BENJAMIN J. RAPHAEL
Professor
Department of Computer Science
Princeton University
35 Olden Street
Princeton, NJ 08540

Phone: (609) 258-6314   Email: braphael@princeton.edu
Web: http://compbio.cs.brown.edu

EDUCATION

1996-2002   **Ph.D.** in Mathematics, University of California, San Diego.

Thesis Title: *A Computational Investigation of Spectral Sets and Rational Dilations over Multiply-Connected Domains.* Advisor: Professor Jim Agler.

1992-1996   **S.B.** in Mathematics, **S.B. Minor** in Biology, Massachusetts Institute of Technology.

EXPERIENCE

2016-   **Professor**, Department of Computer Science, Princeton University
2013-2016   **Director**, Center for Computational Molecular Biology, Brown University
2011-2016   **Associate Professor**, Department of Computer Science & Center for Computational Molecular Biology, Brown University
2006-2011   **Assistant Professor**, Department of Computer Science & Center for Computational Molecular Biology, Brown University
2005-2006   **Burroughs Wellcome Postdoctoral Fellowship** in Computer Science (Bioinformatics), University of California, San Diego. Sponsor: Professor Pavel Pevzner.
2002-2004   **Alfred P. Sloan Postdoctoral Fellowship** in Computer Science (Bioinformatics), University of California, San Diego. Sponsor: Professor Pavel Pevzner.

PUBLICATIONS

Author order generally follows convention in biology, with senior/corresponding author listed last. Underlined authors are trainees. † indicates undergraduates. *indicates joint first or last author.

Refereed Journal and Conference Research Papers

M.A. Reyna, …, ICGC Pan-Cancer Analysis of Whole Genomes, J. Reimand, J.M. Stuart, **B.J. Raphael.** (2020) Pathway and network analysis of more than 2,500 whole cancer genomes. *Nature Communications.* [In Press]

G. Satas, S. Zaccaria, G. Mon, and **B.J. Raphael.** (2020) Single-cell tumor phylogeny inference with copy-number constrained mutation losses. *International Conference on Research in Computational Molecular Biology (RECOMB) 2020* [In press].

M.A. Reyna*, U. Chitra*, R. Elyanow, **B.J. Raphael.** (2020) NetMix: A network-structured mixture model for less biased identification of altered subnetworks. *International Conference on Research in Computational Molecular Biology (RECOMB) 2020*. [In press]

B. Li, S.W. Brady, X. Ma, S. Shen, Y. Zhang, Y. Li, K. Szlachta, L. Dong, Y. Liu, F. Yang, N. Wang, D.A. Flasch, M.A. Myers, H.L. Mulder, L. Ding, Y. Liu, L. Tian, K. Hagiwara, K. Xu, X. Zhou, E. Sioson, T. Wang, L. Yang, J. Zhao, H. Zhang, Y. Shao, H. Sun, L. Sun, J. Cai, H. Sun, T. Lin, L. Du, H. Li, M. Rusch, M.N. Edmonson, J. Easton, X. Zhu, J. Zhang, C. Cheng, **B.J. Raphael**, J. Tang, J.R. Downing, L.B. Alexandrov, B.S. Zhou, C. Pui, J.J. Yang, J. Zhang (2020) Therapy-induced mutations drive the genomic landscape of relapsed acute lymphoblastic leukemia. *Blood* 135 (1), 41-55.

U. Chitra, **B.J Raphael** (2019). Random Walks on Hypergraphs with Edge-Dependent Vertex Weights. *International Conference on Machine Learning (ICML) 2019.*

M. Myers, G. Satas, **B.J. Raphael** (2019). Inferring tumor evolution from longitudinal samples. *Cell Systems* 8 (6), 514-522.e5 and *International Conference on Research in Computational Molecular Biology* (RECOMB) 2019.

R. Elyanow, B. Dumitrascu and B. Engelhardt, **B.J. Raphael** (2019). netNMF: A network regularization algorithm for dimensionality reduction and imputation of single-cell expression data. *Genome Research* [In Press] and *International Conference on Research in Computational Molecular Biology* (RECOMB) 2019.

B Li, SW Brady, X Ma, S Shen, Y Zhang, Y Li, Y Liu, N Wang, D Flasch, M. Myers, ..., **B.J Raphael**, ..., J. Yang, J. Zhang (2019). Acquisition of drug resistance mutations during chemotherapy treatment in pediatric acute lymphoblastic leukemia. *Cancer Research* 79 (13 Supplement), 2872-2872.

SW Brady, X Ma, A Bahrami, G Satas, G Wu, S Newman, M Rusch, DK Putnam, HL Mulder, DA Yergeau, MN Edmonson, J Easton, LB Alexandrov, X Chen, ER Mardis, RK Wilson, JR Downing, AS Pappo, **B.J. Raphael**, MA Dyer, J. Zhang (2019) The clonal evolution of metastatic osteosarcoma as shaped by cisplatin treatment. *Molecular Cancer Research* 17 (4), 895-906

M.R. Reyna, M.D.M. Leiserson, **B.J. Raphael**. (2018) Hierarchical HotNet: identifying hierarchies of altered subnetworks. *Bioinformatics* [ECCB 2018 Proceedings] 34(17): i972–i980.

M.M. Parks, **B.J. Raphael**, C.E. Lawrence. (2018) Using controls to limit false discovery in the era of big data. *BMC Bioinformatics* 19 (1), 323.

M. El-Kebir, G. Satas, **B.J. Raphael**. (2018) Inferring parsimonious migration histories for metastatic cancers. *Nature Genetics* (5):718-726.

G. Satas, **B.J. Raphael**. (2018) Haplotype phasing in single-cell DNA-sequencing data. *Bioinformatics* [Proceedings of ISMB 2018] 34 (13), i211-i217.

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C.S. Grasso, et al. (2018) Genetic mechanisms of immune evasion in colorectal cancer. *Cancer Discovery* 8 (6), 730-749.

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S. Zaccaria*, M. El-Kebir*, G.W. Klau, **B.J Raphael**. (2018) Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. *Journal of Computational Biology*

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R. Elyanow, H.T. Wu, **B.J Raphael**. (2017) Identifying structural variants using linked-read sequencing data. *RECOMB Computational Cancer Biology 2017* and *Bioinformatics*, 34 (2), 353-360.

J. Kuipers, K. Jahn, **B.J. Raphael**, N. Beerenwinkel. (2017) Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors. *Genome Research,* 27 (11), 1885-1894.

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BJ Raphael*, RH Hruban*, AJ Aguirre*, TCGA Research Network (2017). Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell,* 32 (2), 185-203. e13.

R.J. Mashl, A.D. Scott, K. Huang, M.A. Wyczalkowski, C.J. Yoon, B. Niu, E. DeNardo, V.D. Yellapantula, R.E. Handsaker, K. Chen, D.C. Koboldt, K. Ye, D. Fenyö, **B.J. Raphael**, M.C. Wendl, L. Ding. (2017) GenomeVIP: a cloud platform for genomic variant discovery and interpretation**.** *Genome Research,* (8):1450-1459.

M El-Kebir, **BJ Raphael**, R Shamir, R Sharan, S Zaccaria, M Zehavi, R Zeira. (2017) Complexity and algorithms for copy-number evolution problems. *Algorithms for Molecular Biology,* 12 (1), 13.

P. Nakka, N.P. Archer, H. Xu, P.J. Lupo, **B.J. Raphael**, J.J. Yang, S. Ramachandran. (2017) Novel gene and network associations found for lymphoblastic leukemia using case-control and family-based studies in multi-ethnic populations. *Cancer Epidemiology and Prevention Biomarkers* (10):1531-1539.

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M. El-Kebir*, G. Satas*, L. Oesper, **B.J. Raphael** (2016). Inferring the Mutational History of a Tumor using Multi-State Perfect Phylogeny Mixtures. *Cell Systems*, 3(1):43-53.

On the Sample Complexity of Cancer Pathways Identification. (2016)
F. Vandin, **B.J. Raphael**, E.Upfal. *Journal of Computational Biology* 23(1):30-41.

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M. El-Kebir, G. Satas, L. Oesper, **B.J. Raphael** (2016). Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing. *RECOMB 2016*

S. Zheng, A.D. Cherniack, N. Dewal, R.A. Moffitt, L. Danilova, B.A. Murray, A.M. Lerario, T. Else, T.A. Knijnenburg, G. Ciriello, S. Kim, G. Assie, O. Morozova, R. Akbani, J. Shih, K.A. Hoadley, T.K. Choueiri, J. Waldmann, O. Mete, A.G. Robertson, **B.J. Raphael**, M. Meyerson, M.J. Demeure, F. Beuschlein, A.J. Gill, A.C. Latronico, M.C. Fragoso, L.M. Cope, E. Kebebew, M.A. Habra, T.G. Whitsett, K.J. Bussey, W.E. Rainey, S.L. Asa, J. Bertherat, M. Fassnacht, D.A. Wheeler, The Cancer Genome Atlas Research Network, G.D. Hammer*, T.J. Giordano*, R.G.W. Verhaak*. (2015) Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*. (2016) 29(5):723-36.

C. Weinreb[†] and **B.J. Raphael** (2016). Identification of hierarchical chromatin domains. *Bioinformatics*. 32(11):1601-9.

M.D. Leiserson, F. Vandin, H.T. Wu, **B.J. Raphael**. (2016) Reply: Co-occurrence of MYC amplification and TP53 mutations in human cancer. *Nature Genetics*, 48(2):106-8.

C.Lu*, M. Xie*, M.C. Wendl*, J. Wang*, M.D. McLellan*, M.D.M. Leiserson*, M.A. Wyczalkowski, R. Jayasinghe, K. Huang, T. Banerjee , J.Ning, P.Tripathi, Q. Zhang, B. Niu, K. Ye, H.K. Schmidt , R.S. Fulton, J.F. McMichael , P. Batra , C. Kandoth , M. Bharadwaj , D.C. Koboldt , C.A. Miller , K.L. Kanchi , J.M. Eldred , D.E. Larson, J.S. Welch, M. You, B.A. Ozenberger, R. Govindan, M.J. Walter, M.J. Ellis, E.R. Mardis, T.A. Graubert, J.F. Dipersio, T.J. Ley, R.K. Wilson, P.J. Goodfellow, **B.J. Raphael**, F. Chen, K.J. Johnson, J.D. Parvin, L. Ding. (2015) Patterns and Functional Implications of Rare Germline Variants across 12 Cancer Types. *Nature Communications*. 6:10086.

The Cancer Genome Atlas Research Network. (2015) Comprehensive Molecular Characterization of Papillary Renal Cell Carcinoma. *New England Journal of Medicine*. 374(2):135-45.

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M.D.M. Leiserson, C.C. Gramazio, J. Hu[†], H. Wu, D.H. Laidlaw, **B.J. Raphael.** (2015) MAGI: Visualization and Collaborative Annotation of Genomic Aberrations. *Nature Methods* 12(6):483-484.

M. El-Kebir*, L. Oesper*, H. Acheson-Field†, **B.J. Raphael**. (2015) Reconstruction of clonal trees and tumor composition from multi-sample cancer sequencing data. *Bioinformatics [Proceedings of ISMB 2015]*. 31(12):i62-i70.

S.M. Doris, D.R. Smith, J.N. Beamesderfer, **B.J. Raphael**, J.A. Nathanson, S.A. Gerbi. (2015) Universal and Domain-Specific Sequences in 23S-28S Ribosomal RNA Identified by Computational Phylogenetics. *RNA*. (10):1719-30.

B.J. Raphael, F. Vandin (2015). Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. *Journal of Computational Biology* 22(6):510-27.

M.M. Parks, C.E. Lawrence, **B.J. Raphael**. (2015) Detecting non-allelic homologous recombination from high-throughput sequencing data. *Genome Biology* 16 (1), 72.

F. Vandin, A. Papoutsaki, **B.J. Raphael***, E. Upfal*. (2015) Accurate Computation of Survival Statistics in Genome-wide Studies. *PLOS Computational Biology*. 11(5):e1004071. *corresponding authors

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. *19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)*, 202-204.

F. Vandin, **B.J. Raphael**, E. Upfal (2015) On the Sample Complexity of Cancer Pathways Identification. *19th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2015)*, 326-337.

M.D.M Leiserson*, F. Vandin*, H. 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.

L. Oesper, G. Satas, **B.J. Raphael**. (2014) Quantifying Tumor Heterogeneity in Whole-Genome and Whole-Exome Sequencing Data. *Bioinformatics.* 30(24):3532-40.

A. Ritz, A. Bashir, S. Sindi, D. Hsu, I. Hajirasouliha, **B.J. Raphael**. (2014). Characterization of Structural Variants with Single Molecule and Hybrid Sequencing Approaches. *Bioinformatics*. 30(24):3458-66.

Integrated Genomic Characterization of Papillary Thyroid Carcinoma. (2014) The Cancer Genomic Atlas Research Network. *Cell* 159(3):676-90.

C. Weinreb†, L. Oesper, **B.J. Raphael**. (2014) Open adjacencies and k-breaks: detecting simultaneous rearrangements in cancer genomes . *BMC Genomics* 15(Suppl 6):S4. *Special issue for the 12th Annual Research in Computational Molecular Biology (RECOMB) Satellite Workshop on Comparative Genomics (RECOMB-CG 2014)*

K.A. Hoadley*, C. Yau*, D.M. Wolf*, A.D. Cherniack*, D. Tamborero, S. Ng, M.D.M. Leiserson, B. Niu, M.D. McLellan, E.O. Paull, V.Uzunangelov, C.Kandoth, R.Akbani, H.Shen, TCGA Network, L.van't Veer,

N.Lopez-Bigas, P.W. Laird, **B. J. Raphael**, L.Ding, E.A. Collisson, L.A. Byers, G.B. Mills, J.Weinstein, C. Van Waes, Z. Chen, C. Benz#, C.M. Perou#, J.M. Stuart# (2014) Multi-platform integration of 12 cancer types reveals cell-of-origin classes with distinct molecular signatures. *Cell* 158(4):929-944.

I. Hajirasouliha, **B.J. Raphael.** (2014) Reconstructing mutational history in multiply sampled tumors using perfect phylogeny mixtures. *14th Workshop on Algorithms in Bioinformatics (WABI)*.

The Cancer Genome Atlas Research Network. (2014) Comprehensive molecular characterization of gastric adenocarcinoma. *Nature* 513:202-209.

H. Wu, I. Hajirasouliha, **B. J. Raphael.** (2014) Detecting independent and recurrent copy number aberrations using interval graphs. *Bioinformatics* 30 (12), i195-i203.
[Special issue for the 22nd Annual International Conference on Intelligent Systems in Molecular Biology (ISMB 2014)]

I. Hajirasouliha*, A. Mahmoody*, **B. J. Raphael**. (2014) A combinatorial approach for analyzing intra-tumor heterogeneity from high-throughput sequencing data. *Bioinformatics* 30 (12), i78-i86. [Special issue for the 22nd Annual International Conference on Intelligent Systems in Molecular Biology (ISMB 2014)] *equal contribution.

A.S. Brodsky, A. Fischer, D.H. Miller, S.Vang, S.Maclaughlan, H.T. Wu, J.Yu, M.Steinhoff, C.Collins, P.J.Smith, **B.J. Raphael**, L.Brard. (2014) Expression profiling of primary and metastatic ovarian tumors reveals differences indicative of aggressive disease. *PLoS One.* (2014) 9(4):e94476.

B.J. Raphael, F. Vandin (2014) Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. *18th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*.

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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):333-9. **[Publisher Link]**

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The Cancer Genome Atlas Research Network. (2013) Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. *New England Journal of Medicine.* 368(22):2059-74. **[Publisher Link]**. [**Interative visualization**]

L. Oesper, A. Mahmoody, **B.J. Raphael**. (2013) Estimating Tumor Purity and Cancer Subpopulations from High-Throughput DNA Sequencing Data. *17th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2013)*. **[Publisher Link]**

F. Vandin, A. Papoutsaki, **B.J. Raphael***, E.Upfal*. (2013) Genome-Wide Survival Analysis of Somatic Mutations in Cancer. *17th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2013)*. [**Best Paper Award, RECOMB 2013**] **[Publisher Link]** *equal contribution.

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A. Mahmoody, C.L. Kahn, **B.J. Raphael**. (2012) Reconstructing Genome Mixtures From Partial Adjacencies. BMC Bioinformatics 13 Suppl 19:S9. [*Proceedings of the Tenth Annual RECOMB Satellite Workshop on Comparative Genomics.]*

C. Grasso , Y.Wu , D. Robinson , X. Cao , S. Dhanasekaran , A. Khan , M. Quist , X. Jing , R. Lonigro , J.C. Brenner , I. Asangani , B. Ateeq , S. Chun , J. Siddiqui , L. Sam , M. Anstett , R. Mehra , J. Prensner , N. Palanisamy , G. Ryslik , F. Vandin , **B. J. Raphael** , L. Kunju , D. Rhodes , K. Pienta , A. M. Chinnaiyan, S.A. Tomlins. (2012) The Mutational Landscape of Lethal Castrate Resistant Prostate Cancer. *Nature* 487(7406):239-43.

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A. Stuckey, A. Fischer, D. H Miller, S. Hillenmeyer, K. K Kim, A. Ritz, R. K Singh, **B. J. Raphael**, L. Brard and A.S. Brodsky. (2011) Integrated Genomics of Ovarian Xenograft Tumor Progression and Chemotherapy Response. *BMC Cancer.* Jul 22;11:308

K.H. Lim, L. Ferraris, M. Filloux, **B.J. Raphael**, W. Fairbrother. (2011) Using positional distribution to identify splicing elements and predict mRNA processing defects in human genes. *Proceedings of the National Academy of Sciences (PNAS).* 108(27):11093-8.

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V. Nguyen, L. Cao,J.T. Lin, N. Hung, A. Ritz, K. Yu, R. Jianu, S.P. Ulin, **B.J. Raphael**, D.H. Laidlaw, L.Brossay, A.R. Salomon. (2009) A New Approach for Quantitative Phosphoproteomic Dissection of Signaling Pathways Applied to T cell Receptor Activation. *Molecular and Cellular Proteomics*. 8(11):2418-31.

S. Sindi, E. Helman†, A. Bashir, **B.J. Raphael**. (2009) A Geometric Approach for Classification and Comparison of Structural Variants. *Bioinformatics* 25: i222-i230. *[Proceedings of the Joint 17th Annual International Conference on Intelligent Systems in Molecular Biology and 8th Annual International European Conference on Computational Biology (ISMB/ECCB 09*)]

S. Sindi and **B.J. Raphael**. Identification and Frequency Estimation of Inversion Polymorphisms from Haplotype Data. (2009) *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009).*

A. Bashir, Q. Liu, **B.J. Raphael**, D. Carson, Y.T. Liu, V. Bafna. Optimizing PCR assays for DNA based cancer diagnostics. (2009) *Proceedings of the 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2009).*

C.L. Kahn and **B. J. Raphael.** A Parsimony Approach to Analysis of Human Segmental Duplications. (2009) *Pacific Symposium on Biocomputing.* 14:126-137.

B.T. Messmer*, **B. J. Raphael***, S.J. Aerni†, G.F Widhopf, L.Z Rassenti, T.L Toy, T.J Kipps. (2009) Computational Identification And Clinical Relevance Of CDR3 Sequence Archetypes Among CLL IGHV Sequences. *Leukemia Research*. 33(3):368-76.
*equal contribution

A. Ritz, G. Shakhnarovich, A.R. Salomon, **B.J. Raphael**. (2009) Identification of Phosphorylation Motif Mixtures in Phosphoproteomics Data. *Bioinformatics*. 25(1):14-21.

C.L. Kahn and **B. J. Raphael.** Analysis of Segmental Duplications via Duplication Distance. (2008) *Bioinformatics*. 24(16):i133-8 (Proceedings of the European Conference on Computational Biology).

B. J. Raphael, S. Volik, G. Huang, F.Waldman, J. Costello, S.Aerni†, R.P. Brown†, A. Bashir, K. Pienta, G. Mills, K. Bajsarowicz, P. Paris, Q. Tao, W. Kuo, J.W. Gray, J. Cheng, M. Nefedov, P. de Jong, and C. Collins. (2008). A sequence based survey of the complex structural organization of tumor genomes. *Genome Biology*. 9(3):R59. [Designated "Highly Accessed]

A. Bashir, S. Volik, C.C. Collins, V. Bafna, **B. J. Raphael**. (2008) Evaluation of Paired-end Sequencing Strategies for Detection of Genome Rearrangements in Cancer. *PLOS Computational Biology*. 4(4):e1000051.

J. Agler, J. Harland, **B. J. Raphael**. (2008) Classical Function Theory, Operator Dilation Theory, and Machine Computation on Multiply-Connected Domains. *Memoirs of the American Mathematical Society.* Vol. 191, No. 892.

A. Bashir, Y.T. Liu, **B. J. Raphael**, D. Carson, V. Bafna. (2007) Optimization of primer design for the detection of variable genomic lesions in cancer. *Bioinformatics.* 23(21):2807-15.

L. Cao, K. Yu, V. Nguyen, A. Ritz, **B. J. Raphael**, Y. Kawakami, T. Kawakami, A.R. Salomon, (2007) Quantitative Time-Resolved Phosphoproteomic Analysis of Mast Cell Signaling. *Journal of Immunology*. 179(9):5864-76.

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S. Yooseph, G. Sutton, D.B. Rusch, A.L. Halpern, S.J. Williamson, K.Remington, J.A. Eisen, K..B. Heidelberg, G. Manning, W. Li, L. Jaroszewski, P. Cieplak, C.S. Miller, H. Li, S. T. Mashiyama, M. P. Joachimiak, C. van Belle, J. Chandonia, D. A. Soergel, Y. Zhai, K. Natarajan, S. Lee, **B. J. Raphael**, V. Bafna, R. Friedman, S. E. Brenner, A. Godzik, D. Eisenberg, J.E. Dixon, S. S. Taylor, R.L. Strausberg, M. Frazier, J.C. Venter. (2007) The Sorcerer II Global Ocean Sampling Expedition: Expanding the Universe of Protein Families. *PLOS Biology*. 5(3):e16.

M. Chaisson, **B. J. Raphael**, and P. Pevzner. (2006) Micro-inversions in Mammalian Evolution. *Proceedings of the National Academy of Sciences, USA*. 103(52):19824-9.

N.C. Jones, D. Zhi, **B. J. Raphael**. (2006) AliWABA: Alignment on the Web through an A-Bruijn Approach. *Nucleic Acids Research*. July 1;34:W613-6.

S. Volik, **B. J. Raphael**, Huang, G., Stratton, M.R., Bignel, G., Murnane, J., Brebner, J.H., Bajsarowicz, K., Paris, P.L., Tao, Q., Kowbel, D., Lapuk, A., Shagin, D.A., Shagina, I.A., Gray, J.W., Cheng, J., de Jong, P.J., Pevzner, P., and Collins, C. (2006) Decoding the Fine-scale Architecture of a Breast Cancer Genome and Transcriptome. *Genome Research*, 16(3):394-404.

D. Zhi, **B. J. Raphael**, A. Price, H. Tang, P. Pevzner. (2006) Identifying Repeat Domains in Large Genomes. *Genome Biology*, 7(1):R7. [Designated "Highly Accessed"]

B. J. Raphael, D. Zhi, H. Tang, P. Pevzner. (2004) A Novel Method for Multiple Alignment of Sequences with Repeated and Shuffled Domains. *Genome Research*, 14(11):2336-46.

B. J. Raphael and P. Pevzner. (2004) Reconstructing Tumor Amplisomes. *Bioinformatics*, 20 Suppl 1:I265-I273. (Special ISMB/ECCB 2004 Issue). [Selected by "Faculty of 1000"]

B. J. Raphael, L. Liu, and G. Varghese. (2004) A Uniform Projection Method for Motif Discovery in DNA Sequences. *IEEE Transactions on Computational Biology and Bioinformatics*, 1(2): 91-94.

B. J. Raphael, S. Volik, C. Collins, P. Pevzner. (2003) Reconstructing Tumor Genome Architectures. *Bioinformatics*, Suppl 2:ii162-171. (Special ECCB 2003 Issue). [Selected by "Faculty of 1000"]

Books and Edited Volumes

B.J. Raphael (Ed). (2018) Proceedings of Research in Computational Molecular Biology: 22nd Annual International Conference, RECOMB 2018, Paris, France, April 21-24, 2018.

B.J. Raphael, J. Tang (Eds.). (2012) Algorithms in Bioinformatics - 12th International Workshop, WABI 2012, Ljubljana, Slovenia, September 10-12, 2012. Proceedings. Lecture Notes in Computer Science 7534, Springer.

E. Eskin, T. Ideker, **B. J. Raphael**, C. Workman (eds.), (2006) *Systems Biology and Regulatory Genomics. Joint Annual RECOMB 2005 Satellite Workshops on Systems Biology and on Regulatory Genomics*. Lecture Notes in Computer Science , Vol. 4023. Springer-Verlag.

Book Chapters and Review Articles

L. Cowen, T. Ideker, **B.J Raphael**, R Sharan (2017). Network propagation: a universal amplifier of genetic associations. *Nature Reviews Genetics.* 18(9):551-562.

P.Creixell, J.Reimand, S.Haider, G.Wu, T. Shibata, M. Vazquez, V.Mustonen, A.Gonzalez-Perez, J. Pearson, C. Sander, **B.J. Raphael**, D.S. Marks, B.F.F. Ouellette, A. Valencia, G.D. Bader, P.C. Boutros, J.M. Stuart, R. Linding, N. Lopez-Bigas, L.D. Stein, Mutation Consequences and Pathway Analysis Working Group of the International Cancer Genome Consortium. (2015) Pathway and Network Analysis of Cancer Genomes. *Nature Methods.* 12(7):615-621.

S. Brunak, F.M. De La Vega, A. Margolin, **B.J. Raphael**, G. Raetsch, J.M. Stuart. (2015) Cancer Panomics: Computational Methods and Infrastructure for Integrative Analysis of Cancer High-Throughput "Omics" Data. *Pacific Symposium on Biocomputing (PSB) 2015.* 20:8-9.

M.D.M. Leiserson and **B.J. Raphael**. (2015) Analyzing Combinations of Somatic Mutations in Cancer Genomes. In: Integrating -omics data: Statistical and Computational Methods. G.C. Tseng, D. Ghosh, X.J. Zhou, (Eds.) Cambridge University Press.

L. Ding L, M.C. Wendl, J.F. McMichael, **B.J. Raphael**. (2014) Expanding the computational toolbox for mining cancer genomes. *Nature Reviews Genetics.* (8):556-70.

B.J. Raphael, J.R. Dobson, L. Oesper, and F. Vandin (2014) Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. *Genome Medicine.* 6:5.

S.S. Sindi, **B.J. Raphael** (2014). Identification of Structural Variation. In *Genome Analysis: Current Procedures*. M.S. Poptsova (ed). Caister Academic Press.

M.D.M. Leiserson, J.V. Eldridge, S.Ramachandran, **B.J. Raphael**. Network Analysis of GWAS Data. *Current Opinion in Genetics & Development* (2013) 23(6):602-10. **[Publisher Link]**

B.J.Raphael (2013). Making connections: using networks to stratify human tumors (News and Views). *Nature Methods* 10(11):1077-8. **[Publisher Link]**

L. Ding, **B.J. Raphael**, F. Chen, M.C. Wendl. (2013) Advances for Studying Clonal Evolution in Cancer. *Cancer Letters*. pii: S0304-3835(13)00034-7. **[Publisher Link]**

E. Batchelor, M.G. Kann, T.M. Przytycka, **B.J. Raphael**, D. Wojtowicz. (2013) Modeling cell heterogeneity: from single-cell variations to mixed cells. *Pacific Symposium on Biocomputing (PSB) 2013*. 18:445-50. **[Publisher Link]**

G. Bebek, M. Koyutürk, T. Laframboise, **B.J. Raphael**, M.R. Chance (2013). Post-NGS: Interpretation and Analysis of Next Generation Sequencing Data for Basic and Translational Science. *Pacific Symposium on Biocomputing (PSB) 2013.* 18:307-309.

B.J. Raphael. (2012) Structural Variation and Medical Genomics. *PLOS Computational Biology.* 8(12): e1002821.

F. Vandin, E. Upfal, **B.J. Raphael**. (2012) Algorithms and Genome Sequencing: Identifying Driver Pathways in Cancer. *IEEE Computer* March 2012 (vol. 45 no. 3) pp.39-46.

B. J. Raphael, S. Volik, C. Collins (2007). Analysis of Genomic Alterations in Cancer. In *Genome Sequencing Technology and Algorithms*. H. Tang, S. Kim, E.Mardis (eds). Artech House Publishers.

Work in Review

S. Zaccaria, **B.J Raphael** (2018) Accurate quantification of copy-number aberrations and whole-genome duplications in multi-sample tumor sequencing data. *Nature Methods* (in review)

Patents

B.J. Raphael, M.D.M. Leiserson, F.Vandin, H.Wu (2015). Heat Diffusion Based Genetic Network Analysis. U.S. Patent Application No.: 62/057,479.

B.J. Raphael, M. El-Kebir. G. Satas. (2016). Phylogeny Tree Generation From Mixed Samples. U.S. Provisional Patent Application No.: 62/440,563.

Invited Talks

2019   Memorial Sloan Kettering Cancer Center
    UCLA Computational Medicine Department
    Advances in Genome Biology and Technology (AGBT) 2019
    M.D. Anderson Cancer Center, Computational Biology Department
    Seoul National University Bioinformatics Workshop
    UCLA Computational Genomics Summer Institute
    CNIO – "la Caixa" Frontiers Meeting: Heterogeneity and Evolution in Cancer
    Bertinoro Computational Biology Meeting
    International Symposium on Mathematical and Computational Oncology (ISMCO)
    Mathematical Biology Institute, Ohio State University

2018   Harvard Biostatistics - Biomedical Informatics - Big Data (B3D) Seminar
    St. Jude's Children's Research Hospital
    New York Genome Center
    American Association for Cancer Research (AACR) Annual Meeting, Methods Workshop
    Lewis Sigler Institute Cancer Symposium, Princeton University
    Lorentz Institute, Leiden, Netherlands
    Gordon Research Conference on Human Genetic Variation and Disease, Biddeford, ME
    Computational ONcology TRaining Alliance (CONTRA) Workshop, Bertinoro, Italy
    Computational Genomics Summer Institute (CGSI), University of California, Los Angeles
    Cell Mapping Symposium, University of California San Diego
    Future Forum, Beijing China
    Symposium on Advances in Cancer Genomics, Cancer Institute of New Jersey, Rutgers
        University
    Princess Margaret Cancer Centre, Toronto, ON

2017   NIPS Workshop on Machine Learning in Computational Biology
    Biomedical Data Science Industry Day, Princeton University
    CPTAC 3.0 PI Meeting, National Institutes of Health
    Bertinoro Computational Biology
    Distinguished Lecture: Department of Computer Science, University of Illinois,
        Urbana Champaign,
    Francis Crick Institute, Systems Genetics of Cancer Workshop
    Cell Mapping Symposium, University of California, San Francisco
    Simons Institute for the Theory of Computing, Genomics Reunion
    UCLA Computational Genomics Summer Institute
    Lake Como Workshop and School on Cancer Development and Complexity
    Keynote: RECOMB 2017
    Boston University Bioinformatics Student Symposium
    Mathematical Methods in Cancer Evolution and Heterogeneity Workshop, Institute

for Advanced Study, Princeton
Keynote: Informatics Technology for Cancer Research (ITCR) Annual Meeting,
     University of California, Santa Cruz
New York Genome Center, Five Points Lecture
Data Science Seminar, Brown University
MIT Mathematics and CSAIL Bioinformatics Seminar
Statistical and Computational Challenges in Large Scale Molecular Biology, Banff
Princeton-Rutgers Cancer Genomics Retreat
Rutgers Cancer Institute of New Jersey
Mount Sinai, Department of Genetics
University of California, San Diego Bioinformatics Program, Student invited speaker

2016   Simons Institute for the Theory of Computing, Genomics Bootcamp
Simons Institute for the Theory of Computing, Networks Biology Workshop
Michael Waterman 75th Birthday Symposium
Systems Approaches to Cancer Biology Conference.
Weill Cornell, Institute for Computational Biomedicine (ICB) Seminar
University of Pennsylvania, Penn Bioinformatics Forum
International Symposium on Pancreatic Cancer
5th Seoul National University Bioinformatics Workshop
UCLA Computational Genomics Summer Institute
1st Annual Cancer Cell Map Initiative Symposium
Simons Foundation, New York. Invited Lecture
Microsoft Research New England. Computational Aspects of Biological Information (CABI)
    Conference
University of Toronto, Molecular Genetics Seminar.

2015   Princeton, Department of Computer Science, Seminar
Rhode Island Hospital, Department of Pathology Seminar
McGill Barbados Computational Biology Workshop
ETH, Zurich: Department of Biosystems Science and Engineering
Novartis, Basel, Switzerland
AstraZenca, Waltham, MA
MIT, Mathematics and CSAIL Bioinformatics Seminar
Pompeu Fabra University, Barcelona.
COST Action for Pancreas Cancer Workshop, Barcelona.
Foundation Medicine, Cambridge, MA.
The Cancer Genome Atlas (TCGA), Steering Committee Meeting.
Stanford University, Cancer Systems Biology Symposium
Carnegie Mellon University, Computational Biology Seminar
European Laboratory for Molecular Biology (EMBL), Cancer Genetics Meeting
RECOMB Workshop on Bioinformatics Education (RECOMB-BE)
CAS-MPG Partner Institute for Computational Biology, Shanghai
CSHA/AACR Joint Meeting: Big Data, Computation and Systems Biology in Cancer
Indiana University, Department of Computer Science Seminar
Jackson Laboratory for Genomic Medicine, Seminar

2014   Vanderbilt University: Department of Seminar
U. Illinois Urbana Champaign: Institute for Genomic Biology Seminar
Cambridge Healthtech: Molecular Medicine Tri-Conference

Keynote: RECOMB Workshop on Massively Parallel Sequencing.
Invited Talk: American Association of Cancer Research (AACR) Annual Meeting
Tufts University: Department of Computer Science Seminar
Seminar: Novartis, Cambridge
Invited Talk: Institute for Pure and Applied Mathematics (IPAM)
Invited Talk: GE Research
Keynote: VarI-SIG at Intelligent Systems for Molecular Biology (ISMB) conference
BioConductor Annual Meeting
European Conference on Computational Biology (ECCB) Workshop
Kavli Institute for Theoretical Physics: Evolution of Drug Resistance Program
Brown University MPPB Department
Beyond the Genome Conference
UNC Charlotte: Department of Bioinformatics Seminar
Broad Institute
EMBL: Causal Inference Workshop
Keynote: UW Department of Genome Sciences Symposium
Boston University: Systems Biology Seminar

2013 Cold Spring Harbor Systems Biology: Networks Meeting
American Association of Cancer Research (AACR) Annual Meeting
TCGA Pan-Cancer Symposium
Illumina Sequencing Expert Panel
Institute for Pure and Applied Mathematics, UCLA, Program Reunion
Bertinoro Computational Biology Conference
Rhode Island College Biology Symposium
Genentech
International Cancer Genome Consortium (ICGC) Annual Meeting
American Society Human Genetics (ASHG) Annual Meeting
Microsoft Research, New England

2012 International Cancer Genome Consortium (ICGC) Annual Meeting
Cold Spring Harbor Quantitative Biology Seminar
The Cancer Genome Atlas (TCGA) Second Scientific Symposium
Vancouver Bioinformatics Group (VanBUG)
TCGA Pan-Cancer Workshop
Beyond the Genome Conference, Boston, MA
Joint Statistical Meetings Session on "Design and Analysis Issues with Next-Generation
   Sequencing Data on Complex Traits", San, Diego, CA.
Pacific Symposium on Biocomputing, Genomic Medicine Session.
Canadian Institute for Advanced Research, Genetic Networks Meeting.

2011 Program Final Retreat, Institute for Pure and Applied Mathematics, UCLA
Bioinformatics Rendezvous, Genome Quebec, Montreal, Canada
The Cancer Genome Atlas' 1st Annual Scientific Symposium
Cancer Genomics Workshop, Institute for Pure and Applied Mathematics, UCLA
Workshop, Statistical Analysis for Next Generation Sequencing, Birmingham, AL
Knight Cancer Center, Oregon Health Sciences University, Seminar
Third RECOMB Satellite Conference on Bioinformatics Education
Ascona, Swizerland Workshop: "Statistical Challenges and Biomedical Applications of Deep
Sequencing Data".

Cambridge Healthtech Institute, "X-Gen Congress and Exposition"
University of California, San Diego. Bioinformatics Seminar.
University of California, Los Angeles. Computer Science Seminar.
IEEE Workshop on Computational Advances for Next Generation Sequencing (CANGS 2011).
University of Chicago, Departments of Statistics and Cancer Biology Seminar.

2010   Mathematical Association of America, Northeast Section Regional Meeting.
        Washington University in St. Louis, Computer Science Seminar.
        University of Virginia, Biochemistry and Molecular Genetics Seminar.
        Memorial Sloan-Kettering Cancer Center, Computational Biology Seminar.
        Next Generation Sequencing Data Analysis Symposium, Brown University
        Washington University in St. Louis, Genetics Seminar.
        Cold Spring Harbor Laboratory, "Personal Genomes" Meeting
        Massachusetts Institute of Technology, Bioinformatics Seminar.
        University of Rhode Island
        Genome Informatics Alliance (Illumina)
        SIAM Conference on Discrete Mathematics

2009   University of California, Berkeley, Mathematics Colloquium
        Rhode Island Research Alliance Symposium.
        Cambridge Healthtech Institute, "Next-Generation Sequence Data Analysis" Meeting
        Cold Spring Harbor Laboratory, "Biology of Genomes" Meeting
        Helicos BioSciences, Cambridge, MA

2008   Washington University St. Louis Genome Sequencing Center
        SIAM Conference on Discrete Mathematics
        University of Connecticut, Department of Computer Science Colloquium
        University of California, Los Angeles, Bioinformatics Seminar
        Second Annual Bertinoro Systems Biology Meeting

2007   Mathematical Sciences Research Institute, "Mathematical Systems Biology of Cancer II"
        Harvard Medical School - Partners Healthcare Center for Genetics and Genomics
        GEM4 Conference on Cancer, Singapore
        Fifth Annual Bertinoro Computational Biology Meeting
        University of Virginia, Department of Mathematics
        Sixth Annual McGill Workshop on Bioinformatics in Barbados

2006   Tufts University, Department of Computer Science
        Brown University, Center for Statistical Sciences
        Mathematical Sciences Research Institute, "Mathematical Systems Biology of Cancer"
        University of California, San Diego, Department of Mathematics
        University of Southern California, Department of Computational and Molecular Biology
        University of Minnesota, Department of Computer Science
        Washington University St. Louis, Department of Genetics
        Boston University, Bioinformatics Program
        Brown University, Department of Computer Science
        University of California, Irvine, Department of Computer Science
        University of California, Santa Cruz, Department of Bimolecular Engineering
        Fred Hutchinson Cancer Research Center
        Purdue University, Department of Computer Science

University of Wisconsin, Department of Biomedical Informatics
Memorial Sloan-Kettering Cancer Center
University of Maryland, Department of Computer Science
Georgia Tech, Department of Computer Science
University of California, San Diego, Cancer Center

2004　RECOMB Satellite Meeting on Comparative Genomics, Bertinoro, Italy
Duke University, Department of Computer Science
North Carolina State University, Bioinformatics Seminar
Intelligent Systems in Molecular Biology (ISMB), Glasgow, Scotland.

2003　European Conference on Computational Biology (ECCB), Paris, France.

RESEARCH GRANTS

Current

Chan Zuckerberg Initiative　　　　　　　　　　　　　4/1/2018-3/30/2019
Analysis of molecular and cellular interactions by combining network algorithms and human insight
Role: PI
Total Amount: $218,807

National Cancer Institute (NCI) U24-CA211000　　　　　9/15/2016-8/31/2021
Pathway and Network Integration of Cancer Genomics and Clinical Data
Role: PI
Total Amount: $1,680,000

National Cancer Institute (NCI)　　　　　　　　　　　9/15/2016-8/31/2021
Deep Discovery and Clinical Interpretation of the Germline and Somatic Cancer Drivers
Role: Co-investigator.　PI: L. Ding (University of Washington, St. Louis)
Total Amount of Subaward: $50,000

National Science Foundation　　　　　　　　　　　　1/1/2011-12/31/2019
CAREER: Algorithms for Next-Generation Genomics
Role: PI
Total Amount: $450,000

NIH DP1DA042103-01　　　　　　　　　　　　　　9/15/2017 – 8/31/2022
The Kinship Risk Score: An Integrative Tool to Prioritize Alcohol and Drug-Addiction Related Genes for Enhanced Risk prediction
Role: Investigator (PI: Rohan Palmer)

NIH/NHGRI 1R01HG007069　　　　　　　　　　　　9/1/2013-8/31/2019
Computational Characterization of Genetic Heterogeneity
Role: PI
Total Amount: $1,119,000

NIH R01　　　　　　　　　　　　　　　　　　　　4/1/2018 – 3/31/2023
Integrative Prioritization of Alcohol and Drug-Addiction Related Genetic Loci

Role: Investigator (PI: Rohan Palmer)

NIH R01   4/1/2018 – 3/31/2023
Computational methods for identifying non-coding cancer drivers
Role: Investigator (PI: Ekta Khurana)

Pending
NIH U24
Role: PI
Total Amount: $

Completed

NIH/NHGRI 1R01HG005690   1/01/2011-12/31/2016
Computational Approaches for Structural Variation Studies in Genomes
Role: PI
Total Amount: $2,616,370

Sloan Research Fellowship   9/1/2010-8/31/2016
Role: PI
Total Amount: $50,000

Burroughs Wellcome Career Award at the Scientific Interface   1/1/2005-2/15/2017
High-resolution analysis of Tumor Genome Architectures
Role: PI
Total Amount: $500,000

NIH/National Institute of General Medical Sciences   12/1/2014 – 11/30/2019
COBRE Center for Computational Biology of Human Disease
Role: PI of Biomedical Big Data Core (PI: David Rand)
Total Amount: $3,556,896
[PI of the Biomedical Big Data Core. Relinquished this role on move to Princeton.]

National Science Foundation   10/1/2012-9/30/2018
*BIGDATA: Mid-Scale: DA: Analytical Approaches to Massive Data Computation with Applications to
        Genomics*
Role: Co-PI (with PI: Eli Upfal). [Relinquished this role on move to Princeton.]
Total Amount: $1,566,685

NIH/NCI 1R01CA180776-01   6/18/2013-3/31/2017
Role: PI (MPI: with Eli Upfal). [Relinquished this role on move to Princeton.]
Additional funding for the NSF BIGDATA award listed above.
Total Amount: $285,316

National Science Foundation   8/15/2010-07/31/2015
III: Small: Algorithmic Approaches for Pathway and Gene Group Analysis in Genetic Studies
Role: PI
Total Amount: $500,000

NIH/NIAID R01 AI083636-01A1   6/15/10-5/31/15
Phosphoproteomic Analysis of T Cell Activation Pathways
Role: Co-Investigator (PI: Art Salomon, MCB Department, Brown University)
Total Amount: $1,936,800

National Institutes of Health   7/1/2012-6/30/2015
Genome-wide evaluation of therapeutic targets for axonopathies
Role: Co-Investigator (PI: A. DiAntonio, Washington University in St. Louis)
Total Amount of Subcontract: $480,743

DOD Breast Cancer Research Program Idea Expansion Award   9/30/10 - 9/29/12
Origins of DNA Replication and Amplification in the Breast Cancer Genome
Role: co-PI (PI: Susan Gerbi, MCB Department, Brown University)
Total Amount: $607,500.

COBRE Center for Cancer Signaling Networks Pilot Award   4/01/2012-3/31/2013
Computational and Functional Genomic Analysis of the Notch Signaling Pathway in Ovarian Cancer
Role: MPI with Richard Freiman, Brown MCB
Total Amount: $25,000

COBRE Center for Cancer Signaling Networks Pilot Award   9/15/2011-9/30/2012
Mitochondrial Genomics of Cancer
Role: Co-PI (PI: David Rand, Brown MCB)
Total Amount: $52,500

Brown-MBL Partnership Seed Fund   9/15/2011-9/30/2012
Conserved nucleotide elements in ribosomal RNA—target signatures for pathogenic organisms
Role: Co-PI (PI: Susan Gerbi, Brown MCB)
Total Amount: $50,000

Susan G. Komen Foundation   2008-2011
Role of Estrogen in Breast Cancer Gene Amplification
Role: Co-PI (PI: Susan Gerbi)
Total Amount: $480,000

Department of Defense Breast Cancer Research Program   2007-2009
Hormonal Involvement in Breast Cancer Amplification
Role: Co-PI (PI: Susan Gerbi, MCB Department, Brown University)
Total Amount: $500,000

Brown University / Women & Infants Hospital National Center of Excellence In Women's Health
(CoE) Research Seed Grant
Exploring Cisplatin Sensitivity of Primary and Metastatic Ovarian Tumors
Role: Co-PI (PI: Alex Brodsky)
Total Direct Costs: $20,000

Alfred P. Sloan Foundation / DOE Fellowship in Computational Biology   2002-2004
Role: PI
Total Amount: $120,000

EDUCATION GRANTS

National Science Foundation, Research Experiences for Undergraduates (REU)
Supplemental Funding for Summer Undergraduate Research.
2013: $24,000 (Four students)
2012: $15,627 (Two students)

SERVICE

Princeton University
Director of Graduate Studies, Department of Computer Science, 2019-
Chair, Faculty Search Committee, Department of Computer Science, 2017-2018
Admissions Committee, Department of Computer Science, 2019-2020; 2018-2019; 2016-2017
Freshman B.S.E. Advisor, 2017-2018.
Sophomore, B.S.E. Department Advisor, 2018-2019.
Department Undergraduate Advisor, 2019-2020.

Brown University
Director, Center for Computational Molecular Biology, 2013-2016.
Member, Biomedical Informatics Faculty Search Committee, 2015.
Member, Bioinformatics Faculty Search Committee, 2014.
Member, Pediatrics Department Chair Search Committee, 2013-2014.
Director of Graduate Studies, Computational Biology Ph.D. Program, 2011-2013.
Member, Computer Science Department Vision Committee, 2011-13.
Member, Faculty Executive Committee, 2010-2011.
Executive Committee, Center for Computational Molecular Biology, 2006-present.
Member, Faculty Search Committee, Center for Computational Molecular Biology, 2006-09.
Member, Graduate Student Admissions Committee, Dept. of Computer Science, 2006-12.
Member, Research Computing and Support Working Group, 2008.
Sheridan Center Liaison, Computer Science Department, 2008-2009.
Library Liaison, Computer Science Department, 2008-2009.
Member, Strategic Planning Committee on Centers, Programs & Institutes, 2009-10.

To the Profession

Steering Committees:
RECOMB Satellite Workshop on Computational Cancer Biology, 2007-present.
RECOMB Satellite Workshop on Massively Parallel Sequencing, 2012-preesnt.

Program Committees:
Research in Computational Molecular Biology (RECOMB), 2011-2020. 2018 (**Chair)**.
Intelligent Systems in Molecular Biology (ISMB): 2010-2020.
Pacific Symposium on Biocomputing, 2013-2015.
RECOMB Satellite Workshop on Massively Parallel Sequencing, 2014-2015.
Workshop on Algorithms in Bioinformatics (WABI): 2008, 2009, 2012 (**Chair**), 2013, 2015.
IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS): 2011, 2012.
ACM Conference on Bioinformatics, Computational Biology and Biomedicine: 2011.
European Conference on Computational Biology (ECCB): 2010, 2012.
High-Throughput Sequencing (HiTSeq) SiG of ISMB, 2014, 2015

First International Conference on Bioinformatics and Computational Biology (BICoB) 2009.
International Symposium on Bioinformatics Research and Applications, 2008.
RECOMB Satellite Workshop on Computational Cancer Biology. 2007(**Chair**), 2010, 2015 (**Co-chair**).
Sixth IEEE International Workshop on High Performance Computational Biology (HiCOMB) 2007.
VLDB Workshop on Data Mining in Bioinformatics, 2007.
9th Annual Conference on Computational Genomics, 2006.
RECOMB Satellite Workshop on Systems Biology, 2005-2007.
RECOMB Satellite Workshop on and Regulatory Genomics, 2005.
RECOMB Satellite Workshop on Comparative Genomics, 2005-2006.

Organizing Committees:

UCLA Computational Genomics Summer Institute, 2016-present.
Simons Institute for the Theory of Computing, Computational Cancer Biology, 2016.
Mathematical Biosciences Institute, Models for Oncogenesis, Clonality and Tumor Progression, 2016.
Keystone Symposia, The Cancer Genome, 2016.
Institute for Pure and Applied Mathematics, Cancer Genomics Workshop, 2011.
Bertinoro Computational Biology, 2008.
RECOMB Satellite Workshop on Computational Cancer Biology, 2007, 2010,2015.
Sixth Annual McGill Workshop on Bioinformatics in Barbados, 2007.
RECOMB Satellite Workshops on Systems Biology and Regulatory Genomics, 2005.
RECOMB Satellite Workshop on Regulatory Genomics, 2004.

Journal Reviewing:

Nature, Science, Nature Genetics, Nature Biotechnology, Nature Methods, Cell Stem Cell, Proceedings of the National Academy of Sciences, *Genome Research*, *Bioinformatics*, *Journal of Computational Biology* (also guest editor)*, Journal of the Association for Computing Machinery (ACM), ACM Transactions on Algorithms , Genome Biology, Trends in Genetics*, *BMC Bioinformatics*, *BMC Genetics*, *PLOS One, Parallel Computing.*

Grant Review Panels:

National Cancer Institute of Canada, 2008, 2013.
NIH Study Section Member (ad hoc). MABS (2016), BDMA (2012, 2013), GCAT (2012).
National Science Foundation, 2012
National Human Genome Research Institute, 2012.
National Cancer Institute, 2011.
National Science Foundation, 2008, 2010, 2012.
Ministry of Education, Singapore, 2009-2010.
National Institute of General Medical Science, 2008.

Scientific Advisory Committees:

NSF-EPSCoR Rhode Island Genomics and Sequencing Center, 2008-present.

Other:

Co-leader, TCGA Pancreatic Cancer Analysis Working Group, 2014-2017.
Co-leader, ICGC Pan-Cancer Analysis Working Group on Networks, 2014-present.
Leader, Structural Aberration Detection subgroup, International Cancer Genome Consortium (ICGC), 2010-2013.

Member NIH Cancer Genome Atlas, Data Analysis Group, 2008-present.
Career Panel Member, Howard Hughes Medical Institute Interfaces Scholars Meeting, 2008.
Founder/Member, Bioinformatics Consulting Group, UCSD Computer Science Department, 2004-2006.
Founder/Member, Graduate Mathematics Consulting Group, UCSD Mathematics Department, 1999-2002.

Professional Memberships:
   International Society for Computational Biology, 2002-present.
   Association for Computing Machinery, 2016-present
   American Association of Cancer Research, 2013-present.
   American Statistical Society, 2012-2014.
   American Mathematical Society, 1996-2002.

HONORS/AWARDS

Best Paper Award, RECOMB Conference, 2013.

National Science Foundation CAREER Award, 2011.

Sloan Research Fellowship ($50,000), 2010.

Brown Center for Computational Molecular Biology, Research Seed Award ($5000), 2009.

Brown ADVANCE Program Faculty Early Career Development Award ($11,500), 2008.

Institutional Nominee for Packard Foundation Fellowship, 2007.

Brown Center for Computational Molecular Biology, Scholarship Innovator Award ($5000), 2007.

Named one "Tomorrow's PI's" by *Genome Technology* magazine, 2006.

Burroughs Wellcome Career Award at the Scientific Interface, 2005-2010.

Intelligent Systems in Molecular Biology (ISMB), Best Poster Award, 2005.

Alfred P. Sloan Foundation / DOE Fellowship in Computational Biology, 2002-04.

U.S. Department of Education, GAANN Fellowship in Mathematics (declined), 1999.

TEACHING

Enrollments indicated in []

Princeton University
2019	**Instructor**, "*COS Independent Work Seminar*" Fall 2019 [14]
	Instructor, "COS 598E: Computational Biology of Single Cells", Spring 2019 [8]
2018	**Instructor**, "COS343: Algorithms for Computational Biology", Spring 2018 [37]
2017	**Instructor**, "*COS Independent Work Seminar*" Fall 2017 [9]
2017	**Instructor**, "*COS598 : Advanced Topics in Computer Science: Algorithms in Computational Biology*". Spring 2017 [7]

Brown University
2012-2015	**Instructor**, "*CSCI1810: Computational Molecular Biology*." Fall 2015 [34], Fall 2014 [14], Fall 2013 [27]; Fall 2012 [42]; Spring 2012 [23]
2007-2015	**Instructor** (and course creator) "*CSCI2950-C:Topics in Computational Biology: Genomes, Networks, and Cancer*." Spring 2015 [9]; Spring 2013 [6]; Fall 2011 [12]; Fall 2010 [7]; Fall 2009 [6]; Fall 2008, Fall 2007, Spring 2006.

2008, 2011	**Instructor** for "*CSCI0220: Introduction to Discrete Mathematics,*" a core course for CS concentrators. Spring 2011 [86]; Spring 2008 [67].
2009-2011	**Guest lectures** for "*BIOL2010: Quantitative Approaches in Biology.*"
2009	Designed and taught new course "*CSCI1950-Z: Computational Methods for Biology.*" Spring 2009 [14].
2006-2016	*Reading and Research* (*Graduate*): Spring 2016 [ ]; Fall 2015 [ ]; Spring 2015 [5]; Fall 2014 [4]; Spring 2014 [3]; Fall 2013 [4]; Spring 2013 [5]; Fall 2012 [5]; Spring 2012 [6]; Fall 2011 [6]; Spring 2011 [2], Fall 2010 [3]; Spring 2010; Fall 2009; Spring 2009; Fall 2008; Spring 2008; Fall 2007; Spring 2007.
2007-2016	*Individual Independent Study* (*Undergraduate*): Spring 2015 [1]; Fall 2014 [1]; Spring 2014 [6]; Fall 2013 [2]; Fall 2012 [2]; Spring 2012 [1], Fall 2011 [3], Spring 2011 [1], Fall 2010 [1]; Spring 2010; Fall 2009; Spring 2009; Fall 2008; Spring 2008; Fall 2007; Spring 2007; Fall 2006.
1996-2002	**Teaching Assistant**, Department of Mathematics, University of California, San Diego. Four years of experience leading weekly discussion sections in undergraduate courses including: Calculus, Differential Equations, Linear Algebra, and Introduction to Algorithms.
1996	**Lecturer**, Massachusetts Institute of Technology. Designed and taught intersession course *Introduction to Mathematical Proofs* with Henry Cohn.

Advising
Princeton University, Princeton, NJ
Ph.D. Students Research Supervisor:
1. Matthew Myers (Computer Science), 2017-present
2. Tyler Park (Quantitative and Computational Biology), 2018-present
3. Uthsav Chitra (Computer Science), 2018-present
4. Thomas Schaffner (Computer Science), 2016-2017

Postdoctoral Fellows:
1. Ron Zeira, 2018-present
2. Sergey Aganezov, 2017-2018
3. Simone Zaccaria, 2017-present
4. Matthew Reyna, 2016-2018.
5. Mohammed El-Kebir, 2016-2017

Ph.D. Thesis committees
1. Ariel Gerwitz, 2019-present.
2. Borislav Hristov, 2018-2019.
3. Pawel Przytycki, 2018.
4. Joshua Wetzl 2018-2019.
5. Shilpa Nadimpalli, 2016-2018.

Undergraduate Advising
1. Senior Thesis Advisor: 2017-2018 [2 students], 2018-2019 [1 student]

Brown University, Providence RI
Ph.D. Students Research Supervisor:
1. Rebecca Elyanow, 2015-present.
2. Gryte Satas, 2014-present. [Honorable Mention, NSF Graduate Research Fellowship (2015)]

3. Ashley Conard, 2015-2018. Completed Sc.M. [Recipient of NSF Graduate Research Fellowship (2015)
4. Max Leiserson, 2011-2016. [Ph.D. completed, May 2016] [Recipient of NSF Graduate Research Fellowship (2012-2014)]
5. Hsin-Ta Wu, 2010-2016. [Ph.D. completed, May 2016]
6. Layla Oesper, 2010-2015. [Ph.D. completed, May 2015] [Recipient of NSF Graduate Research Fellowship (2011-2013). Recipient of Google Anita Borg Memorial Scholarship 2014].
7. Ahmad Mahmoody, 2011-2013. Completed Sc.M.
8. Matthew Parks [with Chip Lawrence], 2011-2014. [Ph.D. completed, May 2014]
9. Alexandra Papoutsaki, 2011-2013. Completed Sc.M.
10. Fabio Vandin, 2008-2010. [Visiting Ph.D. student from University of Padova]
11. Anna Ritz, 2006-2012. [Ph.D. completed, Oct. 2012] [Recipient of NSF Graduate Research Fellowship (2008-2011)]
12. Crystal Kahn, 2007-2010. [Ph.D. completed, Oct. 2010] [Recipient of NSF Graduate Research Fellowship (2005-2008)]

Postdoctoral Fellows:
1. Dora Erdos, 2015-2016.
2. Mohammed El-Kebir, 2014-2016.
3. Matthew Reyna, 2014-2016.
4. Iman Hajirasouliha, 2013-2014. [Recipient of NSERC Postdoctoral Fellowship, 2014]
5. Jason Dobson, 2013-2014.
6. Fabio Vandin, 2010-2013.
7. Suzanne Sindi, 2006-2012.

Master's Students Research Supervisor:
1. Jeremy Watson, 2014-present
2. John Shen, Sc.M., December 2015.
3. Jonathan Eldridge, Sc.M., Dec. 2014.
4. Hsin-Ta Wu, Sc.M., May 2010.
5. Borislav Hristov, Sc.M., May 2010.
6. Selim Onal, Sc.M., May 2010.
7. Brendan Hickey, Sc.M, May 2009.
8. Eric Lim, Sc.M December 2007.

Ph.D. Thesis committees:
William Jordan (Molecular Biology, Cell Biology, and Biochemistry), 2016-2017.
Connor Gramazio (Computer Science), 2015-2017.
Priyanka Nakka (Computational Biology), 2014-2018.
Michael Hughes (Computer Science), 2014-2016.
Christine Scaduto (Molecular Biology, Cell Biology, and Biochemistry), 2012-2017
John Urban (Molecular Biology, Cell Biology, and Biochemistry), 2012-2016.
Steven Criscione (Molecular Biology, Cell Biology, and Biochemistry), 2012-2016.
Wenjin Zhou (Computer Science), 2009-2012.
Jadrian Miles (Computer Science), 2009-2016.
Radu Jianu (Computer Science), 2009-2012.
Luis Carvalho (Applied Mathematics), 2007-2008.

Ph.D. Research Exam Committees
　　　Kamran Azam (Computer Science), 2008.

Ph.D. Advisory Committees
　　　Priyanka Nakka (Computational Biology), 2014.
　　　Yinghong Lan (Ecology and Evolutionary Biology), 2012.

Master's Student Advising:
　　　Cao Ren, 2015-2016.
　　　Brigitte Harder, 2013-2015.
　　　Aaron Shen, 2010-2011.

Undergraduate Advising
- Honors Theses: Hannah Acheson-Field (2015), Vivian Hsiao (2014), Vishesh Jain (2014), Jovian Yu (2012), Elena Helman (2009)
- Concentration Advisor for Computational Biology. (2008-present)
- Concentration Advisor for Computer Science. (2007-present)
- Sophomore Advising Program. (2009-present).
- Senior Capstone projects: Jihan Chao (2010), Brendan Hickey (2008) and Peter Goldstein (2008).
- Honors Theses (Reader): William Stephanson (2015), Aaron Behr (2015), Glen Scheinberg (EEB), 2008.

External Ph.D. Thesis Committees
Carnegie Mellon University, Department of Computational Biology, Cong Ma, 2018-present
University of Toronto, Department of Computer Science, External Examiner, Amit Deshwar 2018
Worchester Polytechnic University, Nathan Johnson, 2016-2018.

University of California, San Diego

Undergraduate Research Mentoring
　　　Sarah Aerni (2005-2006). [Finalist for Computing Research Association's Outstanding Undergraduate Award Program, 2006]