

Curriculum Vitae

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



December 16, 2015

Signature

Date

I. Personal Information

I.A. Contact Information

Héctor Corrada Bravo

3114F Biomolecular Sciences Building #296

University of Maryland

College Park, MD 20745

hcorrada@umiacs.umd.edu

<http://hcbravo.org>

I.B. Academic Appointments at University of Maryland

- Assistant Professor, Department of Computer Science
University of Maryland, College Park, MD
July 2010-Present
- Assistant Professor, Institute for Advanced Computer Studies
University of Maryland, College Park, MD
July 2010-Present
- Affiliate Assistant Professor, Applied Math, Statistics and Scientific Computation
University of Maryland, College Park, MD
July 2011-Present

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. 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*, *in press*.
2. 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.
3. W. Dinalankara^{^#}, **H. Corrada Bravo*** (2015). Gene expression signatures based on variability can robustly predict tumor progression and prognosis. *Cancer Informatics* 14:71-81.
4. 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.
5. K. Okrah^{^#}, **H. Corrada Bravo*** (2015). Shape analysis for high-throughput transcriptomics experiment data. *Biostatistics*, doi:10.1093/biostatistics/kxv018.
6. 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.
7. 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.

8. 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.
9. 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.
10. 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.
11. 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.
12. E. Alemu[^], J.W. Carl, **H. Corrada Bravo**^{*}, S. Hannenhalli^{*} (2014). Determinants of expression variability. *Nucleic Acids Research* 42 (6), 3503-14.
13. Pop, M.[^], Walker, A.W., Paulson, J.[#], Lindsey, B., Antonio, M., Hossain, M.A., Oundo, J., Tamboura, B., Mai, V., Astrovskaya, I., **Corrada Bravo**, H., Rance, R., Stares, M., Levine, M.M., Panchalingam, S., Kotloff, K., Ikumapayi, U.N., Ebruke, C., Adeyemi, D., Ahmed, F., Alam, M.T., Amin, R., Siddiqui, S., Ochieng, J.B., Ouma, E., Juma, J., Mailu, E., Omore, R., Morris, J.G., Breiman, R.F., Saha, D., Parkhill, J., Stine, O.C.^{*}, Nataro, J.P.^{*} (2014). Diarrhea in young children from low-income countries leads to large-scale alterations in intestinal microbiota composition. *Genome Biology* 15, R76.
14. J. 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.
15. 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).
16. 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.
17. 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.
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. W. Shi[^], 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.
20. T.S. Niranjana[^], A. Adamczyk[^], **H. Corrada Bravo**[^], 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.
21. K. Hansen[^], W. Timp[^], **H. Corrada Bravo**[^], S. Sabunciyan[^], 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.
22. L. Shan[^], 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.
23. 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.

24. 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.
25. M. Taub[^], **H. Corrada Bravo**, R.A. Irizarry* (2010). Overcoming bias and systematic errors in next generation sequencing data. *Genome Medicine* 2 (12):87.
26. H. Wu, R.A. Irizarry*, **H. Corrada Bravo**[^](2010). Intensity normalization improves color calling in SOLiD sequencing. *Nature Methods* 7:336-337.
27. K. H. Eng[^], **H. Corrada Bravo**[^], S. Keles* (2009). A phylogenetic mixture model for the evolution of gene expression. *Molecular Biology and Evolution* 26 (10):2363-2372.
28. **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.
29. **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.
30. M. Acevedo[^], T.M. Aide*, L. J. Villanueva-Rivera, **H. Corrada Bravo**[^], 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.
31. 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.
32. C. Kuang, P. McMurphy, 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. F. Dorri^{^#}, L. Mendelowitz, **H. Corrada Bravo*** (2015). methylFlow: cell-specific methylation pattern reconstruction from high-throughput bisulfite-converted DNA sequencing. *HitSEQ 2015; Bioinformatics, in press*.
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. **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.
4. **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.
5. **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.E. Conferences, Workshops and Talks

II.E.2. Invited Talks

1. What is Biomedical Data Science?. *Symposium of Health Informatics in Latin America and the Caribbean*, San Juan, PR. November 2015.

2. Visualization, Statistical Modeling and Discovery in Computational Epigenomics. *Computer Science Colloquium Series*, College Park, MD. September 2015.
3. Interactive and exploratory visualization of epigenome-wide data. *BioIT World Conference*, Boston, MA. April 2015.
4. Interactive and exploratory visualization of epigenome-wide data. *UMD Campus Visualization Partnership Lecture Series*, College Park, MD. February 2015.
5. Interactive and exploratory visualization of epigenome-wide data. *Epigenomics in Disease, Molecular Medicine Tri-Con*, San Francisco, CA. February 2015.
6. Exploring tumor epigenetic heterogeneity by cell-specific methylation pattern reconstruction. *Department of Biostatistics and Computational Biology, Johns Hopkins Cancer Center*, Baltimore, MD. November 2014.
7. Exploring tumor epigenetic heterogeneity by cell-specific methylation pattern reconstruction. *CMU-Pitt Ph.D. Program in Computational Biology Seminar Series*, Pittsburgh, PA. April 2014.
8. Cell-specific methylation pattern reconstruction using minimum cost network flow algorithms. *Department of Mathematics, George Mason University*, Fairfax, VA. February 2014.
9. 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.
10. 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.
11. 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.
12. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *Innovation Center for Biomedical Informatics, Georgetown University*, Washington, DC. December 2012.
13. Statistical and computational methods for the analysis of pooled, targeted, second-generation re-sequencing data. *Biostatistics Department, University of Alabama*, Birmingham, AL. April, 2012.
14. Modeling gene expression variability for prediction in disease populations. *Department of Biostatistics, Columbia University School of Public Health*, New York, NY. December 2010.
15. Modeling gene expression variability for prediction in disease populations. *Johns Hopkins University School of Medicine*, Baltimore, MD. December 2010.
16. Gene expression variability in disease populations. *National Cancer Institute*, Bethesda, MD. October 2010.
17. Modeling uncertainty in second-generation sequencing data. *Dept. of Biostatistics, Harvard School of Public Health*, Boston, MA. November 2009.
18. Model-based quality assessment and base-calling for second-generation sequencing data. *University of Wisconsin-Milwaukee*, Milwaukee, WI. October 2009.
19. Modeling and managing uncertainty in second-generation sequencing data. *Dept. of Computer Science, University of Maryland*, College Park, MD. October 2009.
20. Model-based quality assessment and base-calling for second-generation sequencing data. *University of Manchester*, Manchester, England. October 2009.

21. Model-based quality assessment and base-calling for second-generation sequencing data. *University of Wisconsin*, Madison, WI. May 2009.
22. 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.
23. Model-based quality assessment and base-calling for second-generation sequencing data. *Case Western Reserve University*, Cleveland, OH. April 2009.
24. Data analysis at the computational/statistical sciences borderland: two examples from genomics. *Johns Hopkins Bloomberg School of Public Health*, Baltimore, MD. February 2009.
25. 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. Differential abundance analysis of metagenomic whole-genome sequencing. *Joint Statistics Meetings*, Seattle, WA. August 2015.
2. Addressing reproducibility in genomic signatures by characterizing variance and estimation stability. *Joint Statistics Meetings*, Seattle, WA. August 2015.
3. Epiviz: a view inside the design of an integrated visual analysis software for genomics. *BioVis*, Dublin, Ireland. July 2015.
4. Interactive and exploratory visual analytics of epigenome-wide data. *ISMB*, Dublin, Ireland. July 2015.
5. methylFlow: cell-specific methylation pattern reconstruction from high-throughput bisulfite-converted DNA sequencing. *HiTSeq*, Dublin, Ireland. July 2015.
6. Interactive and exploratory visualization of epigenome-wide data. *Joint Statistics Meetings*, Boston, MA. July 2014.
7. Interactive, Exploratory Visualization and Statistical Analysis of Genome-Scale Data. *International Biomteric Society ENAR Meeting*, Baltimore, MD. March 2014.
8. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *ISMB '13*, Berlin, Germany. July 2013.
9. Srfim2: using basecalling model parameter estimates to understand sequencing bias. *2012 Joint Statistical Meetings*, San Diego, CA. August 2012.
10. Increased methylation variation in epigenetic domains across cancer types. *16th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, Barcelona, Spain. April 2012.
11. Statistical and computational methods for the analysis of pooled, targeted, second-generation re-sequencing data. *2011 Joint Statistical Meetings*, Miami Beach, FL.. August 2011.
12. Model-based quality assessment and base-calling for second-generation sequencing data. *WNAR/IMS annual meeting*, Portland, OR. June 2009.
13. Tuning regularized kernel estimation parameters for prediction. *SIAM Conference on Optimization*, Boston,

MA. May 2008.

14. Optimizing MPF queries: decision support and probabilistic inference. *26th ACM SIGMOD Intl. Conf. on Management of Data*, Beijing, China. June 2007.
15. 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. Gene expression network anti-profiles. *UMD/NIST Network Science Mini-Symposium*, College Park, MD. January, 2014.
2. Increased methylation variation in epigenetic domains across cancer types. *Omics Day, University of Maryland*, Shady Grove, MD. May 2012.
3. 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. Gene expression network anti-profiles. *UMD/NIST Network Science Mini-Symposium*, College Park, MD. January, 2014.
2. Increased methylation variation in epigenetic domains across cancer types. *Omics Day, University of Maryland*, Shady Grove, MD. May 2012.
3. 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. J. Wagner[#], J.N. Paulson[#], X.S. Wang, B. Bhattacharjee, **H. Corrada Bravo**^{*} (2015). Privacy-Preserving Microbiome Analysis Using Secure Computation. *bioRxiv* <http://dx.doi.org/10.1101/025999>.
2. M. Sharmin[#], **H. Corrada Bravo**^{*}, S. Hannenhalli^{*} (2015). Distinct genomic and epigenomic features demarcate hypomethylated blocks in colon cancer. *bioRxiv* <http://dx.doi.org/10.1101/028803>.

3. M. Sharmin^{^#}, **H. Corrada Bravo**, S. Hannenhalli* (2015). Heterogeneity of Transcription Factor binding specificity models within and across cell lines. *biorxiv* <http://dx.doi.org/10.1101/028787>.
4. H.S. Parker[^], **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].
5. W. Dinalankara^{^#}, **H. Corrada Bravo** (2013). Anomaly classification with the anti-profile support vector machine. *arXiv preprint server* arXiv:1301.3514 [stat.ML].
6. S. Boca[^], **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>.
7. R.A. Irizarry, **H. Corrada Bravo**[^] (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. Epiviz: Interactive visualization for genomics data.
Released June 2013. <http://github.com/epiviz>.
2. Epivizr: interactive visualization of genomics data in R/Bioconductor.
Released June 2013. <http://bioconductor.org/packages/release/bioc/html/epivizr.html>.
3. 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>.
4. Healthvis: Interactive visualization in health.
Released April 2013. <http://healthvis.org>.
5. Minfi: Analyze Illumina's 450k methylation arrays.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/minfi.html>.
6. metagenomeSeq: Statistical analysis for sparse high-throughput sequencing.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/metagenomeSeq.html>.
7. bumphunter: Tools for finding bumps in genomic data.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/bumphunter.html>.
8. Servic4e: Effective detection of rare variants in pooled DNA samples.
Released November 2011. <http://www.cbcb.umd.edu/~hcorrada/secgen>.
9. Rsolid: Intensity normalization for SOLiD sequencing.
Released April 2010. <http://www.cbcb.umd.edu/~hcorrada/secgen>.
10. Srfim: Model-based base-calling and quality assessment for second-generation sequencing.
Released April 2010. <http://www.cbcb.umd.edu/~hcorrada/secgen>.
11. Rcsdp: An interface to the CSDP semidefinite programming library for R.
Released Dec. 2008. <http://cran.r-project.org/web/packages/Rcsdp/index.html>.
12. 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
Recipient Institution: University of Maryland, College Park
Amount Awarded: \$1,800,421
Dates: September 2015-August 2019
Role: PI
3. 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
4. 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. Manuscripts under Review

1. M. Sharmin[^], H. Corrada Bravo*, S. Hannenhalli*. Characterizing the regulatory landscape of large hypomethylated blocks in colon cancer. *BMC Cancer*, revision submitted.

2. J. Wagner^{^#}, J. Paulson[#], X.S. Wang, B. Bhattacharjee, **H. Corrada Bravo**^{*}. Privacy preserving human microbiome analysis using secure computation. *Bioinformatics*, revision submitted.
3. 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^{*}. Transcriptome Remodeling in *Trypanosoma cruzi* and Human Cells during Intracellular Infection. *PLOS Pathogens*, revising to resubmit.
4. M. Sharmin^{^#}, **H. Corrada bravo**, S. Hannenhalli^{*}. Heterogeneity of TF binding specificity models within and across cell lines. *Genome Research*, revising to resubmit.
5. M.C. Fernandes[^], L.A. Dillon[^], A.T. Belew, **H. Corrada Bravo**, D.M. Mosser, N. El-Sayed^{*}. Dual transcriptome profiling of human macrophages infected with *Leishmania* parasites reveals transient reprogramming events followed by a generic phagocytic response. *Nucleic Acids Research*, submitted.
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^{*}. Individual-specific changes in the human gut microbiota after challenge with enterotoxigenic *Escherichia coli* and subsequent ciprofloxacin treatment. *Gut*, submitted.

III. Teaching, Advising and Mentoring

III.A. Courses Taught

| Term | Course | Enrollment | Description |
|-------------|-----------|------------|---|
| Spring 2015 | CMSC 498T | 32 | Introduction to Data Science II |
| Spring 2015 | CMSC 899 | 2 | Doctoral dissertation research (Individual instruction) |
| Spring 2015 | CMSC 898 | 1 | Pre-candidacy research (Individual instruction) |
| Spring 2015 | AMSC 899 | 2 | Doctoral dissertation research (Individual instruction) |
| Fall 2014 | CMSC 423 | 35 | Bioinformatics Databases, Tools and Algorithms |
| Spring 2014 | CMSC 702 | 30 | Computational Systems Biology and Functional Genomics |
| Fall 2014 | CMSC 899 | 2 | Doctoral dissertation research (Individual instruction) |
| Fall 2014 | AMSC 899 | 2 | Doctoral dissertation research (Individual instruction) |
| Fall 2014 | AMSC 760 | 1 | Applied Statistics Practicum (Individual instruction) |
| Fall 2014 | CMSC 798 | 1 | Graduate seminar (Individual instruction) |
| Fall 2014 | CMSC 898 | 1 | Pre-candidacy research (Individual instruction) |
| Spring 2014 | AMSC 899 | 3 | Doctoral dissertation research (Individual instruction) |
| Spring 2014 | CMSC 898 | 3 | Pre-candidacy research (Individual instruction) |
| Spring 2014 | CMSC 899 | 1 | Doctoral dissertation research (Individual instruction) |
| Fall 2013 | CMSC 423 | 48 | Bioinformatics Databases, Tools and Algorithms |
| Fall 2013 | AMSC 689 | 1 | Research Interactions: Regularized Regression Methods |
| Spring 2013 | CMSC 702 | 35 | Computational Systems Biology and Functional Genomics |
| Spring 2013 | CMSC 798 | 1 | Graduate seminar (Individual instruction) |
| Spring 2013 | AMSC 899 | 1 | Pre-candidacy research (Individual instruction) |
| Spring 2013 | AMSC 898 | 3 | Pre-candidacy research (Individual instruction) |
| Spring 2013 | CMSC 898 | 2 | Pre-candidacy research (Individual instruction) |
| 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 858B | 26 | Computational Systems Biology and Functional Genomics |
| Spring 2012 | CMSC 351 | 90 | Introduction to Algorithms |
| Spring 2012 | CMSC 898 | 1 | Pre-candidacy research (Individual instruction) |

| Term | Course | Enrollment | Description |
|---------------|-----------|------------|--|
| 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) |
| 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 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 |
| Mihai Sirbu | CS | Current | advisor |

III.C.2. Master's

III.C.3. Doctoral

| Name | Department | Stage | Role |
|--------------|------------|---------------|---------|
| Faezeh Dorri | CS | Pre-candidacy | advisor |

| Name | Department | Stage | Role |
|-----------------------|------------|---|------------------|
| Justin Wagner | CS | Candidacy | advisor |
| Senthil Muthiah | CBMG | Candidacy | co-advisor |
| Mohammed Gunady | CS | Pre-candidacy | advisor |
| Mahfuza Sharmin | CS | Candidacy | co-advisor |
| 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 Center | |
| Chengxi Ye | CS | Pre-candidacy | committee member |
| Viet-An Nguyen | CS | Completed | committee member |
| | | Data Scientist, Facebook | |
| Justin Malin | CBMG | Completed | committee member |
| | | Postdoc, National Institutes of Health | |
| Ted Gibbons | CBMG | Candidacy | committee member |
| Steven Smith | CBMG | Candidacy | committee member |
| Cody Buntain | CS | Candidacy | committee member |
| David Kelley | CS | Completed | committee member |
| | | Postdoc, Broad Institute | |
| Guillaume Marcais | CS | Completed | committee member |
| | | Research Scientist, University of Maryland | |
| Bhargav Kanagal | CS | Completed | committee member |
| Yuan Li | CBMG | Completed | committee member |
| Mohammadreza Ghodsi | CS | Completed | |
| | | Software Engineer, Facebook | |
| Ginger Houston-Ludlam | CBMG | Candidacy | committee member |
| Louis Licamele | CS | Completed | committee member |
| Benjamin Langmead | CS | Completed | committee member |
| | | Assistant Professor, Johns Hopkins University | |
| Rob Partro | CS | Completed | committee member |
| | | Postdoc, Carnegie Mellon University | |
| Bo Liu | CS | Completed | committee member |
| | | Software Engineer, Google | |
| Charles Dawkins | CBMG | Pre-candidacy | committee member |
| Daehwan Kim | CS | Completed | committee member |
| | | Postdoc, Johns Hopkins University | |
| Laura Dillon | CBMG | Completed | committee member |
| Shane Squires | Physics | Completed | committee member |
| Srutii Surda | CBMG | Candidacy | committee member |
| Kun Wang | CBMG | Candidacy | committee member |
| Vahid Liaghat | CS | Completed | committee member |
| Adam Bazinet | CS | Completed | committee member |
| | | Research Scientist, University of Maryland | |
| Sameh Khamis | CS | Completed | committee member |
| Snighda Chaturvedi | CS | Candidacy | committee member |
| Alex Malozemoff | CS | Candidacy | committee member |
| Chris Hill | CS | Completed | committee member |
| | | Postdoc, University of Washington | |

| Name | Department | Stage | Role |
|-----------------|------------|-----------|------------------|
| Jose Carrillo | ANSC | Candidacy | committee member |
| Stephen Xi Chen | CS | Completed | committee member |

III.F. Professional and Extension Education

III.F.3. 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.

IV. Service and Outreach

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

IV.A.1. Editorships

1. Special Issue Editor, *Proceedings IEEE*. 2013-2015

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. *Manning Publications Press*
18. *Chapman & Hall/CRC*

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

1. *NSF review panel 2011*
2. *NIH ad-hoc review panel 2014*
3. *Austrian Science Fund*

IV.A.5. Reviewing Activities for Conferences

1. *ISMB/ECCB 2013*
2. *ISMB 2014*
3. *ISMB/ECCB 2015*
4. *ACM-BCB 2014*
5. *AMC-BCB 2015*

IV.B. Committees, Professional and Campus Service

IV.B.1. Campus Service - Department

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

IV.B.2. Campus Service - College

- Computer Science Chair Search Committee. December 2011-March 2012

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

- Organizing Committee, Biovis Workshop. 2015-2016

IV.C. External Service and Consulting

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

- City of Hyattsville Council Educational Advisory Committee. September 2014-August 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, *Geneticstimes*, 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.