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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
- 2016- **Founder and Consultant**, Medley Genomics, Providence, RI
- 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

S. Zaccaria*, M. El-Kebir*, G.W. Klau, **B.J. Raphael**. (2017) The Copy-Number Tree Mixture Deconvolution Problem and Applications to Multi-Sample Bulk Sequencing Tumor Data. RECOMB 2017.

The Cancer Genome Atlas Research Network. (2017) Integrated genomic characterization of oesophageal carcinoma. *Nature* 541(7636):169-175.

M.D.M. Leiserson, M.A. Reyna, **B.J. Raphael**. (2016). A Weighted Exact Test for Mutually Exclusive Mutations in Cancer. *ECCB 2016/Bioinformatics*, 32(17):i736-i745.

P.Nakka, **B.J. Raphael***, S Ramachandran* (2016) Gene and Network Analysis of Common Variants Reveals Novel Associations in Multiple Complex Diseases. *Genetics*, 204(2):783-798.

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.

M. El-Kebir, **B.J. Raphael**, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi, R. Zeira. (2016) Copy-Number Evolution Problems: Complexity and Algorithms *Workshop on Algorithms for Bioinformatics (WABI) 2016*.

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.

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.

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.

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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.

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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.

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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.

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Kanchi KL, Johnson KJ, Lu C, McLellan MD, Leiserson MD, Wendl MC, Zhang Q, Koboldt DC, Xie M, Kandoth C, McMichael JF, Wyczalkowski MA, Larson DE, Schmidt HK, Miller CA, Fulton RS, Spellman PT, Mardis ER, Druley TE, Graubert TA, Goodfellow PJ, **Raphael BJ**, Wilson RK, Ding L. (2014) Integrated analysis of germline and somatic variants in ovarian cancer. *Nature Communications* 5:3156.

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](#)]

The Cancer Genome Atlas Research Network. (2013) The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics* 45(10):1113-20. [[Publisher Link](#)]

L. Oesper, A. Mahmoody, **B.J. Raphael**. (2013) THetA: Inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. *Genome Biology* 14:R80. [[Publisher Link](#)] [[Supplemental Material](#)]

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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](#)]. [[Interactive 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.

L. Cao, Y. Ding, N. Hung, K. Yu, A. Ritz, **B.J. Raphael**, A.R. Salomon. (2012) Quantitative Phosphoproteomics Reveals SLP-76 Dependent Regulation of PAG and Src Family Kinases in T Cells. *PLoS One*. 7(10):e46725.

R.H. Palmer, J.E. McGeary, S. Francrazio, **B.J. Raphael**, A.D. Lander, A.C. Heath, V.S. Knopik. (2012) The genetics of alcohol dependence: Advancing towards systems-based approaches. *Drug Alcohol Depend.* 125(3):179-91.

S. Sindi, S. Onal, L. Peng, H. Wu, **B.J. Raphael**. (2012) An Integrative Probabilistic Model for Identification of Structural Variation in Sequencing Data. *Genome Biology* 13(3):R22.

L. Oesper, A. Ritz, S.J. Aerni, R. Drebin[†], **B.J. Raphael** (2012) Reconstructing Cancer Genome Organization. *BMC Bioinformatics (Proceedings of 2nd RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq))*. 13(Suppl 6):S10

A. Caceres, S.S Sindi, **B.J Raphael**, M. Caceres and J.R Gonzalez. (2012) Identification of Polymorphic Inversions from Genotypes. *BMC Bioinformatics* 13(1):28

F. Vandin, P. Clay[†], E. Upfal, **B.J. Raphael**. (2012) Discovery of Mutated Subnetworks Associated with Clinical Data in Cancer. *Pacific Symposium on Biocomputing*. 55-66.

The Cancer Genome Atlas Research Network. (2011) Integrated Genomic Analyses of Ovarian Carcinoma. *Nature*. 474(7353):609-15.

F. Vandin, E. Upfal, **B.J. Raphael**. (2011) *De novo* Discovery of Mutated Driver Pathways in Cancer. *Genome Research*.22(2):375-85. [Journal version of paper accepted at *Proceedings of the 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2011)*].

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.

F. Vandin, E. Upfal, **B.J. Raphael**. (2011) Finding Driver Pathways in Cancer: Models and Algorithms. *Proceedings of the Workshop on Algorithms in Bioinformatics (WABI)*. Lecture Notes in Computer Science, Vol. 6833. 314-315.

A. Ritz, P.L. Paris, M.M. Ittmann, C. Collins, and **B.J. Raphael**. (2011) Detection of Recurrent Rearrangement Breakpoints from Copy Number Data. *BMC Bioinformatics*. 12:114.

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F. Vandin, E. Upfal, and **B.J. Raphael**. (2010) Algorithms for Detecting Significantly Mutated Pathways in Cancer. *Proceedings of the 14th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2010)*. Lecture Notes in Computer Science, Volume 6044, 506-521.

C.L. Kahn, S. Mozes, and **B.J. Raphael**. (2010) Efficient Algorithms for Analyzing Segmental Duplications with Deletions and Inversions in Genomes. *Algorithms for Molecular Biology*. 5(1):11.

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Book Chapters and Review Articles

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

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

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 Biomolecular 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

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 1/1/2011-12/31/2017
CAREER: Algorithms for Next-Generation Genomics
Role: PI
Total Amount: \$450,000

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

NIH/NHGRI 1R01HG007069 9/1/2013-8/31/2017
Computational Characterization of Genetic Heterogeneity
Role: PI
Total Amount: \$1,119,000

National Institutes of Health R01GM118652-01 6/1/2016-5/31/2021
Novel statistical methods to localize genomic elements underlying adaptive evolution
Role: Co-investigator (PI: Ramachandran)

NIH 9/1/2015-8/31/2018

Mapping Origins of DNA Replication in the Genome

Role: Co-Investigator (PI: Gerbi)

Direct Costs to subaward: ~\$100K

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

Pending

National Cancer Institute 1U24CA209858A01

7/1/2016 – 6/30/2021

Cloud-enabled Integration Platform for Proteogenomic Discovery in Cancer

Role: PI (MPI with Ding and Fenyo)

Completed

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

10/1/2012-9/30/2016

BIGDATA: Mid-Scale: DA: Analytical Approaches to Massive Data Computation with Applications to Genomics

Role: Co-PI (with PI: Eli Upfal)

Total Amount: \$1,566,685

NIH/NCI 1R01CA180776-01

6/18/2013-3/31/2017

Role: PI (MPI: with Eli Upfal)

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

Admissions Committee, Department of Computer Science 2016-2017

Brown University

Director, Center for Computational Molecular Biology, 2013-
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-present.

Program Committees:

Research in Computational Molecular Biology (RECOMB), 2011-2017.
Intelligent Systems in Molecular Biology (ISMB): 2010-2016.
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 (ICABS): 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-present.

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 []

- 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 “*BIOL210: Quantitative Approaches in Biology.*”
2009 Designed and taught new course “*CSCI1950-Z: Computational Methods for Biology.*” Spring 2009 [14].
- 2006-present *Reading and Research (Graduate)*: 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-present *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

Brown University, Providence RI

Ph.D. Students Research Supervisor:

1. Thomas Schaffner, 2016-present.
2. Ashley Conard, 2015-present. [Recipient of NSF Graduate Research Fellowship (2015-)]
3. Rebecca Elyanow, 2015-present.
4. Gryte Satas, 2014-present. [Honorable Mention, NSF Graduate Research Fellowship (2015)]
5. Max Leiserson, 2011-2016. [Ph.D. completed, May 2016] [Recipient of NSF Graduate Research Fellowship (2012-2014)]
6. Hsin-Ta Wu, 2010-2016. [Ph.D. completed, May 2016]
7. 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].
8. Ahmad Mahmoody, 2011-2013. Completed Sc.M.
9. Matthew Parks [with Chip Lawrence], 2011-2014. [Ph.D. completed, May 2014]
10. Alexandra Papoutsaki, 2011-2013. Completed Sc.M.
11. Fabio Vandin, 2008-2010. [Visiting Ph.D. student from University of Padova]
12. Anna Ritz, 2006-2012. [Ph.D. completed, Oct. 2012] [Recipient of NSF Graduate Research Fellowship (2008-2011)]

13. 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-present.
3. Matthew Reyna, 2014-present.
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-present.
Connor Gramazio (Computer Science), 2015-present.
Priyanka Nakka (Computational Biology), 2014-present.
Michael Hughes (Computer Science), 2014-present.
Christine Scaduto (Molecular Biology, Cell Biology, and Biochemistry), 2012-present
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-present.
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.

University of California, San Diego

Undergraduate Research Mentoring

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