Pupko Tal, Ph.D.

CURRICULUM VITAE

Faculty:	The George S. Wise Faculty of Life Sciences
School:	The Shmunis School of Biomedicine and Cancer Research
	Phone: 972-3-640-7683 Fax: 972-3-642-2046
E-mail:	talp@tauex.tau.ac.il
Home Address:	21 Haim Levanon Street, Tel-Aviv, 69975, Israel
Date and Place of Birth:	April 14, 1972, Israel
Zahal (Israeli) Military Service	1990-1993. Rank: Captain. Honor officer at officer course

EDUCATION

Period of Study	Name of University	Subject	Degree	Date of Award
1988-1990	Tel Aviv University, Israel	Life Sciences	B.Sc.	Oct. 15, 1990
1993-1995	Tel Aviv University	Biochemistry	M.Sc. *magna cum laude*	Sept. 1, 1995
1995-1997	Tel Aviv University	Mathematics	B.Sc. *summa cum laude*	Feb. 1, 1998
1995-2000	Tel Aviv University	Zoology	Ph.D.	June 5, 2001

Title Of Master's Thesis	The effects of lyophilization on regular and bioadhesive liposomes
Names of Supervisor	Prof. Rimona margalit
Title of Doctoral Dissertation	Algorithmic improvements and biological applications of maximum-likelihood methods of reconstruction of ancestral amino-acid sequences with emphasis on the problem of identification of homoplasious sites indicative of positive Darwinian selection
Names of Supervisor	Prof. Dan Graur

FURTHER STUDIES

Period	Name of Institution	Department	Rank / Function
2000-2002	The Institute of Statistical Mathematics, Tokyo, Japan (Prof. Masami Hasegawa)		Postdoctoral fellow
2002-2003	Florida State University. Tallahassee, FL, USA (Prof. David Swofford)	School of Computational Science & Information Technology	Postdoctoral fellow
2003-2006	Tel Aviv University	Department of Cell Research and Immunology	Lecturer
2006-2008	Tel Aviv University	Department of Cell Research and Immunology	Senior Lecturer
2008-2013	Tel Aviv University	Department of Cell Research and Immunology	Associate Professor
2010-2011	National Evolutionary Synthesis Center (NESCent), Durham, NC, USA		Sabbatical Scholar (Associate Professor)
2016-2017	College of Agricultural Sciences, Oregon State University, Corvallis, OR, USA	Department of Botany and Plant Pathology	Sabbatical Scholar (Full Professor)
2013-	Tel Aviv University	The Shmunis School of Biomedicine and Cancer Research (from 2017-2020: School of Molecular Cell Biology & Biotechnology ; Before 2017, Department of Cell Research and Immunology)	Full Professor

PUBLICATIONS

H-index (Google Scholar 53, ISI Web of Knowledge 46).

REFEREED ARTICLES

1. Pupko, T., and D. Graur. 1999. Evolution of microsatellites in the yeast *Saccharomyces cerevisiaei*: role of length and number of repeated units. Journal of Molecular Evolution 48(3): 313-316.

2. Pupko, T., I. Pe'er, R. Shamir, and D. Graur. 2000. A fast algorithm for joint reconstruction of ancestral amino-acid sequences. Molecular Biology and Evolution 17(6): 890-896.

3. Graur. D. and Pupko, T. 2001. The Permian bacterium that isn't. Molecular Biology and Evolution 18(6): 1143-1146.

4. Pupko, T., Sharan, R., Hasegawa, M., Shamir, R., and Graur, D. 2001. A chemical-distance-based test for positive Darwinian selection. Lecture Notes in Computer Science 2149: 142-155.

5. Pupko, T., and Graur, D. 2002. Fast computation of maximum likelihood trees by numerical approximation of amino-acid replacement probabilities. Computational Statistics & Data Analysis 40(2): 285-291.

6. Friedman, N., Ninio, M., Pe'er, I., and Pupko, T. 2002. A structural EM algorithm for phylogenetic inference. Journal of Computational Biology 9: 331-353.

7. Pupko, T., Pe'er, I., Graur, D. Hasegawa, M., and Friedman N. 2002. A branch-and-bound algorithm for the inference of ancestral amino-acid sequences when the replacement rate varies among sites: Application to the evolution of five gene families. Bioinformatics 18(8): 1116-1123.

8. Pupko, T., and Galtier, N. 2002. A covarion-based method for detecting molecular adaptation: application to the evolution of primate mitochondrial genomes. Proceedings of the Royal Society B-Biological Sciences 269(1498): 1313-1316.

9. Pupko, T., Bell, RE., Mayrose, I., Glaser, F., and Ben-Tal, N. 2002. Rate4Site: an algorithmic tool for the identification of functional regions on proteins by surface mapping of evolutionary determinants within their homologues. Bioinformatics 17, suppl(1): S71-77.

10. Pupko, T., Huchon, D., Cao, Y., Okada, N., and Hasegawa, M. 2002. Combining multiple data sets in a likelihood analysis: which models are the best? Molecular Biology and Evolution 19(12): 2294-2307.

11. Glaser, F., Pupko, T., Paz, I, Benchor, D., Martz, E., and Ben-Tal, N. 2003. ConSurf: a server for the identification of functional regions in proteins by surface-mapping of phylogenetic information. Bioinformatics 19(1): 163-164.

12. Pupko, T., Sharan, R., Hasegawa, M., Shamir, R., and Graur, D. 2003. Detecting excess radical replacements in phylogenetic trees. Gene 13(319): 127-135.

13. Pe'er, I., Pupko, T., Shamir, R., and Sharan, R. 2004. Incomplete direct perfect phylogeny. SIAM Journal on Computing 33(3): 590-607.

14. Berezin, C., Glaser, F., Rosenberg, J., Paz, I., Pupko, T., Fariselli, P., Casadio, R., and Ben-Tal, N. 2004. ConSeq: The identification of functionally and structurally important residues in protein sequences. Bioinformatics 20(8): 1322-1324.

15. Melamed,D. Mark-Danieli, M., Kenan-Eichler, M., Kraus, O., Castiel, A., Laham, N., Pupko, T., Glaser, F., Ben-Tal, N., and Bacharach, E. 2004. The conserved carboxy-terminus of the human immunodeficiency virus type 1 Gag protein is important for virion assembly and release. Journal of Virology 78(18): 9675-9688.

16. Mayrose, I., Graur, D., Ben-Tal, N., and Pupko, T. 2004. Comparison of site-specific rate-inference methods: Bayesian methods are superior. Molecular Biology and Evolution 21(9): 1781-1791.

17. Glaser, F., Rosenberg, Y., Kessel, A., Pupko, T., and Ben-Tal, N. 2005. The ConSurf-HSSP database: the mapping of evolutionary conservation among homologs onto PDB Structures. Proteins-Structure Function and Bioinformatics 58(3): 610-617.

18. Doron-Faigenboim, A., Stern, A., Mayrose I, Bacharach E, and Pupko, T. 2005. Selecton: a server for detecting evolutionary forces at a single amino-acid site. Bioinformatics 21(9): 2101-2103.

19. Mayrose, I., Mitchell, A., and Pupko, T. 2005. Site-specific evolutionary rate inference: taking phylogenetic uncertainty into account. Journal of Molecular Evolution 60(3): 345-353.

20. Dutheil, J,. Pupko, T., Jean-Marie, A, Galtier, N. 2005. A model-based approach for detecting co-evolving positions in a molecule. Molecular Biology and Evolution. 22(9):1919-1928.

21. Landau, M., Mayrose, I., Rosenberg, Y., Glaser, F., Martz, E., Pupko, T., and Ben-Tal, N. 2005. ConSurf 2005: The projection of evolutionary conservation scores of residues on protein structures. Nucleic Acid Research 33: W299-W302.
* Advocated in the NetWatch Department of the September 6th, 2002 issue of Science and in other magazines

22. Nimrod, G., Glaser, F., Steinberg, D., Ben-Tal, N., and Pupko, T. 2005. *In silico* identification of functional regions in proteins. Bioinformatics 21 Suppl 1: i328-i337.

23. Mayrose, I., Friedman, N., and Pupko, T. 2005. A Gamma mixture model better accounts for among site rate heterogeneity. Bioinformatics 21: Suppl 2: ii151-ii158.

24. Stern, A., and Pupko, T. 2006. Evolutionary space-time model with varying among site dependencies. Molecular Biology and Evolution 23(2): 392-400.

25. Shaul, S., Nussinov, R., and Pupko, T. 2006. Paths of lateral gene transfer of lysyl-aminoacyl-tRNA synthetases with a unique evolutionary transition stage of prokaryotes coding for class I and II varieties by the same organisms. BMC EVOLUTIONARY BIOLOGY 6: 12.

26. Goren, A., Ram, O., Amit, M., Keren, H., Lev-Maor, G., Vig, I., Pupko, T., and Ast, G. 2006. Comparative analysis identifies exonic splicing regulatory sequences - the complex definition of enhancers and silencers. Molecular Cell 22(6): 769-781.

27. Stern, A., Privman, E., Rasis, M., Lavi, S., and Pupko, T. 2007. Evolution of the metazoan protein phosphatase 2C superfamily. Journal of Molecular Evolution 64(1): 61-70.

28. Ninio, M., Privman, E., Pupko, T., and Friedman, N. 2007. Phylogeny reconstruction: increasing the accuracy of pairwise distance estimation using Bayesian inference of evolutionary rates. Bioinformatics 23: e136-e141.

29. Mayrose, I., Shlomi, T., Rubinstein, ND., Gershoni, JM., Ruppin, E., Sharan, R., and Pupko, T. 2007. Epitope mapping using combinatorial phage-display libraries: A graph-based algorithm. Nucleic Acids Research 35(1): 69-78.

30. Doron-Faigenboim, A., and Pupko, T. 2007. A combined empirical and mechanistic codon model. Molecular Biology and Evolution 24(2): 388-497.
*Selected for Faculty of 1000 Biology

31. Bublil, EM., Tarnovitski, TF., Mayrose, I., Penn, O., Roitburd-Berman, A., Rubinstein, ND., Pupko, T., and Gershoni, JM. 2007. Stepwise prediction of conformational discontinuous B-cell epitopes using the Mapitope algorithm. Proteins-Structure Function and Bioinformatics 68(1): 293-304.

32. Stern, A., Doron-Faigenboim, A., Bacharach, E., and Pupko, T. 2007. Selecton 2007: advanced models for detecting positive and purifying selection using a Bayesian inference approach. Nucleic Acids Research 35: W506-W511.

33. Mayrose, I., Doron-Faigenboim, A., Bacharach, E., and Pupko, T. 2007. Towards realistic codon models: among site variability and dependency of synonymous and nonsynonymous rates. Bioinformatics 23: i319-i327.

*Selected for Faculty of 1000 Biology

34. Lev-Maor, G., Goren, A., Sela, A., Kim, E., Keren, H., Doron-Faigenboim, A., Leibman-Barak, S., Pupko, T., and Ast, G. 2007. The "alternative" choice of constitutive exons through evolution. PLoS Genetics 3(11): e203.

35. Mayrose, I., Penn, O., Erez, E., Rubinstein, ND., Shlomi, T., Tarnovitski Freund, N., Bublil, E., Rupin, E., Sharan, R., Gershoni, JM., Martz, E., and Pupko, T. 2007. Pepitope: epitope mapping from affinity-selected peptides. Bioinformatics 23(23): 3244-3246.
* Advocated in the Gen magazine (2008)

36. Schwartz, S., Silva, J., Burstein, D., Pupko, T., Eyras, E., and Ast, G. 2008. Large scale comparative analysis of splicing signals and their corresponding splicing factors in eukaryotes. Genome Research 18(1): 88-103.

37. Rubinstein, ND., Mayrose, I., Halperin, D., Yekutieli, D., Gershoni, JM., and Pupko, T. 2008. Computational characterization of B-cell epitopes. Molecular Immunology 45: 3477–3489.

38. Cohen, O., Rubinstein, ND., Stern, A., Gophna, U., and Pupko, T. 2008. A likelihood framework to analyse phyletic patterns. Proceedings of the Royal Society B-Biological Sciences 363: 3903-3911.

39. Sela, N., Stern, A., Makalowski, W., Pupko, T., and Ast, G. 2008. Transduplication resulted in the incorporation of two protein-coding sequences into the Turmoil-1 transposable element of *C. elegans*. Biology Direct 3: 41.

40. Penn, O., Stern, A., Rubinstein, ND., Galtier, N., Bacharach, E., and Pupko, T. 2008. Evolutionary modeling of rate shifts reveals specificity determinants in HIV-1 subtypes. PLoS Computational Biology 4: e1000214.

41. Rubinstein, ND., Mayrose, I., and Pupko, T. 2009. A machine-learning approach for predicting B-Cell epitopes. Molecular Immunology 46(5): 840-847.

42. Blanga-Kanfi, S., Miranda, H., Penn, O., Pupko, T., DeBry, RW., and Huchon, D. 2009. Rodent phylogeny revised: Analysis of six nuclear genes from all major rodent clades. BMC Evolutionary Biology 9: 71.

43. Burstein, D., Zusman, T., Degtyar, E., Viner, R., Segal, G., and Pupko, T. 2009. Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach. PLoS Pathogens 5(7): e1000508.

44. Stern A., Mayrose I., Shaul S., Gophna U., and Pupko T. 2010. An evolutionary analysis of lateral gene transfer in thymidylate synthase enzymes. Systematic Biology. 59(2): 212-225.

45. Rubinstein, N.D, Mayrose, I, Martz, E, and Pupko, T. 2009. Epitopia: a web-server for predicting B-cell epitopes. BMC Bioinformatics 10: 287.

46. Cohen O, and Pupko, T. 2010. Inference and characterization of horizontally transferred gene families using stochastic mapping. Molecular Biology and Evolution 27(3): 703-713.

47. Penn, O., Privman, E., Landan, G., Graur, D., and Pupko, T. 2010. An alignment confidence score capturing robustness to guide-tree uncertainty. Molecular Biology and Evolution 27(8): 1759-1767.

48. Loe-Mie1, Y., Lepagnol-Bestel, A.D., Maussion, G., Doron-Faigenboim, A., Imbeaud, S., Delacroix, H., Aggerbeck, L., Pupko, T., Gorwood, P., Simonneau, M., and Moalic, J.M. ASMARCA2 and other genome-wide supported schizophrenia-associated genes: regulation by REST/NRSF, network organization and primate-specific evolution. Human Molecular Genetics 19(14): 2841-2857.

49. Ashkenazy, H., Erez, E.,Martz, E., Pupko, T., and Ben-Tal, Nir. 2010. ConSurf 2010: calculating evolutionary conservation in sequence and structure of proteins and nucleic acids. Nucleic Acids Research 38(Web Server issue): W529-W533.

50. Penn, O., Privman, E., Ashkenazy, H., Landan, G., Graur, D., and Pupko, T. 2010. GUIDANCE: a web server for assessing alignment confidence scores. Nucleic Acids Research. 38(Web Server issue): W23-W28.
* A book chapter reviewing GUIDANCE is published in Hall B. G. (2011) *Phylogenetic Trees Made Easy: A How-To Manual* (Sinauer, Sunderland, MA).

51. Cohen, O., Ashkenazy, H., Belinky, F., Huchon, D., and Pupko, T. 2010. GLOOME: gain loss mapping engine. Bioinformatics 26(22): 2914–2915.

52. Keren, H., Donyo, M., Zeevi, D., Maayan, C., Pupko, T., and Ast, G. 2010. Phosphatidylserine increases IKBKAP levels in familial dysautonomia cells. PLoS One 5(12): e15884.

53. Cohen, O., and Pupko, T. 2010. The complexity hypothesis revisited: connectivity rather than function constitutes a barrier to horizontal gene transfer. Molecular Biology and Evolution. 28(4): 1481-1489.

54. Barzel, A., Privman, E., Peeri, M., Naor, A., Shachar, E., Burstein, D., Lazary, R., Gophna, U., Pupko, T., and Kupiec, M. 2011. Native homing endonucleases can target conserved genes in humans and in animal models. Nucleic Acids Research 39(15): 6646-6659.

55. Rubinstein, N.D., Doron-Faigenboim, A., Mayrose, I., and Pupko, T. 2011. Evolutionary models accounting for layers of selection in protein coding genes and their impact on the inference of positive selection. Molecular Biology and Evolution 28(12): 3297-3308.

56. Rubinstein N.D., Zeevi, D., Oren, Y., Segal, G., and Pupko, T. 2011. The operonic location of auto-transcriptional repressors is highly conserved in bacteria. Molecular Biology and Evolution 28(12): 3209-3318.

57. Cohen, O., and Pupko, T. 2011. Inference of gain and loss events from phyletic patterns using stochastic mapping and parsimony – a simulation study. Genome Biology and Evolution 3: 1265-1275.

58. Privman, E., Penn, O., and Pupko, T. 2012. Improving the performance of positive selection inference by filtering unreliable alignment regions. Molecular Biology and Evolution 29(1): 1-5.

59. Turner, D., Amit, S., Chalom, S., Penn, O., Pupko T., Katchman, E., Matus, N., Tellio, H., Katzir, M., Avidor, B. 2012. Emergence of an HIV-1 cluster harboring the major protease L90M mutation among treatment-naive patients in Tel-Aviv, Israel. HIV Medicine. 13(4):202-206.

60. Gelfman, S., Burstein, D., Penn, O., Schwartz, S., Pupko, T., and Ast, G. 2012. Changes in exon-intron structure during vertebrate evolution affects the splicing pattern of exons. Genome Research. 22(1):35-50.
*Co-corresponding author

61. Burstein, D., Gould, S.B., Zimorski, V., Klösges, T., Kiosse, F., Major, P., Martin, W., Pupko, T., Dagan, T. 2012. A machine-learning approach to identify hydrogenosomal proteins in *Trichomonas vaginalis*. Eukaryotic Cell. 11(4):217-228.

62. Amit, M., Donyo, M., Hollander, D., Goren, M., Kim, E., Gelfman, S., Lev-Maor, G., Burstein, D., Schwartz, S., Postolsky, B., Pupko, T., and Ast, G. 2012. Differential GC content between exons and introns establishes distinct strategies of splice-site recognition. Cell Reports. 1(5):543-556.

63. Ashkenazy, H., Penn, O., Doron-Faigenboim, A., Cohen, O., Cannarozzi, G., Zomer, O., and Pupko, T. 2012. FastML: a web server for probabilistic reconstruction of ancestral sequences. Nucleic Acids Research. 40(Web Server issue):W580-W584.

64. Ryvkin, A., Ashkenazy, H., Smelyanski, L., Kaplan, G., Penn, O., Weiss-Ottolenghi, Y., Privman, E., Ngam, P.B., Woodward, J.E., May, G.D., Bell, C., Pupko, T., and Gershoni, J.M. 2012. Deep panning: steps towards probing the IgOme. PLoS ONE.7(8):e41469.

65. Cohen, O., Ashkenazy, H., Burstein, D., and Pupko, T. 2012. Uncovering the co-evolutionary network among microbial gene families. Bioinformatics. 28 ECCB 2012:i389-i394.

66. Lifshitza, Z., Burstein, D., Peeri, M., Zusman, T., Schwartz, K., Shuman, H.A., Pupko, T., and Segal, G. 2013. Computational modeling and experimental validation of the Legionella and Coxiella virulence-related Type-IVB secretion signal. Proceedings of the National Academy of Sciences, USA. *110 (8) E707–E715*.
*Co-corresponding author

67. Cohen, O., Ashkenazy, H., Levy Karin, E., Burstein, D., and Pupko, T. 2013. CoPAP: Coevolution of Presence-Absence Patterns. Nucleic Acids Research. 41(Web Server issue):W232-W237.

68. Mayrose, I., Stern, A., Burdelova, E.O., Sabo, Y., Laham-Karam, N., Zamostiano, R., Bacharach, E., and Pupko, T. 2013. Synonymous site conservation in the HIV-1 genome. BMC Evolutionary Biology. 13:164.

69. Yossef, I., Shitrit, D., Goren, M.G., Burstein, D., Pupko, T., and Qimron, U. 2013. DNA motifs determining the efficiency of adaptation into the *Escherichia coli* CRISPR array. Proceedings of the National Academy of Sciences, USA. 110(35):14396-14401.

70. Lifshitz, Z., Burstein, D., Schwartz, K., Shuman, H.A., Pupko, T., and Segal G. 2014. Identification of novel *Coxiella burnetii* Icm/Dot effectors and genetic analysis of their involvement in modulating a mitogen-activated protein kinase pathway. Infect Immun. 82(9):3740-3752.

71. Levy Karin, E., Susko, E., and Pupko, T. 2014. Alignment errors strongly impact likelihood-based tests for comparing topologies. Mol Biol Evol. 31(11):3057-3067.

72. Oren, Y., Smith, M.B., Johns, N.I., Kaplan Zeevi, M., Biran. D., Ron, E.Z., Corander, J., Wang, H.H., Alm. E.J., and Pupko T. 2014. Transfer of noncoding DNA drives regulatory rewiring in bacteria. Proc Natl Acad Sci USA. 111(45):16112-16117.
* Based on paper the 'Cozzarelli Prize' was awarded.

73. Ashkenazy, H., Cohen, O., Pupko, T., and Huchon D. 2014. Indel reliability in indel-based phylogenetic inference. Genome Biol Evol. 6(12):3199-3209.
*Co-corresponding author

74. Molshanski-Mor, S., Yosef, I., Kiro, R., Edgar, R., Manor, M., Gershovits, M., Laserson, M., Pupko, T., and Qimron, U. 2014. Revealing bacterial targets of growth inhibitors encoded by bacteriophage T7. Proc Natl Acad Sci USA. 111(52):18715-18720.

75. Burstein, D., Satanower, S., Simovitch, M., Belnik ,Y., Zehavi, M., Yerushalmi, G., Ben-Aroya, S., Pupko, T., Banin, E. 2015. Novel type III effectors in *Pseudomonas aeruginosa*. mBio. *6(2):e00161-15*
*Co-corresponding author

76. Sela, I., Ashkenazy, H., Kazutaka, K., and Pupko, T. 2015. GUIDANCE2: accurate detection of unreliable alignment regions accounting for the uncertainty of multiple parameters. Nucleic Acids Research. 43(W1):W7-W14.

77. Bar-Rogovsky, H., Stern, A., Penn, O., Kobl, I., Pupko, T., and Tawfik, D.S. 2015. Assessing the prediction fidelity of ancestral reconstruction by a library approach. Protein Engineering, Design & Selection. 28(11):507-518.
*Selected for Faculty of 1000 Biology

78. Levy Karin, E., Rabin, A., Ashkenazy, H., Shkedy, D., Avram, O., Cartwright, R.A., and Pupko, T. 2015. Inferring indel parameters using a simulation-based approach. *Genome Biol Evol*. 7(12):3226-3238.

79. Faigenbloom, L., Rubinstein, N.D., Kloog, Y., Mayrose, I., Pupko, T., and Stein, R. 2015. Regulation of alternative splicing at the single-cell level . Mol Syst Biol. 11(12):845.

80. Teper, D., Burstein, D., Salomon, D., Gershovitz, M., Pupko, T., and Sessa, G. 2016. Identification of novel *Xanthomonas euvesicatoria* type III effector proteins by a machine-learning approach.
Mol Plant Pathol. 17(3):398-411.
*Co-corresponding author

81. Burstein, D., Amaro, F., Zusman, T., Lifshitz, Z., Cohen, O., Gilbert, J.A., Pupko, T., Shuman, H.A., and Segal, G. 2016. Genomic analysis of 38 Legionella species identifies large and diverse effector repertoires.
Nature Genetics. 48(2):167-175.
*The paper was highlighted in Nature Reviews Microbiology:
http://www.nature.com/nrmicro/journal/vaop/ncurrent/full/nrmicro.2016.8.html
**The paper was highlighted in Nature Genetics' news and views
Comas, I. Legionella effectors reflect strength in diversity. 2016. Nature genetics. 48(2) 2:115-116.

82. Eckshtain-Levi, N., Shkedy, D., Gershovits, M., Da Silva, G.M., Tamir-Ariel, D., Walcott, R., Pupko, T., abd Burdman, S. 2016. Insights from the genome sequence of *Acidovorax citrulli* M6, a group I strain of the causal agent of bacterial Fruit Blotch of cucurbits. Front Microbiol. 7:430

83. Ashkenazy, H., Abadi, S., Martz, E., ; Chay, O., Mayrose, I., Pupko, T., and Ben-Tal, N. 2016. ConSurf 2016: an improved methodology to estimate and visualize evolutionary conservation in macromolecules. Nucleic Acids Research. 44(Web Server issue):W344-W350.

84. McNally, A., Oren, Y., Kelly, D., Pascoe, B., Dunn, S., Sreecharan, T., Vehkala, M., Välimäki, N., Prentice, M.B., Ashour ,A., Avram, O., Pupko, T., Dobrindt, U., Literak, I., Guenther, S., Schaufler, K., Wieler, L.H., Zhiyong, Z., Sheppard, S.K., McInerney, J.O., Corander, J. 2016. Combined analysis of variation in core, accessory and regulatory genome regions provides a super-resolution view into the evolution of bacterial populations. PLoS Genet. 12(9):e1006280.

85. Preisner, H., Levy Karin, E., Poschmann, G., Stühler, K., Pupko, T., and Gould SB. 2016. The cytoskeleton of parabasalian parasites comprises proteins that share properties common to intermediate filament proteins. Protist. 167(6):526-543.

86. Levy Karin, E., Wilcke, S., Pupko, T., and Mayrose, I. 2017. An integrated model of phenotypic trait changes and site-specific sequence evolution. Systematics Biology. 66(6):917-933.

87. Levy Karin, E., Shkedy, D., Ashkenazy, H., Cartwright, R.A., and Pupko, T. 2017. Inferring rates and length-distributions of indels using Approximate Bayesian Computation. Genome Biol Evol. 9(5):1280-1294.

88. Levy Karin, E., Ashkenazy, H., Wilcke, S., Pupko, T., and Mayrose, I. 2017. TraitRateProp: a web server for the detection of trait-dependent evolutionary rate shifts in sequence sites. Nucleic Acids Research. 45(W1):W260-W264.

89. Ashkenazy, H., Levy Karin, E., Mertens, Z., Cartwright, R.A., and Pupko, T. 2017. SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. Nucleic Acids Research. 45(W1):W453-W457.

90. Mushegian, A, Karin, E.L., and Pupko, T. 2018. Sequence analysis of malacoherpesvirus proteins: Pan-herpesvirus capsid module and replication enzymes with an ancient connection to "Megavirales". Virology. 513:114-128.

91. Nissan, G., Gershovits, M., Morozov, M., Chalupowicz, L., Sessa, G., Manulis-Sasson, S., Barash, I., and Pupko, T. 2018. Revealing the inventory of type III effectors in *Pantoea agglomerans* gall-forming pathovars by using draft genome sequences and a machine-learning approach. Molecular Plant Pathology. 19(2):381-392.

92. Danziger, O., Pupko, T., Bacharach, E., and Ehrlich, E. 2018. Interleukin-6 and interferon-α signaling via JAK1-STAT differentially regulate oncolytic versus cytoprotective antiviral states. Frontiers in Immunology. 9:94.

93. Xue, Y.A., DiPizio, A., Levit, A., Yarnitzky, T., Penn, O., Pupko, T., and Niv, M.Y. 2018. Independent evolution of strychnine recognition by bitter taste receptor subtypes. Frontiers in Molecular Biosciences. 5:9.

94. Ryvkin, A., Ashkenazy, H., Weiss-Ottolenghi, Y., Piller, C., Pupko, T., and Gershoni, J. 2018. Phage display peptide libraries: deviations from randomness and correctives. Nucleic Acids Research. 46(9):e52.
*Co-corresponding author

95. Bar, L., Levy Karin, E., Pupko, T., and Hazkani-Covo, E. 2018. The prevalence and evolutionary conservation of inverted repeats in proteobacteria. Genome Biol Evol. 10(3):918-927.

96. Avram, O., Vaisman-Mentesh A, Yehezkel, D., Ashkenazy, H., Pupko, T., and Wine, Y. 2018. ASAP, a webserver for immunoglobulin-sequencing analysis pipeline. Front. Immunol. 9:1686.

97. Davis, E.W., Tabima, J.F., Weisberg, A.J., Lopes, L.C., Wiseman, M.S., Pupko, T., Belcher, M.S., Sechler, A.J., Tancos, M.A., Schroeder, B.K., Murray, T.D., Luster, D.G., Schneider, W.L., Rogers, E.E., Andreote, F.D., Grunwald, N.J., Putnam, M.D., and Chang, J.H. 2018. Evolution of the US biological select agent, *Rathayibacter toxicus*. mBio. 9:e01280-18.

98. Ashkenazy, H., Sela, I., Levy Karin, E., Landan, G., and Pupko, T. 2019. Multiple sequence alignment averaging improves phylogeny reconstruction. Systematics Biology. 1;68(1):117-130.

99. Levy Karin, E., Ashkenazy, H., Jotun, H., and Pupko, T. 2019. A simulation-based approach to statistical alignment. Systematics Biology. 68(2):252-266.

100. Moshe, A., and Pupko, T. 2019. Ancestral sequence reconstruction: accounting for structural information by averaging over replacement matrices. Bioinformatics. 15:2562-2568.

101. Abadi, S., Azouri, D, Pupko, T., and Mayrose, I. 2019. Model selection may not be a mandatory step for phylogeny reconstruction. Nature Communications. 10(1):934.
*Co-corresponding author

102. Avram, O., Rapoport, D., Portugez, S., and Pupko, T. 2019. M1CR0B1AL1Z3R - a user-friendly web server for the analysis of large-scale microbial genomics data. Nucleic Acids Research. 47(Web Server issue):W88-W92.

103. Sugis, E., Dauvillier, J., Leontjeva, A., Adler, P., Hindie, V., Moncion, T., Collura, V., Daudin, R., Loe-Mie, Y., Herault, Y., Lambert, J.C., Hermjakob, H., Pupko, T., Rain, J.C., Xenarios, I., Vilo, J., Simonneau, M., and Peterson, H. 2019. HENA, Heterogeneous network-based data set for Alzheimer's disease. Scientific Data. 6(1):151.

104. Guerrero, I.J., Perez-Montano, F., Mateus da Silva, G., Wagner, N., Shkedy, D., Zhao, M., Pizarro, L., Bar, M., Walcott, R., Sessa, G., Pupko, T., and Burdman, S. 2020. Show me your secret(ed) weapons: a multifaceted approach reveals a wide arsenal of type III-secreted effectors in the cucurbit pathogenic bacterium *Acidovorax citrulli* and novel effectors in the Acidovorax genus. Molecular Plant Pathology. 21(1):17–37.

105. Abadi, S, Avram, O., Rosset, S., Pupko, T., and Mayrose, I. 2020. ModelTeller: model selection for optimal phylogenetic reconstruction using machine learning. Molecular Biology and Evolution. *In press.*

106. Loewenthal, G., Abadi, S., Avram, O., Halabi, K., Ecker, N., Nagar, N., Mayrose, I., and Pupko, T. 2020. COVID-19 pandemic-related lockdown: response time is more important than its strictness. EMBO Molecular Medicine. *Accepted.*

REVIEWS

1. Pupko, T. 2011. Evolution after gene duplication. Trends in Evolutionary Biology, 3:e1.

2. Liberles, D., Teichmann, S., Bahar, I., Bastolla, U., Bloom, J., Bornberg-Bauer, E., Colwell, L., de Koning, A.P.J., Dokholyan, N., Echave, J., Elofsson, A., Gerloff, D., Goldstein, R., Grahnen, J., Holder, M., Lakner, C., Lartillot, N., Lovell, S., Naylor, G., Perica, T., Pollock, D., Pupko, T., Regan, L., Roger ,A., Rubinstein, N., Shakhnovich, E., Sjölander, K., Sunyaev, S., Teufel, A., Thorne, J., Thornton, J., Weinreich, D., and Whelan, S. 2012. The interface of protein structure, protein biophysics, and molecular evolution. Proteins Science. 21(6):769-85.

3. Celniker, G., Nimrod, G., Ashkenazy, H., Glaser, F., Martz, E., Mayrose, I., Pupko, T., and Ben-Tal, N. 2013. ConSurf: using evolutionary data to raise testable hypotheses about protein function. Israel Journal of Chemistry. 53(3-4):199-206.

4. Anisimova, M., Liberles, D.A., Philippe, H., Provan, J., Pupko, T., and von Haeseler, A. 2013. State-of the art methodologies dictate new standards for phylogenetic analysis. BMC Evolutionary Biology. 13:161.

CHAPTERS IN BOOKS

Pupko, T., Doron-Faigenboim, A., Liberles, DA., and Cannarozzi, GM. 2007. Probabilistic models and their impact on the accuracy of reconstructed ancestral protein sequences. In Liberles DA (Editor). Ancestral Sequence Reconstruction. Oxford University Press.

Pupko, T., and Mayrose, I. 2010. Probabilistic methods and rate heterogeneity. In Lodhi H and Muggleton S (Editors). Element of Computational Systems Biology. Wiley Book Series on Bioinformatics.

Rubinstein, N.D., and Pupko, T. 2012. Detection and analysis of conservation at synonymous sites. In Cannarozzi GM and Schneider A (Editors). Codon Evolution: Mechanisms and Models. Oxford University Press.

Cohen, O., Gophna, O., and Pupko, T. 2013. The complexity hypothesis and other connectivity barriers to lateral gene transfer. In Gophna O (Editor). Lateral Gene Transfer in Evolution. Springer Science.

Pupko, T., and Mayrose, I. 2020. A gentle introduction for probabilistic evolutionary models. In Scornavacca C, Delsuc D, and Galtier N (Editors). Phylogenetic in the genomic era. No commercial publisher.

GRANTS

2004-2008 Israel Science Foundation grant. “Comparative genomics using rich probabilistic models of evolution”. $137,000 (Tal Pupko, PI, 2/3 of the sum).

2005-2008 The Wolfson Family Foundation in Israel. “Combining functional genomics and bioinformatics with cell biology and biophysics to unravel the molecular complexity in neurological disorders and cancer”. £250,000 (Tal Pupko, CI, 1/7 of the sum).

2005-2008 Israel Ministry of Science, Culture and Sport, Infrastructure grant. “Viral bioinformatics: combining comprehensive computational tools with empirical molecular and medical virology”. $266,000 (Tal Pupko, PI, 1/3 of the sum).

2006-2008 German Israeli Foundation, Young Scientists’ Program. “Novel codon based evolutionary models and their application to the study of adaptive and purifying selection in proteins”. £40,000 (Tal Pupko, PI, the entire sum).

2007-2008 Israel Ministry of Science, Culture and Sport, Scientific and Technological Cooperation between France-Israel, Research Networks Program in BIOINFORMATICS. “Phylogenomics of urochordata and its application for detection evolutionary shifts in vertebrate proteins”. NIS 217,500 (Tal Pupko, CI)

2007 Israeli Bioinformatics Infrastructure Center. NIS 200,000 (Tal Pupko, PI, 12% of sum). (Money is dedicated to Tel-Aviv Bioinformatics Unit).

2008-2010 Israel Ministry of Science, Culture and Sport, Scientific and Technological Cooperation between Israel and Taiwan. "Codon models and their applications". NIS 202,400 (Tal Pupko, PI, the entire sum).

2009-2010 Saia Foundation. "Revealing the functional adaptations of HIV-1 groups and subtypes to their human host using an evolutionary approach". $5,000 (Tal Pupko, PI the entire sum).

2009-2012 The Wolfson Family Charitable Trust. “MicroRNAs in normal and malignant development”. 1,500,000 Pounds (Tal Pupko, PI 1/17 of the sum).

2009-2013 Israel Science Foundation grant. “Evolutionary models accounting for multi-layer selection pressures and their impact on the inference of positive selection in protein coding genes”. NIS 780,000 (Tal Pupko, PI the entire sum).

2010-2012 Recanati research grant. "Designing optimal innate immune factors to combat retroviral infections". $20,000 (Tal Pupko, PI 1/2 of the sum).

2010-2013 United States-Israel Binational Agricultural Research and Development Fund (BARD). "Discovery and reconstitution of cross-reactive vaccine targets for H5 and H9 avian influenza". $320,000 (Tal Pupko, CI).

2010-2013 United States-Israel Binational Science Grant (BSF). "*Coxiella burnetii* effector proteins" $140,000 (Tal Pupko, PI 1/3 of sum).

2010-2013 Israel Ministry of Science and Technology, Infrastructure grant. “Identification of virulent proteins in bacterial pathogens using machine learning”. 1,800,000 NIS (Tal Pupko, head PI, 1/5 of the sum).

2012-2014 NIH/NIAID R11 grant. “High throughput high resolution profiling of antibody specificities of polyclonal”. $163,055 (Tal Pupko, CI, 1/8 of the sum).

2012-2016 FP7 grant “Systems biology of pathways involving brain ageing”. £6,000,000 (Tal Pupko, PI, £338,000 of the sum).

2013-2015 Saia Foundation. "Quantification and functional characterization of the selective evolutionary constraints acting on HIV-1 at the RNA level". $5,000 (Tal Pupko, PI 1/2 of sum).

2014-2017 German Israeli Foundation. “A combined computational-experimental approach for the identification, characterization, and evolutionary analysis of *T. vaginalis* hydrogenosomal proteins and their localization signals”. £180,000 (Tal Pupko, PI, 1/2 of sum).

2013-2016 Israel Science Foundation grant. “Towards realistic evolutionary models: novel codon models and a multi-locus test for detecting selective shifts”. NIS 696,000 (Tal Pupko, PI the entire sum).

2013-2016 United States-Israel Binational Agricultural Research and Development Fund (BARD). " Identifying pathogenic determinants of *Acidovorax citrulli* toward the control of bacterial fruit blotch of cucurbits ". $290,000 (Tal Pupko, PI, 2/7 of sum).

2015-2018 Israel Ministry of Science and Technology. “The analysis of the impact of age on flu vaccination”. 2,000,000 NIS (Tal Pupko, PI, 1/4 of the sum).

2016-2017 Israel Cancer Association (Excellence Research Grant). “Unraveling the molecular mechanisms of vulnerability of cancer cells to oncolytic viruses”. 150,000 NIS (Tal Pupko, PI, 1/2 of the sum).

2016-2020 United States-Israel Binational Science Grant (BSF). "*Estimating insertions and deletions across the tree of life*" $172,800 (Tal Pupko, PI 1/2 of sum).

2016-2021 Israel Science Foundation grant. “Advanced indel models using approximate Bayesian computing (ABC)”. NIS 1,360,000 (Tal Pupko, PI the entire sum).

2020-2022 Tel-Aviv University Data Center. “The phylogenetic tree reconstruction game: developing reinforcement-learning algorithms for fast and accurate inference of evolutionary trees”. NIS 150,000 (Tal Pupko, PI 1/3 of sum).

FELLOWSHIPS, SCHOLARSHIPS AND PRIZES

FELLOWSHIPS

2003-2006	A fellowship from the Horowitz Foundation (Center for Complexity Science).
2010-2011	National Evolutionary Synthesis Center (NESCent) Sabbatical Fellowship, Durham, NC, U.S.A.

SCHOLARSHIPS

1990	Dean’s Program for the Fostering of Academic Excellence, Tel Aviv University.
1990	Dean’s award for excellent achievements in B.Sc. studies, Tel-Aviv University.
1993-1995	M.Sc. Scholarship, Department of Biochemistry, Tel Aviv University.
1995-2000	Ph.D. Scholarship, Faculty of Life Sciences, Tel Aviv University.
2000-2002	A JSPS postdoctoral fellowship grant for foreign researchers in Japan.
2003	A scholarship to participate in the 53rd Meeting of Nobel Laureates in Lindau, (June 30 until July 4) 2003, Medicine (participants were selected based on academic achievements).

PRIZES

1995 Wolf Prize for M.Sc. Students.
2006 The Krill award (Wolf Foundation) for excellence in scientific research in 2006.
2012 The Hestrin Prize of the Israel Society for Biochemistry and Molecular Biology (ISBMB).
2015 The PNAS Cozzarelli Prize (The National Academy of Science, USA), which "recognizes recently published PNAS papers of outstanding scientific excellence and originality".

EDITORIAL DUTIES

2010-2013	Associated Editor for the journal BMC Evolutionary Biology.
2010-2012	Deputy Editor for the journal BMC Evolutionary Biology.
2012-2013	Section Editor for the journal BMC Evolutionary Biology.
2012-	Associated Editor for the journal Molecular Biology and Evolution.
2013-	Associated Editor for the journal Biology Direct.

SOCIETY DUTIES

2019-	President of the Israeli Society of Evolutionary Biology.

TEACHING

1993-2000	Organic Chemistry, Tel Aviv University (Teaching Assistant).
1997-1998	Calculus, the Israeli College of Insurance (Teaching Assistant).
1998-2000	Calculus for Students of Economics and Physics, Open University of Israel (Lecturer).
2005, 2008	Advanced seminar in bioinformatics (M.Sc. track), Tel Aviv University, Israel (co-Lecturer).
2005	Lecturer. A course on molecular evolution. Invited by the national bioinformatics network (NBN), the University of the Western Cape, South Africa (3-5 Oct, 2005).
2006-2008	From DNA to population, Tel Aviv University, Israel (co- Lecturer).
2009-2010	New horizons in RNA processing (co-Lecturer).
2008-2011	Seminar in bioinformatics, Tel Aviv University, Israel (course coordinator).
2005, 2008, 2012	Advanced cell biology (M.Sc. track) Tel Aviv University, Israel (co-Lecturer).
2004-	Molecular evolution, Tel Aviv University, Israel (course coordinator).
2005-	Introduction to bioinformatics, Tel Aviv University, Israel (course coordinator).
2016-	Tools to bioinformatics, Tel Aviv University, Israel (course coordinator).
2018	Scientific literacy.
2019	Introduction to statistics, Tel Aviv University, Israel (course coordinator)

TEACHING AWARDS

2014	Top 100 lecturers throughout Tel-Aviv University, Israel.
2015	Teaching award from the Faculty of Life Sciences, Tel-Aviv University, Israel.
2015	Top 100 lecturers throughout Tel-Aviv University, Israel.
2015	A teaching award from the Rector of Tel-Aviv University, Israel.
2018	Teaching award from the Faculty of Life Sciences, Tel-Aviv University, Israel.
2019	Top 100 lecturers throughout Tel-Aviv University, Israel.

MEMBERSHIP IN PROFESSIONAL SOCIETIES

2003–	Israeli Society for Bioinformatics and Computational Biology (ISBCB)
2005–	Society for Molecular Biology and Evolution (SMBE)
2009–	Israel Society for Microbiology (ISM)
2012-	Israel Society for Biochemistry and Molecular Biology (ISBMB)
2019-	Israeli Society of Evolutionary Biology

ACTIVE PARTICIPATION IN SCIENTIFIC MEETINGS

1998 Evolution of microsatellites in the yeast *Saccharomyces cerevisiaei*: role of length and number of repeated units. The 4th Meeting of European Ph.D. Students of Evolution. April 1-3, Heraklion, Greece (Lecturer).

2001 A structural EM algorithm for phylogenetic inference. The 5th International Conference on Computational Molecular Biology (RECOMB 2001). April 21-25, Montréal, Canada (the lecture was given be a co-author).

2001 A chemical-distance-based test for positive Darwinian selection. 1st Workshop on Algorithms in BioInformatics BRICS (WABI 2001). August 28-31, University of Aarhus, Aarhus, Denmark (Lecturer).

2002 Analyzing multiple genes in phylogeny. Data Mining Symposium. March 28-29, The Institute of Statistical Mathematics, Tokyo, Japan (Lecturer).

2002 Automated identification of conserved patches. Computational Biology Seminar. November 17-22, Dagstuhl, Germany (Lecturer).

2003. Automatic identification of functional regions in proteins. Annual Israeli Bioinformatics Symposium. June 2, The Technion, Haifa, Israel (Lecturer).

2003 Algorithmic approach for detecting functional regions. Bertinoro Computational Biology Meeting (BCB 2003). June 7-13, Bertinoro (Forli), Italy (Lecturer).

2003 Conservation, covarion and evolutionary models as bioinformatics tools. Tel Aviv University Bioinformatics Symposium. October 1, Tel Aviv University, Tel-Aviv, Israel (Lecturer).

2004 Algorithmic approach for detecting functional regions in proteins. A BigRoc bioinformatics seminar. March 1, Weizmann Institute. Rehovot, Israel (Lecturer).

2004 Finding phylogenetic trees, ancestral sequence reconstruction and conserved regions in proteins using a probabilistic based approach. Bioinformatics Workshop Series 2003-2004. June 3, Weizmann Institute, Rehovot, Israel (Lecturer).

2005 Algorithmic challenges in ancestral sequence reconstruction: Taking variation among sites into account. A meeting on “Using Ancestral Sequence Reconstruction to Understand Protein Function”. March 30-31, Kristineberg, Sweden (Lecturer).

2005 Maximum likelihood estimation of evolutionary rates with applications in phylogeny and biochemistry. The Linnaeus Centre for Bioinformatics. April 5, University of Uppsala, Uppsala, Sweden (Lecturer).

2005 A Gamma mixture model better accounts for among site rate heterogeneity. Joint meeting of Fourth European Conference on Computational Biology (ECCB) and the Sixth Meeting of the Spanish Bioinformatics Network (JBI). Sept 28-Oct 1, Madrid, Spain (Poster).

2006 An evolutionary space-time model with varying among-site dependencies. Annual meeting of the Society for Molecular Biology and Evolution. May 24-28, Arizona State University, Tempe, Arizona, U.S.A (Poster).

2007 Detecting functional sites in proteins using evolutionary models. EuroPathogenomics 2007 Meeting. Feb 28, Tel Aviv University, Tel-Aviv (Lecturer).

2007 An evolutionary model that accounts for selection on synonymous mutations. Annual meeting of The Society of Molecular Biology and Evolution. June 24-28, Halifax, Canada (Invited speaker).

2008 Bayesian framework to analyze phyletic patterns. Invited speaker. The Royal Society Discussion Meeting on Statistical and Computation Challenges in Molecular Phylogenetics and Evolution. April 28-29, London, England (Invited speaker).

2008 HIV-1 bioinformatics using evolutionary models. Invited speaker. One Day Symposium on Phylogenetics. December 8, Technion. Haifa, Israel (Invited speaker).

2009 Evolutionary modeling of rate shifts reveals specificity determinants in HIV -1 subtypes. The Israeli Society for Microbiology (ISM) 2009 annual meeting. March 23-24, Bar Ilan University, Ramat Gan, Israel (Lecturer).

2009 Evolutionary modeling of rate shifts reveals specificity determinants in HIV-1 subtypes. From Darwin till Today meeting. April 5, Hebrew University, Jerusalem, Israel (Invited speaker).

2009 Inference and characterization of phyletic patterns using probabilistic mixture models. Annual meeting of the Society for Molecular Biology and Evolution: Darwin to the Next Generation. June 3-7, Iowa City, Iowa, U.S.A. (Poster).

2009 Evolutionary modeling of rate shifts reveals specificity determinants in HIV-1 subtypes. A one day symposium on "Basic Research and Clinical Treatment in HIV-1 Infection". July 9, Tel Aviv University, Tel-Aviv, Israel (Invited speaker).

2010 Modelling gene content evolution in microbes and the inference of horizontal gene transfer. Invited speaker, COST Training School - Advances in Symbiosis Research. March 13-19, 2010
The Robert H. Smith Faculty of Agriculture, Food & Environment, the Hebrew University of Jerusalem, Israel (Invited speaker).

2010 Genome-wide diversifying selection in SIV from chimpanzees. Poster. The 4th European Congress of Virology. 7-11 April 2010. Villa Erba Confress Centre – Cernobbio, Lake Como, Italy (Lecturer).

2010 Advanced evolutionary models of 0/1 and their applications to study horizontal gene transfer. SMBE 2010 - Annual Meeting of the Society for Molecular Biology and Evolution. July 4-8, 2010. Lyon, France (Invited speaker).

2010 Novel evolutionary models accounting for layers of selection in protein coding genes and their applications. Poster presented at the 5th Annual Duke Systems Biology Symposium. October 7, 2010, Durham, NC, U.S.A (Poster).

2011 The complexity hypothesis revisited: connectivity rather than function constitutes a barrier to horizontal gene transfer. Poster presented at the Penn State SMBE Symposium on Molecular and Genomic Evolution. March 18-20, 2011, Penn State University, State College, PA, U.S.A (Poster).

2011 The operonic location of auto-transcriptional repressors is highly conserved in bacteria. 19th Annual International Conference on Intelligent Systems for Molecular Biology and 10th European Conference on Computational Biology. July 17-19, 2011, Vienna, Austria (Poster).

2011 Teaching bioinformatics for life science undergraduate. Invited speaker. Third RECOMB Satellite Conference on Bioinformatics Education. July 20-21, 2011, Vienna, Austria (Invited speaker).

2011 Swiss Institute of Bioinformatics. PhD Training Networks. September 11-16, 2011, Chandolin, Switzerland (Invited speaker).

2011 Evolutionary models accounting for layers of selection in protein coding genes and their impact on the inference of positive selection. In a "Modeling protein structural and energetic constraints on sequence evolution" Catalysis Meeting. The National Evolutionary Synthesis Center. October 18-21, 2011, Durham, NC, USA (Invited speaker).

2011 Novel bioinformatics tools to mine HIV-1 genomes. Autumn Workshop on Virology, Israeli Society for Microbiology (ISM). December 1-3, Kibbutz Ein Gedi, Israel (Invited speaker).

2012 Advanced probabilistic models to study gain and loss dynamics of gene families among microbial species. The 2012 meeting of the Society for Molecular Biology and Evolution (SMBE), June 23-26, 2012, Dublin, Ireland (Invited speaker).

2012 Modeling the evolutionary dynamics of gene family presence\absence using probabilistic methods: the complexity hypothesis revised. A workshop on protein evolution. July 23-25, 2012, Munich, Germany (Invited speaker).

2012 Computational modeling and experimental validation of the Legionella and Coxiella virulence-related type IVB secretion signal. The Israel Society for Biochemistry and Molecular Biology (ISBMB) 2012 annual meeting. October 10, 2012, Tel-Aviv University, Israel (Prize winning lecture).

2013 Genome-scale identification of pathogenic determinants in Legionella and Coxiella using a machine-learning approach. The First Tel-Aviv University – Freie Universitat Berlin Joint Workshop. March 4-7, 2013, Tel-Aviv University, Israel (Invited speaker).

2014 Transfer of non-coding DNA drives regulatory rewiring in bacteria. The 7th Israel Societies for Experimental Biology (FISEB) meeting (ILANIT). February 10-13, 2014, Eilat, Israel (Invited speaker).

2014 Computational modeling and experimental validation of the *legionella* and *coxiella* virulence-related type IVB secretion signal. The Israeli Society for Microbiology (ISM) Fall Workshop. November 27-29, 2014, Ein-Gedi, Israel (Invited speaker).

2015 Searching for positive selection in genes related to neurodegenerative diseases. International Symposium - Advances in Systems Biology in Neurosciences. February 6, 2015, Geneva, Switzerland (Invited speaker).

2015 Computational modeling and experimental validation of the *legionella* and *coxiella* virulence-related type IVB secretion signal. Frontiers in Microbiome Research. March 8, 2015, Volcani Research Center, Bet-Dagan, Israel (Invited speaker).

2015 Accounting for MSA uncertainties in phylogeny inference. Annual meeting of The Society of Molecular Biology and Evolution. July 12-16, Vienna, Austria (poster).

2016 Transfer of noncoding DNA drives regulatory rewiring in bacteria. The Microbiology Society Annual Conference. March 21-24, Liverpool, UK (Invited speaker).

2016 A novel phylogeny-based algorithm for selective sweeps detection n bacteria. Annual meeting of The Society of Molecular Biology and Evolution. July 3-7, Golden Coast, Australia (my student Oren Avram presented a Fitch symposium).

2017 Inferring rates and length-distributions of indels using approximate Bayesian computation. Annual meeting of The Society of Molecular Biology and Evolution. July 2-6, Austin, Texas, USA (Invited speaker).

2018 SpartaABC –Inferring Indel Parameters. Koret -UC Berkeley -Tel Aviv University Initiative in Computational Biology and Bioinformatics. October 9-11, Simons Institute for the Theory of Computing, Melvin Calvin Laboratory, UC Berkeley, USA (Invited speaker).

2019 Regulatory rewiring in bacteria: transfer of non-coding DNA and selective sweeps. The first UNESP – TAU Research Workshop on Cell Biology. December 4-7, São Paulo, Brazil (Invited speaker).

2020 A machine-learning approach to detect bacterial protein functions. The Annual Meeting of the Advanced Communication Center (ACC). March 3, Tel-Aviv University, Tel-Aviv, Israel (Invited speaker).

OTHER LECTURES AND SEMINARS

2002 From sequence variation to enzyme evolution. Feb, 2002. The Institute of Statistical Mathematics, Tokyo, Japan.

2003 Maximum likelihood estimation of evolutionary rates with applications in phylogeny and biochemistry. Feb 26, 2003. Department of Biochemistry and Molecular Biology, Dalhousie University, Halifax, Nova Scotia, Canada.

2005 Probabilistic evolutionary models and (a few of) their applications. Feb 10, 2005. Complex Networks System Seminar 2005. Tel Aviv University, Tel-Aviv, Israel.

2006 Evolutionary models and their applications for predicting functional sites in proteins. March 9, 2006. Department of Life Sciences, Ben-Gurion University, Beer-Sheva, Israel.

2006 Inferring site-specific evolutionary forces in proteins. March 21, 2006. Department of Molecular Microbiology and Biotechnology, Tel-Aviv University, Israel.

2006 Realistic models of sequence evolution. November 30, 2006. Department of Neurobiology, Tel-Aviv University, Israel.

2007 Probabilistic evolutionary models and their applications. January 16, 2007. Department of Statistics and Operations Research, Tel-Aviv University, Israel.

2007 Codon Models and Selection on Synonymous Substitutions. August 21, 2007. Max Planck Institute for Molecular Genetics, Berlin, Germany (Host, Prof. Martin Vingron).

2007 Probabilistic evolution models and their applications. April 18, 2007. Invited by the Dept. of Ecology and Evolution, University of Lausanne. Lausanne, Switzerland.

2007 Detecting functional sites in proteins using probabilistic methods. April 25, 2007. Invited by the Laboratoire de Biométrie et Biologie Evolutive. Université Claude Bernard - Lyon 1. Lyon, France.

2007 Codon evolutionary models and their applications. November 5, 2007. Invited by the Faculty of Medicine, Hebrew University, Jerusalem, Israel.

2008 Detecting functional sites in proteins using probabilistic methods. March 12, 2008. Faculty of Life Sciences, Bar-Ilan University, Ramat Gan, Israel.

2010 Modeling gene content evolution in microbes. February 25, 2010. CNS seminar. School of Computer Science. Tel-Aviv University, Tel-Aviv, Israel.

2010 Modeling gene content evolution in microbes. March 14, 2010. Computational Biology Seminar. School of Computer Science and Engineering, Alexander Silberman Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem, Israel.

2010 HIV-1 bioinformatics using evolutionary models. April 29, 2010. IMRIC – HUJI The Virus-Host Interactions and Viral Pathogenesis Hub Spring Retreat 2010. Kibbutz Nahsholim, Israel.

2010 HIV-1 bioinformatics using evolutionary models. May 31, 2010. Department of Life Sciences, Ben-Gurion University, Beer-Sheva, Israel.

2010 Evolutionary models provide insights into HIV-1 evolution and function. Oct 22, 2010. Biology Department, Duke University, Durham, NC, U.S.A (Host, Prof. Marcy Uyenoyama).

2010 Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach. Nov 19, 2010. Wyoming University, Laramie, Wyoming, U.S.A. Invited speaker for the Faculty of Life Sciences.

2010 Novel evolutionary models accounting for layers of selection in protein coding genes and their applications. Dec 2, 2010. University of California at Berkeley, U.S.A. Invited Speaker for the Computational Biology Seminar, Department of Molecular and Cell Biology (Host, Prof. Lior Pachter).

2010 Evolutionary models provide insights into HIV-1 evolution and function. Dec 8, 2010. National Evolutionary Synthesis Center (NESCent), Durham, NC, U.S.A.

2011 The complexity hypothesis revisited: connectivity rather than function constitutes a barrier to horizontal gene transfer. April 28, 2011. Duke Systematics Discussion Group, Duke University, Durham, NC, U.S.A.

2011 Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach. Nov 16, 2011. Department of Clinical Microbiology and Immunology, Sackler Faculty of Medicine, Tel-Aviv University, Israel.

2012 Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach. Department of Ecology, Evolution & Behavior. Jan 17, 2012. The Hebrew University of Jerusalem, Israel.

2012 Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach. Dept. of Microbiology and Molecular Genetics. Institute for Medical Research Israel-Canada (IMRIC). April 23, 2012. Hadassah Medical School, The Hebrew University of Jerusalem, Israel.

2012 Fishing for virulent factors: machine learning predictions and experimental validations of bacterial effectors. The Institute of Biochemistry, Food and Nutrition, Robert H. Smith Faculty of Agriculture, Food and Environment. April 29, 2012. The Hebrew University of Jerusalem, Israel.

2012 Fishing for virulent factors: machine learning predictions and experimental validations of bacterial effectors. Dept. of Entomology. June 12, 2012. Newe-Ya'ar Research Center, Agricultural Research Organization, Ministry of Agriculture, Ramat Yishay, Israel.

2012 Gain and loss dynamics of gene families among microbial species. Aix Marseille Université. August 21, 2012, Marseille, France.

2012 Genome-scale identification of *Legionella pneumophila* effectors using a machine-learning approach. Agricultural Research Organization (ARO) Volcani Center. October 14, 2012, Bet-Dagan, Israel.

2013 Comparative genomics analyses provide novel insights on lateral gene transfer. Agricultural Research Organization (ARO) Volcani Center. April 21, 2013, Bet-Dagan, Israel.

2013 Comparative genomics analyses provide novel insights on lateral gene transfer. Department of Molecular Microbiology and Biotechnology, Tel-Aviv University. April 23, 2013, Tel-Aviv, Israel.

2013 Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach, The European Bioinformatics Institute (EBI), The Wellcome Trust Genome Campus. December 19, 2013, Hinxton, United Kingdom.

2014 Genome-scale identification of *Legionella pneumophila* effectors using a machine learning approach, School of Computer Science and Engineering, The Hebrew University. May 11, 2014, Jerusalem, Israel.

2015 Computational insights into lateral gene transfer, NCBI Computational Biology Branch, National Center for Biotechnology Information (NCBI), National Library of Medicine (NLM), National Institutes of Health (NIH), April 23, 2015, Bethesda, Maryland, U.S.A.

2016 Transfer of non-coding DNA drives regulatory rewiring in bacteria, Department of Biology & Biochemistry, University of Houston, Oct 7, 2016, Houston, Texas, USA.

2016 Transfer of non-coding DNA drives regulatory rewiring in bacteria, School of Life Sciences - Arizona State University, Dec 5, 2016, Tempe, Arizona, USA.

2017 Inferring rates and length-distributions of indels using approximate Bayesian computation. Computational Biology Seminar. The Alexander Silberman Institute for Life Sciences – The Hebrew University, Dec 3, 2017, Jerusalem, Israel.

2018 Regulatory rewiring in bacteria: transfer of non-coding DNA and selective sweeps, Department: Evolution, Systematics and Ecology, Alexander Silberman Institute of Life Sciences, Faculty of Science The Hebrew University, April 10, 2018, Jerusalem, Israel.

Lectures to general public

2014 Lecture to high school students on Evolution. Pais-Apple high-school. Organized by Bashaar, the Academic Community for Israeli Society. Emeq Hefer, Israel, February 18, 2014.

2014 Lecture to the general public on the evolution of HIV. Tel-Aviv University, Tel-Aviv, Israel, May 26, 2014.

2018 Lecture to the general public on the evolution of HIV (International Darwin Day, Tel-Aviv), February 12, 2018.

ORGANIZATION OF MEETINGS

*Although I helped organizing these meetings, I did not attend all of them

2005 The Center of Complexity Science Annual Meeting. April 19, Tel Aviv University, Tel-Aviv, Israel.

2006 Symposium on "Lateral Gene Transfer". Dec 27, Tel Aviv University, Tel-Aviv, Israel.

2007 The 5th European Conference on Computational Biology (ECCB). Jan 22-25, Eilat, Israel.

2007 Program committee of the 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 6th European Conference on Computational Biology (ECCB). July 21-25, 2007. Vienna, Austria.

2008 Program committee of the 8th European Conference on Computational Biology (ECCB). September 22-26, 2008. Cagliari, Sardinia-Italy.

2008 Program committee of the 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). July 19-23, 2008. Toronto, Canada.

2009 Program committee of the 17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB) & 8th European Conference on Computational Biology (ECCB). June 27-July 02, 2009. Stockholm, Sweden.

2010 Program chair of the 13th Israeli Bioinformatics Symposium. April 6, 2010, Faculty of Medicine, Technion, Haifa, Israel.

2011 Session organizer and chair in the 2011 meeting of the Federation of the Israel Societies for Experimental Biology (FISEB\ILANT), Feb 7-10, 2011, Eilat, Israel.

2012 Symposium organizer and chair. Multiple sequence alignment, alignment confidence and impact on downstream analyses. The 2012 meeting of the Society for Molecular Biology and Evolution (SMBE), Dublin Ireland, June 23-26, 2012.

2012 Program committee of the International Society for Molecular Biology (ISMB) 2012 in the area of Evolution and Comparative Genomics. Long Beach, CA, U.S.A, July 15-17, 2012.

2012 Program committee of WABI 2012, the 12th Workshop on Algorithms in Bioinformatics. Ljubljana Slovenia, September 11-13, 2012.

2012 Program committee of ECCB 2012, the 11th European Conference on Computational Biology. Basel Switzerland, September 9-12, 2012.

2013 Area chair for the section Evolution and Comparative Genomics. The 12th International Conference on Intelligent Systems for Molecular Biology (ISMB) & 12th European Conference on Computational Biology (ECCB). July 19-23, 2013. Berlin, Germany.

2014 Program committee of the annual meeting of the Israeli Society for Microbiology (ISM) 2014. International Convention Center, Haifa, April 7, 2014.

2014 Symposium organizer and chair. Molecular evolution of microbial genomes. The 2014 meeting of the Society for Molecular Biology and Evolution (SMBE), San Juan, Puerto Rico, June 8-12, 2014.

2014 Program committee of ECCB 2014, the 13th European Conference on Computational Biology. Basel Switzerland, September 7-10, 2014.

2015 Program chair of IBS 2015, THE 17th Israeli Symposium of Bioinformatics. Tel-Aviv University, May 26, 2015.

2018 Program committee of the International Society for Molecular Biology (ISMB) 2018 in the area of Evolution and Comparative Genomics. Chicago, Illinois, USA, July 6-10, 2018.

2019 Program committee of the International Society for Molecular Biology (ISMB) / ECCB 2019 in the area of Evolution and Comparative Genomics. Basel, Switzerland, July 21-25, 2018.

2019 Fitch Award committee and Travel Award committee member of the Society for Molecular Biology and Evolution (SMBE) 2019 annual meeting, Manchester, United Kingdom, July 21-25, 2019.

2019 Program chair of the 1st meeting of the Israeli Society of Evolutionary Biology. The Steindhardt Museum of Natural History, Tel-Aviv University, December 11-12, 2019.

2020 Program chair member of a Workshop on Computational Biology at the Simons Institute in Berkeley, USA. July 27-30, 2020.

STUDENTS SUPERVISED

Students that became faculty member

Four of my former PhD students have obtained faculty positions in Israel (Itay Mayrose, Adi Stern, Eyal Privman, and David Burstein).

DOCTORAL STUDENTS (at Tel-Aviv University)

Dates	**Name**	**Title of thesis/proposal**
2003-2008	Itay Mayrose	Probabilistic algorithms for predicting functional regions in protein-coding genes (*summa cum laude*)
2003-2009	Adi Doron-Faigenboim	Computational methods for mapping evolutionary selection forces onto proteins (*Direct PhD)
2005-2009	Adi Stern	Probabilistic evolutionary models and their application in inferring interactions between host and pathogen proteins
2004-2010	Eyal Privman	Hybrid methods inspired by the mutual dependency of sequence alignment and phylogeny reconstruction (*Direct PhD)
2006-2011	Nimrod Rubinstein	Computational approaches for studying violations of common assumptions regarding the evolutionary regime operating on genes and proteins
2007-2012	Osnat Penn	Computational methods for sequence analysis of HIV evolutionary dynamics
2007-2012	Ofir Cohen	Evolutionary models for analyzing gene content (*Direct PhD, special track for Excellent Students)
2008-2013	David Burstein	Machine-learning approaches for the identification of pathogenic determinants
2010-2015	Haim Ashkenazi	Reliability of multiple sequence alignments: application in molecular evolution
2010-2015	Yaara Oren	Transfer of non-coding DNA drives regulatory rewiring in Bacteria. Joint supervision with Prof. Eliora Ron. (*Direct PhD, special track for Excellent Students)
2012-2017	Eli Levy Karin	Statistical techniques in molecular evolution: improving *in-silico* sequence simulations and detecting genotype-phenotype associations (*Direct PhD) Joint supervision with Dr. Itay Mayrose
2015-2020	Oren Avram	Algorithms and applications in bacterial phylogenomics
2016-	Asher Moshe	
2018-	Natan Nagar	

2019-	Gil Loewenthal	
2019-	Naama Wagner	
2020-	Noa Ecker	(*Direct PhD)

M.Sc STUDENTS (at Tel-Aviv University)

Dates	**Name**	**Title of thesis/proposal**
2003-2005	Adi Stern	Space-time models of protein evolution with site interdependence (*magna cum laude*)
2005-2006	Nimrod Rubinstein	A computational approach for the study of B cell epitopes (*magna cum laude*)
2005-2007	Osnat (Penn) Zomer	An evolutionary model for the detection of site-specific rate-shifts in proteins (*magna cum laude*)
2006-2008	David Burstein	A quest for new *Legionella pneumophila* effectors using a machine learning approach (*magna cum laude*)
2007-2009	Tal Peled	Large-scale analysis of the evolutionary forces acting on silent sites in yeast (*magna cum laude*)
2008-2011	Dayana Alaluf	Identification of protein-protein interactions in the Ibaraki virus: experimental and computational approaches
2009-2011	David Zeevi	Inching towards understanding *E. coli*'s regulon: first step - detecting novel transcription factors using machine learning algorithms (*magna cum laude*)
2012-2014	Alon Rozental	New codon models detect novel functional regions within the Murine Leukemia Virus genome
2012-2015	Michael Gershovitz	Identification of *Pantoea Agglomerans* effectors using a machine-learning approach (*summa cum laude*)
2011-2015	Michael Peeri	Analyzing molecular signals in proteins using hidden semi-Markov models
2012-2015	Michael Dunaevsky	An automated bioinformatics pipeline for the detection of positively selected genes involved in human neuro-degenerative diseases
2013-2015	Avigayel Hefter	Towards simulating realistic multiple sequence alignments
2013-2015	Oren Avram	A novel algorithm for selective sweeps detection in bacteria (*magna cum laude*) *Joint supervision with Prof. Eytan Ruppin
2014-2016	Dafna Shkedy	Inferring indel parameters using Approximate Bayesian Computation
2014-2016	Nareman Abd El Hadi	Searching for positive Darwinian selection among genes involved in human neurodegenerative diseases
2015-2017	Bar Lavi	An evolutionary study of inverted repeats *Joint supervision with Dr. Einat Hazkani-Covo

2016-	Shir Portugez	*Joint supervision with Dr. Einat Hazkani-Covo
2016-	Dafna Gold Binshtok	
2017-	Ora Balber	
2017-2019	Dana Rapoport	Inferring rates of insertions and deletions using approximate Bayesian computation
2017-2019	Naama Wagner	Machine-learning approach for bacterial protein annotation: type III secreted effectors and transcription factors
2017-2019	Shlomtzion Lahav	Improved numerical algorithms for positive selection inference
2020-	Ben Zerach	
2020-	Elya Wygoda	
2020-	Ido Hasson	*Joint supervision with Dr. Einat Hazkani-Covo

POST DOCTORATE STUDENTS (at Tel-Aviv University)

Dates	Name
2008	Itay Mayrose
2009	Adi Doron-Faigenboim
2010	Eyal Privman
2011-2012	Maya Mayrose
2012	Osnat Penn
2013-2014	Itamar Sela
2015-2019	Haim Ashkenazi
2017	Eli Levy Karin
2020-	Oren Avram

ADMINISTRATIVE ACTIVITIES

2003-2006	Coordinator for the research students’ weekly seminar in the Cell-Biology and Immunology Department, Faculty of Life Sciences, Tel Aviv University
2003-2006	Member of the bioinformatics support unit committee, Faculty of Life Sciences, Tel Aviv University
2004-2008	Member of the M.Sc. committee of the Department of Cell Biology and Immunology, Tel Aviv University
2005-2006	Representative of the lecturers in the Tel Aviv University Senate
2008-2009	Head of the M.Sc. committee of the Department of Cell Biology and Immunology, Tel Aviv University
2004-2012	Head of the undergraduate bioinformatics track in the faculty of Life Sciences, Tel Aviv University

2005-2010	Head of the M.Sc. bioinformatics track in the faculty of Life Sciences, Tel Aviv University
2005-2010, 2012-2015	Member of the university committee of the SAFRA program for promoting bioinformatics at Tel Aviv University
2007-2010	Academic head of the bioinformatics support unit, Faculty of Life Sciences, Tel Aviv University
2009-2010	Member of the university committee to increase students' registration to Tel Aviv University
2011	Representative of Tel-Aviv University in BioAbroad meetings in New York and Washington D.C. USA
2013-2014	Member of the PhD committee of the Department of Cell Biology and Immunology, Tel Aviv University
2013-2015	Member of the academic appointment committee in the Faculty of Life Sciences, Tel Aviv University
2014-2016	Member of the special committee to revise the life science curriculum in the Faculty of Life Sciences, Tel Aviv University
2014-2016	Head, Smolarz Family Graduate School of Life Sciences
2017-2018	Substitute member of the academic appointment committee of Tel-Aviv University
2017-2018	Head of the Ph.D. committee of the School of Molecular Cell Biology & Biotechnology, Tel Aviv University
2017-2018	Member of the Faculty Teaching Committee, Faculty of Life Sciences, Tel Aviv University
2018-	Head, The Shmunis School of Biomedicine and Cancer Research (previously, School of Molecular Cell Biology & Biotechnology), Faculty of Life Sciences, Tel Aviv University

PATENTS

Barzel, A., Privman, E., Michael, P., Pupko, T., and Kupiec, M. 2009. Homing endonuclease genes and their targets. Provisional patent application was submitted to the US Patent and Trademark Office.

Barzel, A., Privman, E., Burstein, D., Gophna, U., Pupko, T., and Kupiec, M. 2009. Method for searching for homing endonucleases, their genes and their targets. PCT/IL2009/000172.