Stanford



Susan Holmes

Professor of Statistics, Emerita

Bio

BIO

Trained in the French school of Data Analysis in Montpellier, Susan Holmes has been working in non parametric multivariate statistics applied to Biology since 1985. She has taught at MIT, Harvard and was an Associate Professor of Biometry at Cornell before moving to Stanford in 1998. She created the Thinking Matters class: Breaking Codes and Finding patterns and likes working on big messy data sets, mostly from the areas of Immunology, Cancer Biology and Microbial Ecology. Her theoretical interests include applied probability, MCMC (Monte Carlo Markov chains), Graph Limit Theory, Differential Geometry and the topology of the space of Phylogenetic Trees. She wrote the book Modern Statistics for Modern Biology with Wolfgang Huber from EMBL and teaches the material as a crash course (BIOS221) regularly every year. Her current focus is improving the statistical analyses and reproducibility of data in perturbation studies of the Human Microbiome.

ACADEMIC APPOINTMENTS

- Emeritus Faculty, Acad Council, Statistics
- Member, Bio-X
- Member, Maternal & Child Health Research Institute (MCHRI)
- Member, Wu Tsai Neurosciences Institute

ADMINISTRATIVE APPOINTMENTS

- CoDirector, Mathematical and Computational Sciences IDP, (2002-2017)
- Director, VIGRE program in Statistics, (2005-2014)
- Professor, Member, BioX, (2003- present)

HONORS AND AWARDS

- CASBS Fellow, Center for the Advanced study of the Behavioral Sciences (2017-2018)
- Breiman Lecturer, N(eur)IPS (December, 2016)
- Fellow, Fields Institute in Mathematical Sciences, Toronto, Canada (2015)
- Director's Transformative Research Award, NIH (2013)
- John Henry Samter University Fellow in Undergraduate Education, Stanford (2012)
- Fellow of the Institute of Mathematical Statistics, IMS (2005)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Member and Chair (2010-2012), Science Board, NimBioS (2007 - 2012)

- Science Boards, Fields Research Institute in the Mathematical Sciences (2012 - 2015)
- Council Member, Institute of Mathematical Statistics (2018 - 2021)
- Scientific Advisory Board, Sydney Mathematics Research Institute (2018 - 2024)

PROGRAM AFFILIATIONS

- Symbolic Systems Program

LINKS

- My lab website: https://susan.su.domains/lab-members-recent-and-current.html
- My website: https://susan.su.domains/index.html

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our work focuses on large heterogeneous multi-layer data analyses. Whether using image analysis and segmentation for the study of cancer and immune cell interactions, or brain imaging and DNA sequence analyses for the study of dependencies between genetic and neurological dynamics, all these statistical studies have involved large complex datasets of different types where dynamics of interactions between different components of a system are the key to understanding the underlying biology.

We have generalized methods such as Principal Components Analysis (PCA) to more diverse data incorporating spatial information as well as tree dependency structures. This has proved useful in the study of drug resistant mutations in HIV and in the study of the dynamics of bacterial communities in the Human Microbiome.

The statistical bases for these nonparametric methods are computer intensive methods using optimization and Kernels and we often find useful embeddings of high dimensional data in low dimensional structures, the extreme case being finding a natural ordering in high dimensional data.

In a long term collaboration with Professor David Relman (Stanford Medical School) we are developing a multi-table toolbox of non parametric methods that enable users to normalize and visualize the multiple facets of the microbiota in the human body under different classes of perturbations. The tools developed in this project are all open source packages developed in R and provide an example of reproducible research in action.

PROJECTS

- Study of the dynamics of the human microbiome. - Stanford University (March 1, 2013 - 2018)
- Hierarchical Testing - Stanford University (8/1/2012)
- Multivariate Data Analysis of Drug Resistance in HIV - Stanford University (9/1/2003)
- Multiway Data Analysis for the Human Microbiome - Stanford University (11/1/2013 - 10/31/2018)

Teaching

COURSES

2023-24

- Literature of Statistics: STATS 319 (Aut)
- Modern Statistics for Modern Biology: BIOS 221, STATS 256, STATS 366 (Aut)
- Statistical Models in Biology: STATS 215 (Win)

Publications

PUBLICATIONS

- **Sub-communities of the vaginal microbiota in pregnant and non-pregnant women.** *Proceedings. Biological sciences*
  Symul, L., Jeganathan, P., Costello, E. K., France, M., Bloom, S. M., Kwon, D. S., Ravel, J., Relman, D. A., Holmes, S.
  2023; 290 (2011): 20231461

- **Comparative analysis of cell-cell communication at single-cell resolution.** *Nature biotechnology*
  Wilk, A. J., Shalek, A. K., Holmes, S., Blish, C. A.
  2023

- **Generative Models: An Interdisciplinary Perspective** *ANNUAL REVIEW OF STATISTICS AND ITS APPLICATION*
  Sankaran, K., Holmes, S. P.
  2023; 10: 325-352

- **Latent variable modeling for the microbiome** *BIOSTATISTICS*
  Sankaran, K., Holmes, S. P.
  2019; 20 (4): 599–614

- **Modern Statistics for Modern Biology** *http://bios221.stanford.edu/book/*
  Holmes, S., Huber, W.
  Cambridge University Press.2019

- **Ten quick tips for effective dimensionality reduction.** *PLoS computational biology*
  Nguyen, L. H., Holmes, S. n.
  2019; 15 (6): e1006907

- **TRACKING NETWORK DYNAMICS: A SURVEY USING GRAPH DISTANCES** *ANNALS OF APPLIED STATISTICS*
  Donnat, C., Holmes, S.
  2018; 12 (2): 971–1012

- **Bayesian Nonparametric Ordination for the Analysis of Microbial Communities** *JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION*
  Ren, B., Bacallado, S., Favaro, S., Holmes, S., Trippa, L.
  2017; 112 (520): 1430–42

- **DADA2: High-resolution sample inference from Illumina amplicon data.** *Nature methods*
  Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J., Holmes, S. P.
  2016; 13 (7): 581-583

- **Waste not, want not: why rarefying microbiome data is inadmissible.** *PLoS computational biology*
  McMurdie, P. J., Holmes, S.
  2014; 10 (4)

- **NKp30 and NKG2D contribute to natural killer cell-mediated recognition of HIV-infected cells.** *iScience*
  Pi, R., Zhao, N. Q., Bien, A. J., Ranganath, T., Seiler, C., Holmes, S., Marson, A., Nguyen, D. N., Blish, C. A.
  2025; 28 (10): 113548

- **Randomized trial of multi-strain Lactobacillus crispatus vaginal live biotherapeutic products after antibiotic therapy for bacterial vaginosis: study protocol for VIBRANT (vaginal live biotherapeutic RANdomized trial)** *CONTEMPORARY CLINICAL TRIALS COMMUNICATIONS*
  Chetty, C., Mafunda, N., Happel, A., Khan, A., Demidkina, B., Yende-Zuma, N., Saidi, Y., Polliah, A., Lewis, L., Osman, F., Radebe, P., Passmore, J. S., Kwon, et al
  2025; 48: 101554

- **Microbiota effects and predictors of Lactobacillus crispatus colonization after treatment with a vaginal live biotherapeutic: results from a randomized, double-blinded, placebo-controlled trial.** *medRxiv : the preprint server for health sciences*
  Bloom, S. M., Symul, L., Elsherbini, J., Xu, J., Hussain, S., Shih, J., Sango, A., Mitchell, C. M., Hemmerling, A., Parks, T. P., Kannan, A., Hussain, F. A., Cohen, et al
  2025

- **Guidelines for preventing and reporting contamination in low-biomass microbiome studies.** *Nature microbiology*
  Fierer, N., Leung, P. M., Lappan, R., Eisenhofer, R., Ricci, F., Holland, S. I., Dragone, N., Blackall, L. L., Dong, X., Dorador, C., Ferrari, B. C., Goordial, J., Holmes, et al
  2025
- **Brief antibiotic use drives human gut bacteria towards low-cost resistance.** *Nature*
  Yaffe, E., Dethlefsen, L., Patankar, A. V., Gui, C., Holmes, S., Relman, D. A.
  2025
- **Learning and teaching biological data science in the Bioconductor community.** *PLoS computational biology*
  Drnevich, J., Tan, F. J., Almeida-Silva, F., Castelo, R., Culhane, A. C., Davis, S., Doyle, M. A., Geistlinger, L., Ghazi, A. R., Holmes, S., Lahti, L., Mahmoud, A., Nishida, et al
  2025; 21 (4): e1012925
- **Learning and teaching biological data science in the Bioconductor community.** *ArXiv*
  Drnevich, J., Tan, F. J., Almeida-Silva, F., Castelo, R., Culhane, A. C., Davis, S., Doyle, M. A., Geistlinger, L., Ghazi, A. R., Holmes, S., Lahti, L., Mahmoud, A., Nishida, et al
  2025
- **Learning and teaching biological data science in the Bioconductor community.** *ArXiv*
  Drnevich, J., Tan, F. J., Almeida-Silva, F., Castelo, R., Culhane, A. C., Davis, S., Doyle, M. A., Geistlinger, L., Ghazi, A. R., Holmes, S., Lahti, L., Mahmoud, A., Nishida, et al
  2025
- **Prior vaccination prevents overactivation of innate immune responses during COVID-19 breakthrough infection.** *Science translational medicine*
  Chan, L., Pinedo, K., Stabile, M. A., Hamlin, R. E., Pienkos, S. M., Ratnasiri, K., Yang, S., Blomkalns, A. L., Nadeau, K. C., Pulendran, B., O'Hara, R., Rogers, A. J., Holmes, et al
  2025; 17 (783): eadq1086
- **Sex differences and immune correlates of Long Covid development, symptom persistence, and resolution.** *Science translational medicine*
  Hamlin, R. E., Pienkos, S. M., Chan, L., Stabile, M. A., Pinedo, K., Rao, M., Grant, P., Bonilla, H., Holubar, M., Singh, U., Jacobson, K. B., Jagannathan, P., Maldonado, et al
  2024; 16 (773): eadr1032
- **Microbiota effects of a Lactobacillus crispatus live biotherapeutic to prevent recurrent bacterial vaginosis: Findings from a randomized, placebo-controlled trial**
  Bloom, S., Symul, L., Elsherbini, J., Xu, J., Hussain, S., Shih, J., Sango, A., Mitchell, C., Hemmerling, A., Hussain, F., Kannan, A., Cohen, C., Holmes, et al
  JOHN WILEY & SONS LTD.2024
- **Sex differences and immune correlates of Long COVID development, persistence, and resolution.** *bioRxiv : the preprint server for biology*
  Hamlin, R. E., Pienkos, S. M., Chan, L., Stabile, M. A., Pinedo, K., Rao, M., Grant, P., Bonilla, H., Holubar, M., Singh, U., Jacobson, K. B., Jagannathan, P., Maldonado, et al
  2024
- **Premature skewing of T cell receptor clonality and delayed memory expansion in HIV-exposed infants.** *Nature communications*
  Dzanibe, S., Wilk, A. J., Canny, S., Ranganath, T., Alinde, B., Rubelt, F., Huang, H., Davis, M. M., Holmes, S. P., Jaspan, H. B., Blish, C. A., Gray, C. M.
  2024; 15 (1): 4080
- **Patient-reported Symptoms Do Not Correlate With Immune Profiling in Multi-omics Analysis of Post-acute Sequelae of COVID-19**
  Pienkos, S., Hamlin, R., Chan, L., Holmes, S., Blish, C.
  AMER THORACIC SOC.2024
- **Pro-inflammatory feedback loops define immune responses to pathogenic Lentivirus infection.** *Genome medicine*
  Wilk, A. J., Marceau, J. O., Kazer, S. W., Fleming, I., Miao, V. N., Galvez-Reyes, J., Kimata, J. T., Shalek, A. K., Holmes, S., Overbaugh, J., Blish, C. A.
  2024; 16 (1): 24
- **Longitudinal gut microbiota composition of South African and Nigerian infants in relation to tetanus vaccine responses.** *Microbiology spectrum*

Iwase, S. C., Osawe, S., Happel, A. -., Gray, C. M., Holmes, S. P., Blackburn, J. M., Abimiku, A., Jaspan, H. B.
2024: e0319023

- **Abrupt perturbation and delayed recovery of the vaginal ecosystem following childbirth.** *Nature communications*
  Costello, E. K., DiGiulio, D. B., Robaczewska, A., Symul, L., Wong, R. J., Shaw, G. M., Stevenson, D. K., Holmes, S. P., Kwon, D. S., Relman, D. A.
  2023; 14 (1): 4141

- **Longitudinal gut microbiota composition of South African and Nigerian infants in relation to tetanus vaccine responses.** *Research square*
  Iwase, S. C., Jaspan, H. B., Happel, A. U., Holmes, S. P., Abimiku, A., Osawe, S., Gray, C. M., Blackburn, J. M.
  2023

- **Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios.** *Journal of applied statistics*
  Donnat, C., Holmes, S.
  2023; 50 (11-12): 2518-2546

- **Disrupted memory T cell expansion in HIV-exposed uninfected infants is preceded by premature skewing of T cell receptor clonality.** *bioRxiv : the preprint server for biology*
  Dzanibe, S., Wilk, A. J., Canny, S., Ranganath, T., Alinde, B., Rubelt, F., Huang, H., Davis, M. M., Holmes, S., Jaspan, H. B., Blish, C. A., Gray, C. M.
  2023

- **Profiling the human intestinal environment under physiological conditions.** *Nature*
  Shalon, D., Culver, R. N., Grembi, J. A., Folz, J., Treit, P. V., Shi, H., Rosenberger, F. A., Dethlefsen, L., Meng, X., Yaffe, E., Aranda-Diaz, A., Geyer, P. E., Mueller-Reif, et al
  2023

- **HIV-1 Group M Capsid Amino Acid Variability: Implications for Sequence Quality Control of Genotypic Resistance Testing.** *Viruses*
  Tao, K., Rhee, S. Y., Tzou, P. L., Osman, Z. A., Pond, S. L., Holmes, S. P., Shafer, R. W.
  2023; 15 (4)

- **Highly Ambiguous HIV-1 pol Positions Encoding Multiple Amino Acids Usually Result from Antiviral or Immune Selection Pressure.** *AIDS research and human retroviruses*
  Tao, K., Rhee, S., Tzou, P. L., Holmes, S., Shafer, R. W.
  2022

- **SARS-CoV-2 escapes direct NK cell killing through Nsp1-mediated downregulation of ligands for NKG2D.** *Cell reports*
  Lee, M. J., Leong, M. W., Rustagi, A., Beck, A., Zeng, L., Holmes, S., Qi, L. S., Blish, C. A.
  2022: 111892

- **Genotypic correlates of resistance to the HIV-1 strand transfer integrase inhibitor cabotegravir.** *Antiviral research*
  Rhee, S., Parkin, N., Harrigan, P. R., Holmes, S., Shafer, R. W.
  2022: 105427

- **Chimpanzee and pig-tailed macaque iPSCs: Improved culture and generation of primate cross-species embryos.** *Cell reports*
  Roodgar, M., Suchy, F. P., Nguyen, L. H., Bajpai, V. K., Sinha, R., Vilches-Moure, J. G., Van Bortle, K., Bhadury, J., Metwally, A., Jiang, L., Jian, R., Chiang, R., Oikonomopoulos, et al
  2022; 40 (9): 111264

- **Robust variation in infant gut microbiome assembly across a spectrum of lifestyles.** *Science (New York, N.Y.)*
  Olm, M. R., Dahan, D., Carter, M. M., Merrill, B. D., Yu, F. B., Jain, S., Meng, X., Tripathi, S., Wastyk, H., Neff, N., Holmes, S., Sonnenburg, E. D., Jha, et al
  2022; 376 (6598): 1220-1223

- **Statistical Modeling for Practical Pooled Testing During the COVID-19 Pandemic** *STATISTICAL SCIENCE*
  Comess, S., Wang, H., Holmes, S., Donnat, C.
  2022; 37 (2): 229-250

- **Labeling Self-Tracked Menstrual Health Records With Hidden Semi-Markov Models** *IEEE JOURNAL OF BIOMEDICAL AND HEALTH INFORMATICS*
  Symul, L., Holmes, S.
  2022; 26 (3): 1297-1308

- **Natural Killer Cell Receptors and Ligands Are Associated With Markers of HIV-1 Persistence in Chronically Infected ART Suppressed Patients.** *Frontiers in cellular and infection microbiology*
  Ivison, G. T., Vendrame, E., Martinez-Colon, G. J., Ranganath, T., Vergara, R., Zhao, N. Q., Martin, M. P., Bendall, S. C., Carrington, M., Cyktor, J. C., McMahon, D. K., Eron, J., Jones, et al
  2022; 12: 757846

- **Arcsine laws for random walks generated from random permutations with applications to genomics** *JOURNAL OF APPLIED PROBABILITY*
  Fang, X., Gan, H. L., Holmes, S., Huang, H., Pekoz, E., Rollin, A., Tang, W.
  2021; 58 (4): 851-867

- **Stereotypic Expansion of T Regulatory and Th17 Cells during Infancy Is Disrupted by HIV Exposure and Gut Epithelial Damage.** *Journal of immunology (Baltimore, Md. : 1950)*
  Dzanibe, S., Lennard, K., Kiravu, A., Seabrook, M. S., Alinde, B., Holmes, S. P., Blish, C. A., Jaspan, H. B., Gray, C. M.
  2021

- **Reporting guidelines for human microbiome research: the STORMS checklist.** *Nature medicine*
  Mirzayi, C., Renson, A., Genomic Standards Consortium, Massive Analysis and Quality Control Society, Zohra, F., Elsafoury, S., Geistlinger, L., Kasselman, L. J., Eckenrode, K., van de Wijgert, J., Loughman, A., Marques, F. Z., MacIntyre, D. A., Arumugam, et al
  2021

- **Author Correction: Community-wide hackathons to identify central themes in single-cell multi-omics.** *Genome biology*
  Cao, K. L., Abadi, A. J., Davis-Marcisak, E. F., Hsu, L., Arora, A., Coullomb, A., Deshpande, A., Feng, Y., Jeganathan, P., Loth, M., Meng, C., Mu, W., Pancaldi, et al
  2021; 22 (1): 246

- **Community-wide hackathons to identify central themes in single-cell multi-omics.** *Genome biology*
  Le Cao, K., Abadi, A. J., Davis-Marcisak, E. F., Hsu, L., Arora, A., Coullomb, A., Deshpande, A., Feng, Y., Jeganathan, P., Loth, M., Meng, C., Mu, W., Pancaldi, et al
  2021; 22 (1): 220

- **Multi-omic profiling reveals widespread dysregulation of innate immunity and hematopoiesis in COVID-19.** *The Journal of experimental medicine*
  Wilk, A. J., Lee, M. J., Wei, B., Parks, B., Pi, R., Martinez-Colon, G. J., Ranganath, T., Zhao, N. Q., Taylor, S., Becker, W., Stanford COVID-19 Biobank, Jimenez-Morales, D., Blomkalns, A. L., et al
  2021; 218 (8)

- **Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios** *JOURNAL OF APPLIED STATISTICS*
  Donnat, C., Holmes, S.
  2021

- **A Statistical Perspective on the Challenges in Molecular Microbial Biology.** *Journal of agricultural, biological, and environmental statistics*
  Jeganathan, P., Holmes, S. P.
  2021; 26 (2): 131-160

- **A Statistical Perspective on the Challenges in Molecular Microbial Biology** *JOURNAL OF AGRICULTURAL BIOLOGICAL AND ENVIRONMENTAL STATISTICS*
  Jeganathan, P., Holmes, S. P.
  2021

- **CytoGLMM: conditional differential analysis for flow and mass cytometry experiments.** *BMC bioinformatics*
  Seiler, C., Ferreira, A., Kronstad, L. M., Simpson, L. J., Le Gars, M., Vendrame, E., Blish, C. A., Holmes, S.
  2021; 22 (1): 137

- **Mass Cytometry Analysis of the NK Cell Receptor-Ligand Repertoire Reveals Unique Differences between Dengue-Infected Children and Adults.** *ImmunoHorizons*
  McKechnie, J. L., Beltran, D., Ferreira, A. M., Vergara, R., Saenz, L., Vergara, O., Estripeaut, D., Arauz, A. B., Simpson, L. J., Holmes, S., Lopez-Verges, S., Blish, C. A.
  2020; 4 (10): 634–47

- **Effect of water, sanitation, handwashing and nutrition interventions on enteropathogens in children 14 months old: a cluster-randomized controlled trial in rural Bangladesh.** *The Journal of infectious diseases*

Grembi, J. A., Lin, A., Karim, M. A., Islam, M. O., Miah, R., Arnold, B. F., McQuade, E. T., Ali, S., Rahman, M. Z., Hussain, Z., Shoab, A. K., Famida, S. L., Hossen, et al

2020

- **Microbiota assembly, structure, and dynamics among Tsimane horticulturalists of the Bolivian Amazon.** *Nature communications*

  Sprockett, D. D., Martin, M., Costello, E. K., Burns, A. R., Holmes, S. P., Gurven, M. D., Relman, D. A.

  2020; 11 (1): 3772

- **Cytokine profile in plasma of severe COVID-19 does not differ from ARDS and sepsis.** *JCI insight*

  Wilson, J. G., Simpson, L. J., Ferreira, A., Rustagi, A., Roque, J. A., Asuni, A., Ranganath, T., Grant, P. M., Subramanian, A. K., Rosenberg-Hasson, Y., Maecker, H., Holmes, S., Levitt, et al

  2020

- **Author Correction: Gut microbiota plasticity is correlated with sustained weight loss on a low-carb or low-fat dietary intervention.** *Scientific reports*

  Grembi, J. A., Nguyen, L. H., Haggerty, T. D., Gardner, C. D., Holmes, S. P., Parsonnet, J.

  2020; 10 (1): 11095

- **Variability in the analysis of a single neuroimaging dataset by many teams.** *Nature*

  Botvinik-Nezer, R., Holzmeister, F., Camerer, C. F., Dreber, A., Huber, J., Johannesson, M., Kirchler, M., Iwanir, R., Mumford, J. A., Adcock, R. A., Avesani, P., Baczkowski, B. M., Bajracharya, et al

  2020; 582 (7810): 84-88

- **Microbial biogeography and ecology of the mouth and implications for periodontal diseases.** *Periodontology 2000*

  Proctor, D. M., Shelef, K. M., Gonzalez, A., Davis, C. L., Dethlefsen, L., Burns, A. R., Loomer, P. M., Armitage, G. C., Ryder, M. I., Millman, M. E., Knight, R., Holmes, S. P., Relman, et al

  2020; 82 (1): 26–41

- **Expanded Spectrum of Antiretroviral-Selected Mutations in Human Immunodeficiency Virus Type 2.** *The Journal of infectious diseases*

  Tzou, P. L., Descamps, D., Rhee, S., Raugi, D. N., Charpentier, C., Taveira, N., Smith, R. A., Soriano, V., de Mendoza, C., Holmes, S. P., Gottlieb, G. S., Shafer, R. W.

  2020

- **TIGIT is upregulated by HIV-1 infection and marks a highly functional adaptive and mature subset of natural killer cells.** *AIDS (London, England)*

  Vendrame, E. n., Seiler, C. n., Ranganath, T. n., Zhao, N. Q., Vergara, R. n., Alary, M. n., Labbé, A. C., Guédou, F. n., Poudrier, J. n., Holmes, S. n., Roger, M. n., Blish, C. A.

  2020

- **Learning Weighted Submanifolds with Variational Autoencoders and Riemannian Variational Autoencoders**

  Miolane, N., Holmes, S., IEEE

  IEEE COMPUTER SOC.2020: 14491-14499

- **Estimation of Orientation and Camera Parameters from Cryo-Electron Microscopy Images with Variational Autoencoders and Generative Adversarial Networks**

  Miolane, N., Poitevin, F., Li, Y., Holmes, S., IEEE COMP SOC

  IEEE COMPUTER SOC.2020: 4174-4183

- **Characterization of the Impact of Daclizumab Beta on Circulating Natural Killer Cells by Mass Cytometry.** *Frontiers in immunology*

  Ranganath, T. n., Simpson, L. J., Ferreira, A. M., Seiler, C. n., Vendrame, E. n., Zhao, N. n., Fontenot, J. D., Holmes, S. n., Blish, C. A.

  2020; 11: 714

- **Influenza-Induced Interferon Lambda Response Is Associated With Longer Time to Delivery Among Pregnant Kenyan Women.** *Frontiers in immunology*

  Seiler, C. n., Bayless, N. L., Vergara, R. n., Pintye, J. n., Kinuthia, J. n., Osborn, L. n., Matemo, D. n., Richardson, B. A., John-Stewart, G. n., Holmes, S. n., Blish, C. A.

  2020; 11: 452

- **Treated HIV Infection Alters Phenotype but Not HIV-Specific Function of Peripheral Blood Natural Killer Cells.** *Frontiers in immunology*

  Zhao, N. Q., Ferreira, A., Grant, P. M., Holmes, S., Blish, C. A.

  2020; 11: 829

- **Natural killer cell phenotype is altered in HIV-exposed seronegative women.** *PloS one*
  Zhao, N. Q., Vendrame, E., Ferreira, A., Seiler, C., Ranganath, T., Alary, M., Labbe, A., Guedou, F., Poudrier, J., Holmes, S., Roger, M., Blish, C. A.
  2020; 15 (9): e0238347

- **Analysis of unusual and signature APOBEC-mutations in HIV-1 pol next-generation sequences.** *PloS one*
  Tzou, P. L., Kosakovsky Pond, S. L., Avila-Rios, S. n., Holmes, S. P., Kantor, R. n., Shafer, R. W.
  2020; 15 (2): e0225352

- **Chromosome-level de novo assembly of the pig-tailed macaque genome using linked-read sequencing and HiC proximity scaffolding.** *GigaScience*
  Roodgar, M. n., Babveyh, A. n., Nguyen, L. H., Zhou, W. n., Sinha, R. n., Lee, H. n., Hanks, J. B., Avula, M. n., Jiang, L. n., Jian, R. n., Lee, H. n., Song, G. n., Chaib, et al
  2020; 9 (7)

- **Gut microbiota plasticity is correlated with sustained weight loss on a low-carb or low-fat dietary intervention** *Scientific Reports*
  Grembi, J. A., Nguyen, L. H., Haggerty, T. D., Gardner, C. D., Holmes, S. P., Parsonnet, J.
  2020; 10

- **Successful strategies for human microbiome data generation, storage and analyses** *JOURNAL OF BIOSCIENCES*
  Holmes, S.
  2019; 44 (5)

- **Successful strategies for human microbiome data generation, storage and analyses.** *Journal of biosciences*
  Holmes, S.
  2019; 44 (5)

- **Specific gut microbiome members are associated with distinct immune markers in pediatric allogeneic hematopoietic stem cell transplantation.** *Microbiome*
  Ingham, A. C., Kielsen, K., Cilieborg, M. S., Lund, O., Holmes, S., Aarestrup, F. M., Muller, K. G., Pamp, S. J.
  2019; 7 (1): 131

- **Multitable Methods for Microbiome Data Integration** *FRONTIERS IN GENETICS*
  Sankaran, K., Holmes, S. P.
  2019; 10

- **Multitable Methods for Microbiome Data Integration.** *Frontiers in genetics*
  Sankaran, K., Holmes, S. P.
  2019; 10: 627

- **Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2.** *Nature biotechnology*
  Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., Alexander, H., Alm, E. J., Arumugam, M., Asnicar, F., Bai, Y., Bisanz, J. E., Bittinger, et al
  2019

- **Nuclear degradation dynamics in a nonapoptotic programmed cell death.** *Cell death and differentiation*
  Yalonetskaya, A., Mondragon, A. A., Hintze, Z. J., Holmes, S., McCall, K.
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