Mark D.M. Leiserson

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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

Post-doctoral researcher, Microsoft Research   *2016-*

Publications

* 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., 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. To appear: *Nature Communications*.

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

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

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

February 2016   Computational Cancer Biology Workshop, Simons Institute, Berkeley, CA
April 2015   Bio-IT World Conference & Expo, Boston, MA.

Advising Experience

Co-advised Master's Students

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

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.

PLoS Computational Biology: 2012, 2014-2015.

Nature Genetics: 2016.

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