

Publications during past five years

Héctor Corrada Bravo

3114F Biomolecular Sciences Building #296
University of Maryland
College Park, MD 20745

hcorrada@umiacs.umd.edu
<http://hcbravo.org>

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**^{*} (2018). Analysis and correction of compositional bias in sparse sequencing count data. *BMC Genomics*, *in press*.
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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/s12864-016-27777-0.
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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.

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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*.
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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].