



## Susan Holmes

Professor of Statistics

### Bio

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#### 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

- Professor, 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 - present)

## 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

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### 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. More general manifolds have also proved useful in one of our current projects, joint with Xavier Pennec of INRIA-SophiaAntipolis which focuses on the uses of differential geometry in computational anatomy and image processing.

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

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### COURSES

#### 2021-22

- Introduction to Statistical Learning: STATS 216 (Win)
- Literature of Statistics: STATS 319 (Win)
- Modern Statistics for Modern Biology: BIOS 221, STATS 155, STATS 256, STATS 366 (Aut)

#### 2020-21

- Consulting Workshop: STATS 390 (Spr)
- Modern Statistics for Modern Biology: BIOS 221, STATS 256, STATS 366 (Spr)

#### 2019-20

- Applied Statistics III: STATS 305C (Spr)
- Biostatistics: BIO 141, STATS 141 (Aut)
- Modern Statistics for Modern Biology: BIOS 221, STATS 366 (Aut)
- Statistical Methods in Computational Genetics: STATS 155 (Aut)

### STANFORD ADVISEES

#### Postdoctoral Faculty Sponsor

Laura Marie Symul

#### Doctoral Dissertation Co-Advisor (AC)

Saskia Comess

#### Doctoral (Program)

Fang Cai, Jaime Roquero Gimenez

#### Postdoctoral Research Mentor

Laura Marie Symul

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Informatics (Masters Program)
- Biomedical Informatics (Phd Program)
- Microbiology and Immunology (Phd Program)

### Publications

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#### PUBLICATIONS

- **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
- **Comparative analysis of cell-cell communication at single-cell resolution.** *bioRxiv : the preprint server for biology*  
Wilk, A. J., Shalek, A. K., Holmes, S., Blish, C. A.  
2022
- **Modeling the heterogeneity in COVID-19's reproductive number and its impact on predictive scenarios** *JOURNAL OF APPLIED STATISTICS*  
Donnat, C., Holmes, S.  
2021
- **Latent variable modeling for the microbiome** *BIOSTATISTICS*  
Sankaran, K., Holmes, S. P.  
2019; 20 (4): 599–614
- **Multitable Methods for Microbiome Data Integration** *FRONTIERS IN GENETICS*  
Sankaran, K., Holmes, S. P.  
2019; 10

- **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
- **Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data.** *Microbiome*  
Davis, N. M., Proctor, D. M., Holmes, S. P., Relman, D. A., Callahan, B. J.  
2018; 6 (1): 226
- **TRACKING NETWORK DYNAMICS: A SURVEY USING GRAPH DISTANCES** *ANNALS OF APPLIED STATISTICS*  
Donnat, C., Holmes, S.  
2018; 12 (2): 971–1012
- **Latent variable modeling for the microbiome.** *Biostatistics (Oxford, England)*  
Sankaran, K. n., Holmes, S. P.  
2018
- **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)
- **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
- **Labeling Self-Trackd 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*  
Iverson, 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*  
Mirzayati, C., Renson, A., Genomic Standards Consortium, Massive Analysis and Quality Control Society, Zohra, F., Elsafoury, S., Geistlinger, L., Kasselmann, L. J., Eckenrode, K., van de Wiggert, 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)
- **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
- **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
  - **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
  - **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
  - **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)
  - **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
  - **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
  - **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
  - **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
  - **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: 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.  
2019
- **Treatment-Specific Composition of the Gut Microbiota Is Associated With Disease Remission in a Pediatric Crohn's Disease Cohort.** *Inflammatory bowel diseases*  
Sprockett, D., Fischer, N., Boneh, R. S., Turner, D., Kierkus, J., Sladek, M., Escher, J. C., Wine, E., Yerushalmi, B., Dias, J. A., Shaoul, R., Kori, M., Snapper, et al  
2019
- **Pregnancy-Induced Alterations in NK Cell Phenotype and Function.** *Frontiers in immunology*  
Le Gars, M., Seiler, C., Kay, A. W., Bayless, N. L., Starosvetsky, E., Moore, L., Shen-Orr, S. S., Aziz, N., Khatri, P., Dekker, C. L., Swan, G. E., Davis, M. M., Holmes, et al  
2019; 10: 2469
- **Convex Hierarchical Clustering for Graph-Structured Data**  
Donnat, C., Holmes, S., Matthews, M. B.  
IEEE.2019: 1999–2006
- **Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data** *MICROBIOME*  
Davis, N. M., Proctor, D. M., Holmes, S. P., Relman, D. A., Callahan, B. J.  
2018; 6
- **Gut microbiome transition across a lifestyle gradient in Himalaya** *PLOS BIOLOGY*  
Jha, A. R., Davenport, E. R., Gautam, Y., Bhandari, D., Tandukar, S., Ng, K. M., Fragiadakis, G. K., Holmes, S., Gautam, G., Leach, J., Sherchand, J., Bustamante, C. D., Sonnenburg, et al  
2018; 16 (11)
- **Interactive Visualization of Hierarchically Structured Data.** *Journal of computational and graphical statistics : a joint publication of American Statistical Association, Institute of Mathematical Statistics, Interface Foundation of North America*  
Sankaran, K., Holmes, S.  
2018; 27 (3): 553-563
- **Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome** *GENOME RESEARCH*  
Goltsman, D., Sun, C. L., Proctor, D. M., DiGiulio, D. B., Robaczewska, A., Thomas, B. C., Shaw, G. M., Stevenson, D. K., Holmes, S. P., Banfield, J. F., Relman, D. A.  
2018; 28 (10): 1467–80
- **Differential Induction of IFN-alpha and Modulation of CD112 and CD54 Expression Govern the Magnitude of NK Cell IFN-gamma Response to Influenza A Viruses** *JOURNAL OF IMMUNOLOGY*  
Kronstad, L. M., Seiler, C., Vergara, R., Holmes, S. P., Bish, C. A.  
2018; 201 (7): 2117–31
- **Metagenomic analysis with strain-level resolution reveals fine-scale variation in the human pregnancy microbiome.** *Genome research*  
Goltsman, D. S., Sun, C. L., Proctor, D. M., DiGiulio, D. B., Robaczewska, A., Thomas, B. C., Shaw, G. M., Stevenson, D. K., Holmes, S. P., Banfield, J. F., Relman, D. A.  
2018
- **Differential Induction of IFN-alpha and Modulation of CD112 and CD54 Expression Govern the Magnitude of NK Cell IFN-gamma Response to Influenza A Viruses.** *Journal of immunology (Baltimore, Md. : 1950)*  
Kronstad, L. M., Seiler, C., Vergara, R., Holmes, S. P., Blish, C. A.  
2018
- **Characterization of the impact of daclizumab beta on circulating natural killer cells by mass cytometry**  
Ranganath, T., Seiler, C., Vendrame, E., Le Gars, M., Fontenot, J. D., Fam, S., Holmes, S., Blish, C.  
LIPPINCOTT WILLIAMS & WILKINS.2018

- **A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow.** *Nature communications*  
Proctor, D. M., Fukuyama, J. A., Loomer, P. M., Armitage, G. C., Lee, S. A., Davis, N. M., Ryder, M. I., Holmes, S. P., Relman, D. A.  
2018; 9 (1): 681
- **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
- **Topologically Constrained Template Estimation via Morse-Smale Complexes Controls Its Statistical Consistency** *SIAM JOURNAL ON APPLIED ALGEBRA AND GEOMETRY*  
Miolane, N., Holmes, S., Pennec, X.  
2018; 2 (2): 348–75
- **Multivariate Heteroscedasticity Models for Functional Brain Connectivity** *FRONTIERS IN NEUROSCIENCE*  
Seiler, C., Holmes, S.  
2017; 11: 696
- **Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment.** *PLoS computational biology*  
Fukuyama, J., Rumker, L., Sankaran, K., Jegannathan, P., Dethlefsen, L., Relman, D. A., Holmes, S. P.  
2017; 13 (8): e1005706
- **Parallel imaging of Drosophila embryos for quantitative analysis of genetic perturbations of the Ras pathway.** *Disease models & mechanisms*  
Goyal, Y., Levario, T. J., Mattingly, H. H., Holmes, S., Shvartsman, S. Y., Lu, H.  
2017
- **Mutational Correlates of Virological Failure in Individuals Receiving a WHO-Recommended Tenofovir-Containing First-Line Regimen: An International Collaboration.** *EBioMedicine*  
Rhee, S., Varghese, V., Holmes, S. P., van Zyl, G. U., Steegen, K., Boyd, M. A., Cooper, D. A., Nsanzimana, S., Saravanan, S., Charpentier, C., de Oliveira, T., Etiebet, M. A., Garcia, et al  
2017; 18: 225-235
- **Mass Cytometry Analytical Approaches Reveal Cytokine-Induced Changes in Natural Killer Cells.** *Cytometry. Part B, Clinical cytometry*  
Vendrame, E., Fukuyama, J., Strauss-Albee, D. M., Holmes, S., Blish, C. A.  
2017; 92 (1): 57-67
- **Discussion of "50 Years of Data Science"** *JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS*  
Holmes, S., Josse, J.  
2017; 26 (4): 768–69
- **Multi-Table Differential Correlation Analysis of Neuroanatomical and Cognitive Interactions in Turner Syndrome.** *Neuroinformatics*  
Seiler, C. n., Green, T. n., Hong, D. n., Chromik, L. n., Huffman, L. n., Holmes, S. n., Reiss, A. L.  
2017
- **STATISTICAL PROOF? THE PROBLEM OF IRREPRODUCIBILITY** *Bulletin of the American Mathematical Society*  
Holmes, S. P.  
2017
- **Interactive Visualization of Hierarchically Structured Data** *Journal of Computational and Graphical Statistics*  
Sankaran, K., Holmes, S. P.  
2017
- **Prevalence of Drug-Resistant Minority Variants in Untreated HIV-1-Infected Individuals With and Those Without Transmitted Drug Resistance Detected by Sanger Sequencing.** *The Journal of infectious diseases*  
Clutter, D. S., Zhou, S. n., Varghese, V. n., Rhee, S. Y., Pinsky, B. A., Jeffrey Fessel, W. n., Klein, D. B., Spielvogel, E. n., Holmes, S. P., Hurley, L. B., Silverberg, M. J., Swanstrom, R. n., Shafer, et al  
2017; 216 (3): 387–91
- **Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment** *PLOS Computational Biology*  
Fukuyama, J., Rumker, L., Sankaran, K., Jegannathan, P., Relman, D. A., Holmes, S. P.



2017; 13 (8): e1005706

- **Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women.** *Proceedings of the National Academy of Sciences of the United States of America*  
Callahan, B. J., DiGiulio, D. B., Goltsman, D. S., Sun, C. L., Costello, E. K., Jeganathan, P. n., Biggio, J. R., Wong, R. J., Druzin, M. L., Shaw, G. M., Stevenson, D. K., Holmes, S. P., Relman, et al  
2017
- **Exact sequence variants should replace operational taxonomic units in marker-gene data analysis.** *The ISME journal*  
Callahan, B. J., McMurdie, P. J., Holmes, S. P.  
2017
- **Template Shape Estimation: Correcting an Asymptotic Bias** *SIAM J Imaging Science*  
Miolane, N., Holmes, S., Pennec, X.  
2017; 10 (2): 808-844
- **Bayesian Nonparametric Ordination for the Analysis of Microbial Communities** *Journal of the American Statistical Association*  
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