

Mohammed El-Kebir

Assistant Professor

Department of Computer Science
University of Illinois at Urbana-Champaign
Urbana, IL 61801, USA

Phone: +1 217-300-7369
E-mail: melkebir@illinois.edu
WWW: <http://www.el-kebir.net>

Research interests

Combinatorial optimization, cancer genomics, intra-tumor heterogeneity, phylogenetics, integrative network analysis, computational biology, integer linear programming, exact algorithms, graph algorithms.

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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| 2021 | ◦ National Science Foundation’s CAREER Award |
| 2019 | ◦ National Science Foundation’s CRII Award
◦ Collins Scholar, Grainger College of Engineering, Academy for Excellence in Engineering Education, UIUC
◦ Listed in “List of Teachers Ranked as Excellent by Their Students” for CS 598MEB: Computational Cancer Genomics (Spring 2019, Spring 2020) |
| 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

- 2018–present **Department of Computer Science, University of Illinois at Urbana-Champaign, Urbana, IL, USA.**
Assistant Professor. Algorithm development and combinatorial optimization in computational biology.
 Affiliate appointments in National Center of Supercomputing Applications, Department of Electrical and Computer Engineering, Institute of Genomic Biology (Infection Genomics of One Health theme).
- 2016–2017 **Department of Computer Science, Princeton University, Princeton, NJ, USA.**
Postdoctoral research associate. Research on topics in computational cancer genomics, with a focus on algorithm development and combinatorial optimization. Advised by Ben Raphael.
- 2014–2016 **Department of Computer Science and Center for Computational Molecular Biology, Brown University, Providence, RI, USA.**
Postdoctoral research associate. Research on topics in computational cancer genomics, with a focus on algorithm development and combinatorial optimization. Advised by Ben Raphael.
- 2010–2014 **Life Sciences group, Centrum Wiskunde & Informatica (CWI), Amsterdam, The Netherlands.**
Centre for Integrative Bioinformatics VU (IBIVU), VU University Amsterdam, The Netherlands.
PhD Student. Research on various topics centered around combinatorial optimization problems in computational biology. Topics include network alignment, active module identification, prediction of protein-protein interactions using coevolution, charge group partitioning.
- February 2013 **School of Chemistry and Molecular Biosciences, University of Queensland, Brisbane, Australia.**
Visiting Scholar. Integrated the charge group partitioning algorithm in the Automated Topology Builder under the supervision of Alan Mark.
- July 2011 **Department of Microbiology and Immunology, University of Michigan, Medical School, Ann Arbor, USA.**
Visiting Scholar. Finished work on the agent-based model on tuberculous meningitis (El-Kebir et al., 2013) under the supervision of Denise Kirschner.
- 2009–2010 **Department of Microbiology and Immunology, University of Michigan, Medical School, Ann Arbor, USA.**
Visiting Scholar. Member of the Kirschner lab. Research and development of an agent-based model describing the immune response in tuberculous meningitis and pulmonary tuberculosis.
- 2009 **Keygene N.V., Wageningen, The Netherlands.**
Trainee. Performing research on a combinatorial optimization problem in plant breeding. Developed a heuristic for obtaining minimum-cost crossing schedules with respect to the number of generations, crossings and total population size. The heuristic is in active use by Keygene and its customers.

Research Support

- 2021 ‘CAREER: Algorithms for Comprehensive and Cost-effective Cancer Phylogeny Inference from Multi-omics Single-cell Sequencing Data’. *National Science Foundation (NSF), CISE Directorate, Division of Computing and Communication Foundations*.
PI: **M. El-Kebir** (Assist. Professor, CS, UIUC).
Budget: \$500,000. Award period: 04/01/2021–03/31/2026.
- ‘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** (Assist. Professor, CS, UIUC).
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), CISE Directorate, Division of Computing and Communication Foundations*.
PI: **M. El-Kebir** (Assist. Professor, CS, UIUC). 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), CISE Directorate, Division of Computing and Communication Foundations*.
PI: **M. El-Kebir** (Assist. Professor, CS, UIUC).
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. Koyeko (Assist. Professor, CS, UIUC), **M. El-Kebir** (Assist. Professor, CS, UIUC).
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** (Assist. Professor, CS, UIUC). co-PIs: N. Chia (Assoc. Professor, Mayo), S. Koyeko (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/last author supervised/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.

Peer-reviewed journal

- 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. 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-CCB 2020 conference paper.

- 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-CG 2018 paper entitled “On the Non-uniqueness of Solutions to the Perfect Phylogeny Mixture Problem”.
- N. Aguse^{*}, Y. Qi^{*}** and **M. El-Kebir[‡]**. Summarizing the Solution Space in Tumor Phylogeny Inference by Multiple Consensus Trees. *Bioinformatics*, 35(14):i408–i416, 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 RECOMB 2017 paper entitled “The Copy-Number Tree Mixture Deconvolution Problem and Applications to Multi-Sample Bulk Sequencing Tumor Data”.
- 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 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 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 RECOMB 2013 paper with identical title.
- 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, Mar. 2011.

Peer-reviewed conference

- 2021 **L. Weber***[†], **P. Sashittal*** and **M. El-Kebir**[‡]. *doubletD: Detecting doublets in single-cell DNA sequencing*. ISMB/ECCB 2021, Intelligent Systems in Molecular Biology/European Conference on Computational Biology, Lyon, France, July 27-30, 2021. Acceptance rate: 19%.
- G. Satas*, S. Zaccaria*, **M. El-Kebir***[‡] and B. J. Raphael[‡]. *DeCiFering the Elusive Cancer Cell Fraction in Tumor Heterogeneity and Evolution*. Invited to *Cell Systems*. RECOMB 2021, Annual International Conference on Research in Computational Molecular Biology, Padova, Italy, Aug 29-Sep 1, 2021. Acceptance rate: 21%.
- 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 **D. Pradhan** and **M. El-Kebir**^{†,‡}. *On the Non-uniqueness of Solutions to the Perfect Phylogeny Mixture Problem*.
RECOMB-CG 2018, RECOMB Comparative Genomics, Magog-Orford (Sherbrooke), Quebec, Canada, October 9-12, 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.
- S. Zaccaria*, **M. El-Kebir***, G. W. Klau, B. J. Raphael. *The Copy-Number Tree Mixture Deconvolution Problem and Applications to Multi-Sample Bulk Sequencing Tumor Data*.
RECOMB 2017, Annual International Conference on Research in Computational Molecular Biology, Hong Kong, China, May 3-7, 2017.
- 2016 **M. El-Kebir**, B.J. Raphael, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi, R. Zeira. *Copy-Number Evolution Problems: Complexity and Algorithms*.
WABI 2016, Workshop on Algorithms in Bioinformatics, Aarhus, Denmark, August 22-24 2016.
- M. El-Kebir**[†], G. Satas, L. Oesper, B. J. Raphael. *Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing*.
RECOMB 2016, Annual International Conference on Research in Computational Molecular Biology, Santa Monica, CA, April 18-21 2016.
- 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.

[†]oral presentation

Selected presentations

- 2021 **Combinatorial Algorithms for Tumor Phylogenetics**
Florida State University. Department of Computer Science. Tallahassee, FL, February 2021.
- 2020 **Characterizing SARS-CoV-2 viral diversity within and between hosts**
CAME: 9th Workshop on Computational Advances in Molecular Epidemiology, virtual, October 2020.
- Counting and Sampling Problems in Computational Biology**
Model Counting Workshop (MCW), part of SAT 2020, virtual, July 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**
RECOMB Computational Cancer Biology 2019, Washington, DC, May 2019.
- 2018 **SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error**
ECCB 2018, Athens, Greece, September 2018.
- Parsimonious Migration History Problem: Complexity and Algorithms**
WABI 2018, Helsinki, Finland, August 2018.
- SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error**
ISMB 2018, Chicago, IL, July 2018.
- Inferring Parsimonious Migration Histories for Metastatic Cancers**
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 Mixtures for Cancer Sequencing**
RECOMB 2016, Santa Monica, CA, April 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.

- 2015 **Reconstructing clonal trees**
ISMB/ECCB 2015, Dublin, Ireland, July 2015.
- 2014 **An integrative network analysis pipeline in Cytoscape**
BioNetVisA workshop, ECCB 2014, Strasbourg, France, September 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.
- 2013 **eXamine: Exploring annotated set-enriched modules in networks**
Poster presentation. Network Biology Symposium and Cytoscape Workshop, Institut Pasteur, Paris, France, October 2013.
- Charge group partitioning in the Automated Topology Builder**
Molecular dynamics group, University of Queensland, Brisbane, Australia, February 2013.
- 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**
Netherlands Bioinformatics conference (NBIC 2011), April 2012.
- 2011 **Lagrangian relaxation applied to network alignment**
International Conference on Operations Research (OR 2011), Zürich, Switzerland, September 2011.

Teaching Experience

- Spring 2021 **Computational Cancer Genomics**, CS 598MEB at UIUC (14 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).
- 2015 **Computational molecular biology**, CS1810 at Brown University.
Lectures on sequence alignment and hidden Markov models.
- Algorithms for cancer genomics**, graduate course at Brown University.
Lectures on perfect phylogeny theory.
- 2014 **Algorithms for biological networks**, postgraduate course by NBIC.
Lecture and lab on integrative network analysis using Heinz and eXamine.
- 2013 **Fundamentals of bioinformatics**, graduate course at VU.
Guest lecture on crossing schedule optimization.

- 2012 **Principles of bioinformatics**, undergraduate course (CS) at VU.
Guest lecture on the stable marriage algorithm.
Bioinformatics of large systems, graduate course at VU.
Guest lecture on network alignment.
- 2011 **Fundamentals of bioinformatics**, graduate course at VU.
Responsible for organizing, setting up and teaching the Python programming labs.

Student mentorship

- present Leah Weber, Ph.D. student, Computer Science. Single-cell cancer genomics.
Yuanyuan Qi, Ph.D. student, Computer Science. Tumor phylogeny estimation from DNA-seq data.
Chuanyi Zhang, Ph.D student, Electrical and Computer Engineering. Co-advised with Idoia Ochoa (Assist. Professor, ECE, UIUC), and supported by a UIUC CompGen fellowship and UIUC/Mayo IT Fellowship. ‘Single-nucleotide variant calling from multi-sample bulk DNA-seq data’
Juho Kim, Ph.D. student (co-advised with Nick Chia and Sanmi Koyeko and supported by UIUC/Mayo IT Fellowship), ‘Pan-cancer AI’
Palash Sashittal, Computer Science, Ph.D./MS student. ‘Phylodynamics and phylogeography’
- 2020 Sarah Christensen, Ph.D. student. Co-advised with Tandy Warnow (Professor, CS, UIUC). ‘Cancer phylogenetics’
Nuraini Aguse, MS student, ‘Study design of tumor sequencing experiments’
Jiaqi Wu, MS student, ‘Tumor visualization’
- 2019 Silas Hsu, Ph.D. student. Independent study. ‘Visualization of copy number data from bulk DNA sequencing samples’
- 2018 Shunping Xie, MS student. ‘Towards characterizing the solution space of the 1-Dollo phylogeny problem’
Amitha Sandur, MS student. Independent study. Co-advised with Kyle Schachtschneider (Research Assist. Professor, Radiology, UIC), ‘RNA-seq analysis of OncoPig xenografts’
- 2016 Samier Merchant, BS student. Co-advised with Ben Raphael (Professor, CS, Princeton), ‘Gene tree-species tree reconciliation’
David Liu, B.S. honor’s thesis student, ‘Clustering mutations in AncesTree’
Michael Mueller, BS student, ‘Reconstructing phylogenetic trees from single-cell sequencing data’
- 2015 Hannah Acheson-Field, BSc honor’s thesis, ‘Reconstructing clonal trees from multi-sample sequencing data’
- 2014 Fedde Schaeffer, MS thesis, ‘A pipeline for integrative network analysis in Cytoscape’
Nam-Binh Nguyen, BS thesis student. Co-advised with Gunnar Klau (Professor, CS, Heinrich-Heine University). ‘Predicting protein-protein interaction networks based on co-evolution of protein families’
Marina Milo, MS thesis student. ‘Benchmarking of crossing schedule optimization algorithms’

	Jimi van der Woning, MS thesis student. Co-advised with Gunnar Klau (Professor, CS, Heinrich-Heine University). ‘Interaction design for fragment-based molecule parameterisation’
2013	Cristina-Iula Bucur, MS thesis student. Co-advised with Gunnar Klau (Professor, CS, Heinrich-Heine University). ‘Finding deregulated signaling modules in human cytomegalovirus’
2012	Marlies van der Wees, MS thesis student. Co-advised with Gunnar Klau (Professor, CS, Heinrich-Heine University). ‘Cross-species alignment of coexpression networks’

Academic Service

Memberships	<ul style="list-style-type: none"> ○ International Society for Computational Biology (ISCB), 2012–present ○ Institute of Electrical and Electronics Engineers (IEEE), 2018–present ○ American Association for the Advancement of Science (AAAS), 2018–present ○ Association for Computing Machinery (ACM), 2018–present
Grant referee	<ul style="list-style-type: none"> ○ Panel member for National Science Foundation (2021) ○ Ad hoc reviewer for National Science Foundation (2021, 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"> ○ Microbial Genomics (2021) ○ Cell Reports Methods (2021) ○ Bioinformatics and Biology Insights (2021) ○ Genome Biology (2020) ○ Nature Communications (2020 [2x], 2019 [2x], 2018 [2x]) ○ Systematic Biology (2021, 2020) ○ Biostatistics (2020) ○ Journal of Graph Algorithms and Applications (2020) ○ Genome Biology (2020) ○ Cell Systems (2020 [2x], 2019) ○ PLOS Computational Biology (2021 [guest editor], 2020 [1x guest editor, 2x reviewer], 2019 [4x], 2018, 2011) ○ Bioinformatics (2021 [2x], 2019 [3x], 2018 [2x], 2017) ○ Communications Biology (2018) ○ Genome Research (2018 [2x]) ○ F1000Research (2018) ○ PeerJ (2018) ○ IEEE/ACM Transactions on Computational Biology and Bioinformatics (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 referee	<ul style="list-style-type: none"> ○ Research in Computational Molecular Biology (RECOMB, 2020-2017, 2015) ○ RECOMB-Comparative Genomics (RECOMB-CG, 2019) ○ Intelligent Systems in Molecular Biology (ISMB, 2018) ○ Asia Pacific Bioinformatics Conference (APBC, 2017, 2012) ○ RECOMB-Computational Cancer Biology, (RECOMB-CCB, 2017) ○ German Conference on Bioinformatics (GCB, 2012) ○ Workshop on Algorithms in Bioinformatics (WABI, 2011) ○ Symposium on Experimental Algorithms (SEA, 2011)
Program committee member	<ul style="list-style-type: none"> ○ Area co-chair for ‘General Computational Biology’ area (ISMB/ECCB 2021) ○ PC co-chair (WABI 2021) ○ Conference on Research in Computational Molecular Biology (RECOMB, 2021, 2020) ○ Pacific Symposium on Biocomputing (PSB, 2020) ○ Current Trends in Theory and Practice of Computer Science (SOFSEM, 2021, 2020) ○ RECOMB-Comparative Genomics, (RECOMB-CG, 2021) ○ RECOMB-Computational Cancer Biology, (RECOMB-CCB, 2020, 2019) ○ Intelligent Systems in Molecular Biology (ISMB, 2020, 2019) ○ Workshop on Algorithms in Biology (WABI, 2021, 2019) ○ Great Lakes Bioinformatics Conference (GLBIO, 2021, 2019) ○ International Symposium on Mathematical and Computational Oncology (ISMCO, 2021, 2020, 2019) ○ ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB, 2021, 2020, 2019, 2018) ○ Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB, 2019, 2017) ○ European Conference on Computational Biology (ECCB, 2019, 2016)
Internal service	<ul style="list-style-type: none"> ○ Admissions committee, Carle-Illinois College of Medicine, UIUC (2019) ○ Graduate studies committee, Computer Science, UIUC (2019–present) ○ Graduate awards committee, Computer Science, UIUC (2019–present) ○ Student awards committee, Computer Science, UIUC (2018–2019)

Software

2021	<p>doubletD [link] Tool for detecting doublets in medium to high-coverage single-cell DNA sequencing data. Implementation details: Python</p>
2020	<p>RECAP [link] 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++</p> <p>Phyolin [link] 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</p>

- TiTUS** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 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** [\[link\]](#)
 Reconstruction of tumor evolutionary history of single-nucleotide variants and copy-number aberrations from multi-sample bulk sequencing data.
 Implementation details: C++

- 2015 **AncesTree** [\[link\]](#)
Reconstruction of tumor evolutionary history of single-nucleotide variants from multi-sample bulk sequencing data.
Implementation details: C++, CPLEX
- 2014 **eXamine** [\[link\]](#)
Cytoscape 3.x app that displays set membership as contours on top of a node-link layout.
Implementation details: Java
- xHeinz** [\[link\]](#)
Identification of conserved active modules.
Implementation details: C++, CPLEX
- Heinz 2.0** [\[link\]](#)
Identification of active modules.
Implementation details: C++, CPLEX
- NatalieQ** [\[link\]](#)
Web server for protein-protein interaction network querying.
Implementation details: C++, Perl
- 2013 **CUPID** [\[link\]](#)
Method for mapping paralogs using units of coevolution.
Implementation details: C++
- Automated topology builder** [\[link\]](#)
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
- 2012 **Charge-group partitioning game** [\[link\]](#)
Game illustrating the charge group partitioning problem. Used as a demo on CWI's in-house days. Also available as an Android app.
Implementation details: C++
- 2011 **Natalie 2.0** [\[link\]](#)
Method for network alignment based on Lagrangian relaxation.
Implementation details: C++

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