

Education

2018 –	Postdoc. Advisor: Dr. Johannes Söding	Quantitative & Computational Biology, MPIBPC
2013 – 2017	Ph.D. Advisors: Prof. Tal Pupko and Prof. Itay Mayrose <i>Dissertation: Statistical Techniques in Molecular Evolution: Improving in-silico Sequence Simulations & Detecting Genotype-Phenotype Associations</i>	Faculty of Life Sciences, TAU
2012 – 2014	M.Sc in Theoretical and Mathematical Biology (direct Ph.D track) Grade average: 98	Faculty of Life Sciences, TAU
2008 – 2011	B.Sc in Computer Science. Grade average: 90 (magna cum laude) - Participated in “ First Steps in Research for Excellent Students ”. Studied the human metabolic network at Prof. Eytan Ruppín’s lab. Grade: 97 - Participated in “ Parallel Computation of Computer Vision Algorithms ” workshop. Project: accelerating calculation of optical flow fields . Grade: 99	Faculty of Exact Sciences, TAU
2005 – 2008	B.Sc in Biology. Grade average: 90	Faculty of Life Sciences, TAU

Publications

* denotes equal contribution / * denotes co-correspondence

- 15 Zhang R, Mirdita M, [Levy Karin E](#), Norroy C, Galiez C, & Söding J. SpacePHARER: Sensitive identification of phages from CRISPR spacers in prokaryotic hosts. *Submitted*. 2020.
- 14 Halabi K, [Levy Karin E*](#), Guéguen L, & Mayrose I*. TraitRELAX - A codon model for associating phenotypic traits with altered selective patterns of sequence evolution. *Submitted*. 2020.
- 13 [Levy Karin E](#), Mirdita M, & Söding J. MetaEuk - sensitive, high-throughput gene discovery and annotation for large-scale eukaryotic metagenomics. *Microbiome*. 2020; 8:48.
- 12 [Levy Karin E](#), Ashkenazy H, Hein J, & Pupko T. A simulation-based approach to statistical alignment. *Systematic Biology*. 2019; 2:252-266.
- 11 Ashkenazy H, Sela I, [Levy Karin E](#), Landan G, & Pupko T. Multiple sequence alignment averaging improves phylogeny reconstruction. *Systematic Biology*. 2019; 1:117-130.
- 10 Mushegian A, [Levy Karin E](#), & Pupko T. Sequence analysis of malacoherpesvirus proteins: pan-herpesvirus capsid module and replication enzymes with an ancient connection to "Megavirales". *Virology*. 2018; 513: 114-128.
- 9 Lavi B, [Levy Karin E](#), Pupko T, & Hazkani-Covo E. The prevalence and evolutionary conservation of inverted repeats in proteobacteria. *Genome Biology and Evolution*. 2018; 3: 918–927.
- 8 [Levy Karin E*](#), Ashkenazy H*, Wicke S, Pupko T, & Mayrose I. TraitRateProp: a web server for the detection of associations between phenotypic trait changes and specific sequence sites. *Nucleic Acids Research*. 2017; 45:W260-W264.
- 7 Ashkenazy H*, [Levy Karin E*](#), Mertens Z, Cartwright R, & Pupko T. SpartaABC: a web server to simulate sequences with indel parameters inferred using an approximate Bayesian computation algorithm. *Nucleic Acids Research*. 2017; 45:W453-W457.

- 6 [Levy Karin E](#), Wicke S, Pupko T, & Mayrose I. An integrated model of phenotypic trait changes and site-specific sequence evolution. *Systematic Biology*. 2017; 6:917–933.
- 5 [Levy Karin E*](#), Shkedy D*, Ashkenazy H, Cartwright R, & Pupko T. Inferring rates and length-distributions of indels using approximate Bayesian computation. *Genome Biology and Evolution*. 2017; 9:1280-1294.
- 4 Preisner H, [Levy Karin E](#), Poschmann G, Stühler K, Pupko T, & Gould S. The cytoskeleton of parabasal parasites comprises proteins that share properties common to intermediate filament proteins. *Protist*. 2016; 167:526–543.
- 3 [Levy Karin E*](#), Rabin A*, Ashkenazy H, Shkedy D, Avram O, Cartwright R, & Pupko T. Inferring indel parameters using a simulation-based approach. *Genome Biology and Evolution*. 2015; 7:3226-3238.
- 2 [Levy Karin E](#), Susko E, & Pupko T. Alignment errors strongly impact likelihood-based tests for comparing topologies. *Molecular Biology and Evolution*. 2014; 31:3057-3067.
- 1 Cohen O, Ashkenazy H, [Levy Karin E](#), Burstein D, & Pupko T. CoPAP: co-evolution of presence-absence patterns. *Nucleic Acids Research*. 2013; 41:W232-W237.

Awards and Scholarships

2018 – 2020	FEBS long-term postdoctoral fellowship	Federation of European Biochemical Societies
2018	EMBO long-term non-stipendiary postdoctoral fellowship	European Molecular Biology Organization
2017	Ernst Mayr award for best talk	Society of Systematic Biologists
2017	Travel scholarship	Society for Molecular Biology and Evolution
2017	Travel scholarship	Constantiner Institute for Molecular Genetics
2016	Travel scholarship	Manna Center, Faculty of Life Sciences, TAU
2015	Award for excellent achievements in teaching	Faculty of Life Sciences, TAU
2015	Dan David Prize for Ph.D students, <i>Future – Bioinformatics</i> category	Dan David Foundation
2015	Excellent Research Student Prize for the academic year 2014-2015	Edmond J. Safra Center, TAU
2014	Walter M. Fitch award finalist for Ph.D and post-doctoral students	Society for Molecular Biology and Evolution
2014 – 2017	Ph.D fellowship	Edmond J. Safra Center
2013	Award for excellent achievements in teaching, research and studies	TAU graduate school

Posters and Oral Presentations (international meetings)

Levy Karin E , Mirdita M, & Soeding J. MetaEuk – sensitive, high-throughput gene discovery and annotation for large-scale eukaryotic metagenomics. Microbiome COSI. <i>ISMB/ECCB</i> . July 21-25, 2019, Basel, Switzerland.	talk
Levy Karin E , Wicke S, Pupko T, & Mayrose I. An integrated model of phenotypic trait changes and site-specific sequence evolution. Mayr symposium. <i>Evolution</i> . June 23-27, 2017, Portland, Oregon, USA.	talk
Levy Karin E , Wicke S, Pupko T, & Mayrose I. An integrated model of phenotypic trait changes and site-specific sequence evolution. <i>SMBE</i> . July 2-6, 2017, Austin, Texas, USA.	poster
Levy Karin E* , Rabin A*, Ashkenazy H, Shkedy D, Avram O, Cartwright R, & Pupko T. Inferring indel parameters using a simulation-based approach. <i>SMBE</i> . July 12-16, 2015, Vienna, Austria.	poster
Levy Karin E , Susko E, & Pupko T. Alignment errors strongly impact likelihood-based tests for comparing topologies. Fitch symposium. <i>SMBE</i> . June 8-12, 2014, San Juan, Puerto Rico, USA.	talk

Student supervision

Vladyslav Dembrovskyi	The EukBook project: Large-scale search for novel eukaryotic proteins from public sequencing data	MSc thesis Oct19 – Apr20
-----------------------	---	--------------------------

Teaching Experience

2013 – 2015	Introductory course in Math for Biology students (8888-42002) I developed and taught a course aiming to better prepare new Biology undergrads for the first year of their studies.	Kahanoff Foundation, Faculty of Life Sciences, TAU
2012 – 2016 (fall semesters)	Perl Programming for Biology (0455-3065) I was responsible for the entire course for which I received an award from the Tel-Aviv University Graduate school.	Faculty of Life Sciences, TAU
Oct 2010 – Jun 2011	Computer Science for middle school students As part of my studies for an additional B.Sc in Computer Science, I developed lesson plans and taught for a year on a weekly basis	Bialik Rogozin School, Tel-Aviv

Academic Experience

2015, 2016	Visiting scholar at the Molecular Evolution institute, Heinrich-Heine-Universität, Düsseldorf, Germany
2016	Visiting scholar at the IEB, Westfälische Wilhelms-Universität, Münster, Germany

Referee Service (for scientific journals)

<i>Journal of Molecular Biology & Evolution</i>	01.2019, 03.2020
<i>Journal of Molecular Evolution</i>	06.2016, 12.2017, 06.2018
<i>Journal of Microbial Genomics</i>	02.2016
<i>Journal of BMC Evolutionary Biology</i>	06.2015, 09.2016, 01.2018
<i>Journal of Bioinformatics</i>	04.2015

Employment

2011 – 2012	Computational genomics scientist	Evogene Ltd.
Nov 2007 – Mar 2008	Molecular biology researcher	Prof. Gil Segal's lab, Faculty of Life Sciences TAU
2005 – 2006	Business intelligence researcher	Adkit Ltd.

Non-Academic Activity

2011 – 2015	Volunteer at the open clinic	Physicians for Human Rights
2014 – 2015	Volunteer private tutor for math	
Feb 2014 – Jul 2014	Volunteer computers instructor	Migrant Worker & Refugee Community Education Center (CEC)
Oct 2013 – Jan 2014	Volunteer Hebrew teacher	CEC