

Johann Gagnon-Bartsch

Curriculum Vitae

April 2021

Address: Department of Statistics, 323 West Hall
1085 South University, Ann Arbor, MI 48109-1107
Phone: (734) 763-1427
Email: johanngb@umich.edu
WWW: <http://dept.stat.lsa.umich.edu/~johanngb/>

Positions

2015– Assistant Professor Department of Statistics, University of Michigan
2012–2015 Neyman Assistant Professor Department of Statistics, UC Berkeley

Affiliations

Michigan Institute for Data Science (MIDAS)
Center of Computational Medicine and Bioinformatics

Education

2012 PhD Statistics UC Berkeley
2007 MS Statistics UC Berkeley
2003 BS, BA Math, Physics, International Relations Stanford University

Publications

Refereed Articles

1. Hunt, G. J., and Gagnon-Bartsch, J. A. (2021). “The role of scale in the estimation of cell-type proportions.” *The Annals of Applied Statistics*, 15, 270–286. <http://dx.doi.org/10.1214/20-AOAS1395>.
2. Wu, E., and Gagnon-Bartsch, J. A. (2021). “Design-based covariate adjustments in paired experiments.” *Journal of Educational and Behavioral Statistics*, 46, 109–132. <https://doi.org/10.3102/1076998620941469>.
3. Hunt, G. J., Dane, M. A., Korkola, J. E., Heiser, L. M., and Gagnon-Bartsch, J. A. (2020). “Automatic transformation and integration to improve visualization and discovery of latent effects in imaging data.” *Journal of Computational and Graphical Statistics*, 29, 929–941. <https://www.tandfonline.com/doi/full/10.1080/10618600.2020.1741379>.
4. Deeke, J., and Gagnon-Bartsch, J. A. (2020). “Stably expressed genes in single-cell RNA-sequencing.” *Journal of Bioinformatics and Computational Biology*, 18. <https://doi.org/10.1142/S0219720020400041>.
5. Conrad*, F. G., Gagnon-Bartsch*, J. A., Ferg, R. A., Schober, M. F., Pasek, J., and Hou, E. (2019). “Social media as an alternative to surveys of opinions about the economy.” *Social Science Computer Review*. <https://doi.org/10.1177/0894439319875692>. denotes co-first authorship.
6. Gagnon-Bartsch, J. A., and Shem-Tov, Y. (2019). “The classification permutation test: A flexible approach to testing for covariate imbalance in observational studies.” *The Annals of Applied Statistics*, 13, 1464–1483. <https://projecteuclid.org/euclid.aos/1571277760>.

7. Molania, R., Gagnon-Bartsch, J. A., Dobrovic, A., and Speed, T. P. (2019). "A new normalization for the nanostring nCounter gene expression assay." *Nucleic Acids Research*, 47, 6073–6083. <https://academic.oup.com/nar/advance-article/doi/10.1093/nar/gkz433/5494770>.
8. Lin, Y., Ghazanfar, S., Wang, K. Y. X., Gagnon-Bartsch, J. A., Lo, K. K., Su, X., Han, Z.-G., Ormerod, J. T., Speed, T. P., Yang, P., and Yang, J. Y. H. (2019). "scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets." *Proceedings of the National Academy of Sciences*, 116, 9775–9784. <https://www.pnas.org/content/116/20/9775>.
9. Hunt, G. J., Freytag, S., Bahlo, M., and Gagnon-Bartsch, J. A. (2019). "dtangle: accurate and robust cell type deconvolution." *Bioinformatics*, 35, 2093–2099. <https://doi.org/10.1093/bioinformatics/bty926>.
10. Wu, E., and Gagnon-Bartsch, J. A. (2018). "The LOOP estimator: Adjusting for covariates in randomized experiments." *Evaluation Review*, 42, 458–488. <https://doi.org/10.1177/0193841X18808003>.
11. Jacob, L., Gagnon-Bartsch, J. A., and Speed, T. P. (2016). "Correcting gene expression data when neither the unwanted variation nor the factor of interest are observed." *Biostatistics*, 17, 16–28. <http://biostatistics.oxfordjournals.org/content/17/1/16.abstract>.
12. Tonks, K. T., Coster, A. C., Christopher, M. J., Chaudhuri, R., Xu, A., Gagnon-Bartsch, J. A., Chisholm, D. J., James, D. E., Meikle, P. J., Greenfield, J. R., and Samocha-Bonet, D. (2016). "Skeletal muscle and plasma lipidomic signatures of insulin resistance and overweight/obesity in humans." *Obesity*, 24, 908–916. <http://dx.doi.org/10.1002/oby.21448>.
13. De Livera, A. M., Sysi-Aho, M., Jacob, L., Gagnon-Bartsch, J. A., Castillo, S., Simpson, J. A., and Speed, T. P. (2015). "Statistical methods for handling unwanted variation in metabolomics data." *Analytical Chemistry*, 87, 3606–3615. <http://dx.doi.org/10.1021/ac502439y>.
14. Freytag, S., Gagnon-Bartsch, J. A., Speed, T. P., and Bahlo, M. (2015). "Systematic noise degrades gene co-expression signals but can be corrected." *BMC Bioinformatics*, 16, 1–17. <http://dx.doi.org/10.1186/s12859-015-0745-3>.
15. Lin, S. J., Gagnon-Bartsch, J. A., Tan, I. B., Earle, S., Ruff, L., Pettinger, K., Ylstra, B., Grieken, N. van, Rha, S. Y., Chung, H. C., Lee, J.-S., Cheong, J. H., Noh, S. H., Aoyama, T., Miyagi, Y., Tsuburaya, A., Yoshikawa, T., Ajani, J. A., Boussioutas, A., Yeoh, K. G., Yong, W. P., So, J., Lee, J., Kang, W. K., Kim, S., Kameda, Y., Arai, T., Hausen, A. zur, Speed, T. P., Grabsch, H. I., and Tan, P. (2015). "Signatures of tumour immunity distinguish asian and non-asian gastric adenocarcinomas." *Gut*, 64, 1721–1731. <http://gut.bmj.com/content/early/2014/11/09/gut.jn1-2014-308252.abstract>.
16. Maksimovic, J., Gagnon-Bartsch, J. A., Speed, T. P., and Oshlack, A. (2015). "Removing unwanted variation in a differential methylation analysis of illumina HumanMethylation450 array data." *Nucleic Acids Research*, 43, e106–e106. <http://nar.oxfordjournals.org/content/early/2015/05/18/nar.gkv526.abstract>.

17. Gagnon-Bartsch, J. A., and Speed, T. P. (2012). "Using control genes to correct for unwanted variation in microarray data." *Biostatistics*, 13, 539–552. <http://biostatistics.oxfordjournals.org/content/13/3/539.abstract>.
18. Onoa, B., Li, H., Gagnon-Bartsch, J. A., Elias, L. A., and Edwards, R. H. (2010). "Vesicular monoamine and glutamate transporters select distinct synaptic vesicle recycling pathways." *The Journal of Neuroscience*, 30, 7917–7927. <http://www.jneurosci.org/content/30/23/7917.short>.

Submitted Manuscripts

1. Hunt, G. J., and Gagnon-Bartsch, J. A. "Containerized analyses enable interactive and reproducible statistics."
2. Mann, C. Z., Abshire, C., Yost, M., Kaatz, S., Swaminathan, L., Flanders, S. A., Prescott, H. C., and Gagnon-Bartsch, J. A. "Derivation and external validation of a simple risk score to predict in-hospital mortality in patients hospitalized for COVID-19."
3. Pan, Y., and Gagnon-Bartsch, J. A. "Separating and reintegrating latent variables to improve classification of genomic data."
4. Ferg, R. A., Conrad, F. G., and Gagnon-Bartsch, J. A. "A critical evaluation of tracking surveys with social media: A case study in presidential approval."
5. Ferg, R. A., and Gagnon-Bartsch, J. A. "Unbiased survey estimation with population auxiliary variables."

Software

R Packages

1. `cpt`: Classification Permutation Test (CPT), a nonparametric test for equality of multivariate distributions.
<https://cran.r-project.org/web/packages/cpt>
2. `dtangle`: Deconvolving cell types from high-throughput gene profiling data.
<https://cran.r-project.org/web/packages/dtangle>
3. `rrscale`: Non-linear transformations of data to better discover latent effects. Applies a sequence of three transformations (1) a Gaussianizing transformation, (2) a Z-score transformation, and (3) an outlier removal transformation.
<https://cran.r-project.org/web/packages/rrscale>
4. `ruv`: Removes Unwanted Variation (RUV) from high-dimensional data using negative controls.
<https://cran.r-project.org/web/packages/ruv>

Shiny Apps

1. Mi-COVID19 COVID-19 In-Hospital Mortality Risk Score Model.
Accompanies manuscript [Mann, et. al. \(2021\)](#).
<https://micovidriskcalc.org/>
2. Relationship between 'jobs' tweets and the ICS.
Accompanies manuscript [Conrad, et. al. \(2019\)](#).
<https://robynferg.shinyapps.io/Twitter-ICS/>

Docker Images

1. rep-int: A base image for interactive reproducible analyses.
<https://hub.docker.com/r/johanngb/rep-int>

Funding

Current Funding

Improving the Power of Education Experiments with Auxiliary Data

Institute of Education Sciences

Role: PI (with Co-PI Adam Sales)

Total award: \$576,429

3/1/2021–2/29/2024

New Approaches to Analyzing Social Media Content for Enhancing Census Bureau Data

US Department of Commerce

Role: Co-PI (with Fred Conrad and Michael Schober)

Total award: \$2,097,076

9/1/2020–8/31/2025

Transforming Analytical Learning in the Era of Big Data

National Institutes of Health

Role: Co-I (PI: Bhramar Mukherjee)

Individual award: \$14,335. Total award: \$752,922.

3/15/2019–2/28/2022

RTG: Understanding dynamic big data with complex structure

National Science Foundation

Role: Faculty affiliate (PI: Liza Levina)

Total award: \$2,500,000

9/1/2017–8/31/2022

Completed Funding

Causal Modeling of Human Drivers

Toyota Research Institute

Role: PI (with Co-PI Richard Frazin)

Total award: \$519,768

1/1/2019–3/31/2021

Michigan Center for Single-Cell Genomic Data Analytics

Michigan Institute for Data Science

Role: Co-I (PIs: Jun Li, Anna Gilbert)

Individual award: \$108,480, with 12.5% investigator cost share. Total award: \$1,249,232.

3/1/2017–2/28/2021

Illinois Pay for Success

Illinois Department of Children and Family Services

Role: Co-I (subcontract; PI, Joe Ryan)

Individual award: \$42,182. Total award: \$277,685.85.

9/2/2015–6/30/2017

Selected Talks

Parsing Latent Factors in High-Dimensional Classification

ENAR Virtual Meeting, 2021

Using Large-scale Pharmacogenomic Databases to Predict Drug Effectiveness

MIDAS-Owkin Workshop, 2021

Choice of Scale in the Estimation of Cell-type Proportions

International Chinese Statistical Association Virtual Meeting, 2020

Everyday reproducibility: A multi-pronged approach to ensure analyses are fully reproducible, easy to access, and easy to use

MIDAS Research Reproducibility Virtual Showcase Series, 2020

Automatic transformation and integration to improve visualization and discovery of latent effects in imaging data

ENAR Virtual Meeting, 2020

Stably expressed genes in single-cell RNA-sequencing

GIW/ABACBS, Sydney, Australia, 2019

Improving the Power of Randomized Experiments with Auxiliary Data

Genentech, South San Francisco, 2019

Parsing latent variables in high dimensional classification

Departmental Seminar, Biostatistics and Medical Informatics, University of Wisconsin, 2019

Improving the Power of Education Experiments with Auxiliary Data

Department of Statistics Seminar, University of Wisconsin, 2019

Improved Classification Accuracy through Inclusion of Latent Variables

Ecosta, Taichung, Taiwan, 2019

Parsing Latent Factors in High-dimensional Classification

Computational Biology Workshop, Ascona, Switzerland, 2019

Integrating Experimental and Observational Data through Machine Learning

European Causal Inference Meeting, 2019

Removing Unwanted Variation with Negative Controls and Replicates

Oregon Health and Science University, 2019

Robust Rescaling of Microenvironment Microarray Data

Oregon Health and Science University, 2019

Integrating Experimental and Observational Data through Machine Learning

Machine Learning Seminar, Michigan State University, 2019

The Duality of Negative Controls and Replicates

Microsoft Research New England, 2018

The Duality of Negative Controls and Replicates

Applied Statistics Workshop, Harvard University, 2018

The Duality of Negative Controls and Replicates

Epidemiology and Biostatistics Department Seminar, Michigan State University, 2018

Endogenous Single Cell Controls

Single Cell Genomic Data Analytics Symposium, University of Michigan, 2018

Using the RUV Package in R

Keynote Speaker. Towards Greater Reproducibility in Medical Research, Olivia Newton-John Cancer Research Institute, 2018

Removing Unwanted Variation with R

useR!, Brisbane, Australia, 2018

The LOOP Estimator: Adjusting for Covariates in Randomized Experiments

Bioinformatics Seminar, Walter and Eliza Hall Institute, 2018

The LOOP Estimator: Adjusting for Covariates in Randomized Experiments

Statistics Department Seminar, University of Sydney, 2018

Removing Unwanted Variation in Cell Image Data

Texas A&M Health Science Center, 2018

The Duality of Negative Controls and Replicates

Atlantic Causal Inference Conference, Carnegie Mellon University, 2018

The RUV Package: Tools to Remove Batch Effects and other Unwanted Variation

Tools and Technology Seminar, University of Michigan, 2018

Removing Unwanted Variation with Negative Controls and Replicates

2017 Single-Cell Genomic Data Analytics Symposium, University of Michigan, 2017

Research Ethics and Statistics

University of Michigan Undergrad Research Opportunity Program (UROP) Student Invited Speaker, 2017

Removing Unwanted Variation with Negative Controls and Replicates

A Symposium on Big Data, Human Health, and Statistics, University of Michigan, 2017

The Classification Permutation Test: A Nonparametric Test for Equality of Multivariate Distributions

Atlantic Causal Inference Conference, University of North Carolina, 2017

Removing Unwanted Variation with Negative Controls and Replicates

Departmental Seminar, University of Michigan, 2017

Removing Unwanted Variation with Negative Controls and Replicates

Network of Mind Symposium, University of Sydney, 2017

Three Topics in Removing Unwanted Variation

Bioinformatics Seminar, Walter and Eliza Hall Institute, 2017

Removing Unwanted Variation with Replicates and Negative Controls

ICSA, Shanghai Jiao Tong University, 2016

Normalization of Microenvironment Microarrays

NIH LINCS Retreat, Oregon Health and Science University, 2016

The Classification Permutation Test

Atlantic Causal Inference Conference, New York University, 2016

Classification, Cross Normalization, and the Number-of-Factors Problem

Departmental Seminar, University of Victoria, 2015

Removing Unwanted Variation with Negative Controls

Departmental Seminar, EPFL, Lausanne, Switzerland, 2015

Departmental Seminar, Stanford University, 2015

Departmental Seminar, Texas A&M University, 2015

Departmental Seminar, University of California, Davis, 2015

Departmental Seminar, University of California, Santa Barbara, 2015

Departmental Seminar, University of Victoria, 2015

Departmental Seminar, University of Michigan, Ann Arbor, 2014

Neyman Seminar, University of California, Berkeley, 2014

Removing Unwanted Variation from High Dimensional Data with Negative Controls

Joint Statistical Meetings, 2013.

Using Control Genes to Correct for Unwanted Variation in Microarray Data

Statistics and Genomics Seminar, Berkeley, 2011.

Correcting for Unwanted Variation in Microarray Data

Bioinformatics Seminar, Walter and Eliza Hall Institute, 2009.

Teaching

University of Michigan

Winter 2021	Stat 700	Special Topics in Applied Statistics
Fall 2020	Stat 500	Statistical Learning I: Regression
Fall 2020	Stat 499	Honors Seminar
Winter 2020	Stat 280	Honors Introduction to Statistics & Data Analysis
Fall 2019	Stat 500	Statistical Learning I: Regression
Fall 2018	Stat 500	Statistical Learning I: Regression
Winter 2018	Stat 280	Honors Introduction to Statistics & Data Analysis
Fall 2017	Stat 280	Honors Introduction to Statistics & Data Analysis
Winter 2017	Stat 280	Honors Introduction to Statistics & Data Analysis
Fall 2016	Stat 280	Honors Introduction to Statistics & Data Analysis
Winter 2016	Stat 500	Applied Statistics I
Fall 2015	Stat 500	Applied Statistics I

UC Berkeley

Spring 2015	Stat 240	Nonparametric and Robust Methods
Spring 2014	Stat 240	Nonparametric and Robust Methods
Fall 2013	Stat 272	Statistical Consulting
Spring 2013	Stat 154	Modern Statistical Prediction and Machine Learning
Summer 2011	Stat 132	Practical Machine Learning
Fall 2010	Stat 21	Introductory Probability and Statistics for Business Students

As Teaching Assistant (UC Berkeley)

Spring 2012	Stat C245F	Statistical Genomics
Spring 2009	Stat 215B	Applied Statistics
Fall 2007	Stat 215A	Applied Statistics
Summer 2007	Stat 21	Introductory Probability and Statistics for Business Students
Spring 2007	Stat 20	Introduction to Probability and Statistics
Fall 2006	Stat 2	Introduction to Statistics
Spring 2006	Stat 21	Introductory Probability and Statistics for Business Students
Fall 2005	Stat 2	Introduction to Statistics
Summer 2005	Stat 2	Introduction to Statistics

Mentoring

PhD Students

Robyn Ferg	Thesis advisor	1/2016 – 08/2020
Julie Deeke	Thesis advisor	8/2016 – 11/2019
Gregory Hunt	Thesis advisor	3/2016 – 11/2018
Charlotte Mann	Research project	3/2020 –
Yujia Pan	Thesis advisor	3/2017 –
Zoe Rehnberg	Thesis advisor	3/2017 –
Ed Wu	Thesis advisor	5/2017 –

Masters Students

Alex Shawn	Research project	4/2020 – 9/2020
Kaifeng Chen	Research project	5/2016 – 4/2019
Ed Wu	Research project	5/2016 – 5/2017

Undergraduate Students

Juejue Wang	Honors Thesis	1/2021 –
Zhanning Zhu	Research project	1/2021 –
Allister Ho	Research project	1/2021 –
Vivian Wang	Research project	1/2021 –
Kathy Huo	Research project	1/2021 –
Melody Wu	Research project	1/2020 – 5/2020
Siwei Sun	Research project	1/2020 – 5/2020
Ben Rappoport	Research project	1/2020 – 5/2020
Nicole Kim	Research project	1/2020 – 5/2020
Qian Lin	Research project	1/2020 – 5/2020
Junshan Chen	Research project	1/2020 – 5/2020
Zhihao Guo	Research project	1/2019 – 12/2019
Ashwin Pothukuchi	Research project	1/2019 – 5/2019
Emma Pomeranz	Research project	1/2019 – 5/2019
Sharanya Jayendraprasad	Research project	5/2016 – 5/2018
Xia Wu	Research project	5/2016 – 7/2017

Thesis and Exam Committees

Nicholas Wang	Progress Review Cmte. Meeting	01/2021
Enes Dilber	PhD Prelim Exam	01/2021
Elnaz Kabir	Thesis Defense	12/2020
Robyn Ferg	Thesis Defense	07/2020
Joseph Dickens	Thesis Defense	05/2020
Adam Hall	Thesis Defense	08/2019
Yura Kim	Thesis Defense	05/2019
Yujia Pan	PhD Prelim Exam	04/2019
Zoe Rehnberg	PhD Prelim Exam	04/2019
Julie Deeke	Thesis Defense	04/2019
Gregory Hunt	Thesis Defense	11/2018
Yilai Li	Thesis Defense	04/2018
Ed Wu	PhD Prelim Exam	04/2018
Teal Guidici	Thesis Defense	03/2018
Shweta Ramdas	Progress Review Cmte. Meeting	11/2017
Robyn Ferg	PhD Prelim Exam	11/2017
Julie Deeke	PhD Prelim Exam	09/2017
Joseph Dickens	PhD Prelim Exam	09/2017
Yilai Li	Progress Review Cmte. Meeting	08/2017
Shweta Ramdas	Progress Review Cmte. Meeting	01/2017
Gregory Hunt	PhD Prelim Exam	12/2016
Yura Kim	PhD Prelim Exam	12/2016
Adam Hall	PhD Prelim Exam	09/2016

Student Talks and Posters

Student Talks

1. Pan, Y., and Gagnon-Bartsch, J. A. (2021), "Separating and reintegrating latent variables for improved classification of genomic data," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor MI.
2. Rehnberg, Z., and Gagnon-Bartsch, J. (2021), "Computationally efficient classification in large drug screening studies," Meeting of the Eastern North American Region of The International Biometric Society, Virtual Meeting.
3. Mann, C., Charlotte Z. Abshire, Yost, M., Kaatz, S., Swaminathan, L., Flanders, S. A., Prescott, H. C., and Gagnon-Bartsch, J. A. (2021), "Derivation and external validation of a simple risk score to predict in-hospital mortality in patients hospitalized for COVID-19," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor MI.
4. Rehnberg, Z., and Gagnon-Bartsch, J. (2020), "Irreproducibility in large-scale drug sensitivity data," Meeting of the Eastern North American Region of The International Biometric Society, Virtual Meeting.
5. Rehnberg, Z., and Gagnon-Bartsch, J. (2019), "Irreproducibility in large-scale drug sensitivity data," Michigan Institute for Data Science Symposium, Ann Arbor, MI.

6. Wu, E., Gagnon-Bartsch, J., Sales, A., Botelho, A., Heffernan, N., Miratrix, L., and Patikorn, T. (2019), "Integrating experimental and observational data through machine learning," MIDAS Annual Symposium, Ann Arbor, MI.
7. Hunt, G. J., and Gagnon-Bartsch, J. A. (2019), "Determining brain cell-types in the presence of complex biology," Joint Statistical Meetings 2019, Denver CO.
8. Ferg, R. A., Gagnon-Bartsch, J. A., and Conrad, F. (2019), "Tracking public opinion with twitter: A critical comparison of cross-sectional and longitudinal analyses," Joint Statistical Meetings, Denver.
9. Ferg, R. A., Gagnon-Bartsch, J., and Fred, C. (2019), "Tracking presidential approval with twitter: A critical comparison of cross-sectional and longitudinal analyses," European Survey Research Association, Zagreb.
10. Pan, Y. (2019), "Learning from unobserved covariates for improved classification accuracy," Joint Statistical Meetings, Denver.
11. Rehnberg, Z., and Gagnon-Bartsch, J. A. (2019), "Characterizing irreproducibility in drug sensitivity data from a large pharmacogenomic study," Joint Statistical Meetings, Denver.
12. Wu, E. (2019), "The p-loop estimator: Covariate adjustment for paired experiments," Joint Statistical Meetings, Denver.
13. Ferg, R. A. (2019), "An introduction to obtaining tweets and analyzing their sentiment," US Census Bureau, Washington, D.C.
14. Hunt, G. J., Dane, M. A., Korkola, J. E., Heiser, L. M., and Gagnon-Bartsch, J. A. (2019), "Robust transformation of mema data," Western North American Region of the International Biometric Society, Portland OR.
15. Rehnberg, Z., and Gagnon-Bartsch, J. (2019), "Irreproducibility in drug sensitivity data from a large pharmacogenomic study," Meeting of the Western North American Region of The International Biometric Society (WNAR), Portland, OR.
16. Ferg, R. A., Gagnon-Bartsch, J. A., and Conrad, F. G. (2019), "Tracking presidential approval with twitter: A critical comparison of cross-sectional and longitudinal analyses," American Association for Public Opinion Research, Toronto.
17. Wu, E. (2019), "The loop estimator: Adjusting for covariates in randomized experiments," 2nd Annual Data for Public Good Symposium, University of Michigan.
18. Deeke, J. M. (2018), "Identifying endogenous reference genes for single-cell rna-sequencing," Western North American Region of the International Biometric Society, Edmonton.
19. Hunt, G. J., Freytag, S., Bahlo, M., and Gagnon-Bartsch, J. A. (2017), "Estimating cell-type proportions using gene expressions," Mathematics Colloquium and EXTREEMS-QED Lecture, College of William and Mary, Williamsburg VA.
20. Hunt, G. J., Freytag, S., Bahlo, M., and Gagnon-Bartsch, J. A. (2017), "Dtangle: A simple and fast cell type deconvolution estimator," Joint Statistical Meetings, Baltimore MD.
21. Hunt, G. J., Freytag, S., Bahlo, M., and Gagnon-Bartsch, J. A. (2017), "Dtangle: A simple and fast cell type deconvolution estimator," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor MI.

Student Posters

1. Mann, C., Charlotte Z. Abshire, Yost, M., Kaatz, S., Swaminathan, L., Flanders, S. A., Prescott, H. C., and Gagnon-Bartsch, J. A. (2021), "Derivation and external validation of a simple risk score to predict in-hospital mortality in patients hospitalized for COVID-19," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor MI.
2. Rehnberg, Z. L., and Gagnon-Bartsch, J. A. (2021), "Empirical maximum likelihood normalization for drug screening data," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor, MI.
3. Rehnberg, Z. L., and Gagnon-Bartsch, J. A. (2020), "Irreproducibility in large-scale drug sensitivity data," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor, MI.
4. Wu, E. (2020), "The p-loop estimator: Covariate adjustment for paired experiments," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor, MI.
5. Pan, Y. (2019), "Improving high-dimensional classification in the presence of latent variables," MIDAS Annual Symposium.
6. Wu, E. (2019), "The p-loop estimator: Covariate adjustment for paired experiments," Atlantic Causal Inference Conference, Montreal.
7. Ferg, R. A., Gagnon-Bartsch, J., and Conrad, F. (2019), "A longitudinal analysis of politically active twitter users," Michigan Student Symposium for Interdisciplinary Statistical Sciences, University of Michigan.
8. Deeke, J., and Gagnon-Bartsch, J. (2018), "Identifying endogenous reference genes from single-cell rna-sequencing," Women in Big Data at Michigan, Ann Arbor, MI.
9. Deeke, J., and Gagnon-Bartsch, J. (2018), "Identifying endogenous reference genes from single-cell rna-sequencing," Michigan Institute for Data Science Annual Symposium, Ann Arbor, MI.
10. Ferg, R. A., Gagnon-Bartsch, J., and Conrad, F. (2018), "A cross-sectional vs. Longitudinal case study of twitter and presidential approval," BigSurv: Big Data Meets Survey Science, Barcelona.
11. Ferg, R. A., Gagnon-Bartsch, J., and Conrad, F. (2018), "A cross-sectional vs. Longitudinal case study of twitter and presidential approval," Michigan Institute of Data Science 2018 Data Science Symposium, University of Michigan.
12. Deeke, J., and Gagnon-Bartsch, J. (2018), "Identifying endogenous reference genes from single-cell rna-sequencing," Health Sciences Challenge Symposium of Michigan Institute for Data Science, Ann Arbor, MI.
13. Deeke, J., and Gagnon-Bartsch, J. (2018), "Identifying endogenous reference genes from single-cell rna-sequencing," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor, MI.
14. Ferg, R. A., Gagnon-Bartsch, J., and Conrad, F. (2018), "A cross-sectional vs. Longitudinal case study of twitter and presidential approval," Michigan Student Symposium for Interdisciplinary Statistical Sciences, University of Michigan.

15. Deeke, J., and Gagnon-Bartsch, J. (2017), "Modeling amplification biases in single-cell rna-sequencing," Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor, MI.
16. Wu, E. (2016), "Covariate-adjusted estimation of the average treatment effect in randomized experiments," Nonparametric Statistics Workshop, Ann Arbor.

Professional Activities

Conference Sessions

- *Integration of Imaging and Genomic Data* (2019). Organizer. Meeting of the Western North American Region of The International Biometric Society (WNAR). Invited session.
- *Leveraging Disparate Sources of Data and Machine Learning to Improve Causal Inference* (2019). Co-Organizer and Chair, with Jann Spiess. Joint Statistical Meetings. Sponsor: ENAR. Topic contributed session.
- *Removing Unwanted Variation with R* (2018). Organizer and Session Leader, with additional presenters Anna Quagliari, Marie Trussart, Sepideh Foroutan, and Ramyar Mollania. useR! Tutorial session.
- *Batch Effects in Genomics Data* (2016). Organizer and Chair. Joint Statistical Meetings. Section on Statistics in Genomics and Genetics. Topic contributed session.

Journal Referee

- *Annals of Applied Statistics*
- *Bioinformatics*
- *Biometrics*
- *Biometrika*
- *BMC Bioinformatics*
- *Briefings in Bioinformatics*
- *Cell Reports*
- *Chemometrics and Intelligent Laboratory Systems*
- *Environmental and Ecological Statistics*
- *Gastric Cancer*
- *Genome Biology*
- *Genome Research*
- *International Journal of Public Opinion Research*
- *Journal of the American Statistical Association*
- *Journal of Econometrics*
- *Journal of Educational and Behavioral Statistics*
- *Microbiome*
- *Molecular Psychiatry*

- *Nucleic Acids Research*
- *Nucleic Acids Research: Genomics and Bioinformatics*
- *Plos Computational Biology*
- *Plos One*
- *Public Opinion Quarterly*
- *Proceedings of the National Academies of Sciences*
- *Scientific Reports*
- *Social Science Computer Review*
- *Statistica Sinica*

Grant Review

- NSF, 2018, Ad hoc
- NSF, 2019, Panel

Other Reviewer Activities

- External grant review, University of Queensland Diamantina Institute (Australia)
- External thesis review, University of Melbourne (Australia)
- Textbook review, Wiley

Memberships

- American Statistical Association
- Institute of Mathematical Statistics

Service

Big Data Science Institute (BDSI)

Departmental Service

2021	Masters Admissions Committee
2020–2021	Undergraduate Advising
2020	Seminar Committee
2019	Seminar Committee (chair)
2018	Undergraduate Curriculum Committee
2018	Undergraduate Advising
2017–2018	Masters Admissions Committee
2017–2018	Masters Advising
2017–2018	Seminar Committee
2016–2017	Masters Admissions Committee
2016–2017	Undergraduate Advising
2016–2017	Committee for Undergraduate Research in Statistics
2016–2017	Seminar Committee
2015–2016	Undergraduate Advising
2015–2016	Committee for Undergraduate Research in Statistics
2015–2016	Seminar Committee
2015	Graduate Curriculum Committee

First Year PhD Student Advising

2020–2021 Avery Winn
2019–2020 Brian Manzo
2017–2018 Daniel Iong
2016–2017 Yujia Pan
2015–2016 Nick Zaborek

Other Service

2021–2022 Michigan Student Symposium for Interdisciplinary Statistical Sciences (MSSISS)
Faculty Advisor
2020 Introduction to Data Science (Stat 206) Task Force
2019 Graduate Curriculum Task Force
2019 Course planning discussion leader, LSA Teaching Academy
2017 Course planning discussion leader, LSA Teaching Academy
2017 Conducted Skype interviews for the PhD admissions committee
2016 NextProf host

Awards

- **MIDAS Reproducibility Challenge Winner (2020)**
Recognizes work in developing workflows for reproducible research, in enabling a deeper understanding of issues of reproducibility, and in providing tools and templates that others can follow.
- **Thomas R. Ten Have Award (2016)**
Recognizes “exceptionally creative or skillful research on causal inference.” Awarded at the Atlantic Causal Inference Conference.
- **Evelyn Fix Prize (2013)**
Awarded to the PhD student on the Berkeley campus showing the greatest promise in statistical research, with preference for applications to biology and problems of health.
- **Outstanding Graduate Student Instructor Award (2010)**
Given to at most 9% of Berkeley teaching assistants.
- **Elizabeth Scott Award (2007)**
Given as warranted, but at most annually, to the M.A. student in the Statistics Department showing the greatest promise in statistical research.

Other Activities

- Consulting experience (2008–2013)
Berkeley Statistics Department’s free consulting service. Four semesters as a consultant, one semester as the course instructor.
- Summer Statistics Intern (2009)
Genentech. South San Francisco, CA
- The Cancer Genome Atlas (TCGA) Batch Effects Working Group (BEWG) participant (2010–2011).
- Summer Research Intern (2002)

DESY Particle Accelerator. Hamburg, Germany.

- Stanford Overseas Studies Program (2001–2002)
Moscow, Russia and Berlin, Germany.