practical applications of bioinformatics are presented by J. BŁAŻEWICZ and P. ŁUKASIAK who talk about a genetic vaccine support system and by K. PAWŁOWSKI who covers applications in the drug discovery process.

Bioinfomatics part of this issue of "Kosmos", organized by members of the recently formed Polish Bioinformatics Society (www.ptbi.org.pl), offers a broad, though by necessity not complete, overview of today's bioinformatics, with special focus on areas represented in Poland. We hope other fields of bioinformatics represented in Poland will soon be published in "Kosmos". It gives also an opportunity to propose to the scientific community a Polish vocabulary for disciplines that are not often addressed in the Polish language.

Krzysztof Pawłowski