CURRICULUM VITAE

Eric F. Lock

IDENTIFYING INFORMATION

Academic Rank

Assistant Professor of Biostatistics

Education

Degree	Institution	Date Degree Granted
B.A.	Hamilton College Mathematics	2006
Ph.D	University of North Carolina Statistics Advisors: Andrew B. Nobel and J.S. Marron	2012

Positions/Employment

University of Minnesota, Twin Cities Assistant Professor	2014-present
Duke University Postdoctoral Associate	2012-2014

Current Membership in Professional Organizations

Sigma Xi

Phi Beta Kappa

American Statistical Association (ASA)

Institute of Mathematical Statistics (IMS)

International Biometric Society, Eastern North America Region (ENAR)

American Association for the Advancement of Science (AAAS)

HONORS AND AWARDS FOR RESEARCH/CREATIVE WORK, TEACHING, PUBLIC ENGAGEMENT, AND SERVICE

Teaching Award, UNC Department of Statistics and Operations Research, Fall 2011

Wassily Hoeffding Award, Outstanding First Year Student in Statistics, UNC, Fall 2008

Sigma Xi Inductee, Spring 2006

Phi Beta Kappa Inductee, Spring 2006

Huntington Memorial Mathematical Prize Scholarship, Hamilton College, Fall 2005

Deans List (Spring 2003, Fall 2003, Spring 2004, Fall 2004, Fall 2005, Spring 2006)

Top Senior, Pi Mu Epsilon regional high school mathematics competition, Spring 2002

RESEARCH, SCHOLARSHIP, AND CREATIVE WORK

Publications

§ = mentored or supervised student author

Refereed Journal Articles

1. **EF Lock**, N Kohli, and §M Bose. Detecting Multiple Random Changepoints in Bayesian Piecewise Growth Mixture Models. *Psychometrika*, to appear, 2017.

2. **EF Lock**. Tensor-on-tensor regression. *Journal of Computational and Graphical Statistics*, to appear, 2017.

3. R Rao, K Ennis, G Lubach, **EF Lock**, M Georgieff, and C Coe. Metabolomic Analysis of CSF Indicates Brain Metabolic Impairment Precedes Hematological Indices of Anemia in the Iron-Deficient Infant Monkey. *Nutritional Neuroscience*, 21(1): 40-48, 2018.

4. §A Kaplan and **EF Lock**. Prediction with Dimension Reduction of Multiple Molecular Data Sources for Patient Survival. *Cancer Informatics*, 16: 1-11, 2017.

5. §T Lyu, **EF Lock**, and LE Eberly. Discriminating sample groups with multi-way data. *Biostatistics*, 18(3): 434-450, 2017.

6. **EF Lock** and DB Dunson. Bayesian Genome- and Epigenome-wide Association Studies with Gene-Level Dependence. *Biometrics*, 73(3): 1018-1028, 2017.

7. §MJ O'Connell and **EF Lock**. R.JIVE for exploration of multi-source molecular data. *Bioinformatics*, 32(18): 2877-2879, 2016.

8. **EF Lock** and DB Dunson. Shared kernel Bayesian screening. *Biometrika*, 102(4): 829-842, 2015.

9. **EF Lock**, CA Markunas, K Soldano, H Cope, G Grant, H Fuchs, DB Dunson, SG Gregory and AE Ashley-Koch. Joint eQTL Assessment of Whole Blood and Dura Mater Tissue from Individuals with Chiari Type I Malformation. *BMC Genomics*, 16(1):11, 2015.

10. J Kuligowski, D Perez-Guaita, A Sánchez-Illana, Z Leon, M De La Guardia, M Vento, **EF Lock**, G Quintas. Multi-source metabolomic data analysis using Joint and Individual Variation Explained (JIVE). *Analyst*, 140(13): 4521-4529, 2015.

11. CA Markunas, **EF Lock**, CC Ding, K Soldano, H Cope, DS Enterline, G Grant, H Fuchs,AE, Ashley-Koch, and SG Gregory. Identification of Chiari Type I Malformation subtypes using whole genome expression profiles and cranial base morphometrics. *BMC Medical Genomics*, 7(1): 39, 2014.

12. J Zhang, D Jima, Q Liu, A Moffitt, M Czader, Y Fedoriw, K Richards, Z Sun, C Love, P Scotland, **EF Lock**, S Levy, DB Dunson, and S Dave. The genomic landscape of mantle cell lymphoma is related to the epigenetically determined chromatin state of normal B cells. *Blood*, 123(19): 2988-2996, 2014.

13. **EF Lock** and DB Dunson. Bayesian consensus clustering. *Bioinformatics*, 29(20): 2610-2616, 2013.

14. **EF Lock**, KA Hoadley, JS Marron, and AB Nobel. Joint and Individual Variation Explained (JIVE) for integrated analysis of multiple datatypes. *Annals of Applied Statistics*, 7(1): 523-542, 2013.

15. DM Reif, M Sypa, **EF Lock**, FA Wright, A Wilson, T Cathey, RR Judson, and I Rusyn. ToxPi GUI: An interactive visualization tool for transparent integration of data from diverse sources of evidence. *Bioinformatics*, 29(3): 402-403, 2013.

16. **EF Lock**, N Abdo, O Kosyk, SH OShae, R Huang, M Xia, YH Zhou, A Sedykh, A Tropsha, CP Austin, RR Tice, FA Wright, and I Rusyn. Quantitative high-throughput screening for chemical toxicity in a population-based in vitro model. *Toxicological Sciences*, 126(2):578-588, 2012.

17. BU Bradford, **EF Lock**, O Kosyk, S Kim, T Uehara, D Harbourt, M DeSimone, DW Threadgill, V Tryndyak, IP Pogribny, L Bleyle, DR Koop, and I Rusyn. Inter-strain differences in the liver effects of trichloroethylene in a multi-strain panel of inbred mice. *Toxicological Sciences*, 120(1), 2010.

18. **EF Lock**, R Ziemiecki, D Dittmer, and JS Marron. Efficiency clustering for low-density microarrays and its application to QPCR. *BMC Bioinformatics*, 11:386, 2010.

19. S Yeo, J Cisewski, **EF Lock**, and JS Marron. Exploratory analysis of exercise adherence patterns with sedentary pregnant women. *Nursing Research*, 59(4): 280-287, 2010.

20. RM Frongillo, **EF Lock**, and DM Brown. Symmetric fractal trees in three dimensions. *Chaos, Solitons & Fractals*, 32(2): 284-295, 2007.

Invited discussion articles

21. **EF Lock**, AB Nobel, and JS Marron. Comment: Population Value Decomposition, a framework for the analysis of image populations. *Journal of the American Statistical Association*, 106(495), 2011.

Book Chapters

22. **EF Lock** and AB Nobel. Exploratory methods to integrate multisource data. In GC Tseng, D Ghosh & XJ Zhou (Eds), *Integrating Omics Data*, pp. 242-268. Cambridge University Press, Cambridge, UK. 2015.

Books or Monographs

23. RH Lock, PF Lock, KL Morgan, **EF Lock**, and DF Lock. <u>Statistics: Unlocking the Power of Data.</u> John Wiley & Sons, Hoboken, NJ, 2012.

Submitted articles and preprints

1. §MJ O'Connell and **EF Lock**. Linked Matrix Factorization. *arXiv Preprint*, arXiv:1710.02931, 2017.
   (A version of this manuscript won the 2018 ENAR Student Paper Award)

2. **EF Lock** and G Li. Supervised multiway factorization. *arXiv Preprint*, arXiv: 1609.03228, 2017.

3. BJ Sandri, §A Kaplan, SW Hodgson, M Peterson, S Avdulov, LA Higgins, T Markowski, P Yang, AH Limper, TJ Griffin, P Bitterman, **EF Lock** and CH Wendt**.** Multi-Omic Molecular Profiling of Lung Cancer Risk in Chronic Obstructive Pulmonary Disease.

4. AM Tauer, MJ Liles, S Chavarria, M Valle, S Amaya, G Quijada, O Melendez, S Rodriguez, **EF Lock,** AV Henriquez, AR Gaos, and JA Seminoff. Hematology, biochemistry, and toxicology of wild hawksbill turtles (*Eretmochelys imbricata*) nesting in mangrove estuaries in the eastern Pacific Ocean.

Grant and Contracts

University Sources

1. **Title:** Methods Development for the Integration of Multi-way Array Datasets
   Source: Grant in Aid of Scholarship, Artistry and Scholarship
   Role: PI and sole author of proposal
   Period: January 2015 – May 2016
   Award: $33,902

External Sources

2. **Title:** Biomarkers for Multi-Source, Multi-Way Data
   Source: NIH Clinical and Translational Science Institute at UMN, KL2
   Role: PI
   Period: September 2015 – August 2018
   Award: $100,000 salary support and $25,000 research costs per year

3. **Title:** Evaluating Natural Experiments in Healthcare to Improve Diabetes Prevention and Treatment
   Source: NIH R18
   Role: Co-investigator
   PIs: Kevin Peterson (UMN)
   Period: 2016-2021
   Award: 10% salary support

3. **Title:** Detection and Correction of Iron Deficiency Induced Abnormal Brain Metabolism
   Source: NIH R01
   Role: Co-investigator
   PIs: Raghu Rao (UMN)
   Period: 2017-2022
   Award: 10% salary support

Software Development

1. **MultiwayRegression:** an R package to predict one multi-way array (e.g., a tensor) from another multi-way array.

2. **MultiwayClassification**: an R package to perform linear classification for data with multi-way structure.

3. **BayesianScreening**: an R package to screen for group differences in high-dimensional data using Bayesian nonparametrics.

4. **JIVE.R:** an R package to perform the joint and individual variation explained (JIVE) method for integrating multiple high-dimensional datasets and visualize the results.

5. Bayesian consensus clustering (BCC): Publicly available, documented R functions to implement the BCC method for clustering multi-source data.

6. Primer efficiency analysis (PEA): Publicly available, documented R functions to account for variability among different quantitative polymerase chain-reaction (qPCR) technologies.

Presentations, Posters, and Exhibits

Invited Presentations

1. "Tensor-on-tensor regression." ICSA Applied Statistics Symposium in Chicago, June, 2017.

2. "Bayesian Screening for Group Differences in High-Throughput Data." Columbia University, December, 2016.

3. "Integrative Analysis of High-Throughput Toxicity Screening Data." Joint Statistical Meetings in Chicago, August, 2016.

4. "Exploratory Factorization of Multi-Source Data." ICSA Applied Statistics Symposium in Atlanta, June, 2016.

5. "Bayesian Screening for Group Differences in High-Throughput Data." Iowa State University, November, 2015.

6. "Subtyping from Multi-Source High-Throughput Data." iBright Conference, MD Anderson Cancer Center, November 2015.

7. "Exploratory Integrative Analysis of Multi-Source Genomic Data." Johns Hopkins University, September, 2015.

8. "Shared Kernel Bayesian Screening." Department of Statistics, UMN, November 2014.

9. "Integrated Analysis of Multi-Source Biological Data." Department of Plant Biology, UMN, October 2014.

10. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." EXTREEMS-QED colloquium, College of William & Mary, April 2014.

11. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Cornell University, February 2014.

12. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Emory University, February 2014.

13. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Minnesota, February 2014.

14. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Washington State University, February 2014.

15. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of South Carolina, January 2014.

16. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Michigan, January 2014.

17. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Notre Dame, January 2014.

18. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." Colorado State University, January 2014.

19. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Florida, January 2014.

20. "Exploratory Methods for the Integrated Analysis of Multi-Source Data." University of Chicago, January 2014.

21. "Sparse low-rank models for the integration of multiple data types." Invited presentation. ASA-IMS Joint Statistical Meetings in Montreal, 2013.

22. "Genetic Dissection of Chiari Type I Malformation." Invited presentation. American Syringomyelia and Chiari Annual Conference in Los Angeles, CA, July 2013.

23. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes." Florida State University, February 2012.

24. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple

Datatypes." UMASS-Amherst, February 2012.

25. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes." MD Anderson Cancer Center, February 2012.

26. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes." Wake Forest University, January 2012.

Contributed Presentations

1. "Supervised Multiway Factorization." Contributed poster presentation. ENAR Spring Meeting, March 2017.

2. "Detecting Multiple Random Knots in Bayesian Piecewise Growth Mixture Models." International Meeting of the Psychometric Society in Asheville, NC, July, 2016.

3. "Bayesian Clustering of Multi-Source Data." Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in Seattle, WA, August 2015.

4. "Bayesian Screening for Group Differences in Methylation Array Data." Contributed presentation. Eastern North American Region of the International Biometrics Society conference in Miami, FL, March 2015.

5. "Bayesian Screening for Group Differences in Methylation Array Data." Contributed presentation. Statistical Modeling and Analysis of Epigenetics Workshop at SAMSI, Raleigh, NC, March 2015.

6. "Bayesian Consensus Clustering." Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in Boston, MA, August 2014.

7. "Technology for teaching bootstraps and randomizations", with RH Lock, PF Lock, DF Lock and KF Lock. Breakout Session. United States Conference on Teaching Statistics in Raleigh, NC, May 2011 & May 2013.

8. "Using randomization methods to build conceptual understanding of statistical inference," with RH Lock, PF Lock, DF Lock and KF Lock. Minicourse. Presented at AMS-MAA Joint Mathematics Meetings, January 2012 & January 2013.

9. "Low-rank modeling across multiple high-dimensional datasets". Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in San Diego, CA, August 2012.

10. "Joint and Individual Variation Explained (JIVE) for Integrated Analysis of Multiple Datatypes." Topic-contributed presentation. ASA-IMS Joint Statistical Meetings in Miami, FL, August 2011.

11. "Fractal Trees in Three Dimensions". Contributed presentation. Hudson River Undergraduate Mathematics Conference in Westfield, MA, April 2006.

TEACHING AND CURRICULUM DEVELOPMENT

University of Minnesota

Courses taught

*PUBH8442 Bayesian Decision Theory and Data Analysis (Spring 2015)

Duke University

Courses taught

STA101 Data Analysis and Statistical Inference (co-taught Spring 2013)

University of North Carolina

Courses taught

STOR155 Introduction to Statistics (Spring 2009, Fall 2011)

Linear Algebra Boot camp (Summer 2011, Summer 2010)

ADVISING AND MENTORING

Name	Degree Program	Major	Date of completion	Role
Michael O'Connell	PhD	Biostatistics	Active	Dissertation Advisor
Adam Kaplan	PhD	Biostatistics	Active	Dissertation Advisor
James Normington	PhD	Biostatistics	Active	Dissertation Advisor
Yadira Peralta	PhD	Ed. Psych	Active	Doctoral Committee
Tsan-Yao Huang	PhD	HSRPA	Active	Doctoral Committee
Tianmeng Lyu	PhD	Biostatistics	Active	Doctoral Committee
Evan Olawsky	PhD	Biostatistics	Active	Academic Advisor
Sungtae Kim	Masters	Biostatistics	Active	Academic Advisor
Adam Kaplan	Masters	Biostatistics	2017	Advisor / Project Director
Nathan Rubin	Masters	Biostatistics	2017	Academic Advisor
Brandon Coombes	PhD	Biostatistics	2016	Doctoral Committee
Abhirup Datta	PhD	Biostatistics	2016	Doctoral Committee
Elizabeth Duffy	Masters	Biostatistics	2015	Project Director

SERVICE AND PUBLIC OUTREACH

Service to The Profession:

Professional Committees

1. Serving on the Eastern North American (ENAR) Regional Advisory Board for the International Biometric society (appointed for term 2018-2020)
2. Program committee member for the ENAR Spring Meeting in Atlanta, GA, March 2018

Editorships/Journal Reviewer Experience

1. Referee, *American Journal of Human Genetics*, 2017
2. Referee, *Annals of Applied Statistics*, 2013-2017 *(4)*
3. Referee, *Biometrics*, 2016-2017 *(4)*
4. Referee, *Bioinformatics*, 2013-2017 *(4)*
5. Referee, *Journal of Chemometrics*, 2016-2017 *(2)*
6. Referee, *Journal of Computational and Graphical Statistics*, 2014-2017 *(2)*
7. Referee, *Journal of Multivariate Analysis*, 2017
8. Referee, *PLOS Computational Biology*, 2016-2017 *(2)*
9. Referee, *Biometrika*, 2016
10. Referee, *Journal of the American Statistical Association,* 2014-2016 *(2)*
11. Referee, *Nature Communications*, 2016
12. Referee, *Biostatistics*, 2015
13. Referee, *The American Statistician*, 2014-2015
14. Referee, *Scientific Reports,* 2015
15. Referee, *IEEE Transactions on Pattern Analysis and Machine Intelligence,* 2015
16. Referee, *IEEE Transactions on Neural Networks and Learning Systems,* 2014
17. Referee, *The Journal of Agricultural, Biological, and Environmental Statistics,* 2014
18. Referee, *IEEE Transactions on Computational Biology and Bioinformatics*, 2013
19. Referee, *Entropy*, 2013

Grant review experience

Ad-hoc reviewer for the National Science Foundation, Fall 2015

Other Review Experience

Evaluator, Banff International Research Station (BIRS) Program, Fall 2016

Organization of conferences, workshops, panels, symposia

1. Program committee member for the ENAR Spring Meeting in Atlanta, GA, March 2018

2. Organizer of invited session "Advancing the Analysis of Multiway (Tensor) Data", ENAR Spring Meeting in Atlanta, GA, March 2018

3. Chair of session "Multi-platform Data Integration: Network and Prediction", ASA-IMS Joint Statistical Meetings in Chicago, IL, August 2016

4. Co-organizer of session "Next Generation Matrix Decompositions: Methods and Applications," with V Zipunnikov. ASA-IMS Joint Statistical Meetings in San Diego, CA, August 2012

Service to The University/College/Department

University of Minnesota

Collegiate Service

Affiliated member, Public Health Practice (2015-present)

Judge, SPH Research Day 2015

Division Service

Reading room coordinator (2014-present)

Curriculum committee (2016-present)

Seminar committee (member, 2014; chair, 2015-2017)

Search committee (2015-2016)

Exam committee (2014-2015)