

Julia Fukuyama

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Current position

Assistant Professor
Department of Statistics
Indiana University, Bloomington

2018-present

Appointments held

Postdoctoral Research Fellow
Department of Computational Biology
Fred Hutchinson Cancer Research Center

2017-2018

Education

PhD Statistics, Stanford University

2017

Advisor: Susan Holmes

MS Statistics, Stanford University

2012

BS Biology, *magna cum laude*, Yale University

2010

Preprints

*Julia Fukuyama**, Kris Sankaran*, Laura Symul*. Multiscale Analysis of Count Data through Topic Alignment. arXiv:2109.05541

Publications

Julia Fukuyama. Local biplots for multidimensional scaling, with application to the microbiome. *Journal of Computational and Graphical Statistics*, 2021.

Brielle Stark and *Julia Fukuyama*. Leveraging big data to understand the interaction of task and language during monologic spoken discourse in speakers with and without aphasia. *Language, Cognition, and Neuroscience*, 2020.

Julia Fukuyama, Branden Olson, Frederick Matsen. Lack of evidence for a substantial rate of templated mutagenesis in B cell diversification. *Journal of Immunology*, 2020.

Julia Fukuyama. Emphasis on the deep or shallow parts of the tree provides a new characterization of phylogenetic distances. *Genome Biology*, 2019.

Julia Fukuyama. Adaptive gPCA: A method for structured dimensionality reduction. *Annals of Applied Statistics*, 2019.

Diana Proctor, *Julia Fukuyama*, Peter Loomer, Gary Armitage, Stacey Lee, Nicole Davis, Mark Ryder, Susan Holmes, David Relman. A spatial gradient of bacterial diversity in the human oral cavity shaped by salivary flow. *Nature Communications*, 2018.

*Julia Fukuyama**, Laurie Rumker*, Kris Sankaran*, Pratheepa Jeganathan, Les Dethlefsen, David A. Relman, Susan Holmes. Multidomain analyses of a longitudinal human microbiome intestinal cleanout perturbation experiment. *PLoS Computational Biology*, 2017.

Elena Vendrame*, *Julia Fukuyama**, Dara Strauss-Albee, Susan Holmes, Catherine Blish. Mass cytometry analytical approaches reveal cytokine-induced changes in natural killer cells. *Cytometry Part B: Clinical Cytometry*, 2016.

Benjamin Callahan, Kris Sankaran, *Julia Fukuyama*, Paul McMurdie, and Susan Holmes. Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. *Frontiers Research*, 2016.

Benjamin Callahan, Diana Proctor, *Julia Fukuyama*, David A. Relman, Susan Holmes. Reproducible research workflow in R for the analysis of personalized human microbiome data. *Pacific Symposium on Biocomputing*, 2016.

Dara Strauss-Albee, *Julia Fukuyama*, Emily Liang, Yi Yao, Justin Jarrell, Alison Drake, John Kinuthia, Ruth Montgomery, Grace John-Stewart, Susan Holmes, Catherine Blish. Human NK cell repertoire diversity reflects immune experience and correlates with viral susceptibility. *Science Translational Medicine*, 2015.

Alex Kay, Nick Bayless, *Julia Fukuyama*, Natali Aziz, Cornelia Dekker, Sally Mackey, Gary Swan, Mark Davis, Catherine Blish. Pregnancy does not attenuate the antibody or plasmablast response to inactivated influenza vaccine. *Journal of Infectious Diseases*, 2015.

Alex Kay, *Julia Fukuyama*, Natali Aziz, Cornelia Dekker, Sally Mackey, Gary Swan, Mark Davis, Susan Holmes, Catherine Blish. Enhanced natural killer-cell and T-cell responses to influenza A virus during pregnancy. *Proceedings of the National Academy of Sciences*, 2014.

Miling Yan, Sunje Pamp, *Julia Fukuyama*, Peter Hwang, Do-Yeon Cho, Susan Holmes, David A. Relman. Nasal microenvironments and interspecific interactions influence nasal microbiota complexity and *S. aureus* carriage. *Cell Host and Microbe*, 2013.

Julia Fukuyama, Paul McMurdie, Les Dethlefsen, David A. Relman, Susan Holmes. Comparisons of Distance Methods for Combining Covariates and Abundances in Microbiome Studies. *Pacific Symposium on Biocomputing*, 2012.

Jeffrey Isenberg, Yifeng Jia, *Julia Fukuyama*, Christopher Switzer, David A. Wink, David D. Roberts. Thrombospondin-1 inhibits nitric oxide signaling via CD36 by inhibiting myristic acid uptake. *Journal of Biological Chemistry*, 2007.

Invited Presentations

Phylogenetically-informed distance methods for microbiome data analysis
Joint Statistical Meetings, Philadelphia, PA, August 2020.

Local biplots and their application to microbiome data
CMStatistics, London, UK, December 2019.

Phylogenetically-informed distance methods for microbial ecology
Notre Dame Department of Statistics, South Bend, IN, October 2019.

Phylogenetically-informed distance methods for microbiome data analysis
University of Louisville Department of Statistics, Louisville, KY, September 2019.

Phylogenetically-informed distance methods: Their uses, properties, and potential
The Fourth Workshop on Higher-Order Asymptotics and Post-Selection Inference
Washington University, St. Louis MO, August 2019.

Unboxing a Black Box: Properties of Phylogenetically-Informed Distances
Workshop on “The Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods”
Banff International Research Station, Banff, Canada, February 2019.

Function-Based Clustering of Amplicon Sequence Variants
CMStatistics, University of Pisa, Pisa, Italy, December 2018.

Using Phylogenetic Information to Understand the Microbiome.
Biostatistics Colloquium, Fred Hutchinson Cancer Research Center, Seattle, WA, May 2018.

Using Phylogenetic Information to Understand the Microbiome

University of California Berkeley Center for Computational Biology, Berkeley, CA,
March 2018.

Using Phylogenetic Information to Understand the Microbiome

University of Vermont Department of Statistics, Burlington, VT, March 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

Wharton Department of Statistics, Philadelphia, PA February 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

Vanderbilt University Department of Biostatistics, Nashville, TN, February 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

Yale University Department of Statistics, New Haven, CT, February 2018.

Learning Interpretable Representations of the Microbiome

Yale University Department of Immunobiology, New Haven, CT, February 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

University of Michigan Department of Biostatistics, Ann Arbor, MI, February 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

University of Toronto Department of Statistics, Toronto, Canada, January 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

Florida State University Department of Statistics, Tallahassee, FL, January 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

University of Virginia Department of Statistics, Charlottesville, VA, January 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

University of Oregon Department of Biology, OR, January 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

Colorado State University Department of Statistics, Fort Collins, CO, January 2018.

Dimensionality Reduction with Structured Variables and Applications to the Microbiome

Columbia University Department of Statistics, New York, NY, January 2018.

Dimension Reduction with Structured Variables

Indiana University Department of Statistics, Bloomington, IN, January 2018.

Adaptive gPCA. Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS), Woods Hole, MA, August 2017.

Beyond UniFrac. Interdisciplinary Microbiome Perspectives, Stanford, CA, June 2017.

Contributed Presentations

Improved phylogenetic ordinations for microbiome data. Joint Statistical Meetings, Chicago, IL, August 2016.

Phylogenetically informed analysis of microbiome data using adaptive gPCA in R, UseR, Stanford, CA, June 2016.

Interpretable ordinations for microbiome data using sparse double principal coordinates analysis. Biomedical Computation at Stanford, Stanford, CA, April 2015.

Comparisons of distance methods for combining covariates and abundances in microbiome studies. Pacific Symposium on Biocomputing, Kona, HI, January 2012.

Teaching

Stat 470/670: Exploratory Data Analysis Spring 2021

Stat 610: Introduction to Statistical Computing Fall 2020

Stat 692: Internship in Statistical Consulting Spring 2020

Stat 610: Introduction to Statistical Computing Fall 2019

Stat 710: Introduction to Statistical Computing Spring 2019

Stat 670: Exploratory Data Analysis Fall 2018

Strategies and Techniques for Analyzing Microbial Population Structures August 2017
Marine Biological Lab, Woods Hole, MA
Research Facilitator

Service to the profession

Referee for the *Annals of Applied Statistics*, *PLoS Computational Biology*, *Microbiome*, *Molecular Ecology Resources*, *PLoS Genetics*, *mSystems*, *Bioinformatics*, *Biometrika*, *Genome Biology*, *Journal*

of Applied Statistics, Nature Methods, Journal of Computational and Graphical Statistics, Journal of the American Statistical Association.

Awards

Bio-X Stanford Interdisciplinary Graduate Fellowship	2014-2017
Yale College William R. Belknap Prize for Excellence in Biology	2010
Yale College Dean's Research Fellowship in the Sciences	2009
Yale College Fellowship for International Research in the Sciences and Health Studies	2008