Hector Corrada Bravo

I. Personal Information

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

Héctor Corrada Bravo
3114F Biomolecular Sciences Building #296
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College Park, MD 20745

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I.B. Academic Appointments at UMD

- 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

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 and Creative Activites

II.C. Articles in Refereed Journals

II.D. Published Conference Proceedings

II.D.1. Refereed Conference Proceedings

1. 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*.
2. **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, 5*33:40.
3. **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.
4. **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 Franciso, CA. February 2013.

12. Gene expression anti-profiles as a basis for accurate universal cancer signatures. *Innovation Center for Biomedical Informatics, Georgetown University,* Washington, DB. 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 Statistical Meetings,* Seattle, WA. August 2015.

2. Addressing reproducibility in genomic signatures by characterizing variance and estimation stability. *Joint Statistical 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 Statistical 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

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

II.F. Professional Publications

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

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 Febraury 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

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

II.L.2. Manuscripts in Preparation

II.L.3. Manuscripts under Review

III. Teaching, Mentoring and Advising

III.A. Courses Taught

III.B. Teaching Innovations

III.B.5. Course or Curriculum Development

III.C. Advising

III.C.1. Undergraduate

III.C.2. Master's

III.C.3. Doctoral

III.F. Professional and Extension Education

III.F.3. Workshops

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. *Nature Scientific Reports*
18. *Manning Publications Press*
19. *Chapman & Hall/CRC*

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

IV.A.5. Reviewing Activities for Conferences

1. *ISMB/ECCB 2013*
2. *ISMB 2014*
3. *ISMB/ECCB 2015*
4. *ISMB 2016*
5. *ACM-BCB 2014*
6. *AMC-BCB 2015*

IV.B. Committees, Professional and Campus Service

IV.B.1. Campus Service - Department

IV.B.2. Campus Service - College

IV.C. External Service and Consulting

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

IV.C.5. Consultancies