

Education

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| 2018 – 2020 | 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 Ruppin’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

- 17 Raghavan V, Eichele G, Larink O, [Levy Karin E](#), & Söding J. RNA sequencing indicates widespread conservation of circadian clocks in marine zooplankton. *NAR*. Accepted 2022.
- 16 Mirdita M, Steinegger M, Breitwieser F, Söding J*, & [Levy Karin E*](#). Fast and sensitive taxonomic assignment to metagenomic contigs. *Bioinformatics*. 2021. 10.1093/bioinformatics/btab184
- 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. 10.1093/bioinformatics/btab222
- 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. *Accepted to Systematic Biology*. 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

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| 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)

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| <u>Levy Karin E</u> , 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 |
| <u>Levy Karin E</u> , 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 |
| <u>Levy Karin E</u> , 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. *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

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

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| 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

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| 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)

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

Employment

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| 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

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| 2011 – 2015 | Volunteer at the open clinic | Physicians for Human Rights |
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| 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 |