



Carlos Bustamante

Professor of Biomedical Data Science, of Genetics and, by courtesy, of Biology

 Curriculum Vitae available Online

CONTACT INFORMATION

- **Alternate Contact**

Email cdbadmin@stanford.edu

Bio

BIO

Dr. Carlos D. Bustamante is an internationally recognized leader in the application of data science and genomics technology to problems in medicine, agriculture, and biology. He received his Ph.D. in Biology and MS in Statistics from Harvard University (2001), was on the faculty at Cornell University (2002-9), and was named a MacArthur Fellow in 2010. He is currently Professor of Biomedical Data Science, Genetics, and (by courtesy) Biology at Stanford University. Dr. Bustamante has a passion for building new academic units, non-profits, and companies to solve pressing scientific challenges. He is Founding Director of the Stanford Center for Computational, Evolutionary, and Human Genomics (CEHG) and Inaugural Chair of the Department of Biomedical Data Science. He is the Owner and President of CDB Consulting, LTD. and also a Director at EdenRoc Sciences, LLC, founder of Arc Bio LLC (formerly IdentifyGenomics LLC and BigData Bio LLC), and an SAB member of Imprinted, Etalon DX, Columbia Care, and Digitalis Ventures.

ACADEMIC APPOINTMENTS

- Professor, Biomedical Data Science
- Professor, Genetics Operations
- Member, Bio-X
- Member, Cardiovascular Institute
- Faculty Affiliate, Institute for Human-Centered Artificial Intelligence (HAI)
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Institute for Computational and Mathematical Engineering (ICME)
- Member, Stanford Cancer Institute

ADMINISTRATIVE APPOINTMENTS

- Founding Director, Stanford Center for Computational, Evolutionary, and Human Genetics (CEHG), (2012-2017)
- Inaugural Chair, Department of Biomedical Data Science, (2015-2019)

HONORS AND AWARDS

- Marshall Sherfield Fellow, Marshall Aid Commemoration Commission (2001-2)
- Sloan Research Fellow in Molecular Biology, Sloan Foundation (2007-9)
- Provost Award for Distinguished Research, Cornell University (2008)

- MacArthur Fellow, John D. and Catherine T. MacArthur Foundation (2010)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Editorial Boards, Genome Research (2008 - present)
- Advisory Board, Slim Initiative for Genomic Medicine in the Americas (2010 - present)
- Editorial Board, Human Biology (2010 - present)
- Advisory Board, External Evaluation Committee NIDDK T2D GENES project (2011 - present)
- Advisory Board, National Human Genome Research Institute Council (2011 - present)
- Advisory Board, Online Mendelian Inheritance in Man (OMIM) (2013 - present)
- Advisory Board, NIH Council of Councils (2013 - present)
- Advisory Board, National Geographic Genographic Project (2013 - present)
- Editorial Board, American Journal of Human Genetics (2013 - present)
- Senior Editor, Evolution, PLoS Genetics (2013 - present)

PROFESSIONAL EDUCATION

- B.A., Harvard University , Biology (1997)
- M.S., Harvard University , Statistics (2001)
- Ph.D., Harvard University , Biology (2001)
- Postdoc, University of Oxford , Mathematical Genetics (2002)

LINKS

- Lab Website: <http://med.stanford.edu/bustamantelab>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

My genetics research focuses on analyzing genome wide patterns of variation within and between species to address fundamental questions in biology, anthropology, and medicine. We focus on novel methods development for complex disease genetics and risk prediction in multi-ethnic settings. I am also interested in clinical data science and development of new diagnostics. I am also interested in disruptive innovation for healthcare including modeling long-term risk shifts and novel payment models.

CLINICAL TRIALS

- Personal Genomics for Preventive Cardiology, Not Recruiting

Teaching

COURSES

2020-21

- Best practices for developing data science software for clinical and healthcare applications: BIODS 235 (Win)

2018-19

- Biomedical Informatics Student Seminar: BIOMEDIN 201 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

John Gorzynski, Guhan Venkataraman

Postdoctoral Faculty Sponsor

Victoria Cepeda Espinoza, Obed Garcia, Alexander Ioannidis, Daniel Mas Montserrat, Babak Moatamed, Sonia Moreno Grau

Doctoral Dissertation Co-Advisor (AC)

Jessica Torres

Postdoctoral Research Mentor

Alice Popejoy

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biology (School of Humanities and Sciences) (Phd Program)
- Biomedical Informatics (Masters Program)
- Biomedical Informatics (Phd Program)
- Genetics (Phd Program)

Publications

PUBLICATIONS

- **Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale.** *Nature genetics*
Li, X., Li, Z., Zhou, H., Gaynor, S. M., Liu, Y., Chen, H., Sun, R., Dey, R., Arnett, D. K., Aslibekyan, S., Ballantyne, C. M., Bielak, L. F., Blangero, et al
2020
- **Native American gene flow into Polynesia predating Easter Island settlement.** *Nature*
Ioannidis, A. G., Blanco-Portillo, J., Sandoval, K., Hagelberg, E., Miquel-Poblete, J. F., Moreno-Mayar, J. V., Rodriguez-Rodriguez, J. E., Quinto-Cortes, C. D., Auckland, K., Parks, T., Robson, K., Hill, A. V., Avila-Arcos, et al
2020
- **Clinical Genetics Lacks Standard Definitions and Protocols for the Collection and Use of Diversity Measures.** *American journal of human genetics*
Popejoy, A. B., Crooks, K. R., Fullerton, S. M., Hindorff, L. A., Hooker, G. W., Koenig, B. A., Pino, N., Ramos, E. M., Ritter, D. I., Wand, H., Wright, M. W., Yudell, M., Zou, et al
2020
- **Development of a small panel of SNPs to infer ancestry in Chileans that distinguishes Aymara and Mapuche components.** *Biological research*
Verdugo, R. A., Di Genova, A., Herrera, L., Moraga, M., Acuna, M., Berrios, S., Llop, E., Valenzuela, C. Y., Bustamante, M. L., Digman, D., Symon, A., Asenjo, S., Lopez, et al
2020; 53 (1): 15
- **Pan-cancer analysis of whole genomes** *NATURE*
Campbell, P. J., Getz, G., Korbel, J. O., Stuart, J. M., Jennings, J. L., Stein, L. D., Perry, M. D., Nahal-Bose, H. K., Ouellette, B., Li, C. H., Rheinbay, E., Nielsen, G., Sgroi, et al
2020; 578 (7793): 82-+
- **LitGen: Genetic Literature Recommendation Guided by Human Explanations.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
Nie, A. n., Pineda, A. L., Wright, M. W., Wand, H. n., Wulf, B. n., Costa, H. A., Patel, R. Y., Bustamante, C. D., Zou, J. n.
2020; 25: 67-78
- **FasTag: Automatic text classification of unstructured medical narratives.** *PloS one*
Venkataraman, G. R., Pineda, A. L., Bear Don't Walk Iv, O. J., Zehnder, A. M., Ayyar, S., Page, R. L., Bustamante, C. D., Rivas, M. A.
2020; 15 (6): e0234647
- **Population history and gene divergence in Native Mexicans inferred from 76 human exomes.** *Molecular biology and evolution*
Avila-Arcos, M. C., McManus, K. F., Sandoval, K., Rodriguez-Rodriguez, J. E., Villa-Islas, V., Martin, A. R., Luisi, P., Penaloza-Espinosa, R. I., Eng, C., Huntsman, S., Burchard, E. G., Gignoux, C. R., Bustamante, et al

2019

- **Xrare: a machine learning method jointly modeling phenotypes and genetic evidence for rare disease diagnosis** *GENETICS IN MEDICINE*
Li, Q., Zhao, K., Bustamante, C. D., Ma, X., Wong, W. H.
2019; 21 (9): 2126–34
- **The inference of sex-biased human demography from whole-genome data.** *PLoS genetics*
Musharoff, S., Shringarpure, S., Bustamante, C. D., Ramachandran, S.
2019; 15 (9): e1008293
- **Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest.** *Current biology : CB*
Lopez, M., Choin, J., Sikora, M., Siddle, K., Harmant, C., Costa, H. A., Silvert, M., Mouguiama-Daouda, P., Hombert, J., Froment, A., Le Bomin, S., Perry, G. H., Barreiro, et al
2019
- **Genetic analyses of diverse populations improves discovery for complex traits.** *Nature*
Wojcik, G. L., Graff, M., Nishimura, K. K., Tao, R., Haessler, J., Gignoux, C. R., Highland, H. M., Patel, Y. M., Sorokin, E. P., Avery, C. L., Belbin, G. M., Bien, S. A., Cheng, et al
2019
- **Structural. Variation Detection by Proximity Ligation from Formalin-Fixed, Paraffin-Embedded Tumor Tissue** *JOURNAL OF MOLECULAR DIAGNOSTICS*
Troll, C. J., Putnam, N. H., Hartley, P. D., Rice, B., Blanchette, M., Siddiqui, S., Ganbat, J., Powers, M. P., Ramakrishnan, R., Kunder, C. A., Bustamante, C. D., Zehnder, J. L., Green, et al
2019; 21 (3): 375–83
- **A genetic counseling needs assessment of Mexico** *MOLECULAR GENETICS & GENOMIC MEDICINE*
Bucio, D., Ormond, K. E., Hernandez, D., Bustamante, C. D., Pineda, A.
2019; 7 (5)
- **Standardized Biogeographic Grouping System for Annotating Populations in Pharmacogenetic Research** *CLINICAL PHARMACOLOGY & THERAPEUTICS*
Huddart, R., Fohner, A. E., Whirl-Carrillo, M., Wojcik, G. L., Gignoux, C. R., Popejoy, A. B., Bustamante, C. D., Altman, R. B., Klein, T. E.
2019; 105 (5): 1256–62
- **A genetic counseling needs assessment of Mexico.** *Molecular genetics & genomic medicine*
Bucio, D., Ormond, K. E., Hernandez, D., Bustamante, C. D., Lopez Pineda, A.
2019: e668
- **Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands** *PLOS ONE*
Fregel, R., Ordonez, A. C., Santana-Cabrera, J., Cabrera, V. M., Velasco-Vazquez, J., Alberto, V., Moreno-Benitez, M. A., Delgado-Darias, T., Rodriguez-Rodriguez, A., Hernandez, J. C., Pais, J., Gonzalez-Montelongo, R., Lorenzo-Salazar, et al
2019; 14 (3)
- **The Genomic Landscape of the Peruvian Andes**
Nieves-Colon, M. A., Rawls, E., Obregon-Tito, A., Tito, R., Lewis, C., Sandoval Mendoza, K., Bustamante, C. D., Wojcik, G. L., Gignoux, C., Baker, J., Fejerman, L., Vidaurre, T., Lizarraga, et al
WILEY.2019: 176
- **Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations.** *Nature communications*
Daya, M., Rafaels, N., Brunetti, T. M., Chavan, S., Levin, A. M., Shetty, A., Gignoux, C. R., Boorgula, M. P., Wojcik, G., Campbell, M., Vergara, C., Torgerson, D. G., Ortega, et al
2019; 10 (1): 880
- **Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations** *NATURE COMMUNICATIONS*
Daya, M., Rafaels, N., Brunetti, T. M., Chavan, S., Levin, A. M., Shetty, A., Gignoux, C. R., Boorgula, M., Wojcik, G., Campbell, M., Vergara, C., Torgerson, D. G., Ortega, et al
2019; 10
- **Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations**

Daya, M., Rafaels, N. M., Brunetti, T. M., Chavan, S., Levin, A. M., Shetty, A., Gignoux, C. R., Boorgula, M., Wojcik, G., Campbell, M., Vergara, C. I., Torgerson, D. G., Ortega, et al
MOSBY-ELSEVIER.2019: AB296

- **Xrare: a machine learning method jointly modeling phenotypes and genetic evidence for rare disease diagnosis.** *Genetics in medicine : official journal of the American College of Medical Genetics*
Li, Q., Zhao, K., Bustamante, C. D., Ma, X., Wong, W. H.
2019
- **Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands.** *PloS one*
Fregel, R., Ordóñez, A. C., Santana-Cabrera, J., Cabrera, V. M., Velasco-Vázquez, J., Alberto, V., Moreno-Benitez, M. A., Delgado-Darias, T., Rodríguez-Rodríguez, A., Hernández, J. C., Pais, J., González-Montelongo, R., Lorenzo-Salazar, et al
2019; 14 (3): e0209125
- **Genetic variation drives seasonal onset of hibernation in the 13-lined ground squirrel.** *Communications biology*
Grabek, K. R., Cooke, T. F., Epperson, L. E., Spees, K. K., Cabral, G. F., Sutton, S. C., Merriman, D. K., Martin, S. L., Bustamante, C. D.
2019; 2 (1): 478
- **Genetic variation drives seasonal onset of hibernation in the 13-lined ground squirrel.** *Communications biology*
Grabek, K. R., Cooke, T. F., Epperson, L. E., Spees, K. K., Cabral, G. F., Sutton, S. C., Merriman, D. K., Martin, S. L., Bustamante, C. D.
2019; 2: 478
- **Ancient DNA reconstructs the genetic legacies of pre-contact Puerto Rico communities.** *Molecular biology and evolution*
Nieves-Colón, M. A., Pestle, W. J., Reynolds, A. W., Llamas, B. n., de la Fuente, C. n., Fowler, K. n., Skerry, K. M., Crespo-Torres, E. n., Bustamante, C. D., Stone, A. C.
2019
- **Author Correction: Association study in African-admixed populations across the Americas recapitulates asthma risk loci in non-African populations.** *Nature communications*
Daya, M. n., Rafaels, N. n., Brunetti, T. M., Chavan, S. n., Levin, A. M., Shetty, A. n., Gignoux, C. R., Boorgula, M. P., Wojcik, G. n., Campbell, M. n., Vergara, C. n., Torgerson, D. G., Ortega, et al
2019; 10 (1): 4082
- **An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos.** *The Journal of allergy and clinical immunology*
Gignoux, C. R., Torgerson, D. G., Pino-Yanes, M. n., Uricchio, L. H., Galanter, J. n., Roth, L. A., Eng, C. n., Hu, D. n., Nguyen, E. A., Huntsman, S. n., Mathias, R. A., Kumar, R. n., Rodríguez-Santana, et al
2019; 143 (3): 957–69
- **Structural Variation Detection by Proximity Ligation from Formalin-Fixed, Paraffin-Embedded Tumor Tissue.** *The Journal of molecular diagnostics : JMD*
Troll, C. J., Putnam, N. H., Hartley, P. D., Rice, B., Blanchette, M., Siddiqui, S., Ganbat, J., Powers, M. P., Ramakrishnan, R., Kunder, C. A., Bustamante, C. D., Zehnder, J. L., Green, et al
2018
- **Polygenic risk scores: a biased prediction?** *Genome medicine*
De La Vega, F. M., Bustamante, C. D.
2018; 10 (1): 100
- **Rapid evolution of a skin-lightening allele in southern African KhoeSan** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Lin, M., Siford, R. L., Martin, A. R., Nakagome, S., Moller, M., Hoal, E. G., Bustamante, C. D., Gignoux, C. R., Henn, B. M.
2018; 115 (52): 13324–29
- **Rapid evolution of a skin-lightening allele in southern African KhoeSan.** *Proceedings of the National Academy of Sciences of the United States of America*
Lin, M., Siford, R. L., Martin, A. R., Nakagome, S., Moller, M., Hoal, E. G., Bustamante, C. D., Gignoux, C. R., Henn, B. M.
2018
- **Standardized biogeographic grouping system for annotating populations in pharmacogenetic research.** *Clinical pharmacology and therapeutics*
Huddart, R., Fohner, A. E., Whirl-Carrillo, M., Wojcik, G. L., Gignoux, C. R., Popejoy, A. B., Bustamante, C. D., Altman, R. B., Klein, T. E.
2018

- **The clinical imperative for inclusivity: Race, ethnicity, and ancestry (REA) in genomics.** *Human mutation*
Popejoy, A. B., Ritter, D. I., Crooks, K., Currey, E., Fullerton, S. M., Hindorff, L. A., Koenig, B., Ramos, E. M., Sorokin, E. P., Wand, H., Wright, M. W., Zou, J., Gignoux, et al
2018; 39 (11): 1713–20
- **DeepTag: inferring diagnoses from veterinary clinical notes** *NPJ DIGITAL MEDICINE*
Nie, A., Zehnder, A., Page, R. L., Zhang, Y., Pineda, A., Rivas, M. A., Bustamante, C. D., Zou, J.
2018; 1
- **Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma.** *Nature communications*
Ioannidis, N. M., Wang, W., Furlotte, N. A., Hinds, D. A., 23andMe Research Team, Bustamante, C. D., Jorgenson, E., Asgari, M. M., Whittemore, A. S., Agee, M., Alipanahi, B., Auton, A., Bell, R. K., et al
2018; 9 (1): 4264
- **Data mining of digitized health records in a resource-constrained setting reveals that timely immunophenotyping is associated with improved breast cancer outcomes.** *BMC cancer*
Lopez-Pineda, A., Rodriguez-Moran, M. F., Alvarez-Aguilar, C., Fuentes Valle, S. M., Acosta-Rosales, R., Bhatt, A. S., Sheth, S. N., Bustamante, C. D.
2018; 18 (1): 933
- **Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies.** *G3 (Bethesda, Md.)*
Wojcik, G. L., Fuchsberger, C., Taliun, D., Welch, R., Martin, A. R., Shringarpure, S., Carlson, C. S., Abecasis, G., Kang, H. M., Boehnke, M., Bustamante, C. D., Gignoux, C. R., Kenny, et al
2018
- **In-solution Y-chromosome capture-enrichment on ancient DNA libraries** *BMC GENOMICS*
Cruz-Davalos, D. I., Nieves-Colon, M. A., Sockell, A., Poznik, G., Schroeder, H., Stone, A. C., Bustamante, C. D., Malaspinas, A., Avila-Arcos, M. C.
2018; 19: 608
- **Network enhancement as a general method to denoise weighted biological networks.** *Nature communications*
Wang, B., Pourshafeie, A., Zitnik, M., Zhu, J., Bustamante, C. D., Batzoglou, S., Leskovec, J.
2018; 9 (1): 3108
- **Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe.** *Proceedings of the National Academy of Sciences of the United States of America*
Fregel, R., Mendez, F. L., Bokbot, Y., Martin-Socas, D., Camalich-Massieu, M. D., Santana, J., Morales, J., Avila-Arcos, M. C., Underhill, P. A., Shapiro, B., Wojcik, G., Rasmussen, M., Soares, et al
2018; 115 (26): 6774–79
- **Spectrum and prevalence of genetic predisposition in medulloblastoma: a retrospective genetic study and prospective validation in a clinical trial cohort** *LANCET ONCOLOGY*
Waszak, S. M., Northcott, P. A., Buchhalter, I., Robinson, G. W., Sutter, C., Groebner, S., Grund, K. B., Brugieres, L., Jones, D. W., Pajtler, K. W., Morrissy, A., Kool, M., Sturm, et al
2018; 19 (6): 785–98
- **Next-Generation Sequencing of the Complete Mitochondrial Genome of the Endangered Species Black Lion Tamarin *Leontopithecus chrysopygus* (Primates) and Mitogenomic Phylogeny Focusing on the Callitrichidae Family** *G3-GENES GENOMES GENETICS*
de Freitas, P., Mendez, F., Chavez-Congrains, K., Galetti, P., Coutinho, L., Pissinatti, A., Bustamante, C.
2018; 8 (6): 1985–91
- **Population structure in Argentina** *PLOS ONE*
Muzzlo, M., Motti, J. B., Sepulveda, P., Yee, M., Cooke, T., Santos, M. R., Ramallo, V., Alfaro, E. L., Dipierri, J. E., Bailliet, G., Bravl, C. M., Bustamante, C. D., Kenny, et al
2018; 13 (5): e0196325
- **Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study** *NATURE COMMUNICATIONS*
DeBoever, C., Tanigawa, Y., Lindholm, M. E., McInnes, G., Lavertu, A., Ingelsson, E., Chang, C., Ashley, E. A., Bustamante, C. D., Daly, M. J., Rivas, M. A.
2018; 9: 1612
- **Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*

- de la Fuente, C., Avila-Arcos, M. C., Galimany, J., Carpenter, M. L., Homburger, J. R., Blanco, A., Contreras, P., Davalos, D., Reyes, O., Roman, M., Moreno-Estrada, A., Campos, P. F., Eng, et al
2018; 115 (17): E4006–E4012
- **Whole-genome sequencing of Atacama skeleton shows novel mutations linked with dysplasia** *GENOME RESEARCH*
Bhattacharya, S., Li, J., Sockell, A., Kan, M. J., Bava, F. A., Chen, S., Avila-Arcos, M. C., Ji, X., Smith, E., Asadi, N. B., Lachman, R. S., Lam, H. K., Bustamante, et al
2018; 28 (4): 423–31
 - **Whole-genome sequencing reveals the extent of heterozygosity in a preferentially self-fertilizing hermaphroditic vertebrate** *GENOME*
Lins, L. F., Trojahn, S., Sockell, A., Yee, M., Tatarenkov, A., Bustamante, C. D., Earley, R. L., Kelley, J. L.
2018; 61 (4): 241–47
 - **Origins and genetic legacies of the Caribbean Taino** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
Schroeder, H., Sikora, M., Gopalakrishnan, S., Cassidy, L. M., Delserc, P., Velasco, M., Schraiber, J. G., Rasmussen, S., Homburger, J. R., Avila-Arcos, M. C., Allentoft, M. E., Moreno-Mayar, J., Renaud, et al
2018; 115 (10): 2341–46
 - **A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth** *SCIENTIFIC REPORTS*
Rappoport, N., Toung, J., Hadley, D., Wong, R. J., Fujioka, K., Reuter, J., Abbott, C. W., Oh, S., Hu, D., Eng, C., Huntsman, S., Bodian, D. L., Niederhuber, et al
2018; 8: 226
 - **An admixture mapping meta-analysis implicates genetic variation at 18q21 with asthma susceptibility in Latinos** *THE JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY*
Gignoux, C. R., Torgerson, D. G., Pino-Yanes, M., Uricchio, L. H., Galanter, J., et al
2018; in press
 - **DeepTag: inferring diagnoses from veterinary clinical notes.** *NPJ digital medicine*
Nie, A. n., Zehnder, A. n., Page, R. L., Zhang, Y. n., Pineda, A. L., Rivas, M. A., Bustamante, C. D., Zou, J. n.
2018; 1: 60
 - **Population genomic analyses of the chocolate tree, *Theobroma cacao* L., provide insights into its domestication process** *COMMUNICATIONS BIOLOGY*
Cornejo, O. E., Yee, M., Dominguez, V., Andrews, M., Sockell, A., Strandberg, E., Livingstone, D., Stack, C., Romero, A., Umaharan, P., Royaert, S., Tawari, N. R., Ng, et al
2018; 1
 - **Gut microbiome transition across a lifestyle gradient in Himalaya.** *PLoS biology*
Jha, A. R., Davenport, E. R., Gautam, Y. n., Bhandari, D. n., Tandukar, S. n., Ng, K. M., Fragiadakis, G. K., Holmes, S. n., Gautam, G. P., Leach, J. n., Sherchand, J. B., Bustamante, C. D., Sonnenburg, et al
2018; 16 (11): e2005396
 - **Population genomic analyses of the chocolate tree, *Theobroma cacao* L., provide insights into its domestication process.** *Communications biology*
Cornejo, O. E., Yee, M., Dominguez, V., Andrews, M., Sockell, A., Strandberg, E., Livingstone, D. 3., Stack, C., Romero, A., Umaharan, P., Royaert, S., Tawari, N. R., Ng, et al
2018; 1: 167
 - **Patterns of genomic and phenomic diversity in wine and table grapes** *HORTICULTURE RESEARCH*
Migicovsky, Z., Sawler, J., Gardner, K. M., Aradhya, M. K., Prins, B. H., Schwaninger, H. R., Bustamante, C. D., Buckler, E. S., Zhong, G., Brown, P. J., Myles, S.
2017; 4: 17035
 - **Complexities of gene expression patterns in natural populations of an extremophile fish (*Poecilia mexicana*, *Poeciliidae*)** *MOLECULAR ECOLOGY*
Passow, C. N., Brown, A. P., Arias-Rodriguez, L., Yee, M., Sockell, A., Schartl, M., Warren, W. C., Bustamante, C., Kelley, J. L., Tobler, M.
2017; 26 (16): 4211–25
 - **Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America** *SCIENCE*
Patin, E., Lopez, M., Grollemund, R., Verdu, P., Harmant, C., Quach, H., Laval, G., Perry, G. H., Barreiro, L. B., Froment, A., Heyer, E., Massougboji, A., Fortes-Lima, et al
2017; 356 (6337): 543–546
 - **Identifying tagging SNPs for African specific genetic variation from the African Diaspora Genome** *SCIENTIFIC REPORTS*

- Johnston, H. R., Hu, Y., Gao, J., O'Connor, T. D., Abecasis, G. R., Wojcik, G. L., Gignoux, C. R., Gourraud, P., Lizee, A., Hansen, M., Genuario, R., Bullis, D., Lawley, et al
2017; 7
- **Using genotype array data to compare multi- and single-sample variant calls and improve variant call sets from deep coverage whole-genome sequencing data** *BIOINFORMATICS*
Shringarpure, S. S., Mathias, R. A., Hernandez, R. D., O'Connor, T. D., Szpiech, Z. A., Torres, R., De La Vega, F. M., Bustamante, C. D., Barnes, K. C., Taub, M. A.
2017; 33 (8): 1147-1153
 - **Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations** *AMERICAN JOURNAL OF HUMAN GENETICS*
Martin, A. R., Gignoux, C. R., Walters, R. K., Wojcik, G. L., Neale, B. M., Gravel, S., Daly, M. J., Bustamante, C. D., Kenny, E. E.
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