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## BIOGRAPHICAL SKETCH

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NAME Pavel A. Pevzner	POSITION TITLE Ronald R. Taylor Chair Professor of Computer Science		
CURRENT AFFILIATION			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Moscow Technological Transport Institute	M.S.	1979	Applied Mathematics
Moscow Institute of Physics and Technology	Ph.D.	1985-1988	Mathematics & Physics
University of Southern California	postdoc	1990-1992	Bioinformatics

List of five recent publications by the candidate:

- Tsur, S. Tanner, V. Bafna, **P.A. Pevzner**. (2005) Identification of post-translational modifications by blind search of mass spectra. *Nature Biotech.*, **12**, 1562-7
- S. Tanner, H. Shu, A. Frank, L.C.Wang, E. Zandi, M. Mumby, **P. Pevzner**, V. Bafna (2005) InsPecT: identification of posttranslationally modified peptides from tandem mass spectra. *Anal Chem.* **77**, 4626-39.
- A. Frank, **P. Pevzner** (2005) PepNovo: de novo peptide sequencing via probabilistic network modeling. *Anal Chem.* **77**, 964-73
- N. Bandeira, D. Tsur, A. Frank, **P.A. Pevzner** (2007) Protein identification by spectral networks analysis. *Proc Natl Acad Sci U S A.* **104**:6140-5
- N. Bandeira, K.R. Clauser, **P.A. Pevzner** (2007) Shotgun protein sequencing: assembly of peptide tandem mass spectra from mixtures of modified proteins. *Mol Cell Proteomics.* **6**, 1123-34.

Please indicate in 200 words or less the reason(s) why you would be a suitable candidate for the HUPO Council elections.

For the past 20 years my field of research has been bioinformatics. Within this period computational molecular biology has been transformed from a rather obscure discipline into an area that making a digital revolution in biology. I contributed to many new areas of bioinformatics and in some areas I was lucky enough to be one of the first soldiers to arrive on the battlefield. Below I will sketch a few problems I have studied in the area of computational proteomics .

Together with my postdoc Vlado Dancik I developed the first machine learning approach to de novo peptide sequencing (Dancik et al., 1999) that is now a part of the SpectrumMill software distributed by Agilent. This paper has become the most cited publication on de novo peptide sequencing. With my student Ari Frank we developed PepNovo software (Frank and Pevzner, 2005) that is among the most accurate de novo peptide sequencing algorithms available today. In 2000 I developed the first approach to "blind" identification of post-translational modifications (Pevzner et al., 2000, 2001). This approach recently resulted in MS-Alignment software that enables blind PTM searches (Tsur et al., 2005). In another recent development we proposed the first approach to shotgun sequencing of entire proteins as opposed to sequencing of short peptides that dominates mass-spectrometry approaches today (Bandeira et al., 2004, 2007, 2007). In collaboration with Genentech scientists we used this approach for fully automated sequencing of antibodies.

I authored a graduate textbook "Computational Molecular Biology: An Algorithmic Approach" and an undergraduate textbook "Introduction to Bioinformatics Algorithms" (jointly with Neil Jones). The latter books was used as a required text in over 120 universities worldwide.

