Mohammed El-Kebir

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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.**
PhD in Computer Science and Bioinformatics
Thesis: Networks, modules and breeding schedules: Applications of Combinatorial Optimization to Computational Biology
Honors: BioSB Young Investigator Award (2015), ISCB-RECOMB Travel Fellowship (2012)
Advisors: G. W. Klau and J. Heringa

2006–2010 **VU University Amsterdam, The Netherlands.**
MSc 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: D. Kirschner, M. van der Kuip, A. M. van Furth

2007–2009 **Eindhoven University of Technology, The Netherlands.**
MSc in Computer Science and Engineering, *cum laude*.
Thesis: Crossing Schedule Optimization
Advisors: M. T. de Berg and J. B. Buntjer

2003–2006 **Eindhoven University of Technology, The Netherlands.**
BSc in Computer Science and Engineering.

Research Experience

2016–present **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.

Professional Experience

2013 **Center of expertise for diversity policy (ECHO), Utrecht, The Netherlands.**
Researcher/Data Analyst. Studying the impact of the Dutch government's G5 policy, which aimed at improving the study performance of Dutch minority students at universities and colleges. Given nation-wide, anonymized student enrollment data, I assessed the performance of student groups pooled according to ethnicity, prior education, etc. Used tools: Python, MySQL, LaTeX and gnuplot.

2012–2013 **Moroccan Dutch Leadership Institute, Amsterdam, The Netherlands.**
Project Coordinator. Supervised a team of six young professionals and students in organising a 'Cito-toets training' for Moroccan-Dutch primary school students for the first time in the city of The Hague. My activities involved the coordination of the process as well as the supervision and coaching of my team members. The project was successful and about 200 children participated.

2006–2009 **eventIS Software Solutions B.V., Veldhoven, The Netherlands.**
Software Engineer (0.4 FTE). eventIS (now part of SeaChange International, Inc.) developed software for the back-end of digital television providers. Activities involved developing applications in C++ and C#. In addition, I was in close contact with customers as to identify their requirements and ensure a successful deployment.

Publications

Peer-reviewed journal

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

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, Lecture Notes in Computer Science 7036: 225–236.

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.*
NeFoRS 2007, New forms of reasoning for the Semantic Web: scalable, tolerant and dynamic, pages 60–74, 2007.

*shared first authorship, †oral presentation

Selected presentations

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**
ISBM/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 partioning 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 Services

Memberships	◦ International Society for Computational Biology, 2012–present
Journal referee	◦ 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) ◦ BMC Bioinformatics (2014, 2012*) ◦ Bioinformatics (2014) ◦ Journal of Chemical Information and Modeling (2013) ◦ PLoS Computational Biology (2011†) ◦ Journal of the ACM (2011*)
Conference referee	◦ Conference on Research in Computational Molecular Biology (RECOMB, 2017) ◦ European Conference on Computational Biology (ECCB, 2016) ◦ Conference on Research in Computational Molecular Biology (RECOMB, 2015) ◦ Asia Pacific Bioinformatics Conference (APBC, 2012) ◦ German Conference on Bioinformatics (GCB, 2012) ◦ Workshop on Algorithms in Bioinformatics (WABI, 2011) ◦ Symposium on Experimental Algorithms (SEA, 2011)

*with Gunnar Klau, †with Jaap Heringa

Software

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 partioning 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 December 4, 2016