Eli Levy Karin

June 2019

Max-Planck Institute for Biophysical Chemistry

Am Fassberg 11, Göttingen 37077, Germany

elilevy@post.tau.ac.il

Education

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

Publications

* denotes equal contribution

13   <u>Levy Karin E</u>, Mirdita M, & Söding J. MetaEuk - sensitive, high-throughput gene discovery and annotation for large-scale eukaryotic metagenomics. 2019; *submitted*.

12   <u>Levy Karin E</u>, Ashkenazy H, Hein J, & Pupko T. A simulation-based approach to statistical alignment. *Systematic Biology*. 2019; 2: 252-266.

11   Ashkenazy H, Sela I, <u>Levy Karin E</u>, Landan G, & Pupko T. Multiple sequence alignment averaging improves phylogeny reconstruction. *Systematic Biology*. 2019; 1: 117-130.

10   Mushegian A, <u>Levy Karin E</u>, & 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, <u>Levy Karin E</u>, Pupko T, & Hazkani-Covo E. The prevalence and evolutionary conservation of inverted repeats in proteobacteria. Genome Biology and Evolution. 2018; 3: 918–927.

8   <u>Levy Karin E</u>*, 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*, <u>Levy Karin E</u>*, 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   <u>Levy Karin E</u>, 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 parabasalian 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 – 2019	**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, *Future – Bioinformatics* 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. *ISMB/ECCB*. 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. *Evolution*. 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. *SMBE*. 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. *SMBE*. 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. *SMBE*. June 8-12, 2014, San Juan, Puerto Rico, USA.	talk

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)

Journal of *Molecular Evolution*	Dec 2017
Journal of *Molecular Evolution*	Jun 2016
Journal of *Microbial Genomics*	Feb 2016
Journal of *BMC Evolutionary Biology*	Jun 2015, Sep 2016
Journal of *Bioinformatics*	Apr 2015

Employment

2011 – 2012	**Computational genomics scientist** Developed software for the analysis of biological data.	Evogene Ltd.
Nov 2007 – Mar 2008	**Molecular biology researcher** Studied function of genes in the bacterium *Legionella pneumophila* at Prof. Segal's lab.	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 and Refugee Community Education Center (CEC)
Oct 2013 – Jan 2014	Volunteer Hebrew teacher	CEC