

# Curriculum Vitae

Notarization. I have read the following and certify that this curriculum vitae is a current and accurate statement of my professional record.



March 31, 2018

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Signature

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Date

## I. Personal Information

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

Last Name: Corrada Bravo  
First Name: Héctor  
3114F Biomolecular Sciences Building #296  
University of Maryland  
College Park, MD 20745  
  
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### I.B. Academic Appointments at UMD

- Associate Professor with Tenure, Department of Computer Science  
University of Maryland, College Park, MD  
July 2016-Present
- Associate Professor with Tenure, Institute for Advanced Computer Studies  
University of Maryland, College Park, MD  
July 2016-Present
- Affiliate Associate Professor, Applied Math, Statistics and Scientific Computation  
University of Maryland, College Park, MD  
July 2016-Present
- Assistant Professor, Department of Computer Science  
University of Maryland, College Park, MD  
July 2010-June 2016
- Assistant Professor, Institute for Advanced Computer Studies  
University of Maryland, College Park, MD  
July 2010-June 2016

- Affiliate Assistant Professor, Applied Math, Statistics and Scientific Computation  
University of Maryland, College Park, MD  
July 2011-June 2016

## I.D. Other Employment

- Postdoctoral Fellow, Department of Biostatistics  
Johns Hopkins University School of Public Health, Baltimore, MD  
September 2008-June 2010
- Research and Teaching Assistant, Departments of Computer Science and Statistics  
University of Wisconsin, Madison, WI  
September 2003-August 2008
- Research Intern,  
IBM Research, Almaden, CA  
May 2005-August 2005

## I.E. 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, Creative and Professional Activities

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

## II.C. Articles in Refereed Journals

1. J. Wagner<sup>^</sup>, F. Chelaru<sup>^</sup>, J. Kancherla<sup>^</sup>, J.N. Paulson<sup>^</sup>, A. Zhang<sup>#</sup>, V. Felix, A. Mahurkar, N. Elmqvist, **H. Corrada Bravo**<sup>\*</sup> (2018). Metaviz: interactive statistical and visual analysis of metagenomic data. *Nucleic Acids Research* gky136, doi:10.1093/nar/gky136.
2. S. Hicks<sup>^</sup>, K. Okrah<sup>#</sup>, J. Paulson<sup>#</sup>, J. Quackenbush, R. Irizarry, **H. Corrada Bravo**<sup>\*</sup> (2018). Smooth quantile normalization. *Biostatistics* 19(2): 185-198, doi:10.1093/biostatistics/kxx028.
3. S. Braid<sup>^</sup>, K. Okrah<sup>#</sup>, A. Shetty, **H. Corrada Bravo**<sup>\*</sup> (2017). Differences in DNA methylation patterns in the cord blood of neonates across gestational age are associated with differences in cell-type composition. *Nursing Research* 66(2): 115-122, doi:10.1097/NNR.0000000000000210.
4. M. Pop<sup>^</sup>, J.N. Paulson<sup>#</sup>, 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<sup>\*</sup> (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.

5. S. Manimaran<sup>^</sup>, H.M. Selby, K. Okrah<sup>#</sup>, C. Ruberman, J.T. Leek, J. Quackenbush, B. Haibe-Kains, **H. Corrada Bravo**, W.E. Johnson\* (2016). BatchQC: interactive software for evaluating sample and batch effects in genomic data. *Bioinformatics* 32(24):3836-3838, doi:10.1093/bioinformatics/btw538.
6. M. Sharmin<sup>^</sup>, **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.
7. M.C. Fernandes<sup>^</sup>, L.A. Dillon<sup>^</sup>, A.T. Belew, **H. Corrada Bravo**, D.M. Mosser, N. El-Sayed\* (2016). Dual transcriptome profiling of human macrophages infected with *Leishmania* parasites reveals transient reprogramming events followed by a generic phagocytic response. *mBio* 7(3). pii: e00027-16, doi:10.1128/mBio.00027-16.
8. J. Wagner<sup>^</sup>, J. Paulson<sup>#</sup>, X.S. Wang, B. Bhattacharjee, **H. Corrada Bravo**\* (2016). Privacy preserving human microbiome analysis using secure computation. *Bioinformatics* , doi:10.1093/bioinformatics/btw073.
9. M. Sharmin<sup>^</sup>, **H. Corrada Bravo**\*, S. Hannenhalli\* (2016). Characterizing the regulatory landscape of large hypomethylated blocks in colon cancer. *BMC Cancer* 16:88, doi:10.1186/s12885-016-2128-1.
10. Y. Li<sup>^</sup>, K.L. Caradonna<sup>^</sup>, K. Okrah<sup>^</sup>, 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.
11. L.A. Dillon<sup>^</sup>, R. Suresh, K. Okrah<sup>#</sup>, **H. Corrada Bravo**, D.M. Mosser, N.M. El-Sayed\* (2015). Simultaneous transcriptional profiling of *Leishmania major* and its murine macrophage host cell reveals insights into host-pathogen interactions. *BMC Genomics* 16:1108, doi:10.1186/s12864-015-2237-2.
12. K. Okrah<sup>^</sup>, **H. Corrada Bravo**\* (2015). Shape analysis for high-throughput transcriptomics experiment data. *Biostatistics* 16(4):627-40, doi:10.1093/biostatistics/kxv018.
13. W. Dinalankara<sup>^</sup>, **H. Corrada Bravo**\* (2015). Gene expression signatures based on variability can robustly predict tumor progression and prognosis. *Cancer Informatics* 14:71-81.
14. W. Huber<sup>^</sup>, 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.
15. L. Dillon<sup>^</sup>, K. Okrah<sup>^</sup>, 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.
16. H.S. Parker<sup>^</sup>, **H. Corrada Bravo**, J.T. Leek\* (2014). Removing batch effects for prediction problems with frozen surrogate variable analysis. *PeerJ* 2:e561, doi:10.7717/peerj.561.
17. W. Timp<sup>^</sup>, **H. Corrada Bravo**<sup>^</sup>, 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.
18. F. Chelaru<sup>^</sup>, L. Smith<sup>#</sup>, N. Goldstein<sup>#</sup>, **H. Corrada Bravo**\* (2014). Epiviz: interactive visual analytics for epigenomics data. *Nature Methods* 11 938-940, doi:10.1038/nmeth.3038.
19. N. Akula<sup>^</sup>, J. Barb, X. Jiang, J. Wendland, K. Choi, S. Sen, L. Hou, D. Chen, G. Laje, K. Johnson, B. Lipska, J. Kleinman, **H. Corrada Bravo**, S. Detera-Wadleigh, P.J. Munson, F.J. McMahon\* (2014). RNA-sequencing of brain transcriptome implicates dysregulation of neuroplasticity, circadian rhythms and GTPase binding in bipolar disorder. *Molecular Psychiatry* , doi:10.1038/mp.2013.170.
20. E. Alemu<sup>^</sup>, J.W. Carl, **H. Corrada Bravo**\*, S. Hannenhalli\* (2014). Determinants of expression variability. *Nucleic Acids Research* 42 (6), 3503-14.
21. C. Ye<sup>^</sup>, C. Hsiao<sup>#</sup>, **H. Corrada Bravo**\* (2014). BlindCall: ultra-fast base-calling of second-generation sequencing by blind deconvolution. *Bioinformatics* 30 (9):1214-9.
22. M. Pop<sup>^</sup>, A.W. Walker<sup>^</sup>, J.N. Paulson<sup>^</sup>, B. Lindsey<sup>^</sup>, M. Antonio<sup>^</sup>, M.A. Hossain<sup>^</sup>, J. Oundo<sup>^</sup>, 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.
23. M. Aryee<sup>^</sup>, 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.
24. J.N. Paulson<sup>#</sup>, 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.

25. X. He<sup>^</sup>, R. Chatterjee<sup>^</sup>, S. John, **H. Corrada Bravo**, B.K. Sathyanarayana, S.C. Biddle, P.C. Fitzgerald, J.A. Stamatoyannopoulos, G.L. Hager, C. Vinson\* (2013). Contribution of nucleosome binding preferences and co-occurring DNA sequences to transcription factor binding. *BMC Genomics* 14 (428).
26. S. Boca<sup>^</sup>, **H. Corrada Bravo**, B. Caffo, J.T. Leek\*, G. Parmigiani (2013). A decision-theory approach to interpretable set analysis for high-dimensional data. *Biometrics* 69 (3):614-23, doi:10.1111/biom.12060.
27. M.L. Nickerson<sup>^</sup>, K.M. Im, K.J. Misner, W. Tan, H. Lou, B. Gold, D.W. Wells, **H. Corrada Bravo**, K.M. Fredrikson, T.T. Harkins, P. Milos, B. Zbar, W.M. Linehan, M. Yeager, T. Andersson, M. Dean\*, G.S. Bova\* (2013). Somatic alterations contributing to metastasis of a castration-resistant prostate cancer. *Human Mutation* 34 (9): 1231-41, doi:10.1002/humu.22346.
28. W. Shi<sup>^</sup>, G. Wahba, R.A. Irizarry, **H. Corrada Bravo**, S.J. Wright\* (2012). The Partitioned LASSO-Patternsearch Algorithm with Application to Gene Expression Data. *BMC Bioinformatics* 13:98, doi:10.1186/1471-2105-13-98.
29. **H. Corrada Bravo**<sup>^</sup>, 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.
30. L. Shan<sup>^</sup>, H.C. Yang, S.A. Rabi, **H. Corrada Bravo**, J.D. Siliciano, R.A. Irizarry, H. Zhang, J. Margolick, R.F. Siliciano\* (2011). Influence of host gene transcription level and orientation on HIV-1 latency in a primary cell model. *Journal of Virology* 85 (11):5384-93.
31. T.S. Niranjan<sup>^</sup>, A. Adamczyk<sup>^</sup>, **H. Corrada Bravo**<sup>^</sup>, M. Taub, S.J. Wheelan, R.A. Irizarry, T. Wang\* (2011). Effective detection of rare variants in pooled DNA samples using Srfim and cross-pool tail-curve analysis. *Genome Biology* 12 (9):R93.
32. K. Hansen<sup>^</sup>, W. Timp<sup>^</sup>, **H. Corrada Bravo**<sup>^</sup>, S. Sabunciyani<sup>^</sup>, B. Langmead<sup>^</sup>, 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.
33. A. Rivas<sup>^</sup>, K. Bohane, **H. Corrada Bravo**<sup>^</sup>, 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.
34. M. Taub<sup>^</sup>, **H. Corrada Bravo**, R.A. Irizarry\* (2010). Overcoming bias and systematic errors in next generation sequencing data. *Genome Medicine* 2 (12):87.
35. J.T. Leek<sup>^</sup>, 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.
36. H. Wu, R.A. Irizarry\*, **H. Corrada Bravo**<sup>^</sup> (2010). Intensity normalization improves color calling in SOLiD sequencing. *Nature Methods* 7:336-337.
37. M. Acevedo<sup>^</sup>, T.M. Aide\*, L. J. Villanueva-Rivera, **H. Corrada Bravo**<sup>^</sup>, C. J. Corrada-Bravo\* (2009). Automated classification of bird and amphibian calls using machine learning: a comparison of methods. *Ecological Informatics* 4 (4):206-214.
38. **H. Corrada Bravo**<sup>^</sup>, 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.
39. **H. Corrada Bravo**<sup>^</sup>, 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.
40. K. H. Eng<sup>^</sup>, **H. Corrada Bravo**<sup>^</sup>, S. Keles\* (2009). A phylogenetic mixture model for the evolution of gene expression. *Molecular Biology and Evolution* 26 (10):2363-2372.
41. A. T. Evan, R. Bennartz, V. Bennington, **H. Corrada Bravo**, A. K. Heidinger, N. M. Mahowald, C. S. Velde, G. Myhre, J. P. Kossin (2008). Ocean temperature forcing by aerosols across the Atlantic tropical cyclone development region. *Geochem, Geophys. Geosyst.* 9:Q05V04, doi:10.1029/2007GC001774.
42. C. Kuang, P. McMurry, A. McCormick, F. Eisele, S.H. Lee, L.H. Young, D.R. Benson, et al. (2007). A system for operational aerosol optical depth data assimilation over global oceans. *J. Geophys. Res* 113(D10):D10208.

## II.D. Published Conference Proceedings

### II.D.1. Refereed Conference Proceedings

1. M.K. Gunady<sup>^#</sup>, S. Cornwell<sup>#</sup>, 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. Dorri<sup>^#</sup>, 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.

3. F. Chelaru<sup>^\*</sup>#, **H. Corrada Bravo**<sup>\*</sup> (2015). Epiviz: a view inside the design of an integrated visual analysis software for genomics. *BioVis 2015; BMC Bioinformatics 16(Supl 11):S4*.
4. **H. Corrada Bravo**<sup>^</sup>, 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**<sup>^</sup>, 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**<sup>^</sup>, 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.E. Conferences, Workshops and Talks

### II.E.2. Invited Talks

1. 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.
2. Interactive visual and computational analysis of epigenetic data. *VIZBI 2017, Sdney, Australia.* June 2017.
3. Interactive statistical and computational analysis of functional and metagenomic data. *University of Puerto Rico, Rio Piedras, PR.* April 2017.
4. Challenges and opportunities in metagenomic data analysis. *NE1602 Kickoff Meeting, Washington, DC.* March 2017.
5. Bias in Biomedical Data Science. *University of Maryland Diversity in Computing Summit, College Park, MD.* November 2016.
6. Statistics and visualization for metagenomics data. *Georgetown University ICBI Seminar Series, Washington, DC.* October 2016.
7. Statistics and visualization for metagenomics data. *Johns Hopkins Young Investigator Symposium, Baltimore, MD.* October 2016.
8. Visualization, Statistical Modeling and Discovery in Computational Epigenomics. *Howard University Precision Medicine Workshop, Washington, DC.* March 2016.
9. Visualization, statistical modeling and discovery in computational epigenomics. *Harvard University Department of Biostatistics and Computational Biology, Boston, MA.* February 2016.
10. What is Biomedical Data Science?. *Symposium of Health Informatics in Latin America and the Caribbean, San Juan, PR.* November 2015.
11. Visualization, Statistical Modeling and Discovery in Computational Epigenomics. *Computer Science Colloquium Series, College Park, MD.* September 2015.
12. Interactive and exploratory visualization of epigenome-wide data. *BioIT World Conference, Boston, MA.* April 2015.
13. Interactive and exploratory visualization of epigenome-wide data. *UMD Campus Visualization Partnership Lecture Series, College Park, MD.* February 2015.
14. Interactive and exploratory visualization of epigenome-wide data. *Epigenomics in Disease, Molecular Medicine Tri-Con, San Francisco, CA.* February 2015.

15. Exploring tumor epigenetic heterogeneity by cell-specific methylation pattern reconstruction. *Department of Biostatistics and Computational Biology, Johns Hopkins Cancer Center, Baltimore, MD.* November 2014.
16. Exploring tumor epigenetic heterogeneity by cell-specific methylation pattern reconstruction. *CMU-Pitt Ph.D. Program in Computational Biology Seminar Series, Pittsburgh, PA.* April 2014.
17. Cell-specific methylation pattern reconstruction using minimum cost network flow algorithms. *Department of Mathematics, George Mason University, Fairfax, VA.* February 2014.
18. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *Greenbaum Cancer Center, University of Maryland School of Medicine, Baltimore, MD.* September 2013.
19. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD.* March 2013.
20. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *Department of Bioinformatics and Computational Biology, Genentech, Inc., South San Francisco, CA.* February 2013.
21. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *Innovation Center for Biomedical Informatics, Georgetown University, Washington, DC.* December 2012.
22. Statistical and computational methods for the analysis of pooled, targeted, second-generation re-sequencing data. *Biostatistics Department, University of Alabama, Birmingham, AL.* April, 2012.
23. Modeling gene expression variability for prediction in disease populations. *Department of Biostatistics, Columbia University School of Public Health, New York, NY.* December 2010.
24. Modeling gene expression variability for prediction in disease populations. *Johns Hopkins University School of Medicine, Baltimore, MD.* December 2010.
25. Gene expression variability in disease populations. *National Cancer Institute, Bethesda, MD.* October 2010.
26. Modeling uncertainty in second-generation sequencing data. *Dept. of Biostatistics, Harvard School of Public Health, Boston, MA.* November 2009.
27. Modeling and managing uncertainty in second-generation sequencing data. *Dept. of Computer Science, University of Maryland, College Park, MD.* October 2009.
28. Model-based quality assessment and base-calling for second-generation sequencing data. *University of Wisconsin-Milwaukee, Milwaukee, WI.* October 2009.
29. Model-based quality assessment and base-calling for second-generation sequencing data. *University of Manchester, Manchester, England.* October 2009.
30. Kernel methods for examining the relative influence of familial, genetic and environmental covariate information in risk models: results and (more importantly) extensions. *University of Wisconsin, Madison, WI.* May 2009.
31. Model-based quality assessment and base-calling for second-generation sequencing data. *University of Wisconsin, Madison, WI.* May 2009.
32. Model-based quality assessment and base-calling for second-generation sequencing data. *Case Western Reserve University, Cleveland, OH.* April 2009.
33. Data analysis at the computational/statistical sciences borderland: two examples from genomics. *Johns Hopkins Bloomberg School of Public Health, Baltimore, MD.* February 2009.

34. Estimating tree-structured covariance matrices via mixed-integer programming. *Johns Hopkins School of Public Health*, Baltimore, MD. January 2008.

### II.E.3. Refereed Presentations

1. Visualization and computation over hierarchically organized features for metagenomics and epigenomics. *Joint Statistical Meetings*, Chicago, IL. August 2016.
2. Differential abundance analysis of metagenomic whole-genome sequencing. *Joint Statistical Meetings*, Seattle, WA. August 2015.
3. Addressing reproducibility in genomic signatures by characterizing variance and estimation stability. *Joint Statistical Meetings*, Seattle, WA. August 2015.
4. methylFlow: cell-specific methylation pattern reconstruction from high-throughput bisulfite-converted DNA sequencing. *HiTSeq*, Dublin, Ireland. July 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. Interactive and exploratory visualization of epigenome-wide data. *Joint Statistical Meetings*, Boston, MA. July 2014.
8. Interactive, Exploratory Visualization and Statistical Analysis of Genome-Scale Data. *International Biomteric Society ENAR Meeting*, Baltimore, MD. March 2014.
9. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *ISMB '13*, Berlin, Germany. July 2013.
10. Srfim2: using basecalling model parameter estimates to understand sequencing bias. *2012 Joint Statistical Meetings*, San Diego, CA. August 2012.
11. Increased methylation variation in epigenetic domains across cancer types. *16th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Barcelona, Spain. April 2012.
12. Statistical and computational methods for the analysis of pooled, targeted, second-generation re-sequencing data. *2011 Joint Statistical Meetings*, Miami Beach, FL.. August 2011.
13. Model-based quality assessment and base-calling for second-generation sequencing data. *WNAR/IMS annual meeting*, Portland, OR. June 2009.
14. Tuning regularized kernel estimation parameters for prediction. *SIAM Conference on Optimization*, Boston, MA. May 2008.
15. Optimizing MPF queries: decision support and probabilistic inference. *26th ACM SIGMOD Intl. Conf. on Management of Data*, Beijing, China. June 2007.
16. A framework for set-oriented computation in inductive logic programming and its application in generalizing inverse entailment.. *15th ILP Conf.*, Bonn, Germany. August 2005.

### II.E.7. Non-Refereed Presentations

1. Does Healthcare Insurance Matter? Establishing Insurance Status as a Risk Factor for Trauma Mortality. *INFORMS 2014*, San Francisco, CA. November 2014.
2. Epiviz(r): turning a genome browser into a display device. *Bioconductor conference*, Boston, MA. July 2014.
3. Statistical and computational methods for the analysis of pooled, targeted, second-generation re-sequencing data. *8th International Chinese Statistical Association (ICSA) International Conference*, Guangzhou, China. December 2010.
4. Model-based quality assessment and base-calling for second-generation sequencing data. *Conference on Next-Generation Sequencing*, Barcelona, Spain. October 2009.

### II.E.11. Symposia

1. Metaviz: interactive statistical and visual analysis of Human Microbiome Project data. *Mid-Atlantic Metagenomics Meetup*, College Park, MD. January 2018.
2. Visualization and statistical modeling for metagenomics data. *Human Microbiome Project 2 Symposium*, Bethesda, MD. June, 2016.
3. Gene expression network anti-profiles. *UMD/NIST Network Science Mini-Symposium*, College Park, MD. January, 2014.
4. Increased methylation variation in epigenetic domains across cancer types. *Omics Day, University of Maryland*, Shady Grove, MD. May 2012.
5. Model-based quality assessment and base-calling for second-generation sequencing data. *Third Annual Young Investigators Symposium on Genomics and Bioinformatics*, Baltimore, MD. September 2009.

### II.E.12. Workshops

1. Metaviz: interactive statistical and visual analysis of Human Microbiome Project data. *Mid-Atlantic Metagenomics Meetup*, College Park, MD. January 2018.
2. Visualization and statistical modeling for metagenomics data. *Human Microbiome Project 2 Symposium*, Bethesda, MD. June, 2016.
3. Gene expression network anti-profiles. *UMD/NIST Network Science Mini-Symposium*, College Park, MD. January, 2014.
4. Increased methylation variation in epigenetic domains across cancer types. *Omics Day, University of Maryland*, Shady Grove, MD. May 2012.
5. Model-based quality assessment and base-calling for second-generation sequencing data. *Third Annual Young Investigators Symposium on Genomics and Bioinformatics*, Baltimore, MD. September 2009.

## II.F. Professional Publications

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

1. M.S. Kumar<sup>#</sup>, E.V. Slud, K. Okrah<sup>#</sup>, S.C. Hicks, S. Hannenhalli, **H. Corrada Bravo**<sup>\*</sup> (2017). Analysis and correction of compositional bias in sparse sequencing count data. *bioRxiv* <https://doi.org/10.1101/142851>.



2. J. Wanger<sup>^</sup>, F. Chelaru<sup>^</sup>, J. Kancherla<sup>^</sup>, J. Paulson<sup>^</sup>, V. Felix, A. Mahurkar, **H. Corrada Bravo**<sup>\*</sup> (2017). Metaviz: interactive statistical and visual analysis of metagenomic data. *bioRxiv* <https://doi.org/10.1101/105205>.
3. J. Paulson<sup>^</sup>, H. Talukder<sup>#</sup>, **H. Corrada Bravo**<sup>\*</sup> (2017). Longitudinal differential abundance analysis of microbial marker-gene surveys using smoothing splines. *bioRxiv* <https://doi.org/10.1101/099457>.
4. S. Hicks<sup>^</sup>, K. Okrah<sup>#</sup>, J. Paulson<sup>#</sup>, J. Quackenbush, R. Irizarry, **H. Corrada Bravo**<sup>\*</sup> (2016). Smooth quantile normalization. *bioRxiv* <https://doi.org/10.1101/085175>.
5. M. Sharmin<sup>^</sup>, **H. Corrada Bravo**, S. Hannenhalli<sup>\*</sup> (2015). Heterogeneity of Transcription Factor binding specificity models within and across cell lines. *bioRxiv* <http://dx.doi.org/10.1101/028787>.
6. J. Wagner<sup>^</sup>, J.N. Paulson<sup>#</sup>, X.S. Wang, B. Bhattacharjee, **H. Corrada Bravo**<sup>\*</sup> (2015). Privacy-Preserving Microbiome Analysis Using Secure Computation. *bioRxiv* <http://dx.doi.org/10.1101/025999>.
7. M. Sharmin<sup>^</sup>, **H. Corrada Bravo**<sup>\*</sup>, S. Hannenhalli<sup>\*</sup> (2015). Distinct genomic and epigenomic features demarcate hypomethylated blocks in colon cancer. *bioRxiv* <http://dx.doi.org/10.1101/028803>.
8. W. Dinalankara<sup>^</sup>, **H. Corrada Bravo** (2013). Anomaly classification with the anti-profile support vector machine. *arXiv preprint server* arXiv:1301.3514 [stat.ML].
9. H.S. Parker<sup>^</sup>, **H. Corrada Bravo**, J.T. Leek (2013). Removing batch effects for prediction problems with frozen surrogate variable analysis. *arXiv preprint server* arXiv:1031.3947 [stat.ME].
10. S. Boca<sup>^</sup>, **H. Corrada Bravo**, B. Caffo, J.T. Leek, G. Parmigiani (2010). A decision-theory approach to interpretable set analysis for high-dimensional data. *Johns Hopkins University, Dept. of Biostatistics Working Papers* Working paper 211. <http://biostats.bepress.com/jhubiostat/paper211>.
11. R.A. Irizarry, **H. Corrada Bravo**<sup>^</sup> (2009). Model-based quality assessment and base-calling for second-generation sequencing data. *Johns Hopkins University, Dept. of Biostatistics Working Papers* Working paper 184. <http://biostats.bepress.com/jhubiostat/paper184>.

## II.H. Completed Creative Works

### II.H.8. Software and Applications

1. Metavizr: Interactive visualziation 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. qsmooth: smooth quantile normalization. Released October 2016. <https://github.com/stephaniehicks/qsmooth>.
4. methylFlow: cell-specific methylation pattern reconstruction. Released June 2015. <http://github.com/hcorrada/methylFlow>.
5. Epivizr: interactive visualization of genomics data in R/Bioconductor. Released June 2013. <http://bioconductor.org/packages/release/bioc/html/epivizr.html>.
6. Epiviz: Interactive visualization for genomics data. Released June 2013. <http://github.com/epiviz>.
7. antiProfiles: Gene expression anti-profiles as a basis for accurate universal cancer signatures. Released April 2013. <http://bioconductor.org/packages/release/bioc/html/antiProfiles.html>.
8. Healthvis: Interactive visualization in health. Released April 2013. <http://healthvis.org>.
9. metagenomeSeq: Statistical analysis for sparse high-throughput sequencing. Released February 2013. <http://bioconductor.org/packages/release/bioc/html/metagenomeSeq.html>.
10. Minfi: Analyze Illumina's 450k methylation arrays. Released Febraury 2013. <http://bioconductor.org/packages/release/bioc/html/minfi.html>.

11. **bumphunter**: Tools for finding bumps in genomic data.  
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/bumphunter.html>.
12. **Servic4e**: Effective detection of rare variants in pooled DNA samples.  
Released November 2011. <http://www.cbcb.umd.edu/~hcorrada/secgen>.
13. **Srfim**: Model-based base-calling and quality assessment for second-generation sequencing.  
Released April 2010. <http://www.cbcb.umd.edu/~hcorrada/secgen>.
14. **Rsolid**: Intensity normalization for SOLiD sequencing.  
Released April 2010. <http://www.cbcb.umd.edu/~hcorrada/secgen>.
15. **Rcsdp**: An interface to the CSDP semidefinite programming library for R.  
Released Dec. 2008. <http://cran.r-project.org/web/packages/Rcsdp/index.html>.
16. **Rcplex**: An interface to the CPLEX optimization engine for R.  
Released Jan. 2008. <http://cran.r-project.org/web/packages/Rcplex/index.html>.

## **II.H.9. Websites**

1. **Epiviz**: Interactive visualization for genomics data.  
Released May 2014. <http://epiviz.cbcb.umd.edu/help>.

## **II.J. Sponsored Research**

### **II.J.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 2019  
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 2019  
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: CGDNet: Cancer Gene Drug Network: Using patient-specific drug-gene networks for recommending targeted cancer therapies  
Funding Agency: NIH  
Recipient Institution: Georgetown University, Simina Boca (PI)

Amount Awarded: \$149,051 subcontracted to UMCP  
Dates: September 2017-August 2019  
Role: PI

5. Title: U54: Longitudinal multiomics microbial profiling in healthy and disease individuals  
Funding Agency: NIH DK102556  
Recipient Institution: Stanford University, Michael P. Snyder (PI)  
Amount Awarded: \$100,702 subcontracted to UMCP  
Dates: September 2015-December 2016  
Role: PI
6. Title: R01: Analysis tools and software for second generation sequencing  
Funding Agency: NIH HG005220  
Recipient Institution: Johns Hopkins University, Rafael A. Irizarry (PI)  
Amount Awarded: \$380,400 subcontracted to UMCP (\$1,230,000 total awarded by NIH )  
Dates: August 2010-May 2013  
Role: PI
7. Title: R01: Alignment software for second generation sequencing  
Funding Agency: NIH HG006102  
Recipient Institution: Johns Hopkins University, Steven Salzberg (PI)  
Amount Awarded: \$432,259.00 subcontracted to UMCP (\$3,585,436 total awarded by NIH)  
Dates: May 2011-April 2014  
Role: PI

## **II.K. Fellowships, Gifts and Other Funded Research**

### **II.K.1. Fellowships**

1. Ford Fellowship, National Academies of Science.
2. Advanced Opportunity Fellowship, University of Wisconsin-Madison.

## **II.L. Submissions and Works in Progress**

### **II.L.1. Current Grant Applications**

1. Title: Visualization tools for the BRAIN initiative  
Funding Agency: NIH  
Recipient Institution: University of Maryland, Baltimore, Ronna Hertzano (PI)  
Amount Requested: \$424,280 subcontracted to UMCP  
Dates: November 2017-October 2020  
Role: PI
2. Title: An integrated network analytics and data visualization platform for complex clinical datasets  
Funding Agency: NIH  
Recipient Institution: University of Maryland, College Park, Michelle Girvan (PI)  
Amount Requested: \$450,000  
Dates: September 2018-August 2020  
Role: co-I
3. Title: Macrophage regulation of immune responses  
Funding Agency: NIH  
Recipient Institution: University of Maryland, College Park, David M. Mosser (PI)

Amount Requested:  
 Dates: Septmeber 2018-August 2022  
 Role: co-I

- Title: U19 Center for Translational Research: Discovery and Preclinical Development of Host-Targeted, Small-Molecule, Pan-Respiratory Virus Therapeutics  
 Funding Agency: NIH  
 Recipient Institution: University of Maryland Baltimore and UM College Park, Mathew Frieman (Center PI)  
 Amount Requested: \$1,157,879  
 Dates: March 2019-February 2024  
 Role: PI

## II.L.2. Manuscripts in Preparation

## II.L.3. Manuscripts under Review

- M.S. Kumar<sup>^</sup>, E.V. Slud, K. Okrah<sup>#</sup>, S.C. Hicks, S. Hannenhalli, **H. Corrada Bravo**<sup>\*</sup>. Analysis and correction of compositional bias in sparse sequencing count data. *BMC Genomics*, *submitted*.
- A.A. Ismail<sup>^</sup>, T. Wood<sup>#</sup>, **H. Corrada Bravo**<sup>\*</sup>. Improving long-horizon forecasts with expectation-biased LSTM networks. *KDD 2018*, *under review*.

# III. Teaching, Advising and Mentoring

## III.A. Courses Taught

Term	Course	Enrollment	Description
Spring 2017	CMSC 423	52	Bioinformatic Databases, Tools and Algorithms
Fall 2016	CMSC 899	2	Doctoral Dissertation Research (Individual instruction)
Spring 2016	CMSC 320	50	Introduction to Data Science
Fall 2016	CMSC 320	83	Introduction to Data Science
Spring 2016	CMSC 898	1	Pre-candidacy Research (Individual instruction)
Spring 2016	CMSC 899	1	Doctoral Dissertation Research (Individual instruction)
Fall 2015	CMSC 423	49	Bioinformatics Databases, Tools and Algorithms

Term	Course	Enrollment	Description
Fall 2015	CMSC 499A	1	Independent Undergraduate Research (Individual instruction)
Fall 2015	CMSC 898	3	Pre-candidacy research (Individual instruction)
Spring 2015	CMSC 498T	32	Introduction to Data Science II
Spring 2015	CMSC 898	1	Pre-candidacy research (Individual instruction)
Spring 2015	CMSC 899	2	Doctoral dissertation research (Individual instruction)
Spring 2015	AMSC 899	2	Doctoral dissertation research (Individual instruction)
Fall 2014	CMSC 423	49	Bioinformatics Databases, Tools and Algorithms
Fall 2014	CMSC 423	35	Bioinformatics Databases, Tools and Algorithms
Fall 2014	CMSC 899	2	Doctoral dissertation research (Individual instruction)
Fall 2014	AMSC 760	1	Applied Statistics Practicum (Individual instruction)
Fall 2014	AMSC 899	2	Doctoral dissertation research (Individual instruction)
Fall 2014	CMSC 798	1	Graduate seminar (Individual instruction)

Term	Course	Enrollment	Description
Fall 2014	CMSC 898	1	Pre-candidacy research (Individual instruction)
Spring 2014	CMSC 702	30	Computational Systems Biology and Functional Genomics
Spring 2014	CMSC 899	1	Doctoral dissertation research (Individual instruction)
Spring 2014	AMSC 899	3	Doctoral dissertation research (Individual instruction)
Spring 2014	CMSC 898	3	Pre-candidacy research (Individual instruction)
Spring 2013	CMSC 702	35	Computational Systems Biology and Functional Genomics
Spring 2013	CMSC 798	1	Graduate seminar (Individual instruction)
Spring 2013	AMSC 898	3	Pre-candidacy research (Individual instruction)
Spring 2013	CMSC 898	2	Pre-candidacy research (Individual instruction)
Spring 2013	AMSC 899	1	Pre-candidacy research (Individual instruction)
Fall 2013	CMSC 423	48	Bioinformatics Databases, Tools and Algorithms
Fall 2013	AMSC 689	1	Research Interactions: Regularized Regression Methods

Term	Course	Enrollment	Description
Fall 2013	AMSC 899	3	Doctoral dissertation research (Individual instruction)
Fall 2013	CMSC 898	4	Pre-candidacy research (Individual instruction)
Fall 2013	AMSC 898	1	Pre-candidacy research (Individual instruction)
Fall 2012	CMSC 726	48	Machine Learning
Fall 2012	CMSC 898	1	Pre-candidacy research (Individual instruction)
Fall 2012	AMSC 899	1	Doctoral dissertation research (Individual instruction)
Fall 2012	AMSC 898	3	Pre-candidacy research (Individual instruction)
Spring 2012	CMSC 351	90	Introduction to Algorithms
Spring 2012	CMSC 858B	26	Computational Systems Biology and Functional Genomics
Spring 2012	CMSC 898	1	Pre-candidacy research (Individual instruction)
Spring 2012	AMSC 898	4	Pre-candidacy research (Individual instruction)
Spring 2011	CMSC 858P	17	Computational Methods for High-Throughput Analysis of Biological Systems
Spring 2011	AMSC 898	1	Pre-candidacy research (Individual instruction)

Term	Course	Enrollment	Description
Fall 2011	CBMG 688P	12	Team-taught graduate 'Programming for Biologists' course
Fall 2011	AMSC 898	3	Pre-candidacy research (Individual instruction)
3rd Term 2010	140.644	16	Practical Machine Learning (Johns Hopkins University School of Public Health, Department of Biostatistics)
Fall 2010	CBMG 688P	12	Team-taught graduate 'Programming for Biologists' course

### III.B. Teaching Innovations

#### III.B.5. Course or Curriculum Development

##### **CMSC 498 - Introduction to Data Science II, Exploring, Modeling and Communicating with Data**

This is the second of two new courses covering the practice of data science. This course focuses on exploratory and statistical data analysis, data and information visualization, and the presentation and communication of analysis results. It is heavily assignment-based and draws extensively from applications.

##### **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.

##### **CMSC 858P - Computational Methods for High-Throughput Analysis of Biological Systems**

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. First offering attracted 21 students, including students from ECE, AMSC and BISI. This course was merged with other content to become CMSC 702 (Computational Systems Biology) to be offered as a regular course in the CS department starting in Spring 2012.

##### **140.644 - Practical Machine Learning**

Developed this new advanced graduate-level course as postdoc at the Johns Hopkins University School of Public Health. The course provided students from a variety of backgrounds with practical knowledge of Machine Learning



models and applications.

### III.C. Advising

#### III.C.1. Undergraduate

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

#### III.C.2. Master's

#### III.C.3. Doctoral

Name	Department	Stage	Role
Aya Ismail	CS	Pre-candidacy	advisor
Mohammed Gunady	CS	Pre-candidacy	advisor
Domenick Braccia	CBMG	Pre-candidacy	advisor
Zhe Cui	EE	Candidacy	co-advisor
Faezeh Dorri	CS	Candidacy	advisor
Justin Wagner	CS	Candidacy	advisor
Senthil Muthiah	CBMG	Candidacy	co-advisor
Nathanael Olson	CBMG	Candidacy	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

Name	Department	Stage	Role
Kwame Okrah	AMSC	Completed Biostatistician, Genen- tech Inc.	advisor
Wikum Dinalankara	CS	Completed Postdoc, Johns Hopkins Univer- sity Medicine	advisor
Hisham Talukder	AMSC	Completed Data Scientist, Dow Jones	advisor
Joseph Paulson	AMSC	Completed Postdoc, Harvard/Dana- Farber Cancer Institute	co- advisor
Chengxi Ye	CS	Pre- candidacy	committee member
Viet-An Nguyen	CS	Completed Data Scientist, Facebook	committee member
Justin Malin	CBMG	Completed Postdoc, National Institutes of Health	committee member
Ted Gibbons	CBMG	Candidacy	committee member
Steven Smith	CBMG	Candidacy	committee member
Cody Buntain	CS	Candidacy	committee member
David Kelley	CS	Completed Postdoc, Broad Institute	committee member
Guillaume Marçais	CS	Completed Research Scientist, Univer- sity of Maryland	committee member
Bhargav Kanagal	CS	Completed	committee member
Yuan Li	CBMG	Completed	committee member

Name	Department	Stage	Role
Mohammad Seza Ghodsi	CS	Completed Software Engineer, Facebook	
Ginger Houston-Ludlam	CBMG	Completed	committee member
Louis Licamele	CS	Completed	committee member
Benjamin Langmead	CS	Completed Assistant Professor, Johns Hopkins University	committee member
Rob Partro	CS	Completed Postdoc, Carnegie Mellon University	committee member
Bo Liu	CS	Completed Software Engineer, Google	committee member
Charles Dawkins	CBMG	Pre-candidacy	committee member
Daehwan Kim	CS	Completed Postdoc, Johns Hopkins University	committee member
Laura Dillon	CBMG	Completed	committee member
Shane Squires	Physics	Completed	committee member
Srutii Sarda	CBMG	Candidacy	committee member
Kun Wang	CBMG	Candidacy	committee member
Vahid Liaghat	CS	Completed	committee member
Adam Bazinet	CS	Completed Research Scientist, University of Maryland	committee member
Sameh Khamis	CS	Completed	committee member
Snighda Chaturvedi	CS	Completed	committee member
Alex Malozemoff	CS	Completed	committee member

Name	Department	Stage	Role
Chris Hill	CS	Completed Postdoc, University of Washington	committee member
Jose Carrillo	ANSC	Completed	committee member
Stephen Xi Chen	CS	Completed	committee member
Yang Shen	Chemical Physics	Candidacy	committee member
Jay Pujara	CS	Completed	committee member
Jayanta Mondal	CS	Completed	committee member
Mossaab Bagdouri	CS	Candidacy	committee member
Avinash Sahu	CS	Completed	committee member
Mohamed Rastegari	CS	Completed	committee member
Sana Malek	CS	Completed	committee member
Fan Yang	CS	Completed	committee member
Bahadir Ozdemir	CS	Completed	committee member
Prachi Kulkarni	School of Public Health	Completed	committee member

### III.F. Professional and Extension Education

#### III.F3. Workshops

1. Big Data in Social Sciences: Introduction to Data Science with R. *Monterrey Technological College*, Mexico City, Mexico. June 2015.
2. Computational and statistical challenges in second-generation sequencing data analysis. *Emerging Biotechnologies, Georgetown University Masters in Biotechnology program*, Washington, DC. February and March 2012.
3. Topics in modern biology: omics: new tools and new areas. *Guest lecturer, Department of Biology, University of Puerto Rico*, San Juan, PR. March 2011.
4. Computational and statistical challenges in second-generation sequencing data analysis. *Emerging Biotechnologies, Georgetown University Masters in Biotechnology program*, Washington, DC. March 2011.
5. 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.
6. Introduction to R and Bioconductor for Microarray Analysis. *PASI*, Guanajuato, México. May 4-5, 2010.
7. Clustering and Classification of Gene Expression Data. *Workshop. Johns Hopkins University Center for*

*Computational Genomics*, Baltimore, MD. May 14, 2010.

8. Interactive Visualization of Genomic Data with epiviz(r). *Bioconductor Conference*, Palo Alto, CA. July 2016.

## **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.3. Reviewing Activities for Journals and Presses**

1. *Bioinformatics*
2. *Annals of Applied Statistics*
3. *Journal of Machine Learning Research*
4. *Biostatistics*
5. *Journal of Artificial Intelligence Research*
6. *Genome Biology*
7. *Journal of the Royal Statistical Society (Series C)*
8. *IEEE Transactions on Computational Biology and Bioinformatics*
9. *BMC Genomics*
10. *Biometrics*
11. *BMC Bioinformatics*
12. *Genome Research*
13. *Nucleic Acids Research*
14. *Nature Communications*
15. *Nature Methods*
16. *New England Journal of Medicine*
17. *Nature Scientific Reports*
18. *Manning Publications Press*
19. *Chapman & Hall/CRC*

#### **IV.A.4. Reviewing Activities for Agencies and Foundations**

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

#### **IV.A.5. Reviewing Activities for Conferences**

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

#### **IV.B. Committees, Professional and Campus Service**

##### **IV.B.1. Campus Service - Department**

- Department Council. 2016-
- Computer Science Recruitment Committee. 2014-
- Computational Biology Field Committee. 2010-
- Center for Women in Computing Advisory Board. 2014-
- UMIACS APT Committee. 2013-2015, 2016-
- CBBG Graduate Admissions Committee. 2012-2014
- Strategic Planning Subcommittee on Diversity and Outreach. 2014-2015

##### **IV.B.2. Campus Service - College**

- Computer Science Chair Search Committee. December 2011-March 2012, November 2016-

##### **IV.B.7. Leadership Roles in Meetings and Conferences**

- Organizing Committee, Biovis Workshop. 2015-2016
- Session Organizer, Joint Statistical Meetings. 2016

#### **IV.C. External Service and Consulting**

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

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

##### **IV.C.5. Consultancies**

- Visualization in Bioconductor. *Genentech*, September 2013-December 2014.

### **V. Awards, Honors and Recognition**

#### **V.D. Recognition in Media**

- Researchers develop tool to better visualize, analyze human genomic data, *Genetics Times*, 11 Aug 2014.

- New Tool To Better Visualize, Analyze Human Genomic Data, *Counsel and Heal*, 04 Aug 2014.
- UMD Researchers Develop Tool to Better Visualize, Analyze Human Genomic Data, *Science Newsline*, 04 Aug 2014.
- UMD Researchers Develop Tool to Better Visualize, Analyze Human Genomic Data, *Technobahn*, 04 Aug 2014.
- New web-based tool to better analyse human genomic data, *Vancouver Verdesi*, 04 Aug 2014.
- New web-based tool to better analyse human genomic data, *Yahoo! News India*, 04 Aug 2014.
- New web-based tool to better analyse human genomic data, *Business Standard*, 04 Aug 2014.
- New web-based tool enables researchers to quickly visualize genomic information, *The Medical News*, 04 Aug 2014.
- UMD researchers develop tool to better visualize, analyze human genomic data, *Innovations Report*, 04 Aug 2014.
- Researchers Develop Tool to Analyze Human Genomic Data, *Medindia*, 04 Aug 2014.
- Tool to better visualize, analyze human genomic data developed, *Science Daily*, 03 Aug 2014.
- Team develops tool to better visualize, analyze human genomic data, *MedicalXpress*, 03 Aug 2014.
- UMD researchers develop tool to better visualize, analyze human genomic data, *EurekAlert!*, 03 Aug 2014.