Curriculum Vitae – Maxim Shatsky

Home address: Kadesh Barnea 3-18, Tel-Aviv, 69986, Israel Tel. No. (972)-54-5555-329 E-mail: <u>maxshats@tau.ac.il</u> Family Status: married, one child. Date and place of birth: 3/9/76 Moscow, Russia Immigration date to Israel: 1994

EDUCATION:

- 1995-1998B.Sc. in Computer Science and Mathematics, Tel-Aviv University1998 2001M.Sc. magna cum laude Tel Aviv University
- 1998-2001 M.Sc., magna cum laude, Tel-Aviv University. Title of M.Sc. thesis: Alignment of flexible protein structures. Name of Supervisor: Prof. Haim Wolfson and Prof. Ruth Nussinov.
- 2001-present Ph.D. student, Computer Science Tel-Aviv University Topic of thesis: Efficient Algorithm for the Protein Structural Analysis Name of Supervisor: Prof. Haim Wolfson and Prof. Ruth Nussinov.

WORK EXPERIENCE:

1998-99 Art-In Internet Technologies & Electronic Commerce Ltd. Tel-Aviv. Software Engineer.

TEACHING EXPERIENCE:

2001-Present Teaching Assistant in Tel-Aviv University. Courses: TA in Structural Bioinformatics, Computer science workshop on structural bioinformatics, Bioinformatics Laboratory.

INTERSHIPS AND SUMMER SCHOOLS:

Internship at Weizmann Institute of Science, department of Particle Physics.
Project subject: Applying artificial Neural Networks in high energy physics.
CIME "Mathematical Methods for Protein Structure Analysis and Design" summer school, Martina Franca, Italy.

AWARDS AND SCHOLARSHIPS:

2000	Award for excellence in M.Sc. studies.
2003-2006	Complexity Science Center PhD scholarship.
2003	Wolf scholarship for excellence in PhD studies.
2005	Award for excellence in Ph.D. studies.
2005	Best Structural Poster award at RECOMB 2005

TALKS AT CONFERENCES AND WORKSHOPS:

- 2000 8th International Conference on Intelligent Systems for Molecular Biology, San Diego, CA (ISMB'00)
- 2001 Annual Israeli Bioinformatics Symposium, Tel Aviv Univ. (AIBS'01)
- 2002 2nd Workshop on Algorithms in Bioinformatics, Rome, Italy (WABI'02)
- 2003 Weizmann Institute of Science, Bioinformatics Workshop Series 2002-2003
- 2005 Fourth Workshop on Geometric Computing, Nachsholim, Israel
- 2005 9th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2005) Cambridge, MA
- 2005 The 1st International Symposium on Computational Life Science, Konstanz, Germany (CompLife '05)

LIST OF PUBLICATIONS

- 1. M. Shatsky, Z. Fligelman, R. Nussinov, H.J. Wolfson. Alignment of Flexible Protein Structures. Proc. 8th International Conference on Intelligent Systems for Molecular Biology (ISMB'00), 329-343, The AAAI press, 2000.
- B. Ma, M. Shatsky, H.J. Wolfson, R.Nussinov. Multiple diverse ligands binding at a single protein site: A matter of pre-existing populations. Protein Sci., 11, 2002, 184-197.

- 3. M. Shatsky, R. Nussinov, H. Wolfson. Flexible protein alignment and hinge detection. Proteins: Structure, Function, and Genetics, 48:242-256, 2002.
- 4. M. Shatsky, H.J. Wolfson, R.Nussinov. MultiProt a Multiple Protein Structural Alignment Algorithm. Workshop on Algorithms in Bioinformatics, Springer Verlag, Lecture Notes in Computer Science 2452: 235-250, 2002.
- 5. D. Schneidman-Duhovny, Y. Inbar, V. Polak, M. Shatsky, I. Halperin, H. Benyamini, A. Barzilay, O. Shem-Tov, N. Haspel, R. Nussinov, H. J. Wolfson. Taking Geometry to its Edge: Fast Unbound Rigid (and Hinge-bent) Docking. Proteins: Structure, Function, and Genetics, 2003, 52(1), 107-112.
- 6. M. Shatsky, R. Nussinov, H. Wolfson. FlexProt: Alignment of Flexible Protein Structures Without a Pre-definition of Hinge Regions. Journal of Computational Biology, 2004, 11(1), 83-106.
- M. Shatsky, R. Nussinov, H. Wolfson. A Method for Simultaneous Alignment of Multiple Protein Structures. Proteins: Structure, Function, and Genetics, 2004, 56(1), 143-156.
- 8. M. Shatsky, O. Dror, D. Duhovny, A. Shulman, R. Nussinov, H. Wolfson.BioInfo3D: A Suite of Tools for Structural Bioinformatics. Nucleic Acid Research 32, 503-507, 2004.
- H. Wolfson, M. Shatsky, D. Duhovny, O. Dror, A. Shulman, B.Ma, R. Nussinov. From structure to function: methods and applications. Curr Protein Pept Sci. 2005 Apr;6(2):171-83.
- M.Shatsky, A.Shulman-Peleg, R.Nussinov, H.Wolfson. Recognition of Binding Patterns Common to a Set of Protein Structures. RECOMB 2005, Lecture Notes in Computer Science, Springer, vol. 3500, pp. 440-455.
- 11. A.Shulman-Peleg, M.Shatsky, R.Nussinov, H.Wolfson. MAPPIS: Multiple 3D Alignment of Protein-Protein Interfaces. M.R. Berthold et al. (Eds.): CompLife 2005, Lecture Notes in Computer Science, Volume 3695, pp. 91-103.
- 12. M.Shatsky, R.Nussinov, and H.J. Wolfson. Optimization of Multiple Sequence Alignment Based on Multiple Structure Alignment (to appear in Proteins: Structure, Function, and Bioinformatics).
- 13. M.Shatsky, A.Shulman-Peleg, R.Nussinov, H.Wolfson. The Multiple Common Point Set Problem and its Application to Molecule Binding Pattern Detection (to appear in Journal of Computational Biology).