



МИНИСТЕРСТВО ЭКОНОМИКИ РОССИЙСКОЙ ФЕДЕРАЦИИ
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To the faculty search committee

I am happy to support the application of Dmitry Papatsenko for a position in your department. My research interests lie in various fields of computational biology, including reconstruction of regulatory circuits in cells based on comparison between genomes. Till recently this could be done almost exclusively for prokaryotic genomes, where regulatory signals are rather long and can be identified by comparative analysis of relatively short gene upstream regions.

The problem appeared too complicated in most eukaryotic systems where the signals are shorter and the intergenic regions are much longer. However, now it becomes clear that the problem can be approached in this case as well, owing to the tendency of identical sites, or sites recognized by a very limited number of proteins, to cluster within regulatory segments, e.g. enhancers. Dmitry was among the few researchers who suggested this idea (as a private communication) as far as four years ago. Although my personal contacts with Dmitry were sparse, I followed the development of this idea almost from its beginning and helped to prepare the first manuscript for publication in *Genome Research*. Dmitry gave a very successful talk at the Moscow Seminar on Computer Genetics that I chair since 1993.

Dmitry belongs to a rare type of computational biologists who came from the wet lab and did not cancel entirely their experimental work. They tend to consider *in silico* calculations as a basis for immediate follow-up experiments. Although Dmitry has obtained sufficient proficiency in mathematical and computational issues to work as an independent computational biologist, his research is always directed towards very practical issues of transcription regulation and organism development. To my opinion, this approach is the most promising for future progress of molecular biology and in its medical applications. The persistency with which Dmitry can bring forward an original idea, and his ability to do that in parallel with his experimental studies in a field of molecular genetics, is one of his most remarkable qualities.

Dmitry and his co-workers started from examining the original experimental papers and created two compilations, of experimentally verified binding sites for several *Drosophila* transcription factors, and of regulatory regions involved in early stages of *Drosophila* development. They used these data and their experimental knowledge to design two programs, *ScanSeq* that locates candidate binding sites for (unknown) transcription factor(s) within a regulatory segment, and *CLUSTER* that identifies regulatory segments within genome loci. *ScanSeq* has been successfully reported at several conferences and published in *Genome Research*, and two more manuscripts describing further development of this study are submitted for publication.

In my lab we use both *ScanSeq* and *CLUSTER* to study regulatory segments in prokaryotes and lower eukaryotes. Although in prokaryotes the organization of regulatory regions usually is less complex, several regulatory system, which are very important from the practical point of view, are organized in a way similar to that of eukaryotes. Both *ScanSeq* and *CLUSTER* have demonstrated their efficiency in this case.

I believe that Dmitry will prosper as an independent researcher in both experimental and computational biology. Among his advantages are his research motivation, his very independent way of thinking and his persistency in pursuing his original research objective. However, this independence does not interfere with his ability to work in a group and his willingness to share his ideas as well as his unpublished data and software.

My sporadic direct communication with Dmitry does not allow me to characterize him on a personal level. However, he appears to be a nice person who can motivate students with his scientific enthusiasm.

Overall, I believe that, Dmitry is an excellent choice for an independent position, and I recommend him in the strongest terms. If you need more information, please feel free to contact me directly at misha@imb.ac.ru or +7-(902)-6092971.

Sincerely



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