

Publications, Creative Works and Funding during Past Five Years

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1. Articles in Refereed Journals

1. M.S. Kumar[^], E.V. Slud, K. Okrah[#], S.C. Hicks, S. Hannenhalli, **H. Corrada Bravo**^{*} (2018). Analysis and correction of compositional bias in sparse sequencing count data. *BMC Genomics*, *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^{*} (2018). 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. Kanckerla[^], 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. Kanckerla[^], 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. Omere, 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.

2. Published Conference Proceedings

1. M.K. Gunady^{^#}, S. Cornwell[#], S.M. Mount, **H. Corrada Bravo**^{*} (2017). Yanagi: transcript segment library construction for RNA-seq quantification. *17th Workshop for Algorithms in Bioinformatics (WABI) 2017*.
2. F. 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.

3. Pre-print/Working Paper (Not Work in Progress)

1. M.K. Gunady^{^#}, S. Mount, **H. Corrada Bravo**^{*} (2018). Fast and interpretable alternative splicing and differential gene-level expression analysis using transcriptome segmentation with Yanagi. *biorxiv* <https://doi.org/10.1101/364281>.
2. N.D. Olson^{^#}, M. Senthil Kumar[#], S. Li, S. Hao, W. Timp, M.L. Salit, O.C. Stine, **H. Corrada Bravo**^{*} (2018). Assessing 16S marker gene survey data analysis methods using mixtures of human stool sample DNA extracts. *biorxiv* <https://doi.org/10.1101/400226>.
3. M.S. Kumar^{^#}, E.V. Slud, K. Okrah[#], S.C. Hicks, S. Hannenhalli, **H. Corrada Bravo**^{*} (2017). Analysis and correction of compositional bias in sparse sequencing count data. *biorxiv* <https://doi.org/10.1101/142851>.
4. J. Wanger^{^#}, F. Chelaru^{^#}, J. Kancherla[^], J. Paulson^{^#}, V. Felix, A. Mahurkar, **H. Corrada Bravo**^{*} (2017). Metaviz: interactive statistical and visual analysis of metagenomic data. *biorxiv* <https://doi.org/10.1101/105205>.
5. J. Paulson^{^#}, H. Talukder[#], **H. Corrada Bravo**^{*} (2017). Longitudinal differential abundance analysis of microbial marker-gene surveys using smoothing splines. *biorxiv* <https://doi.org/10.1101/099457>.
6. S. Hicks[^], K. Okrah[#], J. Paulson[#], J. Quackenbush, R. Irizarry, **H. Corrada Bravo**^{*} (2016). Smooth quantile normalization. *biorxiv* <https://doi.org/10.1101/085175>.
7. 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>.
8. 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>.
9. 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>.
10. W. Dinalankara^{^#}, **H. Corrada Bravo**^{*} (2013). Anomaly classification with the anti-profile support vector machine. *arXiv preprint server* arXiv:1301.3514 [stat.ML].
11. 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].

4. Completed Creative Works

4.1. Software and Applications

1. Metavizr: Interactive visualization of metagenomics data in R/Bioconductor. Released December 2016. <http://github.com/epiviz/metavizr>.
2. Metaviz: Interactive visualization for metagenomics data. Released December 2016. <http://metaviz.org>.
3. 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. Epiviz: Interactive visualization for genomics data.
Released June 2013. <http://github.com/epiviz>.
6. Epivizr: interactive visualization of genomics data in R/Bioconductor.
Released June 2013. <http://bioconductor.org/packages/release/bioc/html/epivizr.html>.
7. Healthvis: Interactive visualization in health.
Released April 2013. <http://healthvis.org>.
8. 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>.
9. Minfi: Analyze Illumina's 450k methylation arrays.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/minfi.html>.
10. metagenomeSeq: Statistical analysis for sparse high-throughput sequencing.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/metagenomeSeq.html>.
11. bumphunter: Tools for finding bumps in genomic data.
Released February 2013. <http://bioconductor.org/packages/release/bioc/html/bumphunter.html>.

4.2. Websites

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

5. Sponsored Research, 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 R21CA220398

Recipient Institution: Georgetown University, Simina Boca (PI)
Amount Awarded: \$149,051 subcontracted to UMCP
Dates: September 2017-August 2019
Role: PI

5. Title: Illuminating neurodevelopment through integrate analysis and visualization of multi-omic data
Funding Agency: NIH R24MH114815
Recipient Institution: University of Maryland, Baltimore, Ronna Hertzano (PI)
Amount Awarded: \$415,443 subcontracted to UMCP
Dates: September 2018-May 2021
Role: PI

6. Submissions and Works in Progress

6.1. Current Grant Applications

1. Title: FACT: Application of big data in food safety-integrating whole genome sequencing information into a risk assessment framework
Funding Agency: USDA-National Institute of Food and Agriculture
Recipient Institution: University of Maryland, College Park, Abani K. Pradhan (PI)
Amount Requested: \$489,000
Dates:
Role: co-PI

6.2. Manuscripts under Review

1. N.D. Olson[#], N. Shah, J. Kancherla[#], J.N. Paulson[#], J. Wagner[#], **H. Corrada Bravo***. metagenomeFeatures: An R package for working with 16S rRNA reference databases and marker-gene survey feature data. *Bioinformatics*, *revising to resubmit*.
2. N.D. Olson[#], M. Senthil Kumar[#], S. Li, S. Hao, W. Timp, M.L. Salit, O.C. Stine, **H. Corrada Bravo***. Assessing 16S marker gene survey data analysis methods using mixtures of human stool sample DNA extracts. *Microbiome*, *submitted*.
3. M.K. Gunady[#], S. Mount, **H. Corrada Bravo***. Fast and interpretable alternative splicing and differential gene-level expression analysis using transcriptome segmentation with Yanagi. *BMC Bioinformatics*, *submitted*.
4. A.A. Ismail[#], T. Wood[#], **H. Corrada Bravo***. Improving long-horizon forecasts with expectation-biased LSTM networks. *AAAI 2019*, *under review*.
5. Z. Cui[#], J. Kancherla[#], **H. Corrada Bravo**, N. Elmqvist*. Sherpa: Leveraging User Attention for Computational Steering in Visual Analytics. *CHI 2019*, *under review*.