CHRONICLE

Second Moscow Conference on Computational Molecular Biology MCCMB'05

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Abstract—From first principles, a simple model was derived to describe the reduplication of the molecular structure as a sequence of stages whose probabilities can be estimated using the general theory of molecular transformations. It was shown that the genetic information transfer in time (the phenomenon of life) for a long period is impossible without simultaneous "phenomenon of death" and that taking into account the features of transition states in reactions (quantum beats) leads to self-oscillations.

The Second, now regular, Moscow Conference on Computational Molecular Biology MCCMB'05 was held in Moscow on July 18–21, 2005. A part of the proceedings of this conference is published in this issue of *Biophysics*, and one more collection of meeting papers will come out in the *Journal of Bioinformatics and Computational Biology*. The organizers of the conference were the Faculty of Bioengineering and Bioinformatics, Moscow State University; the Institute for Information Transmission Problems, Russian Academy of Sciences; the Scientific Council on Biophysics, Russian Academy of Sciences; and the International Foundation of Technology and Investment. Financial support was provided by the Russian Academy of Sciences, the Russian Foundation for Basic Research, the French National Institute for Research in Computer Science and Control (INRIA, France), and the Ludwig Institute for Cancer Research (LICR, USA). The participants in the conference were about 200 scientists from all over the world (Canada, France, Germany, Israel, Italy, Japan, Kazakhstan, Poland, Portugal, Republic of Korea, Republic of South Africa, Serbia, Singapore, Sweden, Switzerland, Ukraine, United Kingdom, and United States) and many Russian cities (Birobidzhan, Krasnoyarsk, Moscow, Novosibirsk, Pushchino, Saratov, St. Petersburg, Vladivostok, and Yekaterinburg).

In addition, conference events were visited by students and graduate students of the Faculty of Bioengineering and Bioinformatics and other faculties of the Moscow State University.

The main topics of the conference were the following:

comparative genomics and proteomics;

proteins: structure, evolution, and interactions;

large-scale analysis and genome annotation;

gene recognition and alternative splicing;

systems biology;

molecular evolution, in particular, evolution of regulation and protein families;

bioinformatics algorithms.

The invited speakers delivered lectures on bioinformatics and allied areas of biology. In particular, D. Hatfield (USA) described the functions of selenium-containing proteins, and D. Papatsenko (USA) characterized the early stages of *Drosophila* development and the role played in them by transcription factors. The results of structural studies were presented by A. Finkelstein (Russia) and M. Frank-Kamenetsky (USA).

The theory of molecular evolution was touched on by A. Kondrashov (USA) in his lecture on the strength of stabilizing selection in human genes; A. Grigoriev (Germany), who characterized the role of the domain structure in protein evolution; S. Kumar (USA), who told how confidence limits should be placed on the molecular age of the human–chimpanzee divergence; and J. Bujnicki (Poland), who described the evolution of restriction endonucleases. A noticeable place was occupied by the discussion of genome annotation problems. The keynote was sounded by A. Osterman (USA), who proposed a concept of sequential experimental verification of bioinformatic predictions, with methods for making such predictions described by D. Frishman (Germany) and I. Dubchak (USA). An allied area of analysis of on-chip gene expression was touched on by M. Ochs (USA).

Regulatory interactions were discussed by E. Alm (USA), who characterized their role in the operon formation in bacterial genomes; L. Mirny (USA), who proposed a mechanism whereby transcription factor search for their binding sites on DNA; and M. Galperin (USA), who described protein domains involved in protein–protein interactions in signal transduction networks. Probabilistic problems in the challenge of regulatory signal recognition were reviewed by M. Regnier (France).

Some of the invited speakers presented the works of the international Ludwig Institute for Cancer Research. Yao Chen (USA) spoke about identification of new cancer/testis-antigen genes by massively parallel signature sequencing; W. Hide (RSA), on-chip gene expression data analysis; and A.T. de Vasconcelos (Brasil) and D. Kuznetsov (Switzerland), databases and genome annotation.

The complete conference program is available in the Internet (http://mccmb.belozersky.msu.ru/2005/Program.html). The conference has demonstrated the high level of Russian bioinformatics. Particularly noteworthy is the special role of representatives of the Russian scientific Diaspora—our compatriots from the whole world, from the United States and Canada to the Western Europe, Israel, and even Japan. Many of the papers presented in the conference were co-authored with Russian scientists, which is indicative of the existence of the Russian school of bioinformatics. It seems that such conferences, which favor contacts between scientists form different countries and allow young researchers to see the modern lines of development of bioinformatics and simply to communicate with leading scientists from the world over, are among the most important mechanisms of support of the basic science in Russia.