Eli Levy Karin

Scientist, ELKMO (CVR 43917897)   https://elileka.github.io/   eli.levy.karin@gmail.com

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Education

2018 – 2020	**Postdoc**. Advisor: Dr. Johannes Söding Focus: methods and tools development for eukaryotic metagenomic analysis	Quantitative & Computational Biology, MPIBPC
2013 – 2017	**Ph.D**. Advisors: Prof. Tal Pupko and Prof. Itay Mayrose Dissertation: *Statistical Techniques in Molecular Evolution: Improving in-silico Sequence Simulations & Detecting Genotype-Phenotype Associations*	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**)	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

22   Levy Karin E & Steinegger M. Cutting edge deep-learning based tools for metagenomic research. *National Science Review*. 2025; 10.1093/nsr/nwaf056.

21   Kim RS, Levy Karin E, Mirdita M, Chikhi R & Steinegger M. BFVD—a large repository of predicted viral protein structures. *Nucleic Acids Research*. 2025; 53:D340–D347; 10.1093/nar/gkae1119.

20   Kim W, Mirdita M, Levy Karin E, Gilchrist CL, Schweke H, Söding J, Levy E & Steinegger M. Rapid and Sensitive Protein Complex Alignment with Foldseek-Multimer. *Nature Methods*. 2025; 10.1038/s41592-025-02593-7.

19   Kim G*, Lee S*, Levy Karin E*, Kim H, Moriwaki Y, Ovchinnikov S, Steinegger M & Mirdita M. Easy and accurate protein structure prediction using ColabFold. *Nature Protocols*. 2024; 10.1038/s41596-024-01060-5

18   Lee S, Kim G, Levy Karin E, Mirdita M, Park S, Chikhi R, Babaian A, Kryshtafovych A & Steinegger M. Petabase-Scale Homology Search for Structure Prediction. *Cold Spring Harbor perspectives in biology*. 2024; 16(5), p.a041465

17   Raghavan V, Eichele G, Larink O, Levy Karin E, & Söding J. RNA sequencing indicates widespread conservation of circadian clocks in marine zooplankton. *NAR Genomics and Bioinformatics.* 2023; 10.1093/nargab/lqad007.

16   Mirdita M, Steinegger M, Breitwieser F, Söding J+, & Levy Karin E+. Fast and sensitive taxonomic assignment to metagenomic contigs. *Bioinformatics*. 2021; 18:3029–3031.

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. *Bioinformatics*. 2021; 19:3364–3366.

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. *Systematic Biology*. 2021; 3:608–622.

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*, <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   <u>Levy Karin E</u>*, 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, <u>Levy Karin E</u>, 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   <u>Levy Karin E</u>*, 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   <u>Levy Karin E</u>, 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, <u>Levy Karin E</u>, Burstein D, & Pupko T. CoPAP: co-evolution of presence-absence patterns. *Nucleic Acids Research*. 2013; 41:W232-W237.

Languages

Hebrew	Native
English	Fluent, TOEFL score 116/120 (equivalent to CEFR C2)
Danish	Fluent, PD3 score 12/12 (equivalent to CEFR B2); self-taught
German	Advanced; self-taught
C/C++	>3 years' experience; see for example https://github.com/soedinglab/metaeuk
R	>5 years' experience; mainly for plotting and statistical analysis
Python	1 year's experience
Perl	>5 years' experience

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 & Evolution
2017	Travel scholarship	Constantiner Institute
2016	Travel scholarship	Manna Center, 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 & 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)

<u>Levy Karin E</u>, Mirdita M, & Soeding J. MetaEuk – sensitive, high-throughput gene discovery and annotation for   talk

large-scale eukaryotic metagenomics. Microbiome COSI. *ISMB/ECCB*. July 21-25, 2019, Basel, Switzerland.

Levy Karin E, Wicke S, Pupko T, & Mayrose I. An integrated model of phenotypic trait changes and site-specific   talk
sequence evolution. Mayr symposium. *Evolution*. June 23-27, 2017, Portland, Oregon, USA.

Levy Karin E, Wicke S, Pupko T, & Mayrose I. An integrated model of phenotypic trait changes and site-specific   poster
sequence evolution. *SMBE*. July 2-6, 2017, Austin, Texas, USA.

Levy Karin E*, Rabin A*, Ashkenazy H, Shkedy D, Avram O, Cartwright R, & Pupko T. Inferring indel parameters using   poster
a simulation-based approach. *SMBE*. July 12-16, 2015, Vienna, Austria.

Levy Karin E, Susko E, & Pupko T. Alignment errors strongly impact likelihood-based tests for comparing topologies.   talk
Fitch symposium. *SMBE*. June 8-12, 2014, San Juan, Puerto Rico, USA.

Student supervision

Vladyslav Dembrovskyi	The EukBook project: Large-scale search for novel eukaryotic proteins from public sequencing data	M.Sc 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 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 Biology & Evolution*	01.2019, 03.2020
Journal of *Molecular Evolution*	06.2016, 12.2017, 06.2018
Journal of *Microbial Genomics*	02.2016
Journal of *BMC Evolutionary Biology*	06.2015, 09.2016, 01.2018
Journal of *Bioinformatics*	04.2015

Employment

2023 – present	**Independent scientific consultant**	ELKMO
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

2022 – 2024	Authored a children's book	כך שמעה הלטאה
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