

# 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	<p><b>Department of Computer Science, Princeton University, Princeton, NJ, USA.</b>  <i>Postdoctoral research associate.</i> Research on topics in computational cancer genomics, with a focus on algorithm development and combinatorial optimization. Advised by Ben Raphael.</p>
2014–2016	<p><b>Department of Computer Science and Center for Computational Molecular Biology, Brown University, Providence, RI, USA.</b>  <i>Postdoctoral research associate.</i> Research on topics in computational cancer genomics, with a focus on algorithm development and combinatorial optimization. Advised by Ben Raphael.</p>
2010–2014	<p><b>Life Sciences group, Centrum Wiskunde &amp; Informatica (CWI), Amsterdam, The Netherlands.</b>  <b>Centre for Integrative Bioinformatics VU (IBIVU), VU University Amsterdam, The Netherlands.</b>  <i>PhD Student.</i> 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.</p>
February 2013	<p><b>Molecular Dynamics group, University of Queensland, Brisbane, Australia.</b>  Integrated the charge group partitioning algorithm in the Automated Topology Builder under the supervision of Alan Mark.</p>
July 2011	<p><b>Department of Microbiology and Immunology, University of Michigan, Medical School, Ann Arbor, USA.</b>  Finished work on the agent-based model on tuberculous meningitis (El-Kebir et al., 2013) under the supervision of Denise Kirschner.</p>
2009–2010	<p><b>Department of Microbiology and Immunology, University of Michigan, Medical School, Ann Arbor, USA.</b>  <i>Visiting Scholar.</i> Member of the Kirschner lab. Research and development of an agent-based model describing the immune response in tuberculous meningitis and pulmonary tuberculosis.</p>
2009	<p><b>Keygene N.V., Wageningen, The Netherlands.</b>  <i>Trainee.</i> 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.</p>

## 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- $\alpha$ . *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<sup>†</sup>, 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<sup>\*†</sup>, 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<sup>\*†</sup>, 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\*<sup>†</sup>, 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<sup>†</sup>, 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\*<sup>†</sup>. *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, <sup>†</sup>oral presentation

## Selected presentations

- 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<sup>†</sup>, ‘Gene tree-species tree reconciliation’
- 2016 David Liu<sup>†</sup>, ‘Clustering mutations in AncesTree’
- 2016 Michael Mueller<sup>†</sup>, ‘Reconstructing phylogenetic trees from single-cell sequencing data’
- 2015 Hannah Acheson-Field<sup>†</sup>, 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

- |                          |  |
|--------------------------|--|
| Memberships              | <ul style="list-style-type: none"><li>○ International Society for Computational Biology (ISCB), 2012–present</li><li>○ Institute of Electrical and Electronics Engineers (IEEE), 2018–present</li><li>○ American Association for the Advancement of Science (AAAS), 2018–present</li><li>○ Association for Computing Machinery (ACM), 2018–present</li></ul>   |
| Grant referee            | <ul style="list-style-type: none"><li>○ Bordeaux University, G2P (2016)</li></ul>  |
| Journal referee          | <ul style="list-style-type: none"><li>○ Nature Communications (2018)</li><li>○ Communications Biology (2018)</li><li>○ PeerJ (2018)</li><li>○ IEEE/ACM Transactions on Computational Biology and Bioinformatics (2018, 2017)</li><li>○ Bioinformatics (2018, 2017)</li><li>○ BMC Bioinformatics (2017, 2014, 2012)</li><li>○ Fundamenta Informaticae (2017)</li><li>○ PLoS One (2016)</li><li>○ EURASIP Journal on Bioinformatics and Systems Biology (2016)</li><li>○ Frontiers in Bioengineering and Biotechnology (2014)</li><li>○ Computational Biology and Chemistry (2014)</li><li>○ Scientific Reports (2014)</li><li>○ Journal of Chemical Information and Modeling (2013)</li><li>○ PLoS Computational Biology (2018, 2011)</li><li>○ Journal of the ACM (2011)</li></ul> |
| Conference referee       | <ul style="list-style-type: none"><li>○ Intelligent Systems in Molecular Biology (ISMB, 2018)</li><li>○ Conference on Research in Computational Molecular Biology (RECOMB, 2018, 2017, 2015)</li><li>○ Asia Pacific Bioinformatics Conference (APBC, 2017, 2012)</li><li>○ RECOMB-Computational Cancer Biology, (RECOMB-CCB, 2017)</li><li>○ German Conference on Bioinformatics (GCB, 2012)</li><li>○ Workshop on Algorithms in Bioinformatics (WABI, 2011)</li><li>○ Symposium on Experimental Algorithms (SEA, 2011)</li></ul>  |
| Program committee member | <ul style="list-style-type: none"><li>○ ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB, 2018)</li><li>○ Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB, 2017)</li><li>○ European Conference on Computational Biology (ECCB, 2016)</li></ul>   |

## 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 8, 2018