

Keegan D Korthauer, PhD

CONTACT 450 Brookline Ave 651-274-1132
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.

Peer-Reviewed Journal Articles

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*, in press, 2017.

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.

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	Travel Award, Workshop on Statistical Challenges in Single-Cell Biology	2017
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	Ascona, Switzerland	
	<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	Bioconductor Meeting, Boston, Massachusetts	July 2017
INVITED TALKS	<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>	
	iBRIGHT, M. D. Anderson Cancer Center, Houston, Texas	November 2015
	<i>A statistical approach for identifying differential distributions in single-cell RNA-seq</i>	
TEACHING	Harvard T.H. Chan School of Public Health , Boston, Mass.	Fall 2017
EXPERIENCE	<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