Mark D.M. Leiserson

Curriculum Vitae (February, 2018)

University of Maryland, College Park
Center for Bioinformatics and Computational Biology
3113 Biomolecular Sciences Building
8314 Paint Branch Dr
College Park, MD

Phone: (301) 405-7395
Email: mdml@cs.umd.edu
Homepage: https://lrgr.io/
Publications: [Google Scholar]

Education

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

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

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

Publications

* denotes equal contribution.

Preprints and in-press

Leiserson, M.D.M., Fan, J., Cannistra, A., Fried, I., Lim, T., Schaffner, T., Crovella, M., Hescott, B. (2018) A Multi-Species Functional Embedding Integrating Sequence and Network Structure. *RECOMB 2018* (to appear). [bioRxiv preprint]

Dwork, C., Immorlica, N., Kalai, A.T., **Leiserson, M.D.M.** (2018) Decoupled classifiers for fair and efficient machine learning. *FAT* 2018* (to appear). [arXiv preprint.]

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. *bioRxiv* https://doi.org/10.1101/231316

Peer-Reviewed Journal Articles

Senft, D., **Leiserson, M.D.M.**, Ruppin. E., Ze'ev, A.R. (2017) Precision Oncology: The Road Ahead. *Trends in Molecular Medicine*, 23(10):874-898. [Publisher link.]

The Cancer Genome Atlas Research Network. (2017) Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, 32(2):185-203. [Publisher link.]

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.]

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.]

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].

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].

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

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

2018	Primary instructor	UMD	CMSC 423	Bioinformatic Algorithms, Databases, and Tools
2017	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

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

December 2016	Tufts University, Department of Computer Science
February 2016	Computational Cancer Biology Workshop, Simons Institute, Berkeley, CA
April 2015	Bio-IT World Conference & Expo, Boston, MA.

Advising Experience

* denotes co-advised.

Master's Students

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

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

Jonathan V. Eldridge* (M.Sc., Computer Science, *2014*).

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*).

Service

Leadership

Program Committee	ACM-BCB	2017
	ISMB	2018
	RECOMB	2017, 2018
	RECOMB-CCB	2017, 2018
Poster Committee	RECOMB	2015

Referee

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

Professional Memberships

International Society of Computational Biology, 2012-present.

Association of Computing Machinery, 2014-present.

IEEE, 2014-present.

Open-Source Software

WExT: Weighted Exclusivity Test *2017*
  Source: http://github.com/raphael-group/wext

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

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

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