

Kaiqiong Zhao – Curriculum Vitae

Website

<https://kaiqiong.github.io>
Google Scholar

Email Github

kaiqiong.zhao@utoronto.ca
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Research Interests

Statistical genetics, high-dimensional statistics, statistical computing, robust optimization, data integration, statistical machine learning

Education

2016-2021 Ph.D. in Biostatistics – McGill University, Montréal, QC, Canada

Thesis: Smooth modelling of covariate effects in bisulfite sequencing-derived measures of DNA methylation

Supervisors: [Celia M.T. Greenwood](#), Ph.D. and [Karim Oualkacha](#), Ph.D.

2014-2016 M.Sc. in Computational biology – University of Manitoba, Winnipeg, MB, Canada

Thesis: Gene-pair based statistical methods for testing gene set enrichment in microarray gene expression studies.

Supervisor: [Pingzhao Hu](#), Ph.D.

2013-2014 M.Sc. in Statistics – University of Windsor, Windsor, ON, Canada

Thesis: Confidence interval construction procedures for a difference between two dependent ICCs

Supervisor: [Sudhir Paul](#), Ph.D.

2009-2013 B.Sc. in Statistics – Beijing Institute of Technology, Beijing, China

Project Topic: Hypothesis testings for the exponential distribution parameters

Honors, Awards and Fellowships

2021-2023 CANSSI Distinguished Postdoctoral Fellowships (\$70,000/ year)

2018-2021 Fonds de recherche du Québec – Santé ([FRQS](#)) [Doctoral award](#) (\$21,000/ year)

2018-2019 Graduate Excellence Award, McGill University (\$12,638)

2018 Graduate Research Enhancement and Travel Awards, McGill University (\$415)

2017-2018 Faculty of Medicine Internal Studentship, McGill University (\$12,000)

2016-2017 Graduate Excellence Award, McGill University (\$27,748)

2015 Selected as 1 of 4 departmental presenters, in 2016 Edge of Science & Medicine, U of Manitoba

2015 Graduate Study Travel Award, University of Manitoba (\$750)

2015 Travel award for attending CANSSI workshop “New Horizons in Copula Modeling” (\$1000)

2014 Entrance Scholarship, University of Manitoba (\$4000)

2013 Entrance Scholarship, University of Windsor (\$5500)

2012 Honorable Mention, Undergraduate Mathematical Contest in Modeling, [COMAP](#), USA

2010 Silver Medalist, Beijing Undergraduate Mathematical Contest in Modeling, [CSIAM](#), China

Professional Experience

Nov 2021 - University of Alberta and University of Toronto, Canada

Current *CANSSI Distinguished Postdoctoral Fellow*

Supervisors: [Linglong Kong](#), Ph.D. and [Dehan Kong](#), Ph.D.

Mar 2018 - Jewish General Hospital, Montréal, QC, Canada

Dec 2019 *Statistics Consultant (Part-time)*

Provide statistical support for research projects of the investigator [Marylise Boutros](#), M.D., FRCSC. Duties include conducting data analysis, interpreting results, writing reports, and preparing tables and figures for manuscript or presentations.

Teaching Experience

Course Instructor

Jan 2022 - Department of Mathematical and Statistical Sciences, University of Alberta, AB, Canada

Apr 2022 *STAT 161: Introductory Statistics for Business and Economics*

141 enrolled students (3.8/5.0)

Jan 2020 - Department of Epidemiology, Biostatistics, and Occupational Health, McGill University, QC, Canada

Apr 2020 *EPIB 521: Regression Analysis for Health Sciences*

11 enrolled students (4.5/5.0)

Teaching Assistant

Sep 2017 - Department of Epidemiology, Biostatistics, and Occupational Health, McGill University

Apr 2018 *EPIB 607: Inferential Statistics*

EPIB 621: Data Analysis in Health Sciences

Sep 2013 - Department of Mathematics and Statistics, University of Windsor

Dec 2013 *62-130-01: Elements of Calculus*

Software Development

R packages

- **SOMNiBUS** (<https://www.bioconductor.org/packages/release/bioc/html/SOMNiBUS.html>)
A method for estimating smooth covariate effects and identifying differentially methylated regions, which copes with experimental errors and provides reliable inference.
- **sparseSOMNiBUS** (<https://github.com/kaiqiong/sparseSOMNiBUS>), coded with **Rcpp**
A sparse-smooth modeling method for identifying SNPs associated with methylation levels in a region, which copes with high-dimensional feature space and allows variable selection.
- **MoMotif** (<https://github.com/kaiqiong/MoMotif>)
A bioinformatics tool for a sensitive identification, at the single base-pair resolution, of complex, or subtle, alterations to core binding motifs, discerned from ChIP-seq data.

Shiny Application

- A web-based **Risk Calculator for Readmission for Dehydration following Creation of a Diverting Loop Ileostomy** (https://kaiqiong.shinyapps.io/dehydration_app/)

Publications

1. **Zhao, K.**, Oualkacha, K., Zeng, Y., Shen, C., Lakhal-Chaieb, L., Labbe, A., Klein, K., Hudson, M., Colmegna, I., Pastinen, T., Bernatsky, S., & Greenwood, C.M.T. A hierarchical quasi-binomial varying coefficient mixed model for detecting differentially methylated regions in bisulfite sequencing data: applications to a preclinical study on rheumatoid arthritis. (2022+). Under Review.
2. Chauhan, U., **Zhao, K.**, Walker, J. & Mackey, J.R. Weighted trajectory analysis and application to clinical outcome assessment. *Statistics in Medicine* (2022+). Submitted
3. *Lebeau, B., ***Zhao, K.**, Jangal, M., Zhao, T., Guerra, M., Greenwood, C.M.T. & Witcher, M. Single base-pair resolution analysis of DNA binding motif with MoMotif reveals an oncogenic function of CTCF zinc-finger 1 mutation. *Nucleic Acids Research* (2022). PMID: 35947648. * co-first authorship

4. **Zhao, K.**, Oualkacha, K., Lakhal-Chaieb, L., Labbe, A., Klein, K., Ciampi, A., Hudson, M., Colmegna, I., Pastinen, T., Zhang, T., Daley, D. & Greenwood, C.M.T. A novel statistical method for modeling co-variate effects in bisulfite sequencing derived measures of DNA methylation. *Biometrics* (2021). PMID: 32438470.
5. Zeng, Y., **Zhao, K.**, Oros Klein, K., Shao, X., Fritzler, M.J., Hudson, M., Colmegna, I., Pastinen, T., Bernatsky, S. & Greenwood, C.M.T. Thousands of CpGs Show DNA Methylation Differences in ACPA-Positive Individuals. *Genes* (2021). PMID: 34573331.
6. Caillon, A., **Zhao, K.**, Klein, K., Greenwood, C.M.T., Lu, Z., Paradis, P. & Schiffrin, E. High systolic blood pressure at hospital admission is an important risk factor in models predicting outcome of COVID-19 patients. *American Journal of Hypertension* (2021). PMID: 33386395.
7. Moon, J., Monton, O., Smith, A., Garfinkle, R., **Zhao, K.**, Zekowitz, P., Loisel, C.G., Fiore Jr, J.F., Sender Liberman, A., Morin, N. and Faria, J. Interactive online informational and peer support application for patients with low anterior resection syndrome: patient survey and protocol for a multicentre randomized controlled trial. *Colorectal Disease* (2021). PMID: 33638278
8. Caminsky, N., Hamad, D., He, H.B., **Zhao, K.**, Boutros, M., Feldman, L.S., Lee, L. & Fiore, J.F. Optimizing discharge decision-making in colorectal surgery: a prospective cohort study of discharge practices in a recently implemented enhanced recovery pathway. *Colorectal Dis* (2021). PMID: 33423346.
9. Zhou, S., Butler-Laporte, G., Nakanishi, T., Morrison, D., Afilalo, J., Afilalo, M., Laurent, L., Pietzner, M., Kerrison, N., **Zhao, K.**, ..., Richards, M. A Neanderthal OAS1 Isoform Protects Against COVID-19 Susceptibility and Severity: Results from Mendelian Randomization and Case-Control Studies. *Nature Medicine* (2021). PMID: 33633408
10. Manousaki, D., Forgetta, V., Keller-Baruch, J., **Zhao, K.**, Greenwood, C.M.T., Mooser, V., Bassett, J.D., Leslie, W.D. & Richards, J.B. A polygenic risk score as a risk factor for medication-associated fractures. *Journal of Bone and Mineral Research* (2020). PMID: 32511779.
11. Alqahtani, M., Garfinkle, R., **Zhao, K.**, Vasilevsky, C.A., Morin, N., Ghitulescu, G., Faria, J. & Boutros, M. Can we better predict readmission for dehydration following creation of a diverting loop ileostomy: development and validation of a prediction model and web-based risk calculator. *Surgical Endoscopy* (2020). PMID: 31451920.
12. Al-Masrouri, S., Garfinkle, R., Al-Rashid, F., **Zhao, K.**, Morin, N., Ghitulescu, G.A., Vasilevsky, C.A. & Boutros, M. Readmission for Treatment Failure After Nonoperative Management of Acute Diverticulitis: A Nationwide Readmissions Database Analysis. *Diseases of the Colon & Rectum* (2020). PMID: 31914114.
13. **Zhao, K.**, Jiang, L., Klein, K., Greenwood, C.M.T. & Oualkacha, K. CpG-set association assessment of lipid concentration changes and DNA methylation. *BMC proceedings* (2018). PMID: 30263044.
14. Jiang, L., **Zhao, K.**, Klein, K., Canty, A. J., Oualkacha, K. & Greenwood, C.M.T. Investigating potential causal relationships between SNPs, DNA methylation and HDL. *BMC proceedings* (2018). PMID: 30275877.
15. Lakhal-Chaieb, L., Greenwood, C.M.T., Ouhourane, M., **Zhao, K.**, Abdous, B. & Oualkacha, K. A smoothed EM-algorithm for DNA methylation profiles from sequencing-based methods in cell lines or for a single cell type. *Statistical applications in genetics and molecular biology* (2017). PMID: 29055941.
16. Ye, X., **Zhao, K.**, Wu, C., Hu, P. & Fu, H. Associations between genetic variants in immunoregulatory genes and risk of non-Hodgkin lymphoma in a Chinese population. *Oncotarget* (2017). PMID: 28060727.
17. Patton, M. J., McCorrister, S., Grant, C., Westmacott, G., Fariss, R., Hu, P., **Zhao, K.**, Blake, M., Whitmire, B., Yang, C., Caldwell, H.J. & McClarty, G. Chlamydial Protease-like Activity Factor and Type III Secreted Effectors Cooperate in the Inhibition of p65 Nuclear Translocation. *mBio* (2016). PMID: 27677792.

Talks and Seminars

Invited Talks

Jul 2022	International Chinese Statistical Association (ICSA)-Canada Chapter, Banff, AB
Jun 2022	Statistical Society of Canada (SSC), Virtual
Apr 2021	Jewish General Hospital Epidemiology Seminar Series, Montréal, QC, Virtual
Dec 2020	Bioinformatics-Biostatistics Research Seminar Series, University of Manitoba, Winnipeg, MB, Virtual
Dec 2020	McGill Initiative in Computational Medicine Research Day , Montréal, QC, Virtual
Oct 2020	Statistics Seminar , Département de mathématiques, UQAM, Montréal, QC, Virtual
Feb 2019	Statistical Genetics Group Seminar , Jewish General Hospital, Montréal, QC
Feb 2015	Seminar , Department of Biochemistry and Medical Genetics, University of Manitoba, Winnipeg, MB

Contributed Talks

Sep 2020	(Bio)Statistics Research and Career Day, McGill University, Montréal, QC
Aug 2018	BIRS Workshop: New Statistical Methods for Family-Based Sequencing Studies, Banff, AB
June 2018	7th Annual Canadian Human and Statistical Genetics Meeting, Harrison Hot Spring, BC
June 2018	Statistical Society of Canada, Montréal, QC
June 2017	Statistical Society of Canada, Winnipeg, MB
June 2016	Canadian Society for Epidemiology and Biostatistics, Winnipeg, MB
Jan 2016	Edge of Science & Medicine, Faculty of Health Sciences, University of Manitoba, Winnipeg, MB
Jun 2015	Statistical Society of Canada Student Conference, Halifax, NS

Poster Presentations

Oct 2019	Annual International Genetic Epidemiology Society Meeting, Houston, Texas, USA
June 2019	8th Annual Canadian Human and Statistical Genetics Meeting, Montebello, QC
Sep 2018	(Bio)Statistics Research Day, Montréal, QC
Mar 2017	Genetic Analysis Workshop 20, San Diego, CA, USA
Apr 2016	5th Annual Canadian Human and Statistical Genetics Meeting, Halifax, NS
Oct 2015	11th Annual Canadian Chronic Lymphocytic Leukemia (CLL) Meeting, Winnipeg, MB
Sep 2015	Child Health Research Day, Winnipeg, MB

Journal Review

2022	Article reviewed for <i>Journal of the American Statistical Association; Applications & Case Studies</i>
2020	Article co-reviewed for <i>The Annals of Applied Statistics</i>
2020	Article co-reviewed for <i>Genetic Epidemiology</i>

Community Activities & Service

July 2022	Conference session organizer <i>International Chinese Statistical Association (ICSA) – Canada Chapter Symposium, Banff, Alberta</i> Session: Statistical Learning Methods and Applications
July 2022	Conference session chair <i>International Chinese Statistical Association (ICSA) – Canada Chapter Symposium, Banff, Alberta</i> Session: Recent Advances in Statistical Genetics
Sep 2017 - Aug 2018	Student representative for the Biostatistics PhD Comprehensive Exam Department of Epidemiology, Biostatistics and Occupational Health, McGill University

Last Updated on Nov 23, 2022