

Mohammed El-Kebir

Associate Professor

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Research interests

Combinatorial optimization and its applications to cancer and infection genomics, integer linear programming, exact algorithms, graph algorithms, cancer phylogenetics, intra-tumor heterogeneity, biological network analysis.

Education

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| 2010–2015 | Centrum Wiskunde & Informatica/VU University Amsterdam, The Netherlands.
Ph.D. in Computer Science and Bioinformatics
Thesis: Networks, modules and breeding schedules: Applications of Combinatorial Optimization to Computational Biology
Advisors: Drs. G. W. Klau and J. Heringa |
| 2006–2010 | VU University Amsterdam, The Netherlands.
M.Sc. in Bioinformatics, <i>cum laude</i> .
Thesis: Modeling Tuberculosis in Lung and Central Nervous System
Advisors: Drs. D. Kirschner, M. van der Kuip, A. M. van Furth |
| 2007–2009 | Eindhoven University of Technology, The Netherlands.
M.Sc. in Computer Science and Engineering, <i>cum laude</i> .
Thesis: Crossing Schedule Optimization
Advisors: Drs. M. T. de Berg and J. B. Buntjer |
| 2003–2006 | Eindhoven University of Technology, The Netherlands.
B.Sc. in Computer Science and Engineering. |

Honors and Awards

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| 2025 | ◦ Cancer Center at Illinois' (CCIL) Faculty Leadership Development Program (FLDP) |
| 2024 | ◦ Excellence in Guiding Undergraduate Research Award, UIUC Campus Awards |
| 2021 | ◦ National Science Foundation's CAREER Award
◦ Listed in "List of Teachers Ranked as Excellent by Their Students" for CS 598MEB: Computational Cancer Genomics (Spring 2019, Spring 2020, Spring 2021) |
| 2019 | ◦ Collins Scholar, Grainger College of Engineering, Academy for Excellence in Engineering Education, UIUC |

- 2015
 - BioSB Young Investigator Award for best Ph.D. thesis in computational biology in the Netherlands
 - ISCB ISMB/ECCB Travel Fellowship
- 2014
 - Honorable Mention for Best Paper Award (BioVis 2014)
- 2012
 - ISCB-RECOMB Travel Fellowship
- 2009
 - VU FEW Free mover grant and KNCV Tuberculosis Foundation grant

Positions

- 2024–present
 - Siebel School of Computing and Data Science, University of Illinois at Urbana-Champaign, Urbana, IL, USA.**
 - Associate Professor.* Affiliate appointments in National Center of Supercomputing Applications, Department of Electrical and Computer Engineering, Institute of Genomic Biology (Infection Genomics of One Health [IGOH] and Center for Artificial Intelligence and Modeling [CAIM] themes).
- 2018–2024
 - Department of Computer Science, University of Illinois at Urbana-Champaign, Urbana, IL, USA.**
 - Assistant Professor.* Affiliate appointments in National Center of Supercomputing Applications, Department of Electrical and Computer Engineering, Institute of Genomic Biology (Infection Genomics of One Health [IGOH] and Center for Artificial Intelligence and Modeling [CAIM] themes).
- 2016–2017
 - Department of Computer Science, Princeton University, Princeton, NJ, USA.**
 - Postdoctoral research associate.*
- 2014–2016
 - Department of Computer Science and Center for Computational Molecular Biology, Brown University, Providence, RI, USA.**
 - Postdoctoral research associate.*

Research Support

- 2021
 - ‘CAREER: Algorithms for Comprehensive and Cost-effective Cancer Phylogeny Inference from Multi-omics Single-cell Sequencing Data’. *National Science Foundation (NSF 2046488), CISE Directorate, Division of Computing and Communication Foundations.* PI: M. El-Kebir. Budget: \$500,000. Award period: 04/01/2021–03/31/2026.
 - ‘Algorithms for Single-cell Cancer Phylogenetics’. *Greg Gulick Honorary Research Awards.* PI: M. El-Kebir. Budget: \$25,000 (AWS credits). Award period: 09/01/2021–10/31/2023.
 - ‘Workflows and Tools for Visualizing Tumor Phylogenies in Metastatic Breast Cancer’. *Cancer Center at Illinois (CCIL).* Seed funding program. PI: M. El-Kebir. co-PI: C. Blatti (Research Scientist, NCSA, UIUC), Z. Madak-Erdogan (Assoc. Professor, FSHN, UIUC). Budget: \$198,905. Award period: 07/01/2021–06/30/2023.
 - ‘Mayo Clinic and Illinois Alliance Fellowship for Technology-Based Healthcare Research’. *Interdisciplinary Health Science Institute, University of Illinois at Urbana-Champaign.* PIs: N. Chia (Assoc. Professor, Mayo), M. El-Kebir. Budget: \$40,000. Award period: 01/16/2021–01/15/2023.
- 2020
 - ‘RAPID: Deciphering Within-host Diversity and Multi-strain Infection in COVID-19’. *National Science Foundation (NSF 2027669), CISE Directorate, Division of Computing and Communication Foundations.* PI: M. El-Kebir. co-PI: J. Peng (Assist. Professor, CS, UIUC). Budget: \$100,000. Award period: 05/15/2020–05/14/2021.

- 2019
- ‘CRII: AF: Towards an Accurate and Complete Characterization of the Solution Space in Phylogeny Estimation from Mixed Samples’. *National Science Foundation (NSF 1850502), CISE Directorate, Division of Computing and Communication Foundations*. PI: M. El-Kebir. Budget: \$174,999. Award period: 06/15/2019–05/30/2021.
 - ‘Mayo Clinic and Illinois Alliance Fellowship for Technology-Based Healthcare Research’. *Interdisciplinary Health Science Institute, University of Illinois at Urbana-Champaign*. PIs: N. Chia (Assoc. Professor, Mayo), S. Koyejo (Assist. Professor, CS, UIUC), M. El-Kebir. Budget: \$40,000. Award period: 08/16/2019–08/15/2021.
 - ‘Algorithms for Experimental Study Design in Cancer Genomics’, *Center for Computational Biotechnology and Genomic Medicine (CCBGM)*. PI: M. El-Kebir. co-PIs: N. Chia (Assoc. Professor, Mayo), S. Koyejo (Assist. Professor, CS, UIUC). Budget: \$120,000. Award period: 01/01/2019–12/31/2020.

Publications

Author order generally follows authorship convention in biology, where the first author carried out the majority of the research (joint first authorship is indicated by ‘*’) and the corresponding author supervised and/or conceived the project (indicated by ‘†’). Advised students are indicated in boldface. Many of the papers listed below first appeared in a conference and later in a journal. Only the journal version (with an additional indication of the conference) is listed if the two versions are very similar in content.

Edited conference proceedings

- 2021 | 21st International Workshop on Algorithms in Bioinformatics, WABI 2021, August 2–4, 2021, Virtual Conference. Edited by Alessandra Carbone and Mohammed El-Kebir.

Peer-reviewed journal

- 2026 | **Y. Qi**, H. Schmidt and M. El-Kebir[†]. Inferring and summarizing tumor phylogenies from bulk DNA data. *Algorithms Molecular Biology*. Extended version of WABI 2024 paper.
- L.L. Weber**, **A. Hart**, I. Ochoa[†] and M. El-Kebir[†]. Pharming: Joint Clonal Tree Reconstruction of Single-Nucleotide Variant and Copy Number Aberration Evolution from Single-Cell DNA Sequencing of Tumors. *Journal of Computational Biology* 33, no. 1: 2–18. Extended version of Research in Computational Molecular Biology (RECOMB) 2025 paper.
- 2025 | H. Schmidt*, **Y. Qi***, B.J. Raphael and M. El-Kebir[†]. Fast tumor phylogeny regression via tree-structured dual dynamic programming. *Bioinformatics* 41(Supplement_1), i170–i179, 2025. Special Issue for Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2025.
- V. Vijayakumar[†], T. Joshi, L. Elkhadragey, L.B. Schook, R.C. Gaba, M. El-Kebir and K.M. Schachtschneider. Development of a whole-exome sequencing kit to facilitate porcine biomedical research. *Genome Biology* 26: 118.
- S. Ivanovic**, and M. El-Kebir[†]. CNRein: an evolution-aware deep reinforcement learning algorithm for single-cell DNA copy number calling. *Genome Biology* 26, no. 1: 86.
- 2024 | **L.L. Weber**, D. Reiman, **M.S. Roddur**, **Y. Qi**, M. El-Kebir[†] and A.A. Khan[†]. Isotype-aware inference of B cell clonal lineage trees from single-cell sequencing data. *Cell Genomics*. Extended version of Research in Computational Molecular Biology (RECOMB) 2024 paper.
- Y. Qi**, S. Snir and M. El-Kebir[†]. Enforcing Temporal Consistency in Migration History Inference. *Journal of Computational Biology* 31, no. 5: 396–415. Extended version of WABI 2023 paper.

- X. Gu, Y. Qi** and **M. El-Kebir**[†]. DERNA Enables Pareto Optimal RNA Design. *Journal of Computational Biology* 31, no. 3: 179-196. Extended version of WABI 2023 paper.
- Y. Qi** and **M. El-Kebir**[†]. Consensus Tree Under the Ancestor–Descendant Distance is NP-Hard. *Journal of Computational Biology* 31, no. 1: 58–70.
- 2023 **L.L. Weber**^{*}, **C. Zhang**^{*}, I. Ochoa[†] and **M. El-Kebir**[†]. Phertilizer: Growing a clonal tree from ultra-low coverage single-cell DNA sequencing of tumors. *PLOS Computational Biology* 19, no. 10: e1011544, 2023. Extended version of RECOMB Computational Cancer Biology (RECOMB-CCB) 2023 paper.
- S. Ivanovic** and **M. El-Kebir**[†]. Modeling and Predicting Cancer Clonal Evolution with Reinforcement Learning. *Genome Research*, 33: 1078–1088. Extended version of Research in Computational Molecular Biology (RECOMB) 2023 paper.
- M. Stroet, B. Caron, M.S. Engler, J. van der Woning, A. Kauffmann, M. van Dijk, **M. El-Kebir**, K.M. Visscher, J. Holownia, C. Macfarlane, B.J. Bennion, S. Gelpi-Dominguez, F.C. Lightstone, T. van der Storm, D.P. Geerke, A.E. Mark, G.W. Klau. OFraMP: A Fragment-Based Tool to Facilitate the Parametrization of Large Molecules. *Journal of Computer-Aided Molecular Design*, June 13, 2023.
- 2022 **Z. Lalani**^{*}, **G. Chu**^{*}, S. Hsu, **S. Kagawa**, **M. Xiang**, S. Zaccaria[†] and **M. El-Kebir**[†]. CNAViz: An interactive webtool for user-guided segmentation of tumor DNA sequencing data. *PLOS Computational Biology* 18, no. 10 (October 13, 2022): e1010614, 2022. Invited journal version of RECOMB Computational Cancer Biology (RECOMB-CCB) 2022 paper.
- C. Zhang**^{*}, **P. Sashittal**^{*}, **M. Xiang**, **Y. Zhang**, **A. Kazi** and **M. El-Kebir**[†]. Accurate Identification of Transcription Regulatory Sequences and Genes in Coronaviruses. *Molecular Biology and Evolution* 39, no. 7, July 2022. Extended version of Research in Computational Molecular Biology (RECOMB) 2022 paper.
- P. Sashittal**, S. Zaccaria and **M. El-Kebir**[†]. Parsimonious Clone Tree Integration in Cancer. *Algorithms for Molecular Biology* 17, no. 1 (2022): 3. Extended version of Workshop on Algorithms in Bioinformatics (WABI) 2021 paper.
- C. Oh^{*}, **P. Sashittal**^{*}, A. Zhou, L. Wang, **M. El-Kebir**[†], and Thanh H. Nguyen[†]. Design of SARS-CoV-2 Variant-Specific PCR Assays Considering Regional and Temporal Characteristics. *Applied and Environmental Microbiology*, March 14, 2022, e02289-21.
- 2021 **P. Sashittal**, **C. Zhang**, J. Peng and **M. El-Kebir**[†]. Jumper Enables Discontinuous Transcript Assembly in Coronaviruses. *Nature Communications* 12, no. 1 (December 2021): 6728.
- G. Satas^{*}, S. Zaccaria^{*}, **M. El-Kebir**^{*†} and B.J. Raphael[†]. DeCiFering the elusive cancer cell fraction in tumor heterogeneity and evolution. *Cell Systems*, 12:1004–1018, 2021. Published online August 2021. Extended version of selected papers that appeared in Research in Computational Molecular Biology (RECOMB) 2021.
- L.L. Weber**^{*}, **P. Sashittal**^{*} and **M. El-Kebir**[†]. doubletD: detecting doublets in single-cell DNA sequencing data. *Bioinformatics*. 37(Supplement_1):i214-i221, 2021. Special issue for Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2021.
- L.L. Weber** and **M. El-Kebir**[†]. Distinguishing linear and branched evolution given single-cell DNA sequencing data of tumors. *Algorithms for Molecular Biology*. 16(1):14, 2021. Extended version of Workshop on Algorithms in Bioinformatics (WABI) 2020 paper.
- C. Zhang**, **M. El-Kebir**[†] and I. Ochoa[†]. Moss enables high sensitivity single-nucleotide variant calling from multiple bulk DNA tumor samples. *Nature Communications*, 12(1):2204, 2021.

- S.S. Patel, **A. Sandur**, **M. El-Kebir**, R.C. Gaba, L.B. Schook and K.M. Schachtschneider. Transcriptional Profiling of Porcine HCC Xenografts Provides Insights Into Tumor Cell Microenvironment Signaling. *Frontiers in Genetics*, 12, 2021.
- 2020 **S. Christensen**, **J. Kim**, N. Chia, O. Koyejo and **M. El-Kebir**[†]. Detecting evolutionary patterns of cancers using consensus trees. *Bioinformatics*, 36:i684–i691, 2020. Special issue for European Conference on Computational Biology (ECCB) 2020.
- L.L. Weber**^{*}, **N. Aguse**^{*}, N. Chia and **M. El-Kebir**[†]. PhyDOSE: Design of Follow-up Single-cell Sequencing Experiments of Tumors. *PLOS Computational Biology*, 16(10):e1008240, 2020. Invited journal version of RECOMB Computational Cancer Biology (RECOMB-CCB) 2020 conference paper.
- R. C. Gaba, L. Elkhadragy, F.E. Boas, S. Chaki, H.H. Chen, **M. El-Kebir**, K.D. Garcia, E.F. Giurini, G. Guzman, F.V. LoBianco, M.F. Neto, J.L. Newson, A. Qazi, M. Regan, L.A. und, R.M. Schwind, M.C. Stewart, F.M. Thomas, H.E. Whiteley, **J. Wu**, L.B. Schook and K.M. Schachtschneider. Development and comprehensive characterization of porcine hepatocellular carcinoma for translational liver cancer investigation. *Oncotarget* 11:2686–2701, 2020.
- J. Wu** and **M. El-Kebir**[†]. ClonArch: Visualizing the Spatial Clonal Architecture of Tumors. *Bioinformatics*, 36:i161–i168, 2020. Special issue for Intelligent Systems for Molecular Biology (ISMB) 2020.
- P. Sashittal** and **M. El-Kebir**[†]. Sampling and Summarizing Transmission Trees with Multi-strain Infections. *Bioinformatics*, 36:i362–i370, 2020. Special issue for Intelligent Systems for Molecular Biology (ISMB) 2020.
- 2019 **Y. Qi**, **D. Pradhan** and **M. El-Kebir**[†]. Implications of Non-uniqueness in Phylogenetic Deconvolution of Bulk DNA Samples of Tumors. *Algorithms for Molecular Biology*, 14:19, 2019. Extended version of RECOMB Comparative Genomics (RECOMB-CG) 2018 paper.
- N. Aguse**^{*}, **Y. Qi**^{*} and **M. El-Kebir**[†]. Summarizing the Solution Space in Tumor Phylogeny Inference by Multiple Consensus Trees. *Bioinformatics*, 35(14):i408–i446, 2019. Special issue for Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB) 2019.
- 2018 **M. El-Kebir**[†]. SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error. *Bioinformatics*, 34(17):i671–679, 2018. Special issue for European Conference on Computational Biology (ECCB) 2018.
- P. Spohr, K. Dinkla, G.W. Klau and **M. El-Kebir**[†]. eXamine: Visualizing annotated networks in Cytoscape. *F1000Research*, 7, 519, 2018.
- S. Zaccaria^{*}, **M. El-Kebir**^{*}, G.W. Klau, B.J. Raphael. Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. *Journal of Computational Biology*, 27(0), 2018. Extended version of Research in Computational Molecular Biology (RECOMB) 2017 paper.
- M. El-Kebir**, G. Satas and B.J. Raphael. Inferring parsimonious migration histories for metastatic cancers. *Nature Genetics*, 50:718–726, 2018.
- 2017 **M. El-Kebir**, B.J. Raphael, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi and R. Zeira. Complexity and algorithms for copy-number evolution problems. *Algorithms for Molecular Biology*, 12(1), 2017. Extended version of selected papers that appeared in Workshop on Algorithms in Bioinformatics (WABI) 2016.
- 2016 **The Computational Pan-Genomics Consortium**. Computational pan-genomics: status, promises and challenges. *Briefings in Bioinformatics*, bbw089, 2016.

- M. El-Kebir*, G. Satas*, L. Oesper, B.J. Raphael. Inferring the Mutational History of a Tumor using Multi-State Perfect Phylogeny Mixtures. *Cell Systems*, 3(1):43-53, 2016. Extended version of selected papers that appeared in Research in Computational Molecular Biology (RECOMB) 2016.
- A. May, B. W. Brandt, M. El-Kebir, G. W. Klau, E. Zaura, W. Crielaard, J. Heringa and S. Abeln. metaModules identifies key functional subnetworks in microbiome-related disease. *Bioinformatics*, 32(11):1678–1685, 2016.
- 2015 M. El-Kebir, J. Heringa and G. W. Klau. Natalie 2.0: Sparse Global Network Alignment as a Special Case of Quadratic Assignment. *Algorithms*, 8 (4), 1035-1051, 2015.
- M. El-Kebir*, H. Soueidan*, T. Hume*, D. Beisser, M. Dittrich, T. Müller, G. Blin, J. Heringa, M. Nikolski, L. F. A. Wessels, G. W. Klau. xHeinz: An algorithm for mining cross-species network modules under a flexible conservation model. *Bioinformatics*, 31(19):3147–3155, 2015.
- M. El-Kebir*, L. Oesper*, H. Acheson-Field, B. J. Raphael. Reconstruction of clonal trees and tumor composition from multi-sample sequencing data, *Bioinformatics*, 31(12):i62-i70, 2015. Special issue for Intelligent Systems for Molecular Biology (ISMB) 2015.
- 2014 K. Dinkla*, M. El-Kebir*, C.-I. Bucur, M. Siderius, M. J. Smit, M. A. Westenberg, and G. W. Klau. eXamine: Exploring annotated modules in networks. *BMC Bioinformatics*, 15(1):201, 2014. Extended version of selected papers that appeared in Symposium on Biological Data Visualization (BioVis) 2014.
- M. El-Kebir*, B. W. Brandt*, J. Heringa, and G. W. Klau. NatalieQ: A web server for protein-protein interaction network querying. *BMC Systems Biology*, 8(1):40, 2014.
- 2013 M. El-Kebir*, T. Marschall*, I. Wohlers*, M. Patterson, J. Heringa, A. Schönhuth, and G. W. Klau. Mapping proteins in the presence of paralogs using units of coevolution. *BMC Bioinformatics*, 14(Suppl 15):S18, 2013. Special issue for RECOMB Comparative Genomics (RECOMB-CG) 2013.
- M. El-Kebir*, M. van der Kuip*, A. M. van Furth, and D. E. Kirschner. Computational modeling of tuberculous meningitis reveals an important role for tumor necrosis factor- α . *Journal of Theoretical Biology*, 328(C):43–53, Mar. 2013.
- S. Canzar*, M. El-Kebir*, R. Pool, K. Elbassioni, A. K. Malde, A. E. Mark, D. P. Geerke, L. Stougie, and G. W. Klau. Charge Group Partitioning in Biomolecular Simulation. *Journal of Computational Biology*, 20(3):188–198, Mar. 2013. Extended version of Research in Computational Molecular Biology (RECOMB) 2013 paper.
- 2011 S. Marino, M. El-Kebir, and D. Kirschner. A hybrid multi-compartment model of granuloma formation and T cell priming in Tuberculosis. *Journal of Theoretical Biology*, 280(1):50–62, July 2011.
- M. Fallahi-Sichani, M. El-Kebir, S. Marino, D. E. Kirschner, and J. J. Linderman. Multiscale Computational Modeling Reveals a Critical Role for TNF-Receptor 1 Dynamics in Tuberculosis Granuloma Formation. *The Journal of Immunology*, 186(6):3472–3483, 2011.

Peer-reviewed conferences

Subsequent journal papers that appeared in conference proceedings first have been omitted in the following.

- 2026 **X. Gu**, **S. Ivanovic**, **D.W. Feng** and M. El-Kebir[†]. *Summarizing RNA Structural Ensembles via Maximum Agreement Secondary Structures*. Research in Computational Molecular Biology (RECOMB) 2026, Thessaloniki, Greece, May 26-29, 2026.

- S. Arasti, A.O.B. Şapcı, E. Rachtman, M. El-Kebir and S. Mirarab[†]. *Deconvolving Phylogenetic Distance Mixtures*. Research in Computational Molecular Biology (RECOMB) 2026, Thessaloniki, Greece, May 26-29, 2026.
- 2025 **D.W. Feng** and M. El-Kebir[†]. *Dolphin: A Combinatorial Algorithm for Identifying 1-Dollo Phylogenies in Cancer*. WABI 2025, Workshop on Algorithms in Bioinformatics, College Park, MD, Aug 20-22, 2025.
- M.S. Roddur**, **V. Ramavarapu**, A. Bunkum, A. Huebner, **R. Mineyev**, N. McGranahan, S. Zaccaria[†] and M. El-Kebir[†]. *Characterizing the Solution Space of Migration Histories of Metastatic Cancers with MACH2*. Research in Computational Molecular Biology (RECOMB) 2025, Seoul, Korea, April 26-29, 2025.
- 2022 M. El-Kebir[†], Q. Morris, L. Oesper, and S.C. Sahinalp. *Emerging Topics in Cancer Evolution*, PSB 2022, Pacific Symposium on Biocomputing. The Big Island of Hawaii, January 3-7, 2022.
- 2019 **S. Christensen**, M. D. M. Leiserson and M. El-Kebir[†]. *PhySigs: Phylogenetic Inference of Mutational Signature Dynamics*. PSB 2020, Pacific Symposium on Biocomputing, Mutational Signatures session, The Big Island of Hawaii, January 3-7, 2020.
- P. Sashittal** and M. El-Kebir[†]. *SharpTNI: Counting and Sampling Parsimonious Transmission Networks under a Weak Bottleneck*. RECOMB-CG 2019, RECOMB Comparative Genomics, Montpellier, France, October 1-4, 2019.
- 2018 M. El-Kebir[†]. *Parsimonious Migration History Problem: Complexity and Algorithms*. WABI 2018, Workshop on Algorithms in Bioinformatics, Helsinki, Finland, August 20-24, 2018.
- 2017 M. S. Engler, M. El-Kebir, A. E. Mark, D. P. Geerke and G. W. Klau. *Enumerating common molecular substructures*. GCB 2017, German Conference on Bioinformatics, Tübingen, Germany, September 18-20, 2017.
- 2011 M. El-Kebir, J. Heringa and G. W. Klau. *Lagrangian relaxation applied to sparse global network alignment*. PRIB 2011, International Conference on Pattern Recognition in Bioinformatics, Delft, The Netherlands, November 2-4 2011.
- S. Canzar* and M. El-Kebir*. *A mathematical programming approach to marker-assisted gene pyramiding*. WABI 2011, Workshop on Algorithms in Bioinformatics, Saarbrücken, Germany, September 5-7 2011, Lecture Notes in Computer Science 6833: 26–38.
- 2007 S. Schlobach, E. Blaauw, M. El-Kebir, A. ten Teije, F. Van Harmelen, *et al.* *Anytime classification by ontology approximation*. NFRSW 2007, New forms of reasoning for the Semantic Web: scalable, tolerant and dynamic, pages 60–74, 2007.

Peer-reviewed workshop

- 2020 M. El-Kebir[†], **J. Oh**, **Y. Qi** and **P. Sashittal**. *Counting and Sampling Problems in Computational Biology*. Model Counting Workshop (MCW) 2020, part of the International Conference on Theory and Applications of Satisfiability Testing (SAT) 2020, July 9th, 2020, virtual.

Other (editorials, opinions, etc.)

- 2022 B. Berger, D. Tian, W.V. Li, M. El-Kebir, A.I. Tomescu, R. Singh, N. Beerenwinkel, Y. Li, C. Boucher and Z. Bar-Joseph. What Are the Keys to Succeeding as a Computational Biologist in Today’s Research Climate? *Cell Systems* 13, no. 10 (October 2022): 781–85.

Invited talks

- 2025 **Comparing and Summarizing Cancer Phylogenies**
BIRS Workshop on Novel Mathematical Paradigm for Phylogenomics. Banff, Alberta, Canada, August 2025.
- Comparing and Summarizing Cancer Phylogenies**
NCI Spring School on Algorithmic Cancer Biology. Bethesda, Maryland, August 2025.
- Introduction to Integer Linear Programming**
Computational Genomics Summer Institute (CGSI) 2025. Los Angeles, California, July 2025.
- 2024 **Introduction to Integer Linear Programming**
Computational Genomics Summer Institute (CGSI) 2024. Los Angeles, California, July 2024.
- Introduction to RNA Design**
Computational Genomics Summer Institute (CGSI) 2024. Los Angeles, California, July 2024.
- Combinatorial Algorithms for Cancer Phylogenetics**
University College London, United Kingdom, June 2024.
- Combinatorial Algorithms for Cancer Phylogenetics**
Keynote talk at BioSB Conference, Egmond aan Zee, Netherlands, June 2024.
- TRIBAL: Tree Inference of B cell Clonal Lineages**
Moderna. Boston, Massachusetts, May 2024.
- Algorithms for RNA Design & Structure and Interaction Prediction**
Moderna. Boston, Massachusetts, May 2024.
- Advanced Integer Linear Programming for Cancer Phylogenetics**
NCI Spring School on Algorithmic Cancer Biology. Bethesda, Maryland, April 2024.
- Algorithms for Cancer Phylogenetics**
Center for Bioinformatics Research and IU's Bioinformatics Club, Indiana University. Bloomington, Indiana, February 2024.
- 2023 **Inferring Migration Histories of Metastatic Cancers**
Computational Genomics Summer Institute (CGSI) 2023. Los Angeles, California, July 2023.
- Inferring Migration Histories of Metastatic Cancers**
BIRS Workshop on Mathematical Methods in Cancer Biology, Evolution and Therapy. Banff, Alberta, Canada, May 2023.
- Combinatorial Algorithms for Cancer Phylogenetics**
NCI Spring School on Algorithmic Cancer Biology. Bethesda, Maryland, March 2023.
- 2022 **Accurate Identification of Transcription Regulatory Sequences and Genes in Coronaviruses**
International Society for Computational Biology (ISCB) / Society for Molecular Biology and Evolution (SMBE) Webinar. November 2022.
- Combinatorial Algorithms for Tumor Phylogenetics**
CRC Integromics Group at MD Anderson Cancer Center. Houston, Texas, October 2022.
- Accurate Identification of Transcription Regulatory Sequences and Genes in Coronaviruses**
Computational Genomics Summer Institute (CGSI) 2022. Los Angeles, California, July 2022.

- 2021 **Combinatorial Algorithms for Tumor Phylogenetics**
DePaul University. Department of Computer Science. Chicago, Illinois, October 2021 (virtual).
- Combinatorial Algorithms for Tumor Phylogenetics**
Sorbonne Université. Laboratory of Computational and Quantitative Biology. Paris, France, May 2021 (virtual).
- Combinatorial Algorithms for Tumor Phylogenetics**
Florida State University. Department of Computer Science. Tallahassee, FL, February 2021 (virtual).
- 2020 **Characterizing SARS-CoV-2 viral diversity within and between hosts**
Talk at the 9th Workshop on Computational Advances in Molecular Epidemiology (CAME), virtual, October 2020.
- 2019 **Implications of Non-uniqueness of Solutions in Cancer Phylogenetics**
University of Maryland College Park. Center for Bioinformatics and Computational Biology, College Park, MD, October, 2019.
- Summarizing the Solution Space in Tumor Phylogeny Inference by Multiple Consensus Trees**
Talk at RECOMB Computational Cancer Biology (RECOMB-CCB) 2019, Washington, DC, May 2019.
- SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error**
Late-breaking research talk at Intelligent Systems for Molecular Biology (ISMB) 2018, Chicago, IL, July 2018.
- Inferring Parsimonious Migration Histories for Metastatic Cancers**
Highlight talk at Intelligent Systems for Molecular Biology (ISMB) 2018, Chicago, IL, July 2018.
- Combinatorial Algorithms for Tumor Phylogenetics**
Indiana University Bloomington, Bloomington, IN, April 2018.
- 2017 **Combinatorial Algorithms for Tumor Phylogenetics**
Carnegie Mellon University, Pittsburgh, PA, May 2017.
- Combinatorial Algorithms for Tumor Phylogenetics**
Rice University, Houston, TX, April 2017.
- Combinatorial Algorithms for Tumor Phylogenetics**
University of Illinois at Urbana-Champaign, Urbana, IL, April 2017.
- 2016 **Inferring the Mutational History of a Tumor using Perfect Phylogeny Mixtures**
Univ. degli Studi di Milano-Bicocca, Milan, Italy, September 2016.
- An MILP formulation for the Variant Allele Frequency Factorization Problem**
Simons Institute for the Theory of Computing, Integer Linear Programming in Computational Biology workshop, Berkeley, CA, May 2016.
- Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing**
Simons Institute for the Theory of Computing, Computational Cancer Biology workshop, Berkeley, CA, February 2016.
- 2014 **Solving the maximum-weight connected subgraph problem**
Exact algorithms for bioinformatics meeting, Shonan Village Center, Japan, March 2014.

	Enumerating all maximal common connected subgraphs Exact algorithms for bioinformatics meeting, Shonan Village Center, Japan, March 2014.
2012	Marker-assisted gene pyramiding Rijk Zwaan B.V. (plant breeding company), Fijnaart, The Netherlands, December 2012.
	A web server for topology-aware global protein-protein interaction network comparison Talk at the Netherlands Bioinformatics conference (NBIC 2011), April 2012.
2011	Lagrangian relaxation applied to network alignment Talk at the International Conference on Operations Research (OR 2011), Zürich, Switzerland, September 2011.

Teaching Experience

Spring 2026	Introduction to Bioinformatics , CS 466 at UIUC (51 students).
Fall 2024	Introduction to Bioinformatics , CS 466 at UIUC (95 students).
Spring 2024	Computational Cancer Genomics , CS 598MEB at UIUC (15 students).
	Bioinformatics and Computation , CS 591BIO at UIUC (15 students).
Fall 2023	Introduction to Bioinformatics , CS 466 at UIUC (79 students).
Fall 2022	Introduction to Bioinformatics , CS 466 at UIUC (50 students).
	Bioinformatics and Computation , CS 591BIO at UIUC (10 students).
Spring 2022	Computational Cancer Genomics , CS 598MEB at UIUC (11 students).
Fall 2021	Introduction to Bioinformatics , CS 466 at UIUC (55 students).
Spring 2021	Computational Cancer Genomics , CS 598MEB at UIUC (13 students).
Fall 2020	Introduction to Bioinformatics , CS 466 at UIUC (62 students).
Spring 2020	Computational Cancer Genomics , CS 598MEB at UIUC (16 students).
Fall 2019	Introduction to Bioinformatics , CS 466 at UIUC (46 students).
Spring 2019	Computational Cancer Genomics , CS 598MEB at UIUC (13 students).
Fall 2018	Introduction to Bioinformatics , CS 466 at UIUC (36 students).

PhD thesis adviser

Former:

2024	Leah Weber, Ph.D. student, Computer Science, graduated 6/2024. Thesis title: Algorithms for single-cell phylogenetics to study tumor evolution and adaptive immune response. Now postdoc at MD Anderson Cancer Center.
	Yuanyuan Qi, Ph.D. student, Computer Science, graduated: 5/2024. Thesis title: Quantifying and summarizing tumor phylogeny solution spaces.
2023	Chuanyi Zhang, Ph.D student, Electrical and Computer Engineering, co-advised with Idoia Ochoa, graduated 5/2023. Thesis title: Algorithms for genomic variant identification and interpretation. Now Associate Scientist (Bioinformatics) at Regeneron.
2022	Juho Kim, Ph.D. student, Electrical and Computer Engineering, co-advised with Sanmi Koyejo, graduated 7/2022. Thesis title: Probabilistic subclonal reconstruction for cancer. Now Postdoctoral Research Fellow at the Institute for Systems Biology.
2020	Sarah Christensen, Ph.D. student, Computer Science, co-advised with Tandy Warnow, graduated 12/2020. Thesis title: Algorithms for phylogenetic tree correction in species and cancer evolution. Now Technical Program Manager at D.E. Shaw Research.

Current:

Mrinmoy Roddur, Ph.D. student, Computer Science, expected graduation: 2026. Topic: metastasis and transmission reconstruction.

Stefan Ivanovic, Ph.D. student, Computer Science, expected graduation: 2026. Topic: application of machine learning to cancer phylogenetics.

Xinyu Gu, Ph.D. student, Computer Science, expected graduation: 2029.

Olivia Davis, Ph.D. student, Computer Science, expected graduation: 2030. Olivia won the NSF Graduate Research Fellowship in 2026.

Thea Traw, Ph.D. student, Computer Science, expected graduation: 2030. Thea won the NSF Graduate Research Fellowship in 2026.

MS thesis adviser

Former:

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|------|---|
| 2024 | Nicole Dong, MS student, Computer Science, graduated 12/2024. Thesis title: Clone Tree Visualization. |
| 2021 | Palash Sashittal, MS student, Computer Science, graduated 8/2021. Thesis title: Algorithms for infection and cancer genomics. Now postdoc in the Department of Computer Science at Princeton University → Assistant Professor at Department of Computer Science, Virginia Tech. |
| 2020 | Nuraini Aguse, MS student, Computer Science, graduated 5/2020. Thesis title: Methods to summarize and reduce the solution space of tumor phylogeny inference. Won Siebel Scholar award in 2019. Now Software Engineer at Google. |
| | Jiaqi Wu, MS student, Computer Science, graduated 5/2020. Thesis title: Deciphering the heterogeneity and spatial architecture of tumors. Now Software Engineer at Facebook. |
| 2019 | Shunping Xie, MS student, Computer Science, graduated 5/2019. Towards characterizing the solution space of the 1-Dollo phylogeny problem. Now Software Engineer at Pony.ai. |

Graduate research mentor

While the previous sections listed advised thesis students, the following sections list research activities with more limited scope, typically in the form of a single-semester independent study. Any resulting publications are indicated.

Former:

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|------|--|
| 2024 | Anna Hart, Ph.D. student, Computer Science. Independent study in Fall 2023 and Spring 2024. Topic: simulator for single-cell DNA sequencing data of cancers. Now continuing Ph.D. student at UIUC CS. |
| 2023 | Vikram Ramavarapu, MS Bioinformatics student, Computer Science. Independent study in Spring and Summer 2023 and continuing research in Fall 2023. Topic: visualization of phylogenies and transmission networks in metastasis. |
| | Griffen Mustion, MS Bioinformatics student, Computer Science. Independent study in Spring 2023 and continuing research in Summer and Fall 2023. Topic: motif detection in viral RNA genomes. |
| | Xinyu Gu, MS Bioinformatics student, Computer Science. Independent study in Spring 2022, Fall 2022 and Spring 2023. Topic: mRNA design. Resulted in publication at WABI 2023. Now continuing PhD student at UIUC CS. |

2021	Sophia Yang, Ph.D. student, Computer Science. Independent study in Fall 2021. Topic: adapting sequence alignment algorithms for SQL query assessment in CS education. Resulted in publication at DataEd 2022 conference. Now continuing Ph.D. student at UIUC CS.
2020	James Willson, Ph.D. student, Computer Science. Independent study in Fall 2020. Topic: 1-Dollo phylogeny. Now continuing Ph.D. student at UIUC CS.
2019	Silas Hsu, Ph.D. student, Computer Science. Independent study in Spring 2019. Topic: visualization of copy-number aberrations in cancer genomics data. Resulted in publication in PLOS CB. Now continuing Ph.D. student at UIUC CS.
2018	Amitha Sandur, MS student, Computer Science (Bioinformatics). Independent study in Fall 2018. Co-advised with Kyle Schachtschneider (Research Assist. Professor, Radiology, UIC). Resulted in publication in <i>Frontiers in Genetics</i> . Now Bioinformatics Production Engineer at Natera.

Undergraduate research mentorship

Former:

2025	Daniel Feng, BS student, Computer Science. REU program at UIUC CS in Summer 2023 and independent study in Spring 2023, Fall 2023, Spring 2024, Fall 2024 and Spring 2025. Topic: 1-Dollo linear and branching phylogeny problem for cancer evolution. Daniel won the Goldwater Scholarship in 2024 and the NSF Graduate Research Fellowship in 2025. First author on publication at WABI 2025. Now Ph.D. student at Harvard Medical School.
2024	Sana Naffakh, BS student, Computer Science. CS STARS in Fall 2023 and Spring 2024. Topic: visualization of tumor phylogenies. Divya Koya, BS student, Computer Science. CS STARS in Fall 2023 and Spring 2024. Topic: visualization of tumor phylogenies.
2023	Samuil Donchev, BS student, Computer Science. Independent study in Fall 2022 and Spring 2023. Topic: identify <i>Mesoniviridae</i> transcription regulatory sequences and genes. Akul Joshi, BS student, Computer Science. Independent study in Spring 2023. Topic: visualization of phylogenies and transmission networks in metastasis.
2022	Keshav Gandhi, BS student, UIC Statistics. REU program at UIUC CS in Summer 2022, 2024 and 2025. Topic: phylogenetic deconvolution of PolyG data. Keshav won the Goldwater Scholarship in 2023. Mayank Hirani, BS student, Computer Science. REU program at UIUC CS in Summer 2022. Co-advised with Alicia Kraay (Assist. Professor, Department of Kinesiology and Community Health). Topic: within-host evolution in acute and chronic SARS-CoV-2 infections. Tyler Camp, BS student (Parkland College). GearUP program in Summer 2022. Topic: mining patterns of cancer clonal evolution using CloMu. Sophie Kish, BS student, Computer Science. Independent study in Spring 2022. Topic: relationship between two-state perfect phylogeny and distance-based phylogeny estimation. Michael Xiang, BS student, Computer Science. Independent study in Fall 2021 and Spring 2022. Topic: cancer genomics + web-based visual analytics. Co-author on two publications in PLOS CB and MBE. Nayonika Roy, BS student, Computer Science. CS STARS in Fall 2021 and Spring 2022. Topic: analysis of cancer genomics data. Michelle Jun, BS student, Computer Science. CS STARS in Fall 2021 and Spring 2022. Topic: analysis of cancer genomics data.

2021	<p>Yichi Zhang, BS student, Computer Science. Independent study in Fall 2021. Topic: web-based visual analytics. Co-author on publication in MBE.</p> <p>Ayesha Kazi, BS student, Computer Science. Independent study in Fall 2021. Topic: web-based visual analytics. Co-author on publication in MBE.</p> <p>Zubair Lalani, BS student, Computer Science. REU program at UIUC CS in Summer 2021. Topic: user-guided segmentation in cancer genomics. Resulted in first-author publication in PLOS CB.</p>
2020	<p>Smarak Pattnaik, BS student, Computer Science. REU program at UIUC CS in Summer 2020. Topic: single-cell cancer phylogenetics.</p> <p>Medha Patil, BS student, Computer Science. REU program at UIUC CS in Summer 2020. Topic: workflow development for SARS-CoV-2 genome analysis.</p> <p>Jackie Oh, BS student, Computer Science. Independent study in Spring 2020. Topic: sampling 1-Dollo solutions. Resulted in workshop paper at Model Counting Workshop (MCW) 2020.</p>

High-school research mentorship

Former:

2021	<p>Toluwanimi Aroyo, high-school student. NIH STEP-UP in Summer 2021. Now undergraduate at Princeton University.</p> <p>Keshav Gandhi, high-school student. researchHStart program at Cancer Center at Illinois in Summer 2021. Now undergraduate at UIC Statistics + Guaranteed Professional Program Admissions (to UIC MD program).</p> <p>Raneem Saadah, high-school student. researchHStart program at Cancer Center at Illinois in Summer 2021.</p>
2018	<p>Eman Zwawi, high-school student. researchHStart program at Cancer Center at Illinois (Summer 2018). Now undergraduate at UIUC MCB.</p>

Academic Service

Conference organization	<ul style="list-style-type: none"> ○ PC co-chair (RECOMB-CCB 2024) ○ Area co-chair for ‘General Computational Biology’ track (ISMB/ECCB 2023–2021) ○ Co-organizer NCI Spring School on Algorithmic Cancer Biology, 2025-2023 ○ Co-organizer of ‘Cancer Evolution’ workshop at PSB 2022 ○ PC co-chair (WABI 2021) ○ Poster chair (RECOMB 2021)
Editorial board	<ul style="list-style-type: none"> ○ PLOS Computational Biology ○ Journal of Computational Biology
Grant referee	<ul style="list-style-type: none"> ○ Panel member for National Science Foundation (2022, 2021) ○ Reviewer for Biodata Management and Analysis (BDMA) study section at NIH (2021) ○ Ad hoc reviewer for National Science Foundation (2021 [2x], 2020) ○ Ad hoc reviewer for National Science Centre, Poland (2021) ○ Ad hoc reviewer for Bordeaux University, G2P (2016)

Journal referee	<ul style="list-style-type: none"> ○ Nature Genetics (2025, 2024, 2023) ○ Nature Cancer (2022) ○ Genome Biology and Evolution (2026) ○ GigaScience (2022) ○ Biometrics (2022) ○ eBioMedicine (2022) ○ Journal of Computational Biology (2021) ○ Bioinformatics Advances (2021) ○ Microbial Genomics (2021) ○ Cell Reports Methods (2021) ○ Bioinformatics and Biology Insights (2021) ○ Genome Biology (2025, 2024, 2023 [2x], 2022 [2x], 2021, 2020) ○ Nature Communications (2026, 2025, 2024, 2023, 2022 [3x], 2021 [2x], 2020 [2x], 2019 [2x], 2018 [2x]) ○ Systematic Biology (2025, 2021, 2020) ○ Biostatistics (2020) ○ iScience (2022 [2x], 2020) ○ Journal of Graph Algorithms and Applications (2020) ○ Cell Systems (2020 [2x], 2019) ○ PLOS Computational Biology (2023, 2022 [1x guest editor, 2x reviewer], 2021 [1x guest editor, 3x reviewer], 2020 [1x guest editor, 2x reviewer], 2019 [4x], 2018, 2011) ○ Bioinformatics (2023, 2022, 2021 [2x], 2019 [3x], 2018 [2x], 2017) ○ Communications Biology (2018) ○ Genome Research (2025, 2023 [2x], 2018 [2x]) ○ F1000Research (2018) ○ PeerJ (2018) ○ IEEE/ACM Transactions on Computational Biology and Bioinformatics (2026, 2022, 2018, 2017) ○ BMC Bioinformatics (2017, 2014, 2012) ○ Fundamenta Informaticae (2017) ○ PLOS One (2016) ○ EURASIP Journal on Bioinformatics and Systems Biology (2016) ○ Frontiers in Bioengineering and Biotechnology (2014) ○ Computational Biology and Chemistry (2014) ○ Scientific Reports (2014) ○ Journal of Chemical Information and Modeling (2013) ○ Journal of the ACM (2011)
Conference program committee	<ul style="list-style-type: none"> ○ Conference on Research in Computational Molecular Biology (RECOMB, 2026–2020) ○ Pacific Symposium on Biocomputing (PSB, 2020) ○ Current Trends in Theory and Practice of Computer Science (SOFSEM, 2021, 2020) ○ RECOMB-Comparative Genomics, (RECOMB-CG, 2023–2021) ○ RECOMB-Computational Cancer Biology, (RECOMB-CCB, 2023–2022, 2020–2019) ○ Intelligent Systems in Molecular Biology (ISMB, 2026–2019) ○ Workshop on Algorithms in Biology (WABI, 2025–2021, 2019) ○ Great Lakes Bioinformatics Conference (GLBIO, 2023, 2021, 2019) ○ International Symposium on Mathematical and Computational Oncology (ISMCO, 2021–2019) ○ ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB, 2022–2018)

- Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB, 2019, 2017)
- European Conference on Computational Biology (ECCB, 2019, 2016)
- Bioinformatics and Computational Biology (BCB) area chair (Spring 2026, Fall 2024)
- Coordinator Future Faculty Fellows program (2023–present)
- Graduate awards committee, UIUC (2019–2023)
- Graduate studies committee, Computer Science, UIUC (2019–present)
- Ad hoc committee to conduct 5-year review of CS Department Head. Grainger College of Engineering, UIUC (2023)
- IGB 2024 retreat advisory committee (2023).
- Ad hoc subcommittee to review curriculum proposal. Grainger College of Engineering, UIUC (2022)
- Student awards committee, Computer Science, UIUC (2018–2019)
- Admissions committee, Carle-Illinois College of Medicine, UIUC (2019)

Software

I am committed to making software developed in my lab available on GitHub under an open source license.

- 2026 **Sapling** [<https://github.com/elkebir-group/Sapling>]
 Sapling is a method that infers a small set of backbone trees on a smaller subset of mutations that collectively summarize the entire set of possible phylogenies. Sapling can also grow given backbone trees into full phylogeny. Finally, Sapling can directly output full phylogenies up to a specified fraction $1 - \rho$ away from optimality.
 Implementation details: Python
- 2025 **Dolphin** [<https://github.com/elkebir-group/Dolphin>]
 Dolphin takes in a binary matrix of single cell SNV sequencing data and outputs a 1-Dollo phylogeny on this data, or a rooted tree on which each character/SNV is gained and lost at most once.
 Implementation details: C++
- fastppm** [<https://github.com/elkebir-group/fastppm>]
 fastppm (fast perfect phylogeny mixtures) is a library for the fast estimation of the (unknown) frequency matrix $F \in [0, 1]^{m \times n}$ given variant and total read count matrices $V, D \in \mathbb{N}^{m \times n}$ over a fixed n -clonal tree T . fastppm supports a variety of convex loss functions such as the ℓ_1 loss, ℓ_2 loss, the binomial loss, and the beta-binomial loss.
 Implementation details: C++, Python
- MACH2** [<https://github.com/elkebir-group/MACH2>]
 MACH2 is a computational tool for inferring optimal migration histories of metastatic cancer from clonal trees and observed clone locations. It supports multiple parsimony criteria, including the unobserved clone criterion, and guarantees optimality and completeness by systematically enumerating solutions.
 Implementation details: Python
- Pharming** [<https://github.com/elkebir-group/Pharming>]
 Farming is a heuristic algorithm to solve the joint clonal tree inference problem and infers a joint CNA and SNV tree from low pass single-cell DNA sequencing.
 Implementation details: C++, Python

- CNRein** [<https://github.com/elkebir-group/CNRein>]
 CNRein is a deep reinforcement learning based evolution-aware algorithm for haplotype-specific copy number calling on single cell DNA sequencing data.
 Implementation details: Python
- 2024 **Sapling** [<https://github.com/elkebir-group/Sapling>]
 Sapling is a method that infers a small set of backbone trees on a smaller subset of mutations that collectively summarize the entire set of possible phylogenies. Sapling can also grow given backbone trees into full phylogeny. Finally, Sapling can directly output full phylogenies up to a specified fraction $1 - \rho$ away from optimality.
 Implementation details: Python
- TRIBAL** [<https://github.com/elkebir-group/tribal>]
 TRIBAL is a method to infer B cell clonal lineages and isotype transition probabilities given isotypes and BCR sequences of a set of n B cells clustered into k clonotypes.
 Implementation details: Python
- 2023 **DERNA** [<https://github.com/elkebir-group/derna>]
 DERNA is an algorithm for designing an RNA sequence \mathbf{v} that encodes for a given target protein \mathbf{w} , balancing minimum free energy (MFE) and codon adaptation index (CAI). This plays an important role in messenger RNA (mRNA) vaccine design.
 Implementation details: C++
- Phertilizer** [<https://github.com/elkebir-group/phertilizer>]
 Phertilizer infers a clonal tree with SNV genotypes and a cell clustering given ultra-low coverage single-cell sequencing data.
 Implementation details: Python
- PCCH** [<https://github.com/elkebir-group/PCCH>]
 Parsimonious Consistent Comigration History (PCCH) is a computational framework for inferring migration history from a given phylogeny with leaves labeled with locations.
 Implementation details: Python
- CloMu** [<https://github.com/elkebir-group/clomu>]
 CloMu is a neural network based algorithm for modeling and predicting cancer clonal evolution.
 Implementation details: Python
- 2022 **CNAViz** [<https://elkebir-group.github.io/cnaviz>]
 CNAViz is an interactive webtool for user-guided segmentation of tumor DNA sequencing data.
 Implementation details: React, TypeScript
- CORSID** [<https://github.com/elkebir-group/corsid>]
 CORSID is a computational tool to simultaneously identify TRS sites, the core sequence and gene locations given an unannotated coronavirus genome sequence.
 Implementation details: Python.
- 2021 **JUMPER** [<https://github.com/elkebir-group/jumper>]
 JUMPER solves the Discontinuous Transcription Assembly problem to infer transcripts \mathcal{T} and their abundances \mathbf{c} with maximum likelihood given a *Nidovirales* alignment \mathcal{T} of (paired end) reads.
 Implementation details: Python

- PACTION** [<https://github.com/elkebir-group/paction>]
 PACTION solves the Parsimonious Clone Tree Integration problem of inferring clones $\Pi \subseteq \Pi_1 \times \Pi_2$, a clone tree T and proportions U given input clone trees T_1, T_2 with clones Π_1, Π_2 and proportions U_1, U_2 .
 Implementation details: Python
- doubletD** [<https://github.com/elkebir-group/doubletD>]
 Tool for detecting doublets in medium to high-coverage single-cell DNA sequencing data.
 Implementation details: Python
- 2020 **RECAP** [<https://github.com/elkebir-group/RECAP>]
 RECAP is an iterative, heuristic algorithm for solving the Multiple Choice Consensus Tree (MCCT) problem. The input is a family of sets of patient tumor phylogenies and an integer $k > 0$. RECAP then returns (i) a single expanded tumor phylogeny for each patient, (ii) an assignment of patients into k clusters, and (iii) a consensus tree for each cluster summarizing its repeated evolutionary patterns.
 Implementation details: C++
- Phyolin** [<https://github.com/elkebir-group/phyolin>]
 Phyolin is an algorithm to test for linear evolution given single-cell DNA sequencing data of a tumor. Specifically, Under the assumption that the phylogeny is linear, Phyolin outputs an estimated false negative rate, an inferred linear perfect phylogeny and classification of the tree topology based on the inputted threshold.
 Implementation details: C++, CPLEX
- TiTUS** [<https://github.com/elkebir-group/TiTUS>]
 TiTUS takes as input a timed pathogen phylogeny whose leaves are labeled by hosts along with epidemiological data. It counts and uniformly samples from the set of feasible interval vertex labelings of the timed phylogeny that satisfy the direct transmission constraint while supporting a weak transmission bottleneck.
 Implementation details: C++, Bash
- PhyDOSE** [<https://github.com/elkebir-group/PhyDOSE>]
 Given a set of candidate tumor phylogenies, a frequency matrix obtained from bulk data, and a confidence level, PhyDOSE computes the minimum number of single cells needed in a follow-up single-cell sequencing (SCS) experiment to determine the true phylogeny among the set of given phylogenies with the desired confidence level.
 Implementation details: C++, R
- 2019 **PhySigs** [<https://github.com/elkebir-group/PhySigs>]
 PhySigs solves the Tree-constrained Exposure inference problem to identify a small number of exposure shifts along the edges of a given tumor phylogeny. This problem arises in the analysis of the dynamics of mutational signature exposures in cancer, and has both therapeutic and basic science applications.
 Implementation details: R
- SharpTNI** [<https://github.com/elkebir-group/SharpTNI>]
 SharpTNI is a tool for counting and sampling solutions from the space of parsimonious transmission networks under a weak transmission bottleneck constraint. This problem arises in phylodynamic and phylogeographic analyses.
 Implementation details: C++, Bash

- MCT** [<https://github.com/elkebir-group/MCT>]
MCT contains exact and heuristic algorithms for solving the Multiple Consensus Tree problem. This problem arises in the summarization of the solution space in tumor phylogeny inference.
Implementation details: C++, CPLEX
- 2018 **PMH-S** [<https://github.com/elkebir-group/PMH-S>]
PMH-S is a fixed parameter tractable (FPT) algorithm for the Parsimonious Migration History problem for the case where the migration graph is restricted to a tree (i.e. $\mathcal{P} = \{S\}$). The asymptotic running time is exponential in the number m of locations.
Implementation details: C++
- SPhyR** [<https://github.com/elkebir-group/SPhyR>]
SPhyR is an algorithm for reconstructing phylogenetic trees from single-cell sequencing data. SPhyR employs the k -Dollo phylogeny model, where each single-nucleotide variant can only be gained once but lost k times.
Implementation details: C++, CPLEX
- 2017 **MACHINA** [<http://github.com/raphael-group/machina>]
MACHINA is a computational framework for inferring migration patterns between a primary tumor and metastases using DNA sequencing data.
Implementation details: C++, Gurobi
- 2016 **SPRUCE** [<http://github.com/raphael-group/spruce>]
Reconstruction of tumor evolutionary history of single-nucleotide variants and copy-number aberrations from multi-sample bulk sequencing data.
Implementation details: C++
- 2015 **AncesTree** [<http://github.com/raphael-group/AncesTree>]
Reconstruction of tumor evolutionary history of single-nucleotide variants from multi-sample bulk sequencing data.
Implementation details: C++, CPLEX
- 2014 **eXamine** [<http://apps.cytoscape.org/apps/examine>]
Cytoscape 3.x app that displays set membership as contours on top of a node-link layout.
Implementation details: Java
- xHeinz** [<https://github.com/ls-cwi/xheinz>]
Identification of conserved active modules.
Implementation details: C++, CPLEX
- Heinz 2.0** [<https://github.com/ls-cwi/heinz>]
Identification of active modules.
Implementation details: C++, CPLEX
- NatalieQ** [<http://ibi.vu.nl/programs/natalieq>]
Web server for protein-protein interaction network querying.
Implementation details: C++, Perl
- 2013 **Automated topology builder** [<http://compbio.chemistry.uq.edu.au/atb/>]
The ATB and Repository facilitates the development of molecular force fields for Molecular Dynamics or Monte Carlo simulations of biomolecular systems.
Implementation details: C++, Python
- 2011 **Natalie 2.0** [<https://github.com/ls-cwi/natalie>]
Method for network alignment based on Lagrangian relaxation.
Implementation details: C++

Last updated on April 14, 2026