

# Mark D.M. Leiserson

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Publications: [Google Scholar]

## Education

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

Thesis: *Methods for Identifying Combinations of Driver Mutations in Cancer*

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

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

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

## Honors & Awards

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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 Interests

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My research interests are in developing algorithms and mathematical models for understanding biological processes, in particular those related to disease. For my Ph.D. thesis, I worked on the problem of distinguishing the few key driver mutations responsible for cancer from the hundreds to thousands of random mutations in a cohort of tumors. I am interested in applying my algorithms to biological data as well, and participated in a number of collaborations with cancer biologists for my thesis. My research is interdisciplinary, involving algorithms, statistics, and biology.

## Research Experience

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**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 and released software for identifying the driver mutations responsible for cancer in a cohort of tumors;
- Analyzed cohorts of tumors in collaboration with cancer biologists.

**Undergraduate research assistant**

2008-2011

Department of Computer Science, Tufts University

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

- Developed an algorithm and released software for analyzing genetic mechanisms of compensation in baker's yeast.

## Teaching Experience

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**Guest Lecturer**, Computational Molecular Biology (CSCI1810), Brown University, Fall 2014, 2015: three lectures.

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

## Professional Experience

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**Software Development Engineer Intern**

Summer 2014

Amazon Web Services, Elastic File System

## Publications

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\* denotes equal contribution.

**Peer-Reviewed Journal Articles**

Lu, C.\*, Xie, M.\*, Wendl, M.C.\*, Wang, J.\*, McLellan, M.D.\*, **Leiserson, M.D.M.\***, Huang, K.L., Wyczalkowski, M.A., Jayasinghe, R., Banerjee, T., Ning, J., Tripathi, P., Zhang, Q., Niu, B., Ye, K., Schmidt, H.K., Fulton, R.S., McMichael, J.F., Batra, P., Kandoth, C., Bharadwaj, M., Koboldt, D.C., Miller, C.A., Kanchi, K.L., Eldred, J.M., Larson, D.E., Welch, J.S., You, M., Ozenberger, B.A., Govindan, R., Walter, M.J., Ellis, M.J., Mardis, E.R., Graubert, T.A., Dpersio, J.F., Ley, T.J., Wilson, R.K., Goodfellow, P.A., Raphael, B.J., Chen, F., Johnson, K.J., Parvin, J.D., Ding, L. (2015). Patterns and Functional Implications of Rare Germline Variants across 12 Cancer Types. To appear: *Nature Communications*.

The Cancer Genome Atlas Research Network (2015). Comprehensive Molecular Characterization of Papillary Renal Cell Carcinoma. To appear: *New England Journal of Medicine*.

**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) Gene-centric: 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](#)].

## 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](#)].

### 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

\* denotes presenting author.

**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.

## Presentations

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### 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]

## Professional Service

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### 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.

**Advising Experience**

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**Co-advised Master's Students**

John Shen (M.Sc., Computer Science, *expected 2016*).

Jeremy Watson (M.Sc., Computer Science, *expected 2016*).

Jonathan V. Eldridge (M.Sc., Computer Science, 2014), now at RedFin.

**Co-advised Undergraduate Students**

Sam Brebner (Sc.B. Computer Science, *expected 2016*).

Adrien Deschamps (Sc.B. Applied Math).

Vivian Hsiao (Sc.B. Computer Science, 2014), now at Brown University Medical School.

Jason Hu (Sc.B. Computer Science, 2015).

Alex Wong (Sc.B. Computer Science, *expected 2018*).

**Open-Source Software**

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**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: November 12, 2015  
<http://maxleiserson.com/docs/cv.pdf>