

Héctor Corrada Bravo (Biographical Sketch)

Education and Appointments

- 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
- 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

Honors

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

Extramural Funding

1. NIH. R01: Overcoming bias and unwanted variability in next generation sequencing. March 2015-February 2019. Amount awarded: \$397,903 subcontracted to UMCP
2. NIH. R01: Integrative visual and computational exploratory analysis of genomics data. September 2015-August 2019. Amount awarded: \$1,800,421
3. NSF. NRT-DESE; Network biology: from data to information to insights. September 2016-August 2021. Amount awarded: \$2,999,847
4. NIH. CGDNet: Cancer Gene Drug Network: Using patient-specific drug-gene networks for recommending targeted cancer therapies. September 2017-August 2019. Amount awarded: \$149,051 subcontracted to UMCP
5. NIH. Illuminating neurodevelopment through integrate analysis and visualization of multi-omic data. September 2018-May 2021. Amount awarded: \$415,443 subcontracted to UMCP

Teaching Experience

1. 2015-present Developed and taught undergraduate course CMSC320 : Introduction to Data Science
2. 2017-present Developed and taught graduate course CMSC828O: Mathematical and Computational Modeling of Networks across Biological Scales
3. 2011-2015 Developed and taught graduate course CMSC702: Computational Systems Biology and Functional Genomics
4. 2012 Taught graduate course CMSC726: Machine Learning
5. 2017-present Developed and taught Master's Certificate course CMSC643: Machine Learning and Data Mining

Advising

Major professor for graduate students:

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	advisor
		Research Scientist, NIST	
Justin Wagner	CS	Completed	advisor
		Resarch Scientist, NIST	
Mahfuza Sharmin	CS	Completed	co-advisor
		Postdoc, Stanford University	
Florin Chelaru	CS	Completed	advisor
		Postdoc, MIT Broad Institute	
Chiao-Wen Hsiao	AMSC	Completed	advisor
		Postdoc, University of Chicago	
Kwame Okrah	AMSC	Completed	advisor
		Biostatistician, Genentech Inc.	
Wikum Dinalankara	CS	Completed	advisor
		Postdoc, Johns Hopkins University	
		Medicine	
Hisham Talukder	AMSC	Completed	advisor
		Data Scientist, Dow Jones	
Joseph Paulson	AMSC	Completed	co-advisor
		Postdoc, Harvard/Dana-Farber	
		Cancer Institute	

Publications (last 5 years)

Peer-reviewed journal articles

1. M.S. Kumar[^], E.V. Slud, K. Okrah[#], S.C. Hicks, S. Hannenhalli, **H. Corrada Bravo**^{*} (). Analysis and correction of compositional bias in sparse sequencing count data. *BMC Genomics*, *in press*.
2. J.S. Meisel[^], D.J. Nasko, B. Brubach, V. Cepeda Espinoza, J. Chopyk, **H. Corrada-Bravo**, M. Fedarko, J. Ghurye, K. Javkar, N.D. Olson[#], N. Shah, S.M. Allard, A.L. Bazinet, N.H. Bergman, A. Brown, J.G. Caporaso, S. Conlan, J.

- DiRuggiero, S.P. Forry, N.A. Hasan, J. Kralj, P.M. Leuthy, D.K. Milton, B.D. Ondov, S. Preheim, S. Ratnayake, S.M. Rogers, M.J. Rosovitz, E.G. Sakowski, N.O. Schliebs, D.D. Sommer, K.L. Ternus, G. Uritskiy, S.X. Zhang, M. Pop, T.J. Treangen* (). Current progress and future opportunities in applications of DNA sequencing for biodefense and pathogen detection: Report from the Winter Mid-Atlantic Microbiome Meet-up, College Park, MD January 10th, 2018. *Microbiome*, in press.
3. A.E. Nazario-Toole[^], J. Robalino, K. Okrah[#], **H. Corrada Bravo**, S.M. Mount, L.P. Wu* (2018). The splicing factor RNA-binding Fox Protein 1 mediates the cellular immune response in *Drosophila melanogaster*. *The Journal of Immunology*, doi:10.4049/jimmunol.1800496.
 4. 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.
 5. 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.
 6. 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.
 7. S. Braid[^], K. Okrah[#], A. Shetty, **H. Corrada Bravo*** (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.
 8. S. Manimaran[^], H.M. Selby, K. Okrah[#], 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.
 9. 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/s12864-016-2777-0.
 10. 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.
 11. 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.
 12. 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.
 13. M. Sharmin[^], **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.
 14. M.C. Fernandes[^], L.A. Dillon[^], 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.
 15. K. Okrah[^], **H. Corrada Bravo*** (2015). Shape analysis for high-throughput transcriptomics experiment data. *Biostatistics* 16(4):627-40, doi:10.1093/biostatistics/kxv018.
 16. 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.
 17. L.A. Dillon[^], R. Suresh, K. Okrah[#], **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.
 18. 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.
 19. W. Dinalankara[^], **H. Corrada Bravo*** (2015). Gene expression signatures based on variability can robustly predict tumor progression and prognosis. *Cancer Informatics* 14:71-81.
 20. H.S. Parker[^], **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.
 21. 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.
22. 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.
 23. 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. Omoro, 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.
 24. 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.
 25. C. Ye[^], C. Hsiao[#], **H. Corrada Bravo**^{*} (2014). BlindCall: ultra-fast base-calling of second-generation sequencing by blind deconvolution. *Bioinformatics* 30 (9):1214-9.
 26. N. Akula[^], 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.
 27. E. Alemu[^], J.W. Carl, **H. Corrada Bravo**^{*}, S. Hannenhalli^{*} (2014). Determinants of expression variability. *Nucleic Acids Research* 42 (6), 3503-14.
 28. 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.
 29. X. He[^], R. Chatterjee[^], 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).
 30. M.L. Nickerson[^], 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.
 31. S. Boca[^], **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.

Abstracts and other professional papers presented

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. 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.
3. 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.
4. Visualization and computation over hierarchically organized features for metagenomics and epigenomics. *Joint Statistical Meetings*, Chicago, IL. August 2016.
5. Differential abundance analysis of metagenomic whole-genome sequencing. *Joint Statistical Meetings*, Seattle, WA. August 2015.
6. Addressing reproducibility in genomic signatures by characterizing variance and estimation stability. *Joint Statistical Meetings*, Seattle, WA. August 2015.
7. Epiviz: a view inside the design of an integrated visual analysis software for genomics. *BioVis*, Dublin, Ireland. July 2015.
8. Interactive and exploratory visual analytics of epigenome-wide data. *ISMB*, Dublin, Ireland. July 2015.
9. methylFlow: cell-specific methylation pattern reconstruction from high-throughput bisulfite-converted DNA sequencing. *HiTSeq*, Dublin, Ireland. July 2015.
10. Interactive and exploratory visualization of epigenome-wide data. *Joint Statistical Meetings*, Boston, MA. July 2014.
11. Interactive, Exploratory Visualization and Statistical Analysis of Genome-Scale Data. *International Biomteric Society ENAR Meeting*, Baltimore, MD. March 2014.

12. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *ISMB '13*, Berlin, Germany. July 2013.