

Curriculum Vitae

I. Personal Information

I.A. UID, Last Name, First Name, Middle Name, Contact Information

UID: 107535276

Last Name: Patro

First Name: Robert

Middle Name: Scott

Mailing address:

3220 Brendan Iribe Center for Computer Science and Engineering

8125 Paint Branch Dr, College Park, MD 20740

email: rob@cs.umd.edu

I.B. Academic Appointments at UMD

Associate Professor, Department of Computer Science, University of Maryland

Dates : July 2020 — current

Assistant Professor, Department of Computer Science, University of Maryland

Dates : July 2019 — July 2020

I.D. Other Employment

Assistant Professor, Department of Computer Science, Stony Brook University Dates:

August 2014 — July 2019

Postdoctoral Research Associate, Lane Center for Computational Biology (now the Department of Computational Biology), School of Computer Science, Carnegie Mellon University

Dates: August 2012 — July 2014

Graduate Research Assistant, Department of Computer Science, University of Maryland

Dates: June 2007 — August 2012

Graduate Teaching Assistant, Department of Computer Science, University of Maryland

Dates: September 2006 — June 2007

I.E. Educational Background

Degree: **PhD** in Computer Science

Institute: University of Maryland at College Park

Dates: 2006 — 2012

Degree: **BS** in Computer Science (cum laude & with departmental honors)
Institute: University of Maryland at College Park
Dates: 2003 — 2006

Degree: **Attended**
Institute: Worcester Polytechnic Institute
Dates: 2002

I.G. Professional Certifications, Licenses, and Memberships

International Society for Computational Biology (ISCB) Member
Dates: 2012—2014, 2016—current

ACM SigBIO Member
Dates: 2016, 2017

II. Research, Scholarly, Creative and/or Professional Activities

II.C. Refereed Journals

II.C.1 Refereed Journal Articles

Dongze He, Mohsen Zakeri, Hira Sarkar, Charlotte Soneson, Avi Srivastava, Rob Patro. Alevin-fry unlocks rapid, accurate, and memory-frugal quantification of single-cell RNA-seq data. *Nature Methods* 19, no. 3 (2022): 316-322.

Fatemeh Almodaresi, Jamshed Khan, Sergey Madaminov, Prashant Pandey, Michael Ferdman, Rob Johnson, Rob Patro. An Incrementally Updatable and Scalable System for Large-Scale Sequence Search using the Bentley-Saxe Transformation. *Bioinformatics*, 2022; btac142, <https://doi.org/10.1093/bioinformatics/btac142>

Fan, Jason, Skylar Chan, and Rob Patro. Perplexity: evaluating transcript abundance estimation in the absence of ground truth. *Algorithms for Molecular Biology* 17, no. 1 (2022): 1-23. (*Extended journal version of WABI conference paper of the same title.*)

Giorgos Skoufos, Fatemeh Almodaresi, Mohsen Zakeri, Joseph N Paulson, Rob Patro, Artemis G Hatzigeorgiou, Ioannis S Vlachos. AGAMEMNON: an Accurate metagenomics and metatranscriptomics quantification analysis suite. *Genome biology* 23, no. 1 (2022): 1-27.

Wancen Mu, Hira Sarkar, Avi Srivastava, Kwangbom Choi, Rob Patro, Michael I. Love. Airpart: Interpretable statistical models for analyzing allelic imbalance in single-cell datasets. *Accepted to Bioinformatics* (pre-print available at : bioRxiv 2021.10.15.464546; doi: <https://doi.org/10.1101/2021.10.15.464546>)

Fatemeh Almodaresi, Mohsen Zakeri, Rob Patro. PuffAligner: a fast, efficient and accurate aligner based on the Pufferfish index, *Bioinformatics*, 2021;, btab408, <https://doi.org/10.1093/bioinformatics/btab408>

Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. Charlotte Soneson, Avi Srivastava, Rob Patro, Michael B. Stadler (2021). *PLoS Comput Biol* 17(1): e1008585. <https://doi.org/10.1371/journal.pcbi.1008585>

Compression of quantification uncertainty for scRNA-seq counts. Scott Van Buren, Hira Sarkar, Avi Srivastava, Naim U. Rashid, Rob Patro, And Michael I. Love (2021). , *Bioinformatics*, 2021; btab001, <https://doi.org/10.1093/bioinformatics/btab001>

Avi Srivastava, Laraib Malik, Hira Sarkar, Mohsen Zakeri, Fatemeh Almodaresi, Charlotte Soneson, Mike Love, Carl Kingsford, Rob Patro (2020). Alignment and mapping methodology influence transcript abundance estimation. *Genome biology*, 21(1), 1-29.

Michael I. Love, Charlotte Soneson, Peter F. Hickey, Lisa K. Johnson, N. Tessa Pierce, Lori Shepherd, Martin Morgan, Rob Patro. "Tximeta: Reference sequence checksums for provenance identification in RNA-seq." *PLoS computational biology* 16.2 (2020): e1007664. *PLoS Computational Biology*, 16(2), e1007664, 2020.

Anqi Zhu, Avi Srivastava, Joseph G. Ibrahim, Rob Patro, Michael I. Love. Nonparametric expression analysis using inferential replicate counts. *Nucleic Acids Research*, gkz622, 2019.

Koen Van Den, Katharina M. Hembach, Charlotte Soneson, Simone Tiberi, Lieven Clement, Michael I. Love, Rob Patro, and Mark D. Robinson. "RNA sequencing data: hitchhiker's guide to expression analysis." *Annual Review of Biomedical Data Science* 2, 2019.

Guillaume Marçais, Brad Solomon, Rob Patro, and Carl Kingsford. Sketching and sublinear data structures in genomics. *Annual Review of Biomedical Data Science*, 2, 2019.

Avi Srivastava, Laraib Malik, Tom Smith, Ian Sudbery, and Rob Patro. Alevin efficiently estimates accurate gene abundances from dscrna-seq data. *Genome Biology*, 20(1):65, 2019

Charlotte Soneson, Michael I Love, Rob Patro, Shobbir Hussain, Dheeraj Malhotra, and Mark D Robinson. A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. *Life science alliance*, 2(1):e201800175, 2019.

Michael I. Love, Charlotte Soneson, and Rob Patro. Swimming downstream:

statistical analysis of differential transcript usage following Salmon quantification. *F1000Research*, 7:952, Oct. 2018

Moriah L Jacobson, Lydia A Kim, Robert Patro, Barbara Rosati, and David McKinnon. Common and differential transcriptional responses to different models of traumatic stress exposure in rats. *Nature Translational Psychiatry*, 8(1):165, 2018

Laraib Malik, Fatemeh Almodaresi, and Rob Patro. Grouper: graph-based clustering and annotation for improved de novo transcriptome analysis. *Bioinformatics*, 34(19):3265–3272, 2018.

Laraib Malik and Rob Patro. Rich Chromatin Structure Prediction from Hi-C Data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, pages 1–12, 2018. (**extended** journal version of ACM-BCB paper by the same name)

Prashant Pandey, Fatemeh Almodaresi, Michael A. Bender, Michael Ferdman, Rob Johnson, and Rob Patro. Mantis: A Fast, Small, and Exact Large-Scale Sequence-Search Index. *Cell Systems*, 7, no. 2 (2018): 201-207. (Journal version of RECOMB 2018 paper)

Gruning, B., et al. "Bioconda: sustainable and comprehensive software distribution for the life sciences." *Nature Methods* 15.7 (2018): 475-476. (**listed as part of "The Bioconda Team" available in the Consortium author list**)

Rob Patro, Geet Duggal, Michael I Love, Rafael A Irizarry, and Carl Kingsford. Salmon provides fast and bias-aware quantification of transcript expression. *Nature Methods*, 14(4):417–419, March 2017

Prashant Pandey, Michael A Bender, Rob Johnson, and Rob Patro. Squeakr: an exact and approximate k-mer counting system. *Bioinformatics*, 34(4):568–575, 2017.

Hirak Sarkar and Rob Patro. Quark enables semi-reference-based compression of RNA-seq data. *Bioinformatics*, 33(21):3380–3386, 2017

Avi Srivastava, Hirak Sarkar, Nitish Gupta, and Rob Patro. RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. *Bioinformatics*, 32(12):i192–i200, June 2016. Proceedings of ISMB 2016

Rob Patro, Raquel Norel, Robert J. Prill, Julio Saez-Rodriguez, Peter Lorenz, Felix Steinbeck, Bjoern Ziemis, Mitja Luštrek, Nicola Barbarini, Alessandra Tiengo, Riccardo Bellazzi, Hans-Jürgen Thiesen, Gustavo Stolovitzky, and Carl Kingsford. A computational method for designing diverse linear epitopes including citrullinated peptides with desired binding affinities to intravenous immunoglobulin. *BMC Bioinformatics*, 17(1):1–13, 2016

Richard Smith-Unna, Chris Boursnell, Rob Patro, Julian M Hibberd, and Steven Kelly. TransRate: reference-free quality assessment of de novo transcriptome assemblies.

Genome Research, 26(8):1134–1144, 2016

Carl Kingsford and Rob Patro. Reference-based compression of short-read sequences using path encoding. *Bioinformatics*, 31(12):1920–1928, 2015

Rob Patro and Carl Kingsford. Data-dependent bucketing improves reference-free compression of sequencing reads. *Bioinformatics*, 31(17):2770–2777, 2015.

Runxuan Zhang, Cristiane PG Calixto, Nikoleta A Tzioutziou, Allan B James, Craig G Simpson, Wenbin Guo, Yamile Marquez, Maria Kalyna, Rob Patro, Eduardo Eyras, et al. AtRTD—a comprehensive reference transcript dataset resource for accurate quantification of transcript-specific expression in arabidopsis thaliana. *New Phytologist*, 2015

Darya Filippova^{*}, Rob Patro^{*}, Geet Duggal^{*}, and Carl Kingsford. Identification of Alternative Topological Domains in Chromatin. *Algorithms for Molecular Biology*, 9(1):1, 2014

Rob Patro, Stephen M Mount, and Carl Kingsford. Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. *Nature Biotechnology*, 32(5):462–464, 2014.

Geet Duggal, Rob Patro, Emre Sefer, Hao Wang, Darya Filippova, Samir Khuller, and Carl Kingsford. Resolving spatial inconsistencies in chromosome conformation measurements. *Algorithms for Molecular Biology*, 8(1):8, 2013. (**extended** journal version of WABI 2012 paper which is not listed here).

Rob Patro, John Dickerson, Sujal Bista, Satyandra Gupta, and Amitabh Varshney. Speeding Up Particle Trajectory Simulations under Moving Force Fields using GPUs. *ASME Journal of Computing and Information Science in Engineering*, 12(2), 2012.

Rob Patro and Carl Kingsford. Global network alignment using multiscale spectral signatures. *Bioinformatics*, 28(23):3105–3114, 2012.

Rob Patro, Emre Sefer, Justin Malin, Guillaume Marçais, Saket Navlakha, and Carl Kingsford. Parsimonious reconstruction of network evolution. *Algorithms for Molecular Biology*, 7(1):25, 2012. (**extended** journal version of WABI 2011 paper below).

Youngmin Kim, Rob Patro, Cheuk Yiu Ip, Dianne P. O’Leary, and Andriy Anishkin. Salient Frame Detection for Molecular Dynamics Simulations. In *Scientific Visualization: Interactions, Features, Metaphors*, volume 2 of *Dagstuhl Follow-Ups*, pages 160–175. Schloss Dagstuhl–Leibniz-Zentrum fuer Informatik, Dagstuhl, Germany, 2011.

Andre Maximo, Rob Patro, Amitabh Varshney, and Ricardo Farias. A Robust and Rotationally Invariant Local Surface Descriptor with Applications to Non-local Mesh

Processing. *Graphical Models*, 73(5):231–242, 2011.

Rob Patro, Cheuk Yiu Ip, Sujal Bista, and Amitabh Varshney. Social Snapshot: A System for Temporally Coupled Social Photography. *Computer Graphics and Applications, IEEE*, 31(1):74–84, 2011.

Rob Patro, Cheuk Yiu Ip, and Amitabh Varshney. Saliency Guided Summarization of Molecular Dynamics Simulations. In *Scientific Visualization: Advanced Concepts*, volume 1 of *Dagstuhl Follow-Ups*, pages 321–335. Schloss Dagstuhl–Leibniz-Zentrum fuer Informatik, Dagstuhl, Germany, 2010.

Aswin C. Sankaranarayanan, Rob Patro, Pavan Turaga, Amitabh Varshney, and Rama Chellappa. Modeling and Visualization of Human Activities for Multicamera Networks. *EURASIP Journal on Image and Video Processing*, vol. 2009(Article ID 259860), 2009.

II.D. Published Conference Proceedings

II.D.1 Refereed Conference Proceedings (*denotes equal contribution)

Jamshed Khan, Rob Patro, Cuttlefish: fast, parallel and low-memory compaction of de Bruijn graphs from large-scale genome collections, *Bioinformatics*, Volume 37, Issue Supplement_1, July 2021, Pages i177–i186, <https://doi.org/10.1093/bioinformatics/btab309>. (appeared at ISMB 2021; **won best paper award**)

Hirak Sarkar, Avi Srivastava, Héctor Corrada Bravo, Michael I Love, Rob Patro, Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data, *Bioinformatics*, Volume 36, Issue Supplement_1, July 2020, Pages i102–i110, <https://doi.org/10.1093/bioinformatics/btaa448>. (appeared at ISMB 2020)

Avi Srivastava, Laraib Malik, Hirak Sarkar, Rob Patro, A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification, *Bioinformatics*, Volume 36, Issue Supplement_1, July 2020, Pages i292–i299, <https://doi.org/10.1093/bioinformatics/btaa450>. (appeared at ISMB 2020)

Hirak Sarkar, Avi Srivastava, and Rob Patro Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. *Bioinformatics* 35.14 (2019): i136–i144. (*ISMB 2019 Special Issue*).

Fatemeh Almodaresi, Prashant Pandey, Michael Ferdman, Rob Johnson, and Robert Patro. An efficient, scalable and exact representation of high-dimensional color information enabled via de bruijn graph search. In Lenore J. Cowen, editor, *Research*

in Computational Molecular Biology - 23rd Annual International Conference, RECOMB 2019, Washington, DC, USA, May 5-8, 2019, Proceedings, volume 11467 of *Lecture Notes in Computer Science*, pages 1–18. Springer, 2019. (appeared at RECOMB 2019)

Fatemeh Almodaresi, Hirak Sarkar, Avi Srivastava, and Rob Patro. A space and time-efficient index for the compacted colored de Bruijn graph. *Bioinformatics*, 34(13):i169–i177, 2018. (special Bioinformatics issue with proceedings of ISMB 2018)

Prashant Pandey, Fatemeh Almodaresi, Michael A. Bender, Michael Ferdman, Rob Johnson, and Rob Patro. Mantis: A Fast, Small, and Exact Large-Scale Sequence Search Index. volume 10812 of *Lecture Notes in Computer Science*, pages 271–273. Springer, 2018. (Proceedings of RECOMB 2018; published as extended abstract, since invited to publication in Cell Systems).

Hirak Sarkar, Mohsen Zakeri, Laraib Malik, and Rob Patro. Towards Selective-Alignment: Bridging the Accuracy Gap Between Alignment-Based and Alignment-Free Transcript Quantification. In *Proceedings of the 2018 ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics*, BCB '18, pages 27–36, New York, NY, USA, 2018. ACM.

Laraib Malik and Rob Patro. Rich chromatin structure prediction from Hi-C data. In *Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics*, pages 184–193. ACM, 2017. (**won best paper award**).

Prashant Pandey, Michael A. Bender, Rob Johnson, and Rob Patro. A General-Purpose Counting Filter: Making Every Bit Count. In *Proceedings of the 2017 ACM International Conference on Management of Data*, SIGMOD '17, pages 775–787, New York, NY, USA, 2017. ACM

Prashant Pandey, Michael A Bender, Rob Johnson, and Rob Patro. deBGR: an efficient and near-exact representation of the weighted de bruijn graph. *Bioinformatics*, 33(14):i133–i141, 2017. (special Bioinformatics issue with proceedings of ISMB 2017)

Mohsen Zakeri, Avi Srivastava, Fatemeh Almodaresi, and Rob Patro. Improved data-driven likelihood factor- izations for transcript abundance estimation. *Bioinformatics*, 33(14):i142–i151, 2017. (special Bioinformatics issue with proceedings of ISMB 2017)

Rob Patro and Carl Kingsford. Predicting protein interactions via parsimonious network history inference. *Bioinformatics*, 29(13):i237–i246, 2013. (special Bioinformatics issue with proceedings of ISMB/ECCB 2013)

Hao Wang, Geet Duggal, Rob Patro, Michelle Girvan, Sridhar Hannenhalli, and Carl Kingsford. Topological Properties of Chromosome Conformation Graphs Reflect

Spatial Proximities Within Chromatin. In *Proceedings of the International Conference on Bioinformatics, Computational Biology and Biomedical Informatics*, BCB'13, pages 306:306–306:315, New York, NY, USA, 2013. ACM

Robert Patro*, Geet Duggal*, Emre Sefer, Hao Wang, Darya Filippova, and Carl Kingsford. The missing models: a data-driven approach for learning how networks grow. In *Proceedings of the 18th ACM SIGKDD international conference on Knowledge discovery and data mining*, pages 42–50. ACM, 2012.

Rob Patro, Cheuk Yiu Ip, Sujal Bista, Samuel Cho, Dave Thirumalai, and Amitabh Varshney. MDMMap : A system for data-driven layout and exploration of molecular dynamics simulations. In *Proceedings of the 1st IEEE symposium on biological data visualization*, pages 111–118, Providence, RI, USA, 2011.

II.E. Conferences, Workshops, and Talks

II.E.2. Invited Talks

Rob Patro. Judging a k-mer by The Company it Keeps: Compressing the de Bruijn Graph and Signals That Live On It. *Compression + Computation 2022 workshop*.

Rob Patro. Algorithms you can count on: Accurate, fast, and memory-frugal single-cell processing with alevin-fry. *Tufts University, Bioinformatics and Computational Biology Research Group, 2021*.

Rob Patro. Tell me something I don't know : The role of inferential uncertainty in bulk and single-cell RNA-seq analysis. *CCB Seminar, Duke University, 2021*.

Rob Patro. Tell me something I don't know : The role of inferential uncertainty in RNA-seq analysis. *Quantitative Science Seminar, Johns Hopkins University, 2021*.

Rob Patro. The known unknowns : Addressing uncertainty in bulk and single-cell RNA-seq quantification. *Bioinformatics Brownbag Seminar, Pacific Biosciences, 2020*. (postponed due to COVID-19 pandemic)

Rob Patro. Single-cell transcriptome analysis: opportunities and computational challenges. *Molecular Medicine Tri-Conference, 2020*.

Rob Patro. The known unknowns : Addressing uncertainty in bulk and single-cell RNA-seq quantification. *TorBUG Seminar, 2020*

Rob Patro. Alignment and Mapping Methodology Influence Transcript Abundance Estimation. *Genome Informatics, 2019*

Rob Patro. Mapping and Modeling Methodology Matter: Making the Most of your RNA-seq Data. *CBBG Seminar Series, 2019*

Rob Patro. Alignment: Back to the Future. *CBBG Program Retreat, 2019*

Rob Patro. Alignment: Back to the Future. *BioC conference, 2019*

Rob Patro. Improving Computational Methods for Single-Cell Gene Expression Analysis. *Gloria and Mark Snyder Symposium on Cancer Medicine, 2019*

Rob Patro. From single cells to thousands of genomes: computational challenges and algorithmic solutions in high-throughput genomics. *UMD, February 2019*

Rob Patro. The past, present and future of transcript quantification: recent progress & some remaining challenges. *EMBL-EBI Industry Workshop: The past, present and future of RNA-seq technology and its application to drug discovery, November 2018*

Rob Patro. Drinking from the firehose: lightweight methods and data structures for indexing, searching and analyzing genomic data. *UMD (Computational Biology Seminar), October 2018*

Rob Patro. Drinking from the firehose: lightweight methods and data structures for indexing, searching and analyzing genomic data. *USC (Computational Biology Seminar), October 2018*

Rob Patro. Deconvolution, dictionaries and de Bruijn graphs : algorithm and data structure design for modern genomics. *Penn State Workshop on Emerging Methods for Sequence Analysis, June 2018*

Rob Patro. When less enables more: making models and methods for modern genomics. *MIT (Computational Biology Seminar), March 2018*

Rob Patro. Faster, Smaller, Better: How improved methods can facilitate better biology. *University of Basel (Computational Biology Seminar), November 2017*

Rob Patro. Algorithmic advances in high-throughput transcriptome analysis. *Calico, July 2017*

Rob Patro. Algorithmic advances in high-throughput transcriptome analysis. *GRAIL, July 2017*

Rob Patro. Don't count on it: Pragmatic and theoretical concerns and best practices for mapping and quantifying RNA-seq data. *DIBSI 2017 training (UC Davis), July 2017*

Rob Patro. Algorithmic advances in transcript quantification. *HiCOMB 2017 (IEEE International Workshop on High Performance Computational Biology), May 2017*

Rob Patro. Accurate, fast and bias-aware transcript quantification with Salmon. *Biostatistics & Medical Informatics Seminar Series, University of Wisconsin, Madison*, September 2016

Rob Patro. A New Deal for Transcriptomics: Better Biology through Better Algorithms. *Laufer Center for Quantitative Biology Seminar*, 2016

Rob Patro. Fast Algorithms for Improved Transcriptome Analysis. *Genomics JHU seminar series, Johns Hopkins University*, 2016

Rob Patro. Rethinking the big BAM: Analysis-efficient computing for improved transcriptome analysis. *Weill Cornell Medical School*, 2016

Rob Patro. Rethinking the big BAM: Fast algorithms for improved transcriptome analysis. *Personal Genome Diagnostics*, 2016.

Rob Patro. The wait is over: lightweight methods for accurate, fast and scalable analysis of transcriptomes. *New York Genome Center*, September 2015.

Rob Patro, Stephen Mount, and Carl Kingsford. Salmon spawns the next the next generation of RNAseq analysis with versatile and ultrafast transcript quantification. *Simons Center for Quantitative Biology Seminar*, March 2015.

Rob Patro, Stephen Mount, and Carl Kingsford. Sailfish: Expression Estimates Shouldn't Take Longer than a Cup of Coffee. *Automated Personal Genome Analysis for Clinical Advisors*, 2013.

II.E.3. Refereed Presentations

I include below only the refereed presentations which I have given, not those for which I am a co-author but which were presented by another co-author.

Mohsen Zakeri, Avi Srivastava, Fatemeh Almodaresi, and Rob Patro. Improved data-driven likelihood factorizations for transcript abundance estimation. *ISMB 2017*.

Avi Srivastava, Larib Malik, and Rob Patro. Accurate, Fast and Lightweight Clustering of *de novo* Transcriptomes using Fragment Equivalence Classes. *RECOMB-Seq 2016*.

Komal Sanjeev, Nitish Gupta, Tim Wall, Carl Kingsford, and Rob Patro. Efficient Index Maintenance Under Dynamic Genome Modification. *RECOMB-Seq 2016*.

Rob Patro, Stephen Mount, and Carl Kingsford. Sailfish and Salmon enable alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. *RECOMB 2015 Highlight Talk*, April 2015.

Rob Patro, Stephen Mount, and Carl Kingsford. Sailfish — RNA-seq Expression

Estimates Need Not Take Longer Than a Cup of Coffee. *Genome Informatics*, October 2013.

Rob Patro and Carl Kingsford. Predicting protein interactions via parsimonious network history inference. ISMB 2013.

Rob Patro and Carl Kingsford. Global Network Alignment Using Multiscale Spectral Signatures. *GLBIO Conference*, 2013.

Rob Patro, Cheuk Yiu Ip, Sujal Bista, Samuel Cho, Dave Thirumalai, and Amitabh Varshney. MDMAP : A system for data-driven layout and exploration of molecular dynamics simulations. *IEEE BioVis Conference*, 2011.

Rob Patro and Carl Kingsford. Learning from Diversity: Epitope Prediction with Sequence and Structure Features using an Ensemble of Support Vector Machines. *RECOMB Systems Biology Satellite Conference*, 2010. (presenting our prediction algorithm that won the DREAM5 Challenge 1 competition)

II.E.4. Refereed Workshop Papers (*denotes equal contribution)

Jason Fan, Skylar Chan, and Rob Patro. "Perplexity: Evaluating Transcript Abundance Estimation in the Absence of Ground Truth." 21st International Workshop on Algorithms in Bioinformatics (WABI 2021). Schloss Dagstuhl-Leibniz-Zentrum für Informatik, 2021. (invited journal version currently under revision.)

Fatemeh Almodaresi, Prashant Pandey, and Rob Patro. Rainbowfish: A Succinct Colored de Bruijn Graph Representation. In Russell Schwartz and Knut Reinert, editors, 17th International Workshop on Algorithms in Bioinformatics (WABI 2017), volume 88 of Leibniz International Proceedings in Informatics (LIPIcs), pages 18:1–18:15, Dagstuhl, Germany, 2017. Schloss Dagstuhl–Leibniz-Zentrum fuer Informatik

Komal Sanjeev, Nitish Gupta, Tim Wall, Carl Kingsford, and Rob Patro. Efficient Index Maintenance Under Dynamic Genome Modification. *Proceedings of RECOMB-Seq 2016*, April 2016

Avi Srivastava, Larib Malik, and Rob Patro. Accurate, Fast and Lightweight Clustering of *de novo* Transcriptomes using Fragment Equivalence Classes. *Proceedings of RECOMB-Seq 2016*, April 2016

Zhong Sichen, Lu Zhao, Yan Liang, Mohammadzaman Zamani, Rob Patro, Rezaul Chowdhury, Esther M Arkin, Joseph SB Mitchell, and Steven Skiena. Optimizing Read Reversals for Sequence Compression. In *Algorithms in Bioinformatics* (WABI 2015), pages 189–202. Springer, 2015.

Darya Filippova*, Rob Patro*, Geet Duggal*, and Carl Kingsford. Multiscale Identification of Topological Domains in Chromatin. In *Algorithms in Bioinformatics*

(WABI 2013), pages 300–312. Springer, 2013.

Rob Patro, Emre Sefer, Justin Malin, Guillaume Marçais, Saket Navlakha, and Carl Kingsford. Parsimonious Reconstruction of Network Evolution. In Teresa Przytycka and Marie-France Sagot, editors, *Algorithms in Bioinformatics* (WABI 2011), volume 6833 of *Lecture Notes in Computer Science*, pages 237–249. Springer Berlin / Heidelberg, 2011.

II.E.6. Refereed Posters

Hirak Sarkar, Avi Srivastava, Mohsen Zakeri, Scott Van Buren, Naim U Rashid, Michael Love, Rob Patro. Accurate, efficient, and uncertainty-aware expression quantification of single-cell RNA-seq data. CSHL Biological Data Science 2020.

Giorgos Skoufos, Fatemeh Almodaresi, Mohsen Zakeri, Joseph Paulson, Rob Patro, Artemis Hatzigeorgiou, Ioannis Vlachos. Time and space-efficient k-mer-based microbial abundance quantification at strain resolution. HSCBB 2019.

Avi Srivastava, Laraib Iqbal Malik, Tom Smith, Ian Sudbery and Rob Patro. Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. *BioC* conference 2019.

Fatemeh Almodaresi, Mohsen Zakeri and Rob Patro
Cedar: scalable, accurate and fast metagenomic abundance estimation. *RECOMB* 2019.

Avi Srivastava, Laraib Iqbal Malik, Tom Smith, Ian Sudbery and Rob Patro.
Alevin efficiently estimates accurate gene abundances from dscRNA-seq data.
RECOMB 2019.

Fatemeh Almodaresi, Prashant Pandey, and Rob Patro. Rainbowfish: A Succinct Colored de Bruijn Graph Representation. *WABI*, 2017.

Fatemeh Almodaresi, Hirak Sarkar, and Rob Patro. A space and time-efficient index for the compacted colored de Bruijn graph. *ACM BCB*, 2017.

Laraib Malik and Rob Patro. Graph regularized, semi-supervised learning improves annotation of de novo transcriptomes. *CSHL BioData*, 2016.

Rob Patro and Carl Kingsford. Global Network Alignment Using Multiscale Spectral Signatures. *GLBIO Conference*, 2013.

Rob Patro and Carl Kingsford. Global Network Alignment Using Multiscale Spectral Signatures. *Systems Biology: Networks (Cold Spring Harbor Laboratory Meeting)*, 2013.

Rob Patro and Carl Kingsford. Global Network Alignment Using Multiscale Spectral Signatures. *ISMB*, 2012.

Rob Patro and Carl Kingsford. Learning from Diversity: Epitope Prediction with Sequence and Structure Features using an Ensemble of Support Vector Machines. *RECOMB Systems Biology Satellite Conference*, 2010.

II.F. Professional and Extension Publications

II.F.2. Pre-print / Working Paper (*Not Work in Progress*)

Scalable, ultra-fast, and low-memory construction of compacted de Bruijn graphs with Cuttlefish 2. Jamshed Khan, Marek Kokot, Sebastian Deorowicz, Rob Patro. bioRxiv 2021.12.14.472718; doi: <https://doi.org/10.1101/2021.12.14.472718>

CSI-Microbes: Identifying cell-type specific intracellular microbes from single-cell RNA-seq data. Welles Robinson, Fiorella Schischlik, E. Michael Gertz, Joo Sang Lee, Kaiyuan Zhu, S. Cenk Sahinalp, Rob Patro, Mark DM Leiserson, Alejandro A. Schäffer, and Eytan Ruppin. bioRxiv (2021): 2020-05. doi: <https://doi.org/10.1101/2020.05.14.096230>

A like-for-like comparison of lightweight-mapping pipelines for single-cell RNA-seq data pre-processing. Mohsen Zakeri, Avi Srivastava, Hirak Sarkar, Rob Patro. bioRxiv 2021.02.10.430656; doi: <https://doi.org/10.1101/2021.02.10.430656>

Accounting for fragments of unannotated origin reduces the “effects of transcriptional noise on estimates of gene and transcript expression in RNA sequencing experiments”. Avi Srivastava, Mohsen Zakeri, Hirak Sarkar, Charlotte Sonesson, Carl Kingsford, and Rob Patro. bioRxiv 2021.01.17.426996; doi: <https://doi.org/10.1101/2021.01.17.426996>.

Mikhail Lipatov, Komal Sanjeev, Rob Patro, Krishna R Veeramah. Maximum Likelihood Estimation of Biological Relatedness from Low Coverage Sequencing Data. bioRxiv 023374; doi: <https://doi.org/10.1101/023374>

II.G. Book Reviews, Notes, and Other Contributions

Algorithms meet sequencing technologies– 10th edition of the RECOMB-Seq workshop. Rob Patro, and Leena Salmela. *iScience*. 24(1):101956. 2021.

II.G.6. Manuals

User manual and documentation for the salmon software.
Available at: <https://salmon.readthedocs.io/en/latest/>

User manual and documentation for the sailfish software.
Available at: <https://sailfish.readthedocs.io/en/latest/>

User manual and documentation for the GHOST software.

Available at:

<http://www.cs.cmu.edu/~ckingsf/software/ghost/downloads/UserGuide.pdf>

II.H. Completed Creative Works and Scholarship

II.H.5. Software and Applications

The following software was either developed within my lab, or for papers on which I am the senior author (with significant contributions from myself and my students):

Alevin-fry: An efficient, scalable, and flexible framework for processing single-cell sequencing data

Software available at: <https://github.com/COMBINE-lab/alevin-fry>

Cuttlefish: Cuttlefish is a fast, parallel, and very lightweight memory tool to construct the compacted de Bruijn graph from genome references

Software available at: <https://github.com/COMBINE-lab/cuttlefish>

Mantis: A Fast, Small, and Exact Large-Scale Sequence-Search Index

Software available at: <https://github.com/splatlab/mantis>

Perplexity: evaluating transcript abundance estimation in the absence of ground truth.

Software available at: <https://github.com/COMBINE-lab/perplexity>

pyroe: Python library for preparing splici reference sequences for alevin-fry and for importing alevin-fry data into AnnData objects for use in ScanPy and related tools.

Software available at: <https://github.com/COMBINE-lab/pyroe>

roe: R library for preparing splici reference sequences for alevin-fry and for importing alevin-fry data into Bioconductor SingleCellExperiment objects.

Software available at: <https://github.com/COMBINE-lab/roe>

Usefulaf: functions and utilities that are useful for preparing data for processing with alevin-fry, as well as for reading alevin-fry data into other packages for downstream analysis; pipelines for simplified analysis.

Software available at: <https://github.com/COMBINE-lab/usefulaf>

Squeakr: An Exact and Approximate k -mer Counting System

Software available at: <https://github.com/splatlab/squeakr>

deBGR: An Efficient and Near-Exact Representation of the Weighted deBruijn Graph

Software available at: <https://github.com/splatlab/debgr>

Salmon: Fast and bias-aware quantification of transcript expression
Software available at: <https://github.com/COMBINE-lab/salmon>

Terminus: Robust and accurate data-driven transcriptome analysis
Software available at: <https://github.com/COMBINE-lab/terminus>

Pufferfish: An efficient index for the colored, compacted, de Bruijn Graph
Software available at: <https://github.com/COMBINE-lab/pufferfish>

Wasabi: Prepare Sailfish and Salmon output for downstream analysis
Software available at: <https://github.com/COMBINE-lab/wasabi>

RapMap: Rapid, sensitive and accurate read mapping via quasi-mapping
Software available at: <https://github.com/COMBINE-lab/RapMap>

Grouper: Clustering and quantification of *de novo* transcriptomes
Software available at: <https://github.com/COMBINE-lab/grouper>

Minnow: A principled framework for dscRNA-seq simulation at the read level
Software available at: <https://github.com/COMBINE-lab/minnow>

Quark: Semi-reference-based short-read compression
Software available at: <https://github.com/COMBINE-lab/quark>

LCMLKin: Low-coverage maximum likelihood relatedness estimation
Software available at:
<https://github.com/COMBINE-lab/maximum-likelihood-relatedness-estimation>

Rainbowfish: A succinct colored deBruijn Graph Representation
Software available at: <https://github.com/COMBINE-lab/rainbowfish>

Matryoshka: Automated discovery of hierarchically-structured chromatin domains
Software available at: <https://github.com/COMBINE-lab/matryoshka>

RapClust: Accurate, Lightweight Clustering of *de novo* Transcriptomes using
Fragment Equivalence Classes
Software available at: <https://github.com/COMBINE-lab/RapClust>

SkipPatch: A dynamically-updatable index for text search
Software available at: <https://github.com/COMBINE-lab/SkipPatch>

FQFeeder: A simple multi-threaded FASTA/FASTQ parser
Software available at: <https://github.com/rob-p/FQFeeder>

I either led or substantially contributed to the development of the following software:

Sailfish: Rapid Mapping-based Isoform Quantification from RNA-Seq Reads
Software available at: <https://github.com/kingsfordgroup/sailfish>

Armatus: Multiresolution domain calling software for chromosome conformation capture interaction matrices
Software available at: <https://github.com/kingsfordgroup/armatus>

GrowCode: A non-parametric framework for learning how networks grow
Software available at: <https://github.com/geetduggal/growcode>

PARANA2: Ancestral network reconstruction by summing over parsimonious histories
Software available at: <https://github.com/kingsfordgroup/parana2>

PARANA: Parsimonious Ancestral Reconstruction And Network Analysis
Software available at:
<http://www.cs.cmu.edu/~ckingsf/software/parana/downloads/parana.tgz>

Mince: Reference-free compression of sequencing reads
Software available at: <https://github.com/Kingsford-Group/mince>

GHOST: Global Network Alignment using Multiscale Spectral Signatures
Software available at: <https://github.com/Kingsford-Group/ghost>

II.J Sponsored Research and Programs – Administered by the Office of Research Administration (ORA)

II.J.1 Grants

Title: Salmon: Improving RNA-seq quantification & building an inclusive community

PI: Robert Patro

Agency: Chan Zuckerberg Initiative Foundation

Award Number: CZIF2020-004893

Duration: 01/01/2021 - 12/31/2021

Amount: \$235,000

Note: Awarded through Ocean Genomics, Inc.

Title: Hyperspectral terahertz imaging for cancer tumor delineation through deep neural network learning and geometry-aware curvelet analysis

PI: Hassan Arbab

co-PI: Robert Patro

Agency: Stony Brook Office of the Vice President of Research Seed Funding Program

Duration: 02/25/2019 — 02/24/2020

Amount: \$12,000

Title: A Modular Framework for Accurate, Efficient, and Reproducible Analysis of RNA-seq Data

PI/PD: Robert Patro

co-PI/PD: Michael Love

Agency: NIH

Award Number: R01 HG009937

Duration: 08/18/2018 – 6/30/2023

Amount: \$1,538,195

Title: CSR: Medium: Approximate Membership Query Data Structures in Computational Biology and Storage

PI: Robert Patro

co-PIs: Michael Bender, Michael Ferdman

Agency: NSF

Award Number: 1763680

Duration: 08/15/2018 – 7/31/2022

Amount: \$1,999,995

Title: Efficient tools for quantifying and simulating transcript-level abundance in single-cell RNA-seq

PI: Robert Patro

Agency: SVCF

Award Number: 182752

Duration: 03/01/2018 – 09/30/2019

Amount: \$132,708.00

Title: CAREER: A Comprehensive and Lightweight Framework for Transcriptome Analysis

PI: Robert Patro

Agency: NSF

Award Number: 1750472

Duration: 02/01/2018 – 01/31/2023

Amount: \$625,000.00

Title: Bilateral BBSRC-NSF/BIO: ABI Innovation: Data-driven hierarchical analysis of de novo transcriptomes PI: Robert Patro (co-PI: Julian Hibberd)

Agency: NSF

Award Number: 1564917

Duration: 07/01/2016 – 06/30/2019

Amount: \$639,767.80 (\$310,627 at Stony Brook, £205,713 at Cambridge University)

II.N. Entrepreneurial, Technology Transfer, and Public Engagement Activities

Co-founder and Chief Technology Officer of Ocean Genomics Inc.

Website: <https://oceangenomics.com/>

II.P. Research Fellowships, Prizes, and Awards

CMU Allen Newell Award for Research Excellence 2021 — Awarded for work on efficient methods for transcript quantification (i.e. Sailfish). Co-awardees include Carl Kingsford and Steve Mount.

ISMB2021 — “Cuttlefish” paper received Ian Lawson Van Toch Memorial Award (best paper with a student first author)

Dean’s Millionaires Club (2018, Stony Brook, raising over \$1,000,000 in external funding as PI within a calendar year)

Best Paper Award, ACM BCB ’17, for the paper Rich chromatin structure prediction from Hi-C data. (2017)

ISMB Student Travel Fellowship (2012, 2013)

1st place in DREAM5 (Dialogue on reverse-engineering assessment and methods) Epitope Antibody Recognition Challenge (2010)

Goldhaber Travel Fellowship (2010)

i3D Student Travel Fellowship (2009)

Verizon Fellowship (2007—2008)

Block Fellowship, Department of Computer Science, University of Maryland (2006—2008)

III. Teaching, Extension, Mentoring, and Advising

III.A. Courses Taught

The following courses were taught at the University of Maryland

CMSC858D : Algorithms, Data Structures and Inference for High-throughput Genomics (graduate-level) : Spring 2022, 27 students

CMSC423 : Bioinformatics Algorithms, Databases and Tools : Spring 2020, 94 students; Fall 2021 75 students

CMSC858D : Algorithms, Data Structures and Inference for High-throughput Genomics (graduate-level) : Fall 2020, 10 students; Spring 2022, 27 students

CMSC423 : Bioinformatics Algorithms, Databases and Tools : Spring 2020, 94 students

CMSC858D : Algorithms, Data Structures and Inference for High-throughput Genomics (graduate-level) : Fall 2019, 17 students

The following courses were taught at Stony Brook University:

CSE373 : Analysis of Algorithms (Undergraduate-level) : Spring 2019, ~110 students

CSE642 : Seminar in Algorithms : Fall 2019, ~50 students (co-taught with other faculty seminar leaders)

CSE549 : Computational Biology (Graduate-level) : Fall 2018, ~65 students

CSE642 : Seminar in Algorithms : Fall 2018, ~45 students (co-taught with other faculty seminar leaders)

CSE373 : Analysis of Algorithms (Undergraduate-level) : Spring 2018, ~160 students

CSE642 : Seminar in Algorithms : Spring 2018, ~35 students (co-taught with other faculty seminar leaders)

CSE549 : Computational Biology (Graduate-level) : Fall 2017, ~100 students

CSE642 : Seminar in Algorithms : Fall 2017, ~30 students (co-taught with other faculty seminar leaders)

CSE549 : Computational Biology (Graduate-level) : Fall 2016, ~60 students

CSE549 : Computational Biology (Graduate-level) : Fall 2015, ~75 students

CSE548 : Analysis of Algorithms (Graduate-level) : Spring 2015, ~10 students

CSE549 : Computational Biology (Graduate-level) : Fall 2014, ~60 students

III.B Teaching Innovations

III.B.6. Course or Curriculum Development

CMSC858D : Algorithms, Data Structures and Inference for High-throughput Genomics (graduate-level)

I have developed the curriculum for this new advanced topics graduate-level course, which is being offered for the first time in Fall 2019. While there is some topical overlap with **CSE549** (see below), this course is substantially different, and sacrifices some breadth to provide considerably more depth on topics in algorithmic and computational genomics. The curriculum contains material on state-of-the-art developments in algorithms, data structures and statistical inference procedures that are used in contemporary tools and methods for genomics analysis.

The following courses had curricula developed by me while at Stony Brook University:

CSE549 : Computational Biology (Graduate-level)

While this course existed before I joined the department, I developed the curriculum during all semesters where I taught the course, and the curriculum differed significantly from when the course was previously taught by other faculty. I also updated the curriculum in each year to account for recent research developments in the field.

CSE548 : Analysis of Algorithms (Graduate-level)

While this course existed before I joined the department, I developed the curriculum when I taught the course, and the curriculum differed non-trivially from when the course was previously taught by other faculty.

CSE373 : Analysis of Algorithms (Undergraduate-level)

While this course existed before I joined the department, I developed the curriculum during all semesters where I taught the course. The curriculum differed non-trivially from when the course is taught by other faculty, and I, in fact, use a different book (“Algorithm Design” by Kleinberg and Tardos vs. “The Algorithm Design Manual” by Skiena).

III.C **Advising: Research or Clinical**

III.C.1 Undergraduate

Spiro Razis (Stony Brook)

Undergraduate (non-matriculating) researcher advisor (2016,2017)

First placement: programmer/analyst for NCI (NIH) subcontractor (IMS)

III.C.2 Master’s

Geoffrey Churchill (Stony Brook)

Advisor (2017)

First placement: Google (software engineer)

Nitish Gupta (Stony Brook)

Advisor, MS Thesis committee member (2014—2016)

First placement: Bloomberg LP (software engineer)

Komal Sanjeev (Stony Brook)

Advisor, MS Thesis committee member (2014—2016)

First placement: Amazon (software engineer)

III.C.3 Doctoral

Mohsen Zakeri

Advisor (2015—2021) (**defended Nov. 2021**)

First placement: Postdoctoral Research Associate, Department of Computer Science, Johns Hopkins University (postdoctoral mentor Ben Langmead)

Fatemeh Almodaresi

Advisor, Research Proficiency Exam Committee Member (2016—current)

Advisor, Committee Member (2016—2020) (**defended July. 2020**)

Note: Awarded Larry S. Davis Doctoral Dissertation Award

First placement: Postdoctoral Research Associate, Ontario Institute for Cancer Research (postdoctoral mentor Lincoln Stein)

Hirak Sarkar

Advisor, Research Proficiency Exam Committee Member

Advisor, Committee Member (2014—2020) (**defended July. 2020**)

First placement: Postdoctoral Research Associate, Department of Biomedical Informatics, Harvard Medical School (postdoctoral mentor Peter Kharchenko)

Laraib Malik (Stony Brook)

Advisor, Research Proficiency Exam Committee Member, Preliminary PhD Exam

Advisor, Committee Member (2014—2020) (**defended Jan. 2020**)

First placement: Senior Scientist, AbbVie

Avi Srivastava (Stony Brook)

Advisor, Research Proficiency Exam Committee Member, Preliminary PhD Exam

Advisor, Committee Member (2014—2019) (**defended Dec. 2019**)

First placement: Postdoctoral Research Associate, New York Genome Center (postdoctoral mentor Rahul Satija).

Thu Nguyen (Stony Brook)

co-Advisor (co-advised by Dr. Alexi Soares at Brookhaven National Lab)
(2018—2020)

The following is ongoing advising / co-advising (alphabetical):

Hyeon Jin Cho

Advisor, co-advised with Dan Larson at NIH (2019—current)

Jason Fan

Advisor (2020—current)

Dongze He

Advisor (2020—current)

Jamshed Khan

Advisor (2019—current)

Noor Pratap Singh

Advisor (2019—current)

III.C.4 Other Directed Research (*e.g. K-12 Interactions*)

The following is ongoing advising / co-advising

Skylar Spencer Chan (UMD CS Honors student)
Research advisor (2020—current)

Completed advising (alphabetical):

Geoffrey Glass (Simons Summer Research Program Fellow)
Advisor
First placement: Brown University

Anjalie Kini (Simons Summer Research Program Fellow)
Advisor
First placement: Massachusetts Institute of Technology

Alice Yeh (Simons Summer Research Program Fellow; BISV Senior Project)
Advisor

III.E. **Advising: Other than Directed Research**

III.E.1 Undergraduate

Lise Ho (Stony Brook, practicum in teaching)
Kyeongsoo Kim (Stony Brook, practicum in teaching)
Freeman Lou (Stony Brook, practicum in teaching)
Matthew Weston (Stony Brook, practicum in teaching)

III.E.2 Master's

The following students were advised as part of CSE523/524 at Stony Brook University, and performed research under my direction, but were not MS thesis students:

Srikant Aggarwal
Eshita Bheda
Anuja Bawaskar
Siddhartha Chhabra
Revati Damle
Komal Dhuri
Shreyas Harisha
Nikhil Junneti
Pavan Kottapalli
Anand Kulkarni
Nikhil Mehta
Nikhil Mohan
Rasika Pohankar
Mridul Ranjan
Manu Rao

Aravind Reddy Ravula
Debjyoti Roy
Ayush Sengupta
Siddarth Harinarayanan
Akshat Singhal
Aditya Srivastava
Alok Thatikunta
Shravya Rani Thatipally
Kevin Wasiluk

III.F. Professional and Extension Education

III.F.4. Guest Lectures

CBMG688Y (Cell Biology and Molecular Genetics Graduate Program; 2019)
Guest lecture on methods for single-cell transcriptome analysis
PQB 558 (Seminar in Physical & Quantitative Biology at Stony Brook; 2017)
Guest lecture on sequence alignment and read mapping
BGE 510 (Graduate Genetics at Stony Brook; 2017)
Guest lecture on RNA-seq read mapping
Guest lecture on RNA-seq assembly and quantification
BGE 510 (Graduate Genetics at Stony Brook; 2016)
Guest lecture on high-throughput sequencing and assembly
Guest lecture on RNA-seq quantification

III.H. Other Teaching Activities

Guest lecturer at CSHL Course “Statistical Methods for Functional Genomics” 2019
Gave lecture covering the theory and practice of transcript quantification and a description of common technical biases in RNA-seq data. Presented a detailed assessment of the effect of different mapping and alignment methodologies on the accuracy of transcript abundance estimation.

Guest lecturer at CSHL Course “Statistical Methods for Functional Genomics” 2018
Gave lecture covering aspects of read alignment and mapping, detailed coverage of the theory of transcript quantification and common technical biases in RNA-seq data, and transcript assembly for working in the presence of an incomplete annotation.

Instructor at Next-Gen Sequence Analysis Workshop (ANGUS) 2017

URL: <https://angus.readthedocs.io/en/2017/>

Gave lecture covering aspects of read alignment and mapping and quantification using RNA-seq, and delivered practical tutorial (co-taught with Mike Love) on quantification and differential expression analysis.

Instructor at Next-Gen Sequence Analysis Workshop (ANGUS) 2016

URL: <https://angus.readthedocs.io/en/2016/>
Created course modules (lecture and practical lab) covering
read alignment and mapping and quantification using RNA-seq.

IV. Service and Outreach

IV.A. Editorships, Editorial Boards, and Reviewing Activities

IV.A.1. Editorships

Oxford Bioinformatics: Editorial Board Member (Nov. 2019 — current)
PLOS Computational Biology (guest editor; 2019, 2021)

IV.A.3. Reviewing Activities for Journals and Presses (in alphabetical order)

Algorithms
BMC Bioinformatics
BMC Genomics
Cell Systems
F1000
Genome Biology
Genome Research
IEEE Transactions on Computational Biology and Bioinformatics
Journal of Bioinformatics and Computational Biology
Nature Communications
Nature Genetics
Nature Methods
Nucleic Acids Research
Nucleic Acids Research Genomics and Bioinformatics
Oxford Bioinformatics
PeerJ
PLOS Computational Biology
PLOS One
Proceedings of the National Academy of Sciences of the United States of America

IV.A.4. Reviewing Activities for Agencies and Foundations (in alphabetical order)

American Heart Association Panelist (2018)
National Institutes of Health Panelist (BDMA study section, NHGRI study section,
recurring)
National Science Foundation Panelist (CISE, BIO, recurring)

IV.A.5. Reviewing Activities for Conferences (in alphabetical order)

ACM BCB Conference
ACM SIGGRAPH Conference

Asia Pacific Bioinformatics Conference
IEEE Intl. Workshop on High Performance Computational Biology (HICOMB)
IEEE Visualization Conference
Intelligent Systems for Molecular Biology (ISMB)
Research in Computational Molecular Biology (RECOMB)
RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq)
SIAM Conference on Applied and Computational Discrete Algorithms (ACDA)
Workshop on Algorithms in Bioinformatics (WABI)

IV.B. Committees, Professional & Campus Service

IV.B.1 Campus Service – Department

Department self-assessment, Undergraduate Instruction sub-committee (**chair**) (2021/2022)
Instructor Search Committee (2021/2022)
Learning Outcomes Committee (2020/2021, 2021/2022)
Teaching Evaluation Committee (2020/2021, 2021/2022)
Faculty Hiring committee, Computer Science Department (2020/2021)
Graduate admissions committee (2020 — current)
Colwell Fellowship selection committee (2019 — current)
Graduate admissions committee (at Stony Brook; 2014 — 2019)
Graduate curriculum committee (at Stony Brook; 2017 — 2019)
Faculty hiring committee (at Stony Brook; 2014, 2015, 2016, 2018)

Ongoing committee membership (alphabetical):

Kiran Gajanan Javkar (UMD, Department of Computer Science)
Committee Member, Preliminary PhD Exam (2020)

Completed committee membership (alphabetical):

Dr. Mohammad Amin (Stony Brook, Department of Computer Science)
Research Proficiency Exam Committee Member, Preliminary PhD Exam
Committee Member, PhD Defense Committee Chair (2017—2019)
First placement: Tenure-track assistant professor of computer science at
Fordham University

Dr. Victoria Paz Cepeda Espinoza (UMD, Department of Computer Science)
Committee Member, PhD Defense (2020)
First placement: Postdoctoral Research Associate, Department of Biomedical
Data Science, Stanford University (postdoctoral advisor, Carlos Bustamante)

Dr. Ahmed Elgohary Ghoneim (UMD, Department of Computer Science)
Committee Member, PhD Defense (2021)
Committee Member, PhD Preliminary Proposal (2019)

Dr. Hayan Lee (Stony Brook, Department of Computer Science)
PhD Defense Committee Member (2015)
First placement: Postdoc at DOE Joint Genome Institute, Lawrence Berkeley
National Laboratory

Dr. Brian David Ondov (UMD, Department of Computer Science)
Committee Member, PhD Defense (2020)

Dr. Prashant Pandey (Stony Brook, Department of Computer Science)
Committee Member, PhD Defense Committee (2018)
First placement: Postdoctoral Research Associate, Department of Computational
Biology, Carnegie Mellon University (postdoctoral advisor, Carl Kingsford)

Dr. Welles Robinson (UMD, Department of Computer Science)
Committee Member, Preliminary Exam (2021)
Committee Member, PhD Defense (2021)

Dr. Nidhi Shaha (UMD, Department of Computer Science)
Committee Member, PhD Defense (2021)

IV.B.2 Campus Service – College

CBBG Program: Graduate admissions committee (2020, 2021, 2022)

Participant in CMNS “Future Center Leaders” program (inaugural 2021 class)

Ongoing committee membership outside of the department (alphabetical):

Theresa Alexander, (UMD, Biological Science Graduate Program)
Preliminary Exam Committee Member (2020)
Qualifying Exam Committee Member (2021)

Domenick Braccia (UMD, Biological Science Graduate Program)
Preliminary Exam Committee Member (2020)
Qualifying Exam Committee Member (2020)

Cindy Li (UMD, Biological Science Graduate Program)
Preliminary Exam Committee Member (2020)

Muzi Li (UMD, Biological Science Graduate Program)
Preliminary Exam Committee Member (2019)
Qualifying Exam Committee Member (2020)

Thomas Pranzatelli (UMD, Biological Science Graduate Program)
Preliminary Exam Committee Member (2020)

Qualifying Exam Committee Member (2020)

Bihua Yu (Stony Brook, Department of Applied Mathematics and Statistics)
Preliminary PhD Exam Committee Member (2017)

Bixuan Wang (UMD, Biological Science Graduate Program)
Preliminary Exam Committee Member (2021)
Qualifying Exam Committee Member (2021)

Completed committee membership outside of the department (alphabetical):

Dr. Han Fang (Stony Brook, Department of Applied Mathematics and Statistics)
Preliminary PhD Exam Committee Member, PhD Defense Committee Member
(2015—2017)
First placement: Facebook Data Scientist

Dr. Sanju Sinha (UMD, Biological Science Graduate Program)
Committee Member (Dean's representative), PhD Defense (2021)

IV.B.3. Campus Service – University

Simons Summer Research Program admissions committee (at Stony Brook;
2018, 2019)

IV.B.5 Campus Service — Other

Completed committee membership outside of the college (alphabetical):

Dr. Jason O'rawe (Stony Brook, Department of Genetics)
Preliminary PhD Exam Committee Member, PhD Defense Committee Member
(2016—2017)
First placement: Data Science Associate at Open Data Science Conference

IV.B.6. Inter-institutional and Regional (*e.g. inter-library agencies, regional consortia*)

SUNY Research Foundation Germination Space for Engineering Driven Medicine
participant (at Stony Brook; 2018)

Ongoing committee membership at different universities (alphabetical):

Keffy Kehrli (Stony Brook, Department of Genetics)
PhD Committee Member (2017—current)

Completed committee membership at different universities (alphabetical):

Dr. Camille Scott (UC Davis, Department of Computer Science)
Qualifying Exam Committee Member & Dissertation Committee Member
(2020—2022)

Dr. Luiz Iber (UC Davis, Department of Computer Science)
Qualifying Exam Committee Member (2019)

Dr. Alisa Yurovsky (Stony Brook, Department of Computer Science)
PhD Committee Member (2018—2020)

IV.B.7 Offices and Committee Memberships

Program committee for ACM BCB (2017—2019)
Program committee for Asia Pacific Bioinformatics Conference (2016, 2017)
Program committee for IPDPS (2019)
Program committee for ISMB (2017 — 2022)
Program committee for RECOMB (2019, 2022)
Program committee for RECOMB-Seq (2016 — 2018, 2021, 2022)
Program committee for SCIAM ACDA (2021)
Program committee for Workshop on Algorithms in Bioinformatics (2017, 2018)

IV.B.8. Leadership Roles in Meetings and Conferences

Area **co-Chair** for ISMB 2022 (Genome Sequence Analysis area)
Highlight Track **co-Chair** for ACM-BCB 2020
Program Committee **co-Chair** for RECOMB-Seq 2020
Poster Committee **Chair** for RECOMB 2019
Genome Informatics 2019 Meeting **discussion leader** (transcriptomics session)

IV.D. Media Contributions

IV.D.6. Blogs

RoBlog (personal blog discussing topics related to computational genomics and computer science)
URL: <http://robpatro.com/blog/>