

Mohammed El-Kebir

Assistant Professor

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Research interests

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

Education

- 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
Honors: BioSB Young Investigator Award (2015), Honorable Mention for Best Paper Award (BioVis 2014), ISCB-RECOMB Travel Fellowship (2012)
Advisors: Drs. G. W. Klau and J. Heringa
- 2006–2010 | **VU University Amsterdam, The Netherlands.**
M.Sc. in Bioinformatics, *cum laude*.
Honors: VU FEW Free mover grant (2009), KNCV Tuberculosis Foundation grant (2009)
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, *cum laude*.
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.

Experience

- 2018–present | **Department of Computer Science, University of Illinois at Urbana-Champaign, Champaign, IL, USA.**
Assistant Professor. Algorithm development and combinatorial optimization in computational biology.

- 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 **Molecular Dynamics group, University of Queensland, Brisbane, Australia.**
 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.**
 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.

Publications

Author order generally follows authorship convention in biology, where the first author is the lead author of the project and the corresponding/last author supervises the project.

Peer-reviewed journal

- 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.
- 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.
- 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.
- 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.
- 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*, btv526, 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*, btv316, 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 (Special Issue: Proceedings of ISMB)*, 31(12):i62-i70, 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.
- 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.
- 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.
- 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.

*shared first authorship

Peer-reviewed conference

- 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. *SPhyR: Tumor Phylogeny Estimation from Single-Cell Sequencing Data under Loss and Error*.
ECCB 2018, European Conference on Computational Biology, Athens, Greece, September 9-12, 2018.
M. El-Kebir. *Parsimonious Migration History Problem: Complexity and Algorithms*.
WABI 2018, Workshop on Algorithms in Bioinformatics, Helsinki, Finland, 20-24 August, 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.
- 2015 M. El-Kebir^{*†}, L. Oesper*, H. Acheson-Field, B. J. Raphael. *Reconstruction of clonal trees and tumor composition from multi-sample sequencing data*.
ISMB 2015, Annual International Conference on Intelligent Systems for Molecular Biology, Dublin, Ireland, July 10-14, 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*.
BIOVIS 2014, Symposium on Biological Data Visualization, 11-12 July 2014, Boston, USA.
- 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*.
RECOMB-CG 2013, RECOMB Comparative Genomics, Lyon, France, October 17-19 2013.

- 2012 | 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*.
RECOMB 2012, Annual International Conference on Research in Computational Molecular Biology, Barcelona, Spain, April 21-24 2012.
- 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.

*shared first authorship, [†]oral presentation

Selected presentations

- 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, Champaign, 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.
- 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

- 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 organising, setting up and teaching the Python programming practical.

Student mentorship

- 2016 Samier Merchant[†], ‘Gene tree-species tree reconciliation’
- 2016 David Liu[†], ‘Clustering mutations in AncesTree’
- 2016 Michael Mueller[†], ‘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*, MSc thesis, ‘A pipeline for integrative network analysis in Cytoscape’
- 2013–2014 Nam-Binh Nguyen*, BSc thesis, ‘Predicting protein-protein interaction networks based on coevolution of protein families’
- 2013–2014 Marina Milo, MSc thesis, ‘Benchmarking of crossing schedule optimization algorithms’
- 2013–2014 Jimi van der Woning*, MSc thesis, ‘Interaction design for fragment-based molecule parameterisation’
- 2012–2013 Cristina-Iula Bucur*, MSc thesis, ‘Finding deregulated signaling modules in human cytomegalovirus’
- 2012 Marlies van der Wees*, MSc thesis, ‘Cross-species alignment of coexpression networks’

*with Gunnar Klau, [†]with Ben Raphael

Academic Service

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| 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">◦ Bordeaux University, G2P (2016) |
| Journal referee | <ul style="list-style-type: none">◦ Nature Communications (2018)◦ Communications Biology (2018)◦ Genome Research (2018, 2x)◦ F1000Research (2018)◦ PeerJ (2018)◦ IEEE/ACM Transactions on Computational Biology and Bioinformatics (2018, 2017)◦ 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)◦ PLoS Computational Biology (2018, 2011)◦ Journal of the ACM (2011) |
| Conference referee | <ul style="list-style-type: none">◦ Intelligent Systems in Molecular Biology (ISMB, 2018)◦ Conference on Research in Computational Molecular Biology (RECOMB, 2018, 2017, 2015)◦ 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">◦ ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB, 2018)◦ Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB, 2017)◦ European Conference on Computational Biology (ECCB, 2016) |

Software

- 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++

Last updated on August 28, 2018