

# Mark D.M. Leiserson

Curriculum Vitae (March 2019)

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Publications: [Google Scholar]

## Education

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**Ph.D.**, Computer Science and Computational Biology, Brown University 2013-2016

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

Advisor: Benjamin J. Raphael.

**M.Sc.**, Computer Science, Brown University 2011-2013

**B.Sc.** (*cum laude*), Computer Science, Tufts University 2007-2011

## Experience

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**Assistant Professor**, Department of Computer Science & UMIACS, University of Maryland 2017-

**Post-doctoral researcher**, Microsoft Research 2016-2017

## Publications

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\* denotes equal first author contribution. ^denotes equal senior author contribution. (A) denotes alphabetical author order.

### Preprints and in-press

Sason, I., Wojtowicz, D., Robinson, W., **Leiserson, M.D.M.**, Przytycka, T., Sharan, R. (2019) A sticky multinomial mixture model of strand-coordinated mutational processes in cancer. *RECOMB 2019* (to appear).

Swinger, N., De-Arteaga, M., Heffernan IV, N.T., **Leiserson, M.D.M.**, Kalai, A.T. (2019) What are the biases in my word embedding? *AIES 2019*. [arXiv preprint]

Huang, X., Sason, I., Wojtowicz, D., Kim, Y-A., **Leiserson, M.D.M.**^, Przytycka, T.M.^, Sharan, R.^ (2018) Hidden Markov Models Lead to Higher Resolution Maps of Mutation Signature Activity in Cancer. *bioRxiv* <https://doi.org/10.1101/392639>

Sinha, S., Cheng, K., **Leiserson, M.D.M.**, Wilson, D.M., Ryan, B.M., Lee, J.S., Rupp, E. (2018) A systematic genome-wide mapping of the oncogenic risks associated with CRISPR-Cas9 editing. *bioRxiv* <https://doi.org/10.1101/407767>

### Peer-Reviewed Journal Articles

1. Fan, J., Cannistra, A., Fried, I., Lim, T., Schaffner, T., Crovella, M., Hescott, B.^, **Leiserson, M.D.M.**^ (2019) A Multi-Species Functional Embedding Integrating Sequence and Network Structure. *Nucleic Acids Research* (in press). [Oral presentation at RECOMB 2018.] [bioRxiv preprint]

2. **Leiserson, M.D.M.**, Syrgkanis, V., Gilson, A., Dudik, M., Bajorin, D.F., Rosenberg, J., Funt, S., Snyder, A., Mackey, L. (2018) A Multifactorial Model of T Cell Expansion and Durable Clinical Benefit in Response to a PD-L1 Inhibitor. *PLOS ONE* 13(12): e0208422. [[Publisher link](#)]
3. Persi, E., Wolf, Y.I., **Leiserson, M.D.M.**, Koonin, E.V., Ruppín, E. (2018) Criticality in Tumor Evolution and Clinical Outcome. *PNAS* 115(47): E111101-E111110. [[Publisher link](#)]
4. Reyna, M.R., **Leiserson, M.D.M.**, Raphael, B.J. (2018) Hierarchical HotNet: identifying hierarchies of altered subnetworks. *ECCB/Bioinformatics* 34(17), i972-i980. [[Publisher link](#)]
5. Grasso, C., Giannakis, M., Wells, D., Hamada, T., Mu, X.J., Quist, M., Nowak, J., Nishihara, R., Qian, Z.R., Inamura, K., Morikawa, T., Noshio, K., Abril-Rodriguez, G., Connolly, C., Escuin-Ordinas, H., Geybels, M., Grady, W., Hsu, L., Hu-Lieskova, S., Huyghe, J., Kim, Y.J., Krystofinski, P., **Leiserson, M.D.M.**, Montoya, D., Nadel, B., Pellegrini, M., Pritchard, C., Puig-Saus, C., Quist, E., Raphael, B., Stanford, J., Sun, W., Tsoi, J., Upfill-Brown, A., Wheeler, D., Wu, C., Yu, M., Zaidi, S., Zaretsky, J., Gabriel, S., Lander, E., Garraway, L., Hudson, T., Fuchs, C., Ribas, A., Ogino, S., Peters, U. (2018) Genetic mechanisms of immune evasion in colorectal cancer. *Cancer Discovery*, 10.1158/2159-8290.CD-17-1327. [[Publisher link](#)]
6. Radovich, M., Pickering, C.R., Felau, I., Ha, G., Zhang, H., Jo, H., Hoadley, K.A., Anur, P., Zhang, J., McLellan, M., Bowlby, R., Matthew, T., Danilova, L., Hegde, A.M., Kim, J., **Leiserson, M.D.M.**, Sethi, G., Lu, C., Ryan, M., Su, X., Cherniack, A.D., Robertson, G., Akbani, R., Spellman, P., Weinstein, J.N., Hayes, D.N., Raphael, B., Lichtenberg, T., Leraas, K., Zenklusen, J.C., TCGA Research Network, Fujimoto, J., Scapulatempo-Neto, C., Moreira, A.L., Hwang, D., Huang, J., Marino, M., Korst, R., Giaccone, G., Gokmen-Polar, G., Badve, S., Rajan, A., Strobel, P., Girard, N., Tsao, M.S., Marx, A., Tsao, A.S., Loehrer, P.J. (2018) The Integrated Genomic Landscape of Thymic Epithelial Tumors. *Cancer Cell*, 33(2):244-2458.e10. [[Publisher link](#)]
7. Dwork, C., Immorlica, N., Kalai, A.T., **Leiserson, M.D.M.**<sup>(A)</sup> (2018) Decoupled classifiers for fair and efficient machine learning. *Proceedings of the 1st Conference on Fairness, Accountability and Transparency (FAT 2018)*, PMLR 81:119-133. [[Publisher link](#)] [[arXiv preprint](#)]
8. Senft, D., **Leiserson, M.D.M.**, Ruppín, E., Ze'ev, A.R. (2017) Precision Oncology: The Road Ahead. *Trends in Molecular Medicine*, 23(10):874-898. [[Publisher link](#)]
9. The Cancer Genome Atlas Research Network. (2017) Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, 32(2):185-203. [[Publisher link](#)]
10. **Leiserson, M.D.M.**, Reyna, M., Raphael, B.J. (2016) A weighted exact test for mutually exclusive mutations in cancer. *Bioinformatics/ECCB*, 32(17): i736-i745. [[Publisher link](#)]
11. 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., Dipersio, 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. *Nature Communications*, 6:10086. [[Publisher link](#)]
12. The Cancer Genome Atlas Research Network Group. (2015) Comprehensive Molecular Characterization of Papillary Renal Cell Carcinoma. *New England Journal of Medicine*, doi: 10.1056/NEJMoa1505917. [[Publisher link](#)].

13. **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](#)].
14. **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](#)].
15. **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](#)].
16. 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](#)].
17. 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](#)].
18. 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](#)].
19. 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](#)].
20. **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](#)].
21. 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](#)].
22. 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](#)].
23. **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](#)].
24. 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](#)].

## Honors & Awards

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**National Science Foundation Graduate Research Fellow**, 2012-2016.

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

NSF Travel Award (RECOMB 2013, 2015) and ISCB Travel Award (ISMB 2015).

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.

## Teaching Experience

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2018-2019	Primary instructor	UMD	CMSC 423	Bioinformatic Algorithms, Databases, and Tools
2017-2018	Primary instructor	UMD	CMSC 828P	Algorithms & Machine Learning for Analyzing Mutations in Cancer
2015	Guest lecturer (1)	Brown	CSCI 1810	Computational Molecular Biology
2014	Guest lecturer (2)	Brown	CSCI 1810	Computational Molecular Biology

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

## Presentations

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### Conference Presentations

- M. Leiserson**, M. Reyna, B. Raphael. A Weighted Exact Test for the Significance of Mutually Exclusive Mutations in Cancer. *24rd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2016. [Late breaking research 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. *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]

### Invited Talks

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| June 2018     | SIAM Conference on Discrete Mathematics, Computational Biology Mini-symposium, Denver, CO  |
| November 2017 | Challenges and Synergies in the Analysis of Large-Scale Population-Based Biomedical Data, Banff International Research Station, Oaxaca, Mexico |
| November 2017 | University of Maryland, Department of Computer Science, College Park, MD   |
| October 2017  | University of Maryland, Computational Biology, Bioinformatics, and Genomics Program, College Park, MD  |
| December 2016 | Tufts University, Department of Computer Science, Medford, MA  |
| February 2016 | Computational Cancer Biology Workshop, Simons Institute, Berkeley, CA  |
| April 2015    | Bio-IT World Conference & Expo, Boston, MA   |

## Advising Experience

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### Ph.D. Students

- Tracy Chen (Chemistry & Biochemistry; co-advised with Dr. David Fushman; *expected 2022*).
- Nicholas Franzese (Computer Science; *expected 2023*)
- Jason Fan (Computer Science; *expected 2023*)
- Xuan (Cindy) Li (Computational Biology, Bioinformatics, Genomics; *expected 2022*)
- Welles Robinson\* (Computer Science; co-advised with Dr. Eytan Ruppin, *expected 2021*).

### Undergraduate Students

- Mark Keller\* (Computer Science; *expected 2020*).

## Service

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### Leadership

Program Committee	ACM-BCB	2017
	ISMB	2018-2019
	RECOMB	2017-2019
	RECOMB-CCB	2017-2018, 2019 (PC co-chair)
Poster Committee	RECOMB	2015

### Referee

Conferences	RECOMB	2013-2015
	ISMB	2013
Journals	Bioinformatics–Oxford Journals	2012, 2014-2015, 2018
	Genome Medicine	2016
	Nature Genetics	2016
	PLoS Computational Biology	2012, 2014-2015, 2018
	Scientific Reports	2018
	PLoS ONE	2018

### Professional Memberships

International Society of Computational Biology (ISCB), 2012-present.

Association of Computing Machinery (ACM), 2014-present.

Institute of Electrical and Electronics Engineers, 2014-present.

American Association of Cancer Research (AACR), 2018-present.

## Open-Source Software

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<b>SigMa</b> : Signature Markov model	2018
Source: <a href="http://github.com/lrgr/sigma">http://github.com/lrgr/sigma</a>	
<b>MUNK</b> : Multi-species Network Kernel	2018
Source: <a href="http://github.com/lrgr/munk">http://github.com/lrgr/munk</a>	
<b>WExT</b> : Weighted Exclusivity Test	2017
Source: <a href="http://github.com/raphael-group/wext">http://github.com/raphael-group/wext</a>	
<b>CoMEt</b> : Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer	2015
Source: <a href="http://github.com/raphael-group/comet">http://github.com/raphael-group/comet</a>	
<b>GD3</b> : Javascript library for visualizing genomics data with D3	2014
Source: <a href="http://github.com/raphael-group/gd3">http://github.com/raphael-group/gd3</a>	
<b>MAGI</b> : Interactive visualization and collaborative annotation of genetic aberrations	2014
Web application: <a href="http://magi.cs.brown.edu">http://magi.cs.brown.edu</a> Source: <a href="http://github.com/raphael-group/magi">http://github.com/raphael-group/magi</a>	

**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 2013  
Source: <https://github.com/raphael-group/multi-dendrix>

Last updated: March 4, 2019

<https://lrgr.io/assets/files/Max-Leiserson-CV.pdf>