Eli Levy Karin Jul 2024
Scientist, ELKMO (CVR 43917897) https://elileka.github.io/ eli.levy.karin@gmail.com

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	Faculty of Life Sciences, TAU
	Dissertation: *Statistical Techniques in Molecular Evolution: Improving in-silico Sequence Simulations & 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
2005 – 2008	**B.Sc** in **Biology**. Grade average: 90	Faculty of Life Sciences, TAU

Publications

** denotes equal contribution / ⁺ denotes co-correspondence*

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. *BioRxiv*. 2024. DOI: 10.1101/2024.04.14.589414

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. *Submitted*. 2023. DOI: 10.21203/rs.3.pex-2490/v1

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*, 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 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.

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)

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

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