

Mark D.M. Leiserson

*Ph.D. candidate in Computer Science and Computational Biology
Brown University*

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Research Interests

My research interests are in developing algorithms and mathematical models for understanding biological processes, in particular those related to disease. There are many challenges in analyzing modern biological data sets e.g. scale (every genome is $> 1\text{Gb}$ of information), the relatively low signal-to-noise ratio, and the complexity of biology. As a result, it is imperative that new approaches utilize both biological and quantitative methods and expertise. My goal is to be at the heart of this process, and to develop new methods and algorithms that are efficient, scalable, and easy-to-use (by biologists and computer scientists alike), but that capture the complexity of biological processes.

Education

Ph.D., Computer Science and Computational Biology, Brown University *Expected May 2016*

Advisor: Associate Professor of Computer Science Benjamin J. Raphael.

M.Sc., Computer Science, Brown University *May 2013*

Advisor: Associate Professor of Computer Science Benjamin J. Raphael.

Thesis: *Methods for Identifying Driver Pathways in Cancer.*

B.Sc. (cum laude), Computer Science, Tufts University *May 2011*

Minor: Political Science

Advisor: Assistant Professor of Computer Science Benjamin J. Hescott.

Thesis (*highest honors*): *Inferring Mechanisms of Compensation from E-MAP and SGA Data Using Local Search Algorithms for Max Cut.*

Honors / Awards

Selected to attend Heidelberg Laureate Forum (one of 200 students), 2014.

NSF Travel Award (RECOMB 2013, 2015).

National Science Foundation Graduate Research Fellow, 2012-present.

Tufts University Senior Thesis in Computer Science completed with Highest Honors, 2011.

Runner-up for Computing Research Association Outstanding Undergraduate Award, 2011.

Tufts University Senior Award: Benjamin G. Brown Scholarship for Promise in Scientific Research, 2011.

Designed and implemented <http://TuftScopeJournal.org>, winner of 2010 Tufts Campus Innovation and Imagination Award.

Recipient of research grant from Tufts Undergraduate Research Fund, 2008 and 2010.

Research Experience

National Science Foundation Graduate Research Fellow/Graduate research assistant *2011-present*

Department of Computer Science and Center for Computational Molecular Biology, Brown University

Advisor: **Dr. Benjamin J. Raphael.**

- developed algorithms for distinguishing the driver mutations that cause cancer from the random passenger mutations that have no effect for cancer;
- these algorithms include Multi-Dendrix and CoMEt, which identify mutually exclusive sets of mutated genes in cancer, and HotNet2 for finding significantly mutated subgraphs of protein interaction networks;
- member of The Cancer Genome Atlas's acute myeloid leukemia, pan cancer, and stomach adenocarcinoma analysis working groups.

Undergraduate research assistant

2008-2011

Department of Computer Science, Tufts University

Advisors: **Dr. Benjamin J. Hescott** and **Dr. Lenore J. Cowen.**

- analyzed genetic mechanisms of compensation in baker's yeast;
- implemented an algorithm for scoring putatively compensatory sets of genes using microarray expression data;
- developed an algorithm for identifying putatively compensatory sets of genes from high-throughput pairwise epistasis data.

Research assistant

2007

Molecular, Cellular, and Developmental Biology Department, Yale University

Principal Investigator: **Dr. John Carlson**

- assisted with research of the fruit fly olfactory system;
- performed larval behavioral assays under the supervision of Denis Mathew.

Teaching Experience

Certifications

Teaching Certificate I, Sheridan Center, Brown University, 2015.

Guest lecturer

Fall 2014 Computational Molecular Biology (CSCI1810) Brown University two lectures

Professional Experience

Software Development Engineer Intern*Summer 2014*

Amazon Web Services

Professional Service

Leadership

Poster Committee, Research in Computational Molecular Biology (RECOMB) conference: 2015.

Referee

Intelligent Systems for Molecular Biology (ISMB) conference: 2013.

Research in Computational Molecular Biology (RECOMB) conference: 2013-2015.

Bioinformatics–Oxford Journals: 2012, 2014-2015.

Professional Memberships

International Society of Computational Biology, 2012-present.

Association of Computing Machinery, 2014-present.

IEEE, 2014-present.

Publications

Peer-Reviewed Journal Articles

M.D.M. Leiserson*, H-T. Wu*, F. Vandin, B.J. Raphael. (2015) CoMEt: a statistical approach to identify combinations of mutually exclusive alterations in cancer. *Genome Biology*, 16:160. [[Publisher link](#)].

M.D.M. Leiserson, C.C. Gramazio, J. Hu, H-T. Wu, D.H. Laidlaw, B.J. Raphael. (2015) MAGI: visualization and collaborative annotation of genomic aberrations. *Nature Methods*, 12(6):483-484. [[Publisher link](#)].

M.D.M. Leiserson*, F. Vandin*, H-T. Wu, J.R. Dobson, J.V. Eldridge, J.L. Thomas, A. Papoutsaki, Y. Kim, B. Niu, M. McLellan, M.S. Lawrence, A. Gonzalez-Perez, D. Tamborero, Y. Cheng, G.A. Ryslik, N. Lopez-Bigas, G. Getz, L. Ding, B.J. Raphael. (2015) Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *Nature Genetics*, 47(2):106-114. [[Publisher link](#)].

K.A. Hoadley, C. Yau, D.M. Wolf, A.D. Cherniack, D. Tamborero, S. Ng, **M.D.M. Leiserson**, B. Niu, M.D. McLellan, V. Uzunangelov, J. Zhang, C. Kandoth, R. Akbani, H. Shen, L. Omberg, A. Chu, A.A. Margolin, L.J. van't Veer, N. Lopez-Bigas, P.W. Laird, B.J. Raphael, L. Ding, A.G. Robertson, L.A. Byers, G.B. Mills, J.N. Weinstein, C. Van Waes, Z. Chen, E.A. Collisson, The Cancer Genome

- Atlas Research Network, C.C. Benze, C.M. Peroue, J.M. Stuart.. (2014) Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. *Cell*, 158(4):929-944. [Publisher link].
- K.L. Kanchi, K.J. Johnson, C. Lu, M.D. McLellan, **M.D.M. Leiserson**, M.C. Wendl, Q. Zhang, D.C. Koboldt, M. Xie, C. Kandoth, J.F. McMichael, M.A. Wyczalkowski, D.E. Larson, H.K. Schmidt, C.A. Miller, R.S. Fulton, P.T. Spellman, E.R. Mardis, T.E. Druley, T.A. Graubert, P.J. Goodfellow, B.J. Raphael, R. K. Wilson, L. Ding. (2014) Integrated analysis of germline and somatic variants in ovarian cancer. *Nature Communications*, 5:3156. [Publisher link].
- C. Kandoth, M.D. McLellan, F. Vandin, K. Ye, B. Niu, C. Lu, M. Xie, Q. Zhang, J.F. McMichael, M.A. Wyczalkowski, **M.D.M. Leiserson**, C.A. Miller, J.S. Welch, M.J. Walter, M.C. Wendl, T.J. Ley, R.K. Wilson, B.J. Raphael, L. Ding (2013) Mutational landscape and significance across 12 major cancer types. *Nature*, 502(7471):333-339. [Publisher link].
- The Cancer Genome Atlas Research Network, J.N. Weinstein, E.A. Collisson, G.B. Mills, K.R. Mills Shaw, B.A. Ozenberger, K. Ellrott, I. Shmulevich, C. Sander, J.M. Stuart (2013) The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics*, 45(10):1113-1120. [Publisher link].
- M.D.M. Leiserson**, D. Blokh, R. Sharan*, B. Raphael*. (2013) Simultaneous Identification of Multiple Driver Pathways in Cancer. *PLoS Comp Biol*, 9(5):e1003054. [Publisher link].
- The Cancer Genome Atlas Research Network. (2013) Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. *New England Journal of Medicine*. doi:10.1056/NEJMoa1301689. [Publisher link].
- A. Gallant, **M.D.M. Leiserson**, M. Kachalov, L. Cowen, B. Hescott. (2013) Genecentric: a package to uncover graph-theoretic structure in high-throughput epistasis data. *BMC Bioinformatics*, 14:23. doi:10.1186/1471-2105-14-23. [Publisher link].
- M.D.M. Leiserson**, D. Tatar, L. Cowen, B. Hescott. (2011) Inferring Mechanisms of Compensation from E-MAP and SGA Data Using Local Search Algorithms for Max Cut. *Journal of Computational Biology*, 18(11):1399-1409. [Publisher link].
- B. Hescott, **M.D.M. Leiserson**, D. Slonim, L. Cowen. (2009) Evaluating Between-Pathway Models with Expression Data. *Journal of Computational Biology* 17(3):443-457. [Publisher link].

* equal contribution

Proceedings

- M.D.M. Leiserson***, H-T. Wu*, F. Vandin, B.J. Raphael. (2015) CoMEt: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer. *Proceedings of the 19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)*. *Lecture Notes in Computer Science*, Volume 9029, 202-204. [Publisher link] [arXiv preprint link].
- M.D.M. Leiserson**, D. Tatar, L. Cowen, B. Hescott. (2011) Inferring Mechanisms of Compensation from E-MAP and SGA Data Using Local Search Algorithms for Max Cut. *Proceedings of the 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2011)*. *Lecture Notes in Computer Science*, Volume 6577, 154-167. [Publisher link].
- B. Hescott, **M.D.M. Leiserson**, D. Slonim, L. Cowen. (2009) Evaluating Between-Pathway Models with Expression Data. *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009)*. *Lecture Notes in Computer Science*, Volume 5541, 372-385. [Publisher link].

* equal contribution

Invited Articles and Book Chapters

- M.D.M. Leiserson**, B.J. Raphael. (2015). Analyzing combinations of somatic mutations in cancer genomes. In G.C. Tseng, D. Ghosh, X. J. Zhou (Eds.), *Integrating Omics Data*. New York, NY: Cambridge University Press. [[Publisher link](#)].
- M.D.M. Leiserson**, J.V. Eldridge, S. Ramachandran, B.J. Raphael (2013) Network analysis of GWAS data. *Current Opinion in Genetics & Development*, 23(6):602-610. [[Publisher link](#)].

Conference Abstracts and Posters

- M. Leiserson***, M. Reyna, B. Raphael. A hierarchical clustering approach for identifying high-scoring subnetworks of a protein-protein interaction network. (Abstract and Poster) Presented at the *Systems Biology: Networks Meeting*, Cold Spring Harbor, NY, USA, March 2015.
- M. Leiserson***, C. Gramazio, J. Hu, H. Wu, B. Raphael. MAGI: A Platform for Interactive Visualization and Collaborative Annotation of Combinations of Genetic Aberrations. (Abstract and Poster) Presented at the 1st *Biological Data Science Meeting*, Cold Spring Harbor, NY, USA, November 2014.
- H. Wu*, **M. Leiserson**, V. Hsiao, F. Vandin, B. Raphael. Dendrix++: A Probabilistic Model for Identifying Mutually Exclusive Combinations of Mutations in Cancer. (Abstract and Poster) Presented at the 1st *Biological Data Science Meeting*, Cold Spring Harbor, NY, USA, November 2014.
- M. Leiserson***, H. Wu, J. Hu, C. Gramazio, B. Raphael. Cancer Genome Analysis Tool (CGAT) for the Visualization and Exploration of Combinations of Mutations in Cancer. (Abstract and Poster) Presented at the 4th Annual *The Cancer Genome Atlas Symposium*, Bethesda, MD, USA, May 2014.
- M. Leiserson***, F. Vandin, H. Wu, J. Dobson, A. Papoutsaki, J. Eldridge, B. Raphael. HotNet2 Algorithm Identifies Significantly Mutated Pathways and Protein Complexes Across Cancer Types. (Abstract and Poster) Presented at the 4th Annual *The Cancer Genome Atlas Symposium*, Bethesda, MD, USA, May 2014.
- M. Leiserson**, F. Vandin, H. Wu, J. Dobson*, B. Raphael. Pan-cancer identification of mutated pathways and protein complexes. (Abstract and Poster) Presented at the 105th Annual American Association of Cancer Researchers Meeting. San Diego, CA, USA, Apr 2014.
- M. Leiserson**, F. Vandin, H. Wu, J. Dobson, A. Gonzalez-Perez, D. Tamborero, N. Lopez-Bigas, B. Raphael*. Network Analysis of Mutations Across Cancer Types. (Abstract and Oral Presentation) Presented at the 63rd Annual Meeting of *The American Society of Human Genetics*, Boston, USA, Oct 2013.
- M. Leiserson**, F. Vandin, J. Dobson, H. Wu, A. Papoutsaki, B. Raphael*. Pan-Cancer Network Analysis Identifies Combinations of Rare Somatic Mutations across Pathways and Protein Complexes. (Abstract and Oral Presentation) Presented at the *International Cancer Genome Consortium (ICGC) Annual Meeting*, Toronto, CA, Oct 2013.
- M. Leiserson***, H. Wu, F. Vandin, B. Raphael. Network and pathway analysis of mutations across cancer types. (Abstract and Poster) *The Biology of Genomes: the 26th Annual Meeting on Genome Science*, Cold Spring Harbor, USA, May 2013.
- M. Leiserson***, H. Wu, F. Vandin, B. Raphael. Network analysis of mutations across cancer types. (Poster) *17th International Conference on Research in Computational Molecular Biology (RECOMB)*, Beijing, China, April 2013.

- M. Leiserson**, H. Wu, A. Deschamps, F. Vandin, B. Raphael*. Pathway and Network Analysis of Somatic Mutations Across Cancer Types in TCGA. (Abstract and Oral Presentation) *The Cancer Genome Atlas' 2nd Annual Scientific Symposium: Enabling Cancer Research Through TCGA*, December 2012.
- M. Leiserson***, H. Wu, D. Blokh, F. Vandin, R. Sharan, B. Raphael. Methods for Identifying Driver Pathways in Cancer. (Poster) *3rd Annual Beyond the Genome Conference*, Boston, USA, September 2012.
- M. Leiserson***, D. Tatar*, L. Cowen, B. Hescott. (2009). Inferring Fault Tolerance from E-MAP Data. (Abstract and Poster) *6th Annual Research in Computational Molecular Biology Regulatory Genomics (RECOMB-RG) Conference*, Cambridge, USA, December 2009.
- B. Hescott, **M. Leiserson***, D. Slonim, L. Cowen. (2009). Evaluating between-pathway models with expression data. (Abstract and Poster) *1st Annual Research in Computational Molecular Biology Bioinformatics Education (RECOMB-BE) Conference*, San Diego, USA, March 2009.

* presenting author

Presentations

Conference Presentations

- M. Leiserson** , F. Vandin, H-T. Wu, J. Dobson, J. Eldridge, J. Thomas, A. Papoutsaki, Y. Kim, B. Niu, M. McLellan, M. Lawrence, A. Gonzalez-Perez, D. Tamborero, Y. Cheng, G. Ryslik, N. Lopez-Bigas, G. Getz, L. Ding, B. Raphael. Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *23rd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2015. [Highlight talk]
- M. Leiserson** , F. Vandin, H-T. Wu, J. Dobson, J. Eldridge, J. Thomas, A. Papoutsaki, Y. Kim, B. Niu, M. McLellan, M. Lawrence, A. Gonzalez-Perez, D. Tamborero, Y. Cheng, G. Ryslik, N. Lopez-Bigas, G. Getz, L. Ding, B. Raphael. Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *19th Annual Research in Computational Molecular Biology Conference (RECOMB)*, 2015. [Highlight talk]
- M. Leiserson**, D. Blokh, R. Sharan, B. Raphael. Simultaneous Identification of Multiple Driver Pathways in Cancer. *22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2014. [Highlight talk]

Open-Source Software

- CoMEt**: Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer 2015
Source: <http://github.com/raphael-group/comet>
- GD3**: Javascript library for visualizing genomics data with D3 2014
Source: <http://github.com/raphael-group/gd3>
- MAGI**: Interactive visualization and collaborative annotation of genetic aberrations 2014
Web application: <http://magi.cs.brown.edu> Source: <http://github.com/raphael-group/magi>
- HotNet2**: Identifying significantly altered subnetworks in a large gene interaction network 2014
Source: <http://github.com/raphael-group/hotnet2>

Multi-Dendrix: Rapid identification of multiple driver pathways in cancer
Source: <https://github.com/raphael-group/multi-dendrix>

2013

Last updated: August 9, 2015
<http://maxleiserson.com/docs/cv.pdf>