

Keegan D Korthauer, PhD

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INFORMATION Boston, MA 02115 keegan@jimmy.harvard.edu

EDUCATION **University of Wisconsin**, Madison, Wisconsin 2015
Department of Statistics
Ph.D., Statistics
Dissertation: *Bayesian hierarchical modeling of high-throughput genomic data with applications to cancer bioinformatics and stem cell differentiation*
Advisor: Christina Kendzierski, Ph.D.

University of Minnesota, Minneapolis, Minnesota 2009
Division of Biostatistics, School of Public Health
M.S., Biostatistics
Thesis: *The impact of missing confounders on propensity stratification in observational studies*
Advisor: David Nelson, Ph.D.

University of Minnesota, Minneapolis, Minnesota 2007
College of Biological Sciences
B.S., *summa cum laude*, Biology

RESEARCH **Harvard T.H. Chan School of Public Health, &** 2015 - present
EXPERIENCE **Dana-Farber Cancer Institute**, Boston, Massachusetts
Postdoctoral Research fellow
Advisor: Rafael Irizarry, Ph.D.
Role: Develop statistical & computational tools for high-throughput genomics data

University of Wisconsin, Madison, Wisconsin 2013 - 2015
Department of Biostatistics and Medical Informatics
Graduate Research Assistant
Advisor: Christina Kendzierski, Ph.D.
Role: Collaborate with clinical oncologists and developmental biologists to gain insight into biological processes

University of Wisconsin, Madison, Wisconsin 2010 - 2013
Department of Biostatistics and Medical Informatics
Predoctoral Fellow, NIGMS Biostatistics Training Grant
Rotation Projects:
- *Hidden Markov Modeling of Palindromic Sequences*
Advisor: Bret Larget, Ph.D.
- *SNP-based Genomic Signature of Survival in Ovarian Cancer*
Advisor: Christina Kendzierski, Ph.D.
- *Analysis of Copy Number in Whole Genome Amplified Samples*
Advisor: Michael Newton, Ph.D.

<p>University of Wisconsin, Madison, Wisconsin <i>Institute for Clinical and Translational Research (ICTR)</i> Project Assistant Advisor: Mary Lindstrom, Ph.D. Role: Consult with ICTR investigators on design and analysis plans</p>	<p>2009-2010</p>
<p>Veterans Affairs (VA) Medical Center & University of Minnesota, Minneapolis, Minnesota Statistics Intern Supervisor: David Nelson, Ph.D. Role: Investigate the impact of missing confounders in causal inference</p>	<p>2008-2009</p>
<p>University of Minnesota, Minneapolis, Minnesota <i>Biostatistics Design and Analysis Center</i> Project Assistant Supervisor: Cynthia Davey, M.S. Role: Consult with on-campus investigators on design and analysis plans</p>	<p>2007-2009</p>

PUBLICATIONS

Preprints

- 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. *bioRxiv*, doi: <https://doi.org/10.1101/183210>, 2017. [Invited minor revision from *Biostatistics*, November 2017]
- 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. *bioRxiv*, doi: <https://doi.org/10.1101/189654>, 2017.

Peer-Reviewed Journal Articles

- 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.
- 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.
- 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.
- K. Korthauer**, C. Kendzierski. MADGiC: a model-based approach for identifying driver genes in cancer. *Bioinformatics*, 31(10): 15261535, 2015.

- 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.
- 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.
- 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.
- 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.
- 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.
- 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

- 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.

Manuscripts in Preparation

- P. Kimes*, **K. Korthauer***, A. Reyes, C. Duvallet[†], A. Subramanian[†], M. Teng[†], Chinmay Shukla, R. A. Irizarry and S. C. Hicks. A Practical Guide for Methods Controlling False Discovery Rates. Draft available upon request.

* Denotes co-first authorship.

[†] Denotes equal contribution.

HONORS AND AWARDS	<i>Travel Award</i> , Workshop on Statistical Challenges in Single-Cell Biology Ascona, Switzerland	2017
	<i>Travel Award</i> , Biometrics Section, American Statistical Association Joint Statistical Meetings, Chicago, Illinois	2016
	<i>Poster Award</i> , Regional Advisory Board, International Biometric Society Eastern North American Region Meeting, Miami, Florida	2015
	<i>Travel Grant</i> , Vilas Conference Presentation Trust	2014
	<i>Travel Scholarship</i> , Howard Hughes Medical Institute/NIGMS Jackson Laboratory short course on Systems Genetics, Bar Harbor, Maine	2013
	<i>Travel Award</i> , Genetic Analysis Workshop Stevenson, Washington	2012
	<i>Predoctoral Training Grant</i> in Biostatistics National Institute for General Medical Sciences, University of Wisconsin	2010-2013
	<i>Outstanding Teaching Assistant Award</i> , University of Minnesota	2008
	<i>Phi Beta Kappa Society</i> , University of Minnesota	2007
	<i>Research Grant</i> , Undergraduate Research Opportunities Program University of Minnesota	2006
	<i>National Merit James E. Casey Scholarship</i> National Merit Scholarship Program & United Parcel Service (UPS)	2003-2007
SELECTED INVITED TALKS	Bioconductor Meeting, Boston, Massachusetts	July 2017
	<i>Detection and inference of differentially methylated regions from bisulfite sequencing</i>	
	Festival of Genomics California, San Diego, California	September 2016
	<i>Exploiting heterogeneity in single-cell transcriptomic analyses: how to move beyond comparisons of averages</i>	
TEACHING EXPERIENCE	iBRIGHT, M. D. Anderson Cancer Center, Houston, Texas	November 2015
	<i>A statistical approach for identifying differential distributions in single-cell RNA-seq</i>	
	Harvard T.H. Chan School of Public Health , Boston, Mass.	Fall 2017
	<i>Department of Biostatistics</i>	
	Teaching Assistant for BST 260: Introduction to Data Science - Formulate problem sets, solutions, and exam questions with teaching team - Final project supervision and mentorship	
	University of Puerto Rico , San Juan, Puerto Rico	March 2017
	Co-organizer for the Healthcare Innovation Replicathon	
	- 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	

Cold Spring Harbor Laboratory, Cold Spring Harbor, New York 2016-2017
 Teaching Assistant for Summer Short Course: Statistical Methods for Functional Genomics (2 sessions)
 - Guided students through hands-on laboratory sessions

University of Wisconsin, Madison, Wisconsin Spring 2014
Department of Statistics
 Instructor for STAT 324: Applied Introductory Statistics for Engineers
 - Curated course material and lectured to 120 students
 - Designed problem sets and exams
 - Supervised Teaching Assistants

University of Wisconsin, Madison, Wisconsin Spring 2013
Greater University Tutoring Service
 Volunteer Tutor for STAT 301: Introduction to Statistical Methods
 - Led weekly review sessions for small groups of undergraduate students

University of Minnesota, Minneapolis, Minnesota 2007-2008
Division of Biostatistics, School of Public Health
 Teaching Assistant for PubH 6414: Introduction to Biostatistical Methods I (3 semesters)
 - Taught weekly lab sections, held office hours, and graded homework and exams

JOURNAL *Annals of Applied Statistics, Bioinformatics, Biostatistics, GigaScience*
 REFEREE

PROF. SOCIETY *American Statistical Association, International Biometric Society (ENAR)*
 MEMBERSHIPS