

# Keegan D. Korthauer

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## EDUCATION

- 2015 **Ph.D., Statistics**, University of Wisconsin, Madison, Wisconsin USA  
*Advisor: Christina Kendzierski, Ph.D.*  
*Dissertation: Bayesian hierarchical modeling of high-throughput genomic data with applications to cancer bioinformatics and stem cell differentiation*
- 2009 **M.S., Biostatistics**, University of Minnesota, Minneapolis, Minnesota USA  
*Advisor: David Nelson, Ph.D.*  
*Thesis: The impact of missing confounders on propensity stratification in observational studies*
- 2007 **B.S., Biology**, University of Minnesota, Minneapolis, Minnesota USA  
*Summa cum laude*

## PROFESSIONAL POSITIONS

- 2015 - **Postdoctoral Research Fellow**, Boston, Massachusetts  
Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute  
Department of Biostatistics, Harvard T.H. Chan School of Public Health  
*Mentor: Rafael Irizarry, Ph.D.*  
*Develop statistical & computational tools for high-throughput genomics data*
- 2013 -2015 **Graduate Research Assistant**, Madison, Wisconsin  
Department of Biostatistics and Medical Informatics, University of Wisconsin  
*Advisor: Christina Kendzierski, Ph.D.*  
*Collaborate with clinical oncologists and developmental biologists to gain insight into biological processes*
- 2010-2013 **Predoctoral Fellow, NIGMS Biostatistics Training Grant**, Madison, Wisconsin  
Department of Biostatistics and Medical Informatics, University of Wisconsin  
*Advisors: Bret Larget, Ph.D., Christina Kendzierski, Ph.D., and Michael Newton, Ph.D.*  
*Rotation projects:*  
- *Hidden Markov Modeling of Palindromic Sequences*  
- *SNP-based Genomic Signature of Survival in Ovarian Cancer*  
- *Analysis of Copy Number in Whole Genome Amplified Samples*
- 2009-2010 **Project Assistant**, Madison, Wisconsin  
Institute for Clinical and Translational Research (ICTR), University of Wisconsin  
*Advisor: Mary Lindstrom, Ph.D.*  
*Consult with ICTR investigators on design and analysis plans*
- 2008-2009 **Statistics Intern**, Minneapolis, Minnesota  
Veterans Affairs (VA) Medical Center  
*Advisor: David Nelson, Ph.D.*  
*Investigate the impact of missing confounders in causal inference*

2007-2009 **Project Assistant**, Minneapolis, Minnesota  
Biostatistics Design and Analysis Center, University of Minnesota  
*Advisor: Cynthia Davey, M.S.*  
*Consult with on-campus investigators on design and analysis plans*

## PUBLICATIONS

### Pre-prints

- [1] **K. Korthauer**, R. A. Irizarry. Genome-wide repressive capacity of promoter DNA methylation is revealed through epigenomic manipulation. *bioRxiv*, <https://doi.org/10.1101/381145>, 2018.

### Peer-Reviewed Journal Articles

- [1] D. Y. Takeda\*, S. Spisák\*, J.-H. Seo, C. Bell, E. O'Connor, **K. Korthauer**, D. Ribli, I. Csabai, N. Solymosi, Z. Szállási, P. Cejas, X. Qiu, H. Long, V. Tisza, P. V. Nuzzo, M. Rohanizadegan, M. M. Pomerantz, W. C. Hahn, M. L. Freedman. A somatically acquired enhancer of the androgen receptor is a noncoding driver in advanced prostate cancer. *Cell*, in press, 2018.
- [2] **K. Korthauer**, S. Chakraborty, Y. Benjamini, R. A. Irizarry. Detection and accurate False Discovery Rate control of differentially methylated regions from Whole Genome Bisulfite Sequencing. *Biostatistics*, kxy007, 2018.
- [3] C. J. Shukla, A. L. McCorkindale, C. Gerhardinger, **K. Korthauer**, M. N. Cabili, D. M. Shechner, R. A. Irizarry, P. G. Maass, J. L. Rinn. High-throughput identification of RNA nuclear enrichment sequences. *The EMBO Journal*, 37:e98452, 2018
- [4] J. Choi, S. Ye, K. Eng, **K. Korthauer**, W. H. Bradley, J. S. Rader and C. Kendzierski. IPI59: an actionable biomarker to improve treatment response in serous ovarian carcinoma patients. *Statistics in Biosciences*, 9(1):1-12, 2017.
- [5] **K. Korthauer**, L.-F. Chu, M. A. Newton, Y. Li, J. Thomson, R. Stewart and C. Kendzierski. A statistical approach for identifying differential distributions in single-cell RNA-seq experiments. *Genome Biology*, 17:222, 2016.
- [6] C. Bodelon, M. Horswill, A. K. Chaturvedi, N. Wentzensen, S. Vinokurova, **K. Korthauer**, S. T. Dunn, J. N. Sampson, M. Schiffman, M. A. Newton, J. den Boon, M. E. Sherman, P. Ahlquist, J. L. Walker, R. E. Zuna, S. S. Wang. Copy number alterations and HPV integration in cervical precancer and invasive cancer. *Carcinogenesis*, 37(2):188-196, 2016.
- [7] **K. Korthauer**, C. Kendzierski. MADGiC: a model-based approach for identifying driver genes in cancer. *Bioinformatics*, 31(10): 15261535, 2015.
- [8] Y. J. Sung, **K. Korthauer**, M. Swartz and C. Engelman. Methods for Collapsing Multiple Rare Variants in Whole Genome Sequencing Data. *Genetic Epidemiology*, 38(S1):S13-S20, 2014.
- [9] J. Delgado, E. A. Jacobs, N. E. Adler, **K. Korthauer** and A. Fernandez. The relation between subjective socioeconomic status, depression and self-rated health in a population of African Americans, Hispanics and non-Hispanic whites with diabetes, *Journal of General Internal Medicine*, 28: S209, 2013.

- [10] M. Wuthrich, K. Ersland, J. C. Pick-Jacobs, B. H. Gern, C. A. Frye, T. D. Sullivan, M. B. Brennan, H. I. Filutowicz, K. O'Brien, **K. Korthauer**, S. Schultz-Cherry, B. S. Klein. Limited model antigen expression by transgenic fungi induces disparate fates during differentiation of adoptively transferred T cell receptor transgenic CD4+ T cells: robust activation and proliferation with weak effector function during recall. *Infection and immunity*, 80(2): 787-797, 2012.
- [11] J. Delgado, A. Fernandez, N. E. Adler, **K. Korthauer**, E. Jacobs. Subjective and objective socioeconomic status and control of hypertension and diabetes. *Journal of General Internal Medicine*, 27:S312-S312, 2012.
- [12] D. Z. Bliss, J. Lewis, **K. Hasselmann (now Korthauer)**, K. Savik, A. Lowry, R. Whitebird. Use and evaluation of disposable absorbent products for managing fecal incontinence by community-living people. *Journal of wound, ostomy, and continence nursing*, 38(3):289, 2011.
- [13] L. Wang, R. M. Mitra, **K. Hasselmann (now Korthauer)**, M. Sato, L. Lenarz-Wyatt, J. D. Cohen, F. Katagiri, J. Glazebrook. The genetic network controlling the Arabidopsis transcriptional response to Pseudomonas syringae pv. maculicola: roles of major regulators and the phytotoxin coronatine. *Molecular plant-microbe interactions*, 21(11): 1408-1420, 2008.

## Book Chapters

- [1] **K. Korthauer**, J. Dawson and C. Kendzierski. Predicting cancer subtypes using survival-supervised latent Dirichlet allocation models. In *Advances in Statistical Bioinformatics: Models and Integrative Inference for High-Throughput Data*, K.-A. Do, Z. S. Qin and M. Vannucci (Eds). Cambridge University Press, 2013.

## Ph.D. Dissertation

- [1] **K. Korthauer**. Bayesian hierarchical modeling of high-throughput genomic data with applications to cancer bioinformatics and stem cell differentiation, Ph.D. Thesis, University of Wisconsin, 2015.

## HONORS & AWARDS

2017	Travel award for the Ascona Workshop 2017 on <a href="#">Statistical Challenges in Single-Cell Biology</a> in Ascona, Switzerland
2016	Travel award from the Biometrics Section of the American Statistical Association to attend the Joint Statistical Meetings in Chicago, Illinois
2015	Poster award from the Regional Advisory Board of the International Biometric Society at the Eastern North American Region Meeting in Miami, Florida
2014	Travel grant from the Vilas Conference Presentation Trust
2013	Travel award from the Howard Hughes Medical Institute/NIGMS to attend the Jackson Laboratory short course on Systems Genetics in Bar Harbor, Maine
2012	Travel award for the Genetic Analysis Workshop in Stevenson, Washington
2008	Outstanding Teaching Assistant Award at the University of Minnesota
2007	Phi Beta Kappa Society

## FELLOWSHIPS

### & SCHOL-

### ARSHIPS

- 2010-2013 NIH/NIGMS Predoctoral Training Grant in Biostatistics, University of Wisconsin
- 2006 Undergraduate Research Opportunities Program project grant, University of Minnesota
- 2003-2007 National Merit James E. Casey Scholarship (\$24,000 USD)

## PRESENTATIONS

### Invited Talks (forthcoming)

- [1] *International Conference on Advances in Interdisciplinary Statistics and Combinatorics*. 2018 October 5-7. Greensboro, NC.
- [2] *European Bioconductor Meeting*. 2018 December 6-7. Munich, Germany.

### Invited Talks

- [1] Detection and inference of differentially methylated regions from bisulfite sequencing. *Bioconductor Conference*. 2017 Jul 26-28. Boston, MA, USA.
- [2] Exploiting heterogeneity in single-cell transcriptomic analyses: how to move beyond comparisons of averages. *Festival of Genomics California*. 19-21 September 2016. San Diego, California.
- [3] A statistical approach for identifying differential distributions in single-cell RNA-seq. *iBRIGHT*. 1-3 November 2015. M. D. Anderson Cancer Center, Houston, Texas.

### Selected Contributed Talks

- [1] *De novo* detection and accurate inference of differentially methylated regions. *Joint Statistical Meetings*. 29 July - 2 August 2018. Vancouver, British Columbia, Canada.
- [2] scDD: A Statistical Approach for Identifying Differential Distributions in Single-Cell RNA-Seq Experiments. 30 July - 4 August 2016. *Joint Statistical Meetings*, Chicago, Illinois.
- [3] Identifying driver genes from somatic mutations: an integrative model-based approach. *International Biometric Society Eastern North American Region (ENAR) Annual Meeting*. 16-19 March 2014. Baltimore Maryland.

### Selected Poster Presentations

- [1] **K. Korthauer**, S. Chakraborty, Y. Benjamini, R.A. Irizarry. Detection and accurate False Discovery Rate control of differentially methylated regions from Whole Genome Bisulfite Sequencing. *ENCODE Consortium Meeting*. 3-7 February 2018.
- [2] **K. Korthauer** Exploiting heterogeneity in single-cell transcriptomic analyses: how to move past comparisons of averages. 30 April - 5 May 2017. *Ascona Workshop on Statistical Challenges in Single-Cell Biology*. Ascona, Switzerland.
- [3] **K. Korthauer**, R.A. Irizarry. Assessing Statistical Significance of Differentially Methylated Regions in Whole-Genome Bisulfite Sequencing Experiments. *ENCODE Consortium Meeting*. 15-16 June 2016. La Jolla, California.

- [4] **K. Korthauer**, C.K. Kendzierski. Differential Dynamics in Single-Cell RNA-Seq Experiments. *International Biometric Society Eastern North American Region (ENAR) Spring Meeting*. 15-18 March 2015. Miami, Florida.
- [5] **K. Korthauer**, C.K. Kendzierski. An integrative approach for the identification of somatic mutations that drive cancer. *Genomic Sciences Training Program Retreat*. 14 June 2013. Madison, Wisconsin.

## EDITORIAL ACTIVITIES

### Journal Referee

Annals of Applied Statistics, Bioinformatics, Biometrics, Biostatistics, GigaScience

## PROFESSIONAL SOCIETIES

2012-present Member, American Statistical Association

## SOFTWARE

### Bioconductor and Github

- [1] *dmrseq*: An R package for inference for differentially methylated regions (DMRs) from bisulfite sequencing, available on [Bioconductor](#).
- [2] *scDD*: An R package for the identification of differentially distributed genes in single-cell RNA-seq, available on [Bioconductor](#)
- [3] *MADGiC*: R package for the identification of cancer driver genes by integrating somatic mutation, expression, replication timing, and functional impact, available on [GitHub](#)

## EDUCATIONAL ACTIVITIES

### Masters of Biostatistics (MS) Advisees

2018 - Present Eunice Ye, Biostatistics  
Academic co-advisor

## TEACHING

### Classroom Instruction

- 2017 **Teaching Assistant**, [Introduction to Data Science \(BST 260\)](#).  
Department of Biostatistics, Harvard T.H. Chan School of Public Health, Boston, MA  
*Formulate problem sets, solutions, and exam questions. Supervise final projects.*
- 2014 **Instructor**, Applied Introductory Statistics for Engineers (STAT 324).  
Department of Statistics, University of Wisconsin, Madison, Wisconsin  
*Curated course material and lectured to 120 students. Designed problem sets and exams. Supervised Teaching Assistants.*
- 2013 **Tutor**, Introduction to Statistical Methods (STAT 301).  
Greater University Tutoring Service, University of Wisconsin, Madison, Wisconsin  
*Designed and led weekly review sessions in a small group setting.*

2007-2008 **Teaching Assistant**, Introduction to Biostatistical Methods I (PubH 6414).  
Division of Biostatistics, School of Public Health, University of Minnesota, Minneapolis,  
Minnesota  
*Led weekly lab sections, held office hours, and graded homework and exams.*

### Shortcourses & Workshops

- 2017 **Co-organizer and instructor** for the [Healthcare Innovation Replicathon](#).  
24-27 March 2017. University of Puerto Rico, San Juan, Puerto Rico.  
*Generated course material for a two-day hackathon-style event focusing on reproducibility and replicability in biomedical data science. Led interdisciplinary teams from basic data science skills through reproducible analyses and presentations using R and GitHub.*
- 2016-2017 **Teaching Assistant**, Summer Short Course: Statistical Methods for Functional Genomics.  
23 June-6 July 2016 and 30 June-13 July 2017. Cold Spring Harbor Laboratory, Cold Spring Harbor, New York  
*Led students through hands-on laboratory sessions.*
- 2016 **Co-organizer and instructor** of Workshop on [Dismantling the bulk: examining neuronal heterogeneity using single-cell techniques](#). 19 September 2016. Festival of Genomics California, San Diego, California.  
*Organized and led a one-day workshop for non-computational biologists on the analysis of single-cell RNA-sequencing data.*