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Institute of Information and Computational Technologies

ABSTRACTS

International Conference
"Computational and Informational Technologies
in Science, Engineering and Education"

2015, Almaty, Kazakhstan

EDITORIAL BOARD

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Yu.I. Shokin, B.T. Zhumagulov, T.S. Ramazanov,
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Abstracts of the International Conference "Computational and Informational Technologies in Science, Engineering and Education" (September 24-27, 2015). – Almaty: Қазақ университеті, 2015. – 296 p.
ISBN 978-601-04-1389-4

The book contains abstracts of the participants of the International Conference "Computational and Informational Technologies in Science, Engineering and Education". The proceeding of the Conference will be beneficial for specialists in the field of Mathematics and its applications, as well as for students, undergraduates, doctoral students majoring Computational and Informational Technologies.

Dedicated to the bright memory of the Kazakh outstanding scientist, doctor of physical and mathematical sciences, professor, laureate of the State Prize of the Republic of Kazakhstan in science and technology Nargozy Tursinbaevich Danaev, the specialist of computational hydrodynamics, who made a great contribution into the development of mathematics in Kazakhstan, talented organizer and teacher.

PREFACE

International Scientific and Practical Conference "Computational and Information Technologies in Science, Engineering and Education" has a long and rich tradition and has been regularly held since 2002.

Historically, the conference was organized in close cooperation between Russian and Kazakh scientists and the general area of discussion was the most advanced achievements in the field of computational technology.

Later it expanded the geography of the conference and now it is attended by leading scientists from Europe, the USA, Japan, India, Turkey, etc.

The purpose of the conference is dissemination of new knowledge and scientific advances among the participants. A special feature of this conference is to involve young scientists and an assessment of their scientific achievements through the interaction of the leading scientific schools of the two countries. Participating in the CITech formed a whole galaxy of a new generation of young scientists that are currently conducting serious research work.

In different years CITech was held in Almaty (2002, 2004, 2008, 2015), Pavlodar (2006) and Ust-Kamenogorsk (2003, 2013). Personal friendship of scientists from the Novosibirsk Scientific school with prof. Smagulov Sh., Danaev N., Shokin Yu., Monakhov N., Zhumagulov B. and many others has played an important role in the formation of stable traditions for organizing and conducting CITech. Unfortunately, some of them are no longer among us, but we will always remember their contribution to science and education and keep their unforgettable image in our hearts.

The proceeding of the Conference will be beneficial for specialists in the field of Mathematics and its applications, as well as for students, undergraduates, doctoral students majoring Computational and Informational Technologies.

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Section 1.
HIGH PERFORMANCE
COMPUTING

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Parallelization of algorithm of prediction of miRNA binding sites in mRNA on the cluster computing platform

After opening of an important role of microRNA (miRNA) in regulation of an expression of genes the problem of a prediction of binding sites of miRNA with matrixRNA (mRNA) has arisen. Some programs which predicted binding sites of miRNA were created. However many of them had unreasonable restrictions for search of binding sites. Earlier it was claimed that binding sites are localized only in 3'UTR. It was established later that binding sites are localized in 5'UTR and CDS. Other programs were based on identification of binding sites with the obligatory requirement to have complementary interactions of a guanine (G) and an adenine (A) in a site of "seed" which corresponds 5'-end of miRNA. Many such programs predicted a large number of false positive sites and did not allow revealing the binding sites located in 5'UTR and CDS. On this and other reasons it is inexact the beginning of binding sites was established and incorrectly schemes of interaction of miRNA with mRNA were formed. Now, in a genome of the human more than 2500 miRNAs are known and it is necessary for each of them to find target genes among 30 thousand genes of the human. Large volume of calculations demands creation of the program, allowing processing these huge data files. We created the MirTarget program which has no shortcomings given above and with big reliability finds binding sites of miRNA with mRNA.

During the research by authors the following results were received: the mathematical model of optimum process of scanning of genes and miRNA sequences is developed; the algorithm of scanning of genes with miRNA with one gap in miRNA and maximum (in a percentage ratio) free energy is developed and analyzed at coincidence of miRNA and a gene site on the basis of complementarity properties; the constructed algorithm of scanning of genes with miRNA is parallelized on the computational cluster with use of MPJ tools - the MirTarget program; the assessment of overall performance of the parallelized algorithm on the cluster computing platform with consecutive algorithm is performed when processing large volumes of data; the developed program was used for performing researches by search of binding sites of miRNA with matrix RNA (mRNA).

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ҒЫЛЫМИ БАСЫЛЫМ
Халықаралық конференция
«Ғылымдағы, техникадағы және білім берудегі
есептеулер мен ақпараттар технологиясы»

ИБ №8513

Басуға 19.09.2015 жылы қол қойылды. Формат 60x84 1/8.

Көлемі 24,7 б. т. Тапсырыс № 2616. Таралымы 160 дана.

Әл-Фараби атындағы Қазақ ұлттық университетінің

Алматы қаласы, әл-Фараби даңғылы, 71.

«Қазақ университеті» баспа үйі баспаханасында басылды.

«Қазақ университеті» баспа үйі.