

Curriculum Vitae

I. Personal Information

Héctor Corrada Bravo

Computer Science and UMIACS
3226 Brendan Iribe Center for
Computer Science and Engineering
8125 Paint Branch Drive
College Park, MD 20745

hcorrada@cs.umd.edu
<http://hcbravo.org>

I.A. Academic Appointments

- Associate Professor with Tenure
Department of Computer Science, Institute for Advanced Computer Studies
University of Maryland, College Park, MD
July 2016-Present
- Affiliate Associate Professor
Applied Math, Statistics and Scientific Computation, Department of Mathematics
University of Maryland, College Park, MD
July 2016-Present

I.B. Other Employment

- Research Intern
IBM Research, Almaden, CA
May 2005-August 2005

I.C. Educational Background

- Ph.D., Computer Science, University of Wisconsin, Madison, WI
September 2003 - August 2008
Dissertation: Graph-based data analysis
Advisor: Grace Wahba and Raghu Ramakrishnan
- D.M.A., Indiana University School of Music, Bloomington, IN (ABD)
September 2000 - August 2003
- M.M., Peabody Institute of Music, Baltimore, MD
September 1997 - May 1999
- B.M., Peabody Institute of Music, Baltimore, MD
September 1993 - May 1997

II. Research, Scholarly and Creative Activities

Annotation: corresponding authors*, lead authors^, advisee#

II.A. Selected Articles in Refereed Journals (out of 46)

1. S. Hicks^, K. Okrah#, J. Paulson#, J. Quackenbush, R. Irizarry, **H. Corrada Bravo*** (2018). Smooth quantile normalization. *Biostatistics* 19(2): 185-198, doi:10.1093/biostatistics/kxx028.
2. M.S. Kumar^#, E.V. Slud, K. Okrah#, S.C. Hicks, S. Hannenhalli, **H. Corrada Bravo*** (2018). Analysis and correction of compositional bias in sparse sequencing count data. *BMC Genomics* 19:799, doi:10.1186/s12864-018-5160-5.
3. J. Kancherla^#, A. Zhang#, B. Gottfried#, **H. Corrada Bravo*** (2018). Epiviz Web components: reusable and extensible component library to visualize genomic datasets. *F1000 Research* 7:1096, doi:10.12688/f1000research.15433.1.
4. J. Wagner^#, F. Chelaru^#, J. Kancherla^, J.N. Paulson^#, A. Zhang#, V. Felix, A. Mahurkar, N. Elmqvist, **H. Corrada Bravo*** (2018). Metaviz: interactive statistical and visual analysis of metagenomic data. *Nucleic Acids Research* gky136, doi:10.1093/nar/gky136.
5. Y. Li^, K.L. Caradonna^, K. Okrah^#, J. Choi, P. Padmanabhan, D.M. Ndegwa, S. Shah-Simpson, M.R. Temanni, **H. Corrada Bravo**, N. El-Sayed*, B.A. Burleigh* (2016). Transcriptome Remodeling in Trypanosoma cruzi and Human Cells during Intracellular Infection. *PLOS Pathogens* 12(4):e1005511, doi:10.1371/journal.ppat.1005511.
6. M. Pop^, J.N. Paulson#, S. Chakraborty, I. Astrovskaya, B.R. Lindsay, S. Li, **H. Corrada Bravo**, C. Harro, J. Parkhill, A.W. Walker, R.I. Walker, D.A. Sack, O.C. Stine* (2016). Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic *Escherichia coli* and subsequent ciprofloxacin treatment. *BMC Genomics* 17(1):440, doi:10.1186/s12864-016-27777-0.
7. M. Sharmin^#, **H. Corrada bravo**, S. Hannenhalli* (2016). Heterogeneity of TF binding specificity models within and across cell lines. *Genome Research* 26(8):1110-23, doi:10.1101/gr.199166.115.
8. J. Wagner^#, J. Paulson#, X.S. Wang, B. Bhattacharjee, **H. Corrada Bravo*** (2016). Privacy preserving human microbiome analysis using secure computation. *Bioinformatics*, doi:10.1093/bioinformatics/btw073.
9. W. Huber^, V. Carey, R. Gentleman, M. Carlson, B.S. Carvalho, **H. Corrada Bravo**, S. Davis, L. Gatto, T. Girke, R. Gottardo, F. Hahne, K. Hansen, R.A. Irizarry, M. Lawrence, M.I. Love, J. MacDonald, V. Obenchain, A.K. Olés, H. Pagés, P. Shannon, G. Smyth, D. Tenenbaum, L. Waldron, M. Morgan* (2015). Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods* 12 115-121, doi:10.1038/nmeth.3252.
10. W. Dinalankara^#, **H. Corrada Bravo*** (2015). Gene expression signatures based on variability can robustly predict tumor progression and prognosis. *Cancer Informatics* 14:71-81.
11. L. Dillon^, K. Okrah^#, V. Hughitt, R. Suresh, Y. Li, M. Fernandes, A. Belew, **H. Corrada Bravo**, D. Mosser, N. El-Sayed* (2015). Transcriptomic profiling of gene expression and RNA processing during *Leishmania major* differentiation. *Nucleic Acids Research* 43 (14): 6799-6813, doi:10.1093/nar/gkv656.
12. F. Chelaru^#, L. Smith#, N. Goldstein#, **H. Corrada Bravo*** (2014). Epiviz: interactive visual analytics for epigenomics data. *Nature Methods* 11 938-940, doi:10.1038/nmeth.3038.
13. M. Aryee^, A. Jaffe, **H. Corrada Bravo**, C. Ladd-Acosta, A. Feinberg, K. Hansen*, R.A. Irizarry* (2014). Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA Methylation microarrays. *Bioinformatics* 30 (10):1363-9.
14. E. Alemu^, J.W. Carl, **H. Corrada Bravo***, S. Hannenhalli* (2014). Determinants of expression variability. *Nucleic Acids Research* 42 (6), 3503-14.
15. M. Pop^, A.W. Walker^, J.N. Paulson^#, B. Lindsey^, M. Antonio^, M.A. Hossain^, J. Oundo^, B. Tamboura, V. Mai, I. Astrovskaya, **H. Corrada Bravo**, R. Rance, M. Stares, M.M. Levine, S. Panchalingam, K. Kotloff, U.N. Ikumapayi, C. Ebruke, D. Adeyemi, F. Ahmed, M.T. Alam, R. Amin, S. Siddiqui, J.B. Ochieng, E. Ouma, J. Juma, E. Mailu, R. Omore, J.G. Morris, R.F. Breiman, D. Saha, J. Parkhill, O.C. Stine*, J.P. Nataro* (2014). Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. *Genome Biology* 15, R76.
16. W. Timp^, **H. Corrada Bravo**, O.G. McDonald, M. Goggins, C. Umbricht, M. Zeiger, A.P. Feinberg*, R.A. Irizarry* (2014). Large hypomethylated blocks related to large heterochromatin regions as a universal defining epigenetic alteration in human solid tumors. *Genome Medicine* 6:61, doi:10.1186/s13073-014-0061-y.
17. J.N. Paulson#, O.C. Stein, **H. Corrada Bravo***, M. Pop* (2013). Differential abundance analysis for microbial marker-gene surveys. *Nature Methods* 10 (12):1200-1202, doi:10.1038/nmeth.2658.
18. **H. Corrada Bravo**, V. Pihur, M. McCall, R.A. Irizarry, J.T. Leek* (2012). Gene expression anti-profiles as a basis for cancer diagnostics. *BMC Bioinformatics* 13:272, doi:10.1186/1471-2105-13-272.
19. K. Hansen^, W. Timp^, **H. Corrada Bravo**, S. Sabuncian^, B. Langmead^, O.G. McDonald, B. Wen, H. Wu, D. Diep, E. Briem, K. Zhang, R.A. Irizarry*, A.P. Feinberg* (2011). Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics* 43 (8):768-75.
20. A. Rivas^, K. Bohane, **H. Corrada Bravo**, M. Tan, R. Tamargo, H.W. Francis (2011). A model for early prediction of

- facial nerve recovery after vestibular schwannoma surgery. *Otology & Neurotology* 32 (5):826-33.
21. M. Taub[^], **H. Corrada Bravo**, R.A. Irizarry* (2010). Overcoming bias and systematic errors in next generation sequencing data. *Genome Medicine* 2 (12):87.
 22. J.T. Leek[^], R. Scharpf, **H. Corrada Bravo**, D. Simcha, B. Langmead, W.E. Johnson, D. Geman, K. Baggerly, R.A. Irizarry* (2010). Tackling the widespread and critical impact of batch effects in high-throughput data. *Nature Reviews Genetics* 11 (10):733-739.
 23. **H. Corrada Bravo**[^], K.E. Lee, B.E.K. Klein, R. Klein, S.K. Iyengar, G. Wahba* (2009). Examining the relative influence of familial, genetic and environmental covariate information in flexible risk models. *Proceedings of the National Academy of Science* 106 (20): 8128-8133.
 24. **H. Corrada Bravo**[^], R.A. Irizarry* (2009). Model-based quality assessment and base-calling for second-generation sequencing data. *Biometrics* 66(3):665-74, doi:10.1111/j.1541-0420.2009.01353.x.

II.B. Published Conference Proceedings

II.B.1. Refereed Conference Proceedings

1. M.K. Gunady^{^#}, S. Cornwell[#], S.M. Mount, **H. Corrada Bravo*** (2017). Yanagi: transcript segment library construction for RNA-seq quantification. *17th Workshop for Algorithms in Bioinformatics (WABI) 2017*.
2. F Chelaru^{^*#}, **H. Corrada Bravo*** (2015). Epiviz: a view inside the design of an integrated visual analysis software for genomics. *BioVis 2015; BMC Bioinformatics* 16(Supl 11):S4.
3. F Dorri^{^#}, L. Mendelowitz, **H. Corrada Bravo*** (2015). methylFlow: cell-specific methylation pattern reconstruction from high-throughput bisulfite-converted DNA sequencing. *HitSEQ 2015; Bioinformatics* 32(11):1618-24.
4. **H. Corrada Bravo**[^], K. Eng, S. Keles, G. Wahba, S. Wright (2009). Estimating tree-structured covariance matrices via mixed integer programming. *Twelfth International Conference on Artificial Intelligence and Statistics (AISTATS '09); Journal of Machine Learning Research Workshop and Conference Proceedings*, 533:40.
5. **H. Corrada Bravo**[^], R. Ramakrishnan (2007). Optimizing MPF queries: decision support and probabilistic inference. *26th ACM SIGMOD Intl. Conf. on Management of Data* 701:712.
6. **H. Corrada Bravo**[^], D. Page, R. Ramakrishnan, J. Shavlik, V. Santos Costa (2005). A framework for set-oriented computation in inductive logic programming and its application in generalizing inverse entailment. *15th ILP Conf*:69:86.

II.C. Conferences, Workshops and Talks (last 5 years)

II.C.1. Invited Talks

1. What's next? Beyond integration of visual and statistical analysis of genomic data. *Biological Data Science Meeting, Cold Spring Harbor Laboratory*, Long Island, NY. November 2018.
2. Is this Data Science? Adventures in metagenomic data analysis. *Computation and Informatics in Biology and Medicine Program Annual Retreat, University of Wisconsin*, Madison, WI. October 2017.
3. Interactive visual and computational analysis of epigenetic data. *VIZBI 2017*, Sdney, Australia. June 2017.
4. Interactive statistical and computational analysis of functional and metagenomic data. *University of Puerto Rico*, Rio Piedras, PR. April 2017.
5. Challenges and opportunities in metagenomic data analysis. *NE1602 Kickoff Meeting*, Washington, DC. March 2017.
6. Bias in Biomedical Data Science. *University of Maryland Diversity in Computing Summit*, College Park, MD. November 2016.
7. Statistics and visualization for metagenomics data. *Georgetown University ICBI Seminar Series*, Washington, DC. October 2016.
8. Statistics and visualization for metagenomics data. *Johns Hopkins Young Investigator Symposium*, Baltimore, MD. October 2016.
9. Visualization, Statistical Modeling and Discovery in Computational Epigenomics. *Howard University Precision Medicine Workshop*, Washington, DC. March 2016.
10. Visualization, statistical modeling and discovery in computational epigenomics. *Harvard University Department of Biostatistics and Computational Biology*, Boston, MA. February 2016.
11. What is Biomedical Data Science?. *Symposium of Health Informatics in Latin America and the Caribbean*, San Juan, PR. November 2015.
12. Visualization, Statistical Modeling and Discovery in Computational Epigenomics. *Computer Science Colloquium Series*, College Park, MD. September 2015.
13. Interactive and exploratory visualization of epigenome-wide data. *BioIT World Conference*, Boston, MA. April 2015.

14. Interactive and exploratory visualization of epigenome-wide data. *Epigenomics in Disease, Molecular Medicine Tri-Con*, San Francisco, CA. February 2015.
15. Interactive and exploratory visualization of epigenome-wide data. *UMD Campus Visualization Partnership Lecture Series*, College Park, MD. February 2015.
16. Exploring tumor epigenetic heterogeneity by cell-specific methylation pattern reconstruction. *Department of Bio-statistics and Computational Biology, Johns Hopkins Cancer Center*, Baltimore, MD. November 2014.
17. Exploring tumor epigenetic heterogeneity by cell-specific methylation pattern reconstruction. *CMU-Pitt Ph.D. Program in Computational Biology Seminar Series*, Pittsburgh, PA. April 2014.
18. Cell-specific methylation pattern reconstruction using minimum cost network flow algorithms. *Department of Mathematics, George Mason University*, Fairfax, VA. February 2014.

II.C.2. Presentations, Symposia and Workshops

1. Interactive Statistical and Visual Analysis of Longitudinal Metagenomic Data. *Joint Statistical Meetings*, Vancouver, Canada. August 2018.
2. Visualization and computation over hierarchically organized features for metagenomics and epigenomics. *Joint Statistical Meetings*, Chicago, IL. August 2016.
3. Addressing reproducibility in genomic signatures by characterizing variance and estimation stability. *Joint Statistical Meetings*, Seattle, WA. August 2015.
4. Differential abundance analysis of metagenomic whole-genome sequencing. *Joint Statistical Meetings*, Seattle, WA. August 2015.
5. Interactive and exploratory visual analytics of epigenome-wide data. *ISMB*, Dublin, Ireland. July 2015.
6. Epiviz: a view inside the design of an integrated visual analysis software for genomics. *BioVis*, Dublin, Ireland. July 2015.
7. methylFlow: cell-specific methylation pattern reconstruction from high-throughput bisulfite-converted DNA sequencing. *HiTSeq*, Dublin, Ireland. July 2015.
8. Interactive and exploratory visualization of epigenome-wide data. *Joint Statistical Meetings*, Boston, MA. July 2014.
9. Interactive, Exploratory Visualization and Statistical Analysis of Genome-Scale Data. *International Biomteric Society ENAR Meeting*, Baltimore, MD. March 2014.
10. Metaviz: interactive statistical and visual analysis of Human Microbiome Project data. *Mid-Atlantic Metagenomics Meetup*, College Park, MD. January 2018.
11. Visualization and statistical modeling for metagenomics data. *Human Microbiome Project 2 Symposium*, Bethesda, MD. June, 2016.
12. Gene expression network anti-profiles. *UMD/NIST Network Science Mini-Symposium*, College Park, MD. January, 2014.

II.E. Completed Creative Works

II.E.1. Selected Software and Applications

1. Metavizr: Interactive visualization of metagenomics data in R/Bioconductor. Released December 2016. <http://github.com/epiviz/metavizr>.
2. Metaviz: Interactive visualization for metagenomics data. Released December 2016. <http://metaviz.org>.
3. methylFlow: cell-specific methylation pattern reconstruction. Released June 2015. <http://github.com/hcorrada/methylFlow>.
4. Epivizr: interactive visualization of genomics data in R/Bioconductor. Released June 2013. <http://bioconductor.org/packages/release/bioc/html/epivizr.html>.

5. Epiviz: Interactive visualization for genomics data.
Released June 2013. <http://github.com/epiviz>.
6. metagenomeSeq: Statistical analysis for sparse high-throughput sequencing.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/metagenomeSeq.html>.
7. Minfi: Analyze Illumina's 450k methylation arrays.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/minfi.html>.
8. RcpLx: An interface to the CPLEX optimization engine for R.
Released Jan. 2008. <http://cran.r-project.org/web/packages/RcpLx/index.html>.

II.E.2. Websites

1. Metaviz: Interactive visualization for metagenomic data.
Released September 2017. <http://metaviz.org>.
2. Epiviz: Interactive visualization for genomics data.
Released May 2014. <http://epiviz.org>.

II.G. Sponsored Research

II.G.1. Grants

1. Title: R01: Overcoming bias and unwanted variability in next generation sequencing
Funding Agency: NIH HG005220
Recipient Institution: Dana Farber Cancer Institute, Rafael A. Irizarry (PI)
Amount Awarded: \$397,903 subcontracted to UMCP
Dates: March 2015-February 2020
Role: PI
2. Title: R01: Integrative visual and computational exploratory analysis of genomics data
Funding Agency: NIH GM114267
Recipient Institution: University of Maryland, College Park
Amount Awarded: \$1,800,421
Dates: September 2015-August 2020
Role: PI
3. Title: NRT-DESE; Network biology: from data to information to insights
Funding Agency: NSF 1632976
Recipient Institution: University of Maryland, College Park, Michelle Girvan (PI)
Amount Awarded: \$2,999,847
Dates: September 2016-August 2021
Role: co-PI
4. Title: Illuminating neurodevelopment through integrative analysis and visualization of multi-omic data
Funding Agency: NIH R24MH114815
Recipient Institution: University of Maryland, Baltimore, Ronna Hertzano (PI)
Amount Awarded: \$415,443 subcontracted to UMCP
Dates: September 2018-May 2021
Role: PI
5. Title: Epigenomic regulation of hippocampal transcriptome after experimental traumatic brain injury
Funding Agency: UMD Seed Grant NA
Recipient Institution: University of Maryland, College Park
Amount Awarded: \$50,000
Dates: August 2017-July 2019
Role: co-PI

III. Teaching, Mentoring and Advising

III.A. Courses Taught (last 5 years)

Term	Course	Enrollment	Description
Spring 2019	CMSC644	16	Algorithms for Data Science
Spring 2019	CMSC320	230	Introduction to Data Science
Spring 2018	CMSC 320	183	Introduction to Data Science
Fall 2018	CMSC828O	27	Analysis of Biological Networks across Scales
Fall 2018	CSMC798E	9	Graduate Seminar in Computer Science: Research Colloquium
Fall 2018	CMSC643	18	Machine Learning & Data Mining (Data Mining Professional Master's Certificate)
Spring 2017	CMSC 423	52	Bioinformatic Databases, Tools and Algorithms
Fall 2017	CSMC798E	23	Graduate Seminar in Computer Science: Research Colloquium
Fall 2017	CSMC828O	31	Analysis of Biological Networks across Scales
Fall 2017	CMSC643	11	Machine Learning & Data Mining (Data Mining Professional Master's Certificate)
Spring 2016	CMSC 320	50	Introduction to Data Science
Fall 2016	CMSC 320	83	Introduction to Data Science
Spring 2015	CMSC 498T	32	Introduction to Data Science II
Fall 2015	CMSC 423	49	Bioinformatics Databases, Tools and Algorithms
Fall 2014	CMSC 423	49	Bioinformatics Databases, Tools and Algorithms
Fall 2014	CMSC 423	35	Bioinformatics Databases, Tools and Algorithms
Spring 2014	CMSC 702	30	Computational Systems Biology and Functional Genomics

III.B. Selected Teaching Innovations

III.B.1. Course or Curriculum Development

CSMC828O - Analysis of Biological networks across scales

Developed new course in support of our NSF NRT training grant. This course introduces tools and methods for analysis of network data focusing on the study of molecular, neurological and ecological networks. Students are introduced to methods and tools from network science, statistics, Machine Learning and visualization.

CMSC 320 - Introduction to Data Science

Developed a new undergraduate course covering the practice of data science, and a required course on a new Data Science specialization within the undergraduate program of the Department of Computer Science. This course focuses on data management, exploratory and statistical data analysis, data and information visualization. It is heavily assignment-based and draws extensively from applications.

CMSC 702 - Computational Systems Biology and Functional Genomics

Developed this new advanced graduate-level course concentrating on the use of Statistical Learning methods and algorithms in the analysis of large high-throughput biomedical assays. Core course in the Computational Biology concentration area.

III.C. Advising

III.C.1. Undergraduate

Name	Department	Stage	Role
Yifan Yang	CS	Current	advisor
Brian Gottfried	CS	Completed	advisor
Institute of Genome Science, University of Maryland, Baltimore			

Name	Department	Stage	Role
Alexander Zhang	CS	Completed Facebook	advisor
Tim Wood	CS	Completed Broad Institute	advisor
Daniel Konecki	CS	Completed Baylor College of Medicine	advisor
Mihai Sirbu	CS	Completed Capital One	advisor
Lan Tran	CS	Current	advisor
Morgan Walter	Bioengineering	Current	advisor

III.C.2. Doctoral

Name	Department	Stage	Role
Aya Ismail	CS	Pre-candidacy	advisor
Mohammed Gunady	CS	Candidacy	advisor
Domenick Braccia	CBMG	Pre-candidacy	advisor
Zhe Cui	EE	Candidacy	co-advisor
Faezeh Dorri	CS	Candidacy	advisor
Senthil Muthiah	CBMG	Candidacy	advisor
Nathanael Olson	CBMG	Completed Research Scientist, NIST	advisor
Justin Wagner	CS	Completed Resarch Scientist, NIST	advisor
Mahfuza Sharmin	CS	Completed Postdoc, Stanford University	co-advisor
Florin Chelaru	CS	Completed Postdoc, MIT Broad Institute	advisor
Chiao-Wen Hsiao	AMSC	Completed Postdoc, University of Chicago	advisor
Kwame Okrah	AMSC	Completed Biostatistician, Genentech Inc.	advisor
Wikum Dinalankara	CS	Completed Postdoc, Johns Hopkins University Medicine	advisor
Hisham Talukder	AMSC	Completed Data Scientist, Dow Jones	advisor
Joseph Paulson	AMSC	Completed Postdoc, Harvard/Dana-Farber Cancer Institute	co-advisor

III.D. Professional and Extension Education

III.D.1. Workshops

1. Cloud-based analysis of Human Microbiome Project data using Metaviz. *University of Maryland, Baltimore Institute of Genomic Science*, Baltimore, MD. June 2017.
2. Quantitative methods for humanities and social science with R. *Monterrey Technological College*, Mexico City, Mexico. June 2017.
3. Big Data in Social Sciences: Introduction to Data Science with R. *Monterrey Technological College*, Mexico City, Mexico. June 2015.
4. Computational and statistical challenges in second-generation sequencing data analysis. *Emerging Biotechnologies, Georgetown University Masters in Biotechnology program*, Washington, DC. February and March 2012.
5. Topics in modern biology: omics: new tools and new areas. *Guest lecturer, Department of Biology, University of Puerto Rico*, San Juan, PR. March 2011.

6. Computational and statistical challenges in second-generation sequencing data analysis. *Emerging Biotechnologies, Georgetown University Masters in Biotechnology program*, Washington, DC. March 2011.
7. Model-based base-calling and quality assessment for second-generation sequencing data. *Integrative Statistical Analysis of Genome Scale Data. Cold Spring Harbor Laboratory*, Cold Spring Harbor, NY. June 17, 2010.
8. Introduction to R and Bioconductor for Microarray Analysis. *PASI*, Guanajuato, México. May 4-5, 2010.
9. Clustering and Classification of Gene Expression Data. *Workshop. Johns Hopkins University Center for Computational Genomics*, Baltimore, MD. May 14, 2010.
10. Interactive Visualization of Genomic Data with epiviz(r). *Bioconductor Conference*, Palo Alto, CA. July 2016.
11. Machine Learning for Biomedical Data Analysis. *Centro Internacional de Entrenamiento e Investigaciones Medicas*, Cali, Colombia. October 2018.

IV. Service and Outreach

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

IV.A.1. Editorships

1. Special Issue Editor, *Proceedings IEEE*. 2013-2016

IV.A.2. Reviewing Activities for Journals and Presses

Journals: Bioinformatics Annals of Applied Statistics Journal of Machine Learning Research Biostatistics Journal of Artificial Intelligence Research Genome Biology Journal of the Royal Statistical Society (Series C) IEEE Transactions on Computational Biology and Bioinformatics BMC Genomics Biometrics BMC Bioinformatics Genome Research Nucleic Acids Research Nature Communications Nature Methods New England Journal of Medicine Nature Scientific Reports

Academic Presses: Manning Publications Press Chapman & Hall/CRC

IV.A.3. Reviewing Activities for Agencies and Foundations

1. *Standing member NIH GNOM-G review panel* 2017-
2. *NSF review panel* 2011, 2016 (2x)
3. *NIH ad-hoc review panels* 2014 (NIAID), 2016 (NCII, BD2K Training, NIAID), 2017 (BDMA)
4. *Austrian Science Fund*, 2015

IV.A.4. Reviewing Activities for Conferences

1. *ISMB/ECCB* 2013-2016
2. *ACM-BCB* 2014-2017

IV.B. Committees, Professional and Campus Service

IV.B.1. Campus Service - Department

1. Outstanding Graduate Student Selection Committee. 2017
2. Capital One Chairs Search Committee. 2018-
3. Department Faculty Search Committee. 2017-2018
4. Department Council. 2016-2017
5. Computer Science Recruitment Committee. 2014-
6. Computational Biology Field Committee. 2010-
7. Center for Women in Computing Advisory Board. 2014-
8. UMIACS APT Committee. 2013-2015, 2016-
9. CBBG Graduate Admissions Committee. 2012-2014
10. Strategic Planning Subcommittee on Diversity and Outreach. 2014-2015

IV.B.2. Campus Service - College

1. Task Force for Data Science Undergraduate Degree. 2019
2. Computer Science Chair Search Committee. December 2011-March 2012, November 2016-March 2017

IV.C. External Service and Consulting

IV.C.1. Community Engagements, Local, State, National, International

1. City of Hyattsville Council Educational Advisory Committee. September 2014-December 2016
2. Outreach: computer science education after-school club, Hyattsville Elementary School. March-April 2015

IV.C.2. Consultancies

1. Training in Machine Learning. *Fannie Mae*, June-September 2017
2. Visualization in Bioconductor. *Genentech*, September 2013-December 2014