BERKELEY LAB

Michael B. Eisen, Ph.D.

Life Sciences Division
Lawrence Berkeley National Lab

Department of Molecular and Cell Biology
University of California Berkeley

November 15, 2002

To the members of the search committee,

I am writing in support of the application of Dmitri Papatsenko for a faculty position in your department. I do not know Dmitri personally, currently a postdoctoral fellow in Claude Desplan's lab at NYU, aside from some brief email correspondences. However, he has asked me to provide an independent assessment of his work and his potential, especially regarding the computational aspects of his research. In the Desplan lab, Dmitri has been working on understanding how *cis*-regulatory information is encoded in the *Drosophila* genome, and he has recently made a series of noteworthy contributions to the field.

Dmitri's most recent paper, in the March 2002 issue of *Genome Research*, described a computational method to identify functional transcription factor binding sites in *cis*-regulatory regions in the *Drosophila* genome. The problem is an important one. There is limited experimental data on transcription factor binding specificities, even for an intensively studied organism like *Drosophila*, and researchers interested in *cis*-regulation will be reliant on computational methods to infer these specificities for the foreseeable future.

Dmitri's method (SCANSEQ) is based on the observation that binding sites for a given transcription factor are often clustered within regulatory regions, especially within regions controlling genes involved in pattern formation in the early *Drosophila* embryo. Starting with only the sequence of a regulatory region, SCANSEQ builds models of redundant motifs and predicts occurrences of these motifs in the region being analyzed. The approach is well-conceived, has several original aspects, and, most importantly, appears to be effective.

SCANSEQ, and the paper describing it, are nice examples of how the development of rigorous computational methods can be guided by a solid and nuanced understanding of the relevant biology – something still fairly rare in computational biology. Dmitri's more recent, as of yet unpublished, work on detecting uniform clusters of transcription factor binding sites follows a similar vein and shows a continued interest in and knack for pursuing interesting biological problems by developing, deploying and evaluating new computational approaches and methods. Members of my group (which is interested in very similar questions) follow his work closely, have discussed his papers extensively, and have been positively influenced by his ideas and methods.

I have also been impressed with Dmitri's appreciation for the importance of experimental data in guiding the development of computational methods and testing their effectiveness. He spent considerable time assembling and integrating data on experimentally characterized *Drosophila cis*-regulatory regions and transcription factor binding sites, and has used this data extensively. This publicly available resource makes his computational work more insightful and relevant, and has been of immense value to the members of my lab who are working on this system.

Mailstop 84-171, Lawrence Berkeley National Lab, One Cyclotron Road, Berkeley, CA 94720
Email: MBEISEN@LBL.GOV Voice: (510) 486-5214 FAX: (786) 549-0137

Finally, unlike so many other biologists with computational talents, Dmitri has not leapt onto the job market prematurely. Rather, he has taken the time to develop his skills and to mature as a scientist, and this maturity shows in his work and will contribute significantly to his future successes.

Not having had the opportunity to interact with Dmitri personally, and with no knowledge of him other than that gleaned from his papers, it would be unfair of me to fully project his potential for an independent research career or to comment on the type of colleague he would make. However, from where I sit, he seems like an excellent candidate who mixes computational talents and innovation with a well-developed understanding of the biology of the system he is studying. If he were to apply for a position at Berkeley, and if he has superlative recommendations from Desplan and Small who know him and his work better than I do, I would certainly lobby hard for him to be interviewed.

I hope these comments are useful. Good luck with the search. Please feel free to contact me if you have any questions.

Sincerely,

Michael Eisen

Michael B. Eisen

Scientist
Department of Genome Sciences
Life Sciences Division
Lawrence Berkeley National Lab

Assistant Adjunct Professor of Genetics and Development
Department of Molecular and Cell Biology
University of California Berkeley