

DAVID A. ENGLER

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EDUCATION

Ph.D., Biostatistics; Harvard University, Cambridge Massachusetts
Dissertation: Novel Statistical Modeling and Selection Methodologies for High Dimensional Genomic Data
Advisor: Rebecca Betensky

A.M., Biostatistics; Harvard University, Cambridge, Massachusetts

M.S., Statistics; Brigham Young University, Provo, Utah

B.A., Philosophy; Brigham Young University, Provo, Utah

EXPERIENCE

Associate Professor, Brigham Young University, Department of Statistics, 2013-present.

Assistant Professor, Brigham Young University, Department of Statistics, 2007-2013.

Teaching Assistant, Harvard University, Department of Biostatistics, 2005.

Computing Assistant, Harvard University, Department of Biostatistics, 2002-2007.

Teaching Assistant, Brigham Young University, Department of Statistics, 2001-2002.

RESEARCH INTERESTS

High-dimensional data analysis, time-series analysis and forecasting, with applications in both biomedical and business analytics.

PUBLICATIONS

Engler D A, Chitnis T, Healy B. Joint assessment of dependent discrete disease state processes. (2015). *Statistical Methods in Medical Research*, doi: 10.1177/0962280215569899.

Deng S, Bai L, Reboulet R, Matthew R, **Engler DA**, Teyton L, Bendelac A, Savage PB. A peptide-free, liposome-based oligosaccharide vaccine, adjuvanted with a natural killer T cell antigen, generates robust antibody responses *in vivo*. (2014) *Chemical Science*, 5:1437-1441.

Teixeira J, Kaneko-Tarui T, **Engler DA**, Mohapatra G, Ohguchi Y. Loss of LKB1 and PTEN tumor suppressor genes in the ovarian surface epithelium induces papillary serous ovarian cancer. (2014). *Carcinogenesis*, 35(3):546-553.

He L, Guo L, Vathipadiekal V, Sergent P, Growdan W, **Engler D A**, Rueda B, Birrer M, Orsulic S, Mohapatra G. Identification of LMX1B as a novel oncogene in human ovarian cancer. (2013). *Oncogene*, doi:10.1038/onc.2013.375.

Healy B, **Engler D A**, Musallam A, Chitnis T. Assessment of definitions of sustained disease progression in relapsing-remitting multiple sclerosis. (2013). *Multiple Sclerosis International*, ID 189624.

Engler D A, Gupta S, Growdon, W B, Drapkin R I, Nitta M, Sergent P A, Allred S F, Gross J, Deavers M T, Kuo W, Karlan B Y, Rueda B R, Orsulic S, Gershenson D M, Birrer M J, Gray J W, Mohapatra G. Genome wide DNA copy number analysis of serous type ovarian carcinomas identifies genetic markers predictive of clinical outcome. (2012). *PLoS ONE*, 7:e30996.

Engler D A, Shen Y, Gusella J F, Betensky, R A. Comparison of clinical subgroup aCGH profiles through pseudolikelihood ratio tests. (2011). *Statistical Applications in Genetics and Molecular Biology*, 10:31.

Healy B C, Chitnis T, **Engler D A**. Improving power to detect disease progression in multiple sclerosis through alternative analysis strategies. (2011). *Journal of Neurology*, 258:1812-1819.

Healy B C, **Engler D A**, Weiner H, Bakshi R, Chitnis T. Accounting for disease modifying therapy in models of clinical progression in multiple sclerosis. (2011). *Journal of the Neurological Sciences*, 303:109-113.

Mohapatra G, **Engler D A**, Starbuck K D, Kim J C, Bernay D C, Scangas G A, Bachelor T T, Betensky R A, Louis D N. Genome-wide comparison of paired fresh frozen and formalin-fixed paraffin-embedded glioma by custom BAC array comparative genomic hybridization: facilitating analysis of archival gliomas. (2011). *Acta Neuropathologica*, 121:529-543.

Engler D A, Li Y. Survival analysis with high-dimensional covariates: an application in microarray studies. (2009). *Statistical Applications in Genetics and Molecular Biology*, 8:14.

Healy B C, **Engler D A**. Modeling disease-state transition heterogeneity through Bayesian variable selection. (2009). *Statistics in Medicine*, 28:1353-1368.

Gabeau-Lacet D, **Engler D A**, Gupta S, Scangas G A, Betensky R A, Barker F G, Loeffler J S, Louis D N, Mohapatra G. Genomic profiling of atypical meningiomas associates gain of 1q with poor clinical outcome. (2009). *Journal of Neuropathology & Experimental Neurology*, 68:10.

Shen Y, Nunes F, Stemmer-Rachamimov A, James M, Mohapatra G, Plotkin S, Betensky R A, **Engler D A**, Roy J, Ramesh V, Gusella J. Genomic profiling distinguishes familial multiple and sporadic multiple meningiomas. (2009). *BMC Medical Genomics*, 2:42.

Zhu J J, Mrugala M M, **Engler D A**, Nugent W, Nierenberg K, Hochberg F H, Betensky R A, Bachelor T T. High dose methotrexate for elderly patients with primary central nervous system lymphoma. (2009). *Neuro-Oncology*, 11:211-215.

Engler D A, Mohapatra G, Louis D N, Betensky R A. (2006). A pseudolikelihood approach for simultaneous analysis of array comparative genomic hybridizations. *Biostatistics*, 7:399-421.

Mohapatra G, Betensky R A, Miller E R, Carey B, Gaumont L D, **Engler D A**, Louis, D N. (2006). Glioma test array for use with formalin-fixed, paraffin-embedded tissue: array comparative genomic hybridization correlates with loss of heterozygosity and fluorescence in situ hybridization. *Journal of Molecular Diagnostics*, 8(2):268-276.

PRESENTATIONS

American Statistical Association, Joint Statistical Meetings, Boston MA, August 2014 (Poster)
Title: Joint assessment of dependent discrete disease state processes.

American Statistical Association, Joint Statistical Meetings, Montreal, August 2013 (Contributed paper)
Title: Assessment of jointly dependent Markov processes through Bayes factors and Bayesian variable selection.

Novartis Institute for Biomedical Research, Cambridge MA, April 2013 (Invited paper)
Title: Statistical feature selection in high-dimensional data settings: applications in cancer genomics survival analysis

International Biometric Society, ENAR Meeting, Orlando FL, March 2013 (Contributed paper)
Title: Improved assessment of ordinal transitional data in multiple sclerosis through Bayesian hierarchical Poisson models with a hidden Markov structure.

American Statistical Association, Joint Statistical Meetings, San Diego CA, August 2012 (Poster)
Title: Bayesian modeling of regime-switching models: an application in multi-stream asset pricing.

American Association for Cancer Research, Annual Meeting, Chicago IL, April 2012 (Poster)
Title: Genome wide DNA copy number analysis of serous type ovarian carcinomas identifies genetic markers predictive of clinical outcome.

American Statistical Association, Joint Statistical Meetings, Miami FL, August 2011 (Contributed paper)
Title: Joint modeling assessment of discrete state transitions through Bayes factors and Bayesian variable selection.

Vanderbilt University, Department of Biostatistics, Nashville TN, June 2011 (Invited paper)
Title: Model assessment in multistate transition models: utilization of Bayes factors and Bayesian variable selection.

International Biometric Society, WNAR Meeting, Seattle WA, June 2010 (Contributed paper)
Title: Model-based clustering of array CGH profiles: a recursive-partitioning algorithm for wavelet decompositions.

American Statistical Association, Joint Statistical Meetings, Washington DC, August 2009 (Invited paper)
Title: Model-based clustering of array CGH profiles: a recursive-partitioning algorithm for wavelet decompositions.

American Statistical Association, Joint Statistical Meetings, Denver CO, August 2008 (Contributed paper)
Title: Modeling disease-state transition heterogeneity through Bayesian variable selection.

International Biometric Society, WNAR Meeting, Davis CA, June 2008 (Contributed paper)
Title: Modeling disease-state transition heterogeneity through Bayesian variable selection.

International Biometric Society, ENAR Meeting, Alexandria VA, March 2008 (Invited paper)
Title: Survival analysis with large dimensional covariates: an application in microarray studies.

Massachusetts General Hospital, Boston MA, October 2007 (Invited paper)
Title: Adaptive nonhomogeneous markov chain models through Bayesian variable selection: an application in disease stage prediction.

Conference on Emerging Design and Analysis Issues in Genomic Studies in Population Sciences, Boston MA, October 2007 (Poster)
Title: Survival analysis with large dimensional covariates: an application in microarray studies.

International Biometric Society, ENAR Meeting, Tampa FL, March 2006 (Contributed paper)
Title: A pseudolikelihood approach for the simultaneous analysis of array comparative genomic hybridizations.

Brigham Young University, Department of Statistics, Provo UT, February 2006 (Invited paper)
Title: A pseudolikelihood approach for the simultaneous analysis of array comparative genomic hybridizations.

EXTERNAL FUNDING

2015-2016 (submitted Jan 2015): Society of Actuaries, "Bayesian Prior Specification for Multivariate Regime-switching Models."
Role: Co Principal Investigator
Requested: \$27,185

2012-2014: NIH (R03), "Novel approaches for the modeling of disease progression in multiple sclerosis."
Role: Principal Investigator
Awarded: \$128,000
Grant number: R03NS078700

HONORS

International Biometric Society, Eastern North American Region (ENAR) Distinguished Student Paper Award (2006)
Harvard University Biostatistics Faculty Memorial Award (2006)
NIH Neurostatistics Training Grant (2004-2007)

TEACHING

Undergraduate:

Principles of Statistics (Statistics 121), BYU Department of Statistics, 2011, 2013
Inference (Statistics 340), BYU Department of Statistics, 2012, 2014
Statistical Inference (Statistics 442), BYU Department of Statistics, 2007–2010

Graduate:

Survival Analysis (Statistics 538), BYU Department of Statistics, 2008–2014
Models of Financial Economics (Statistics 595R), BYU Department of Statistics, 2014
Statistical Computation (Statistics 624), BYU Department of Statistics, 2009–2012

UNIVERSITY SERVICE

Department of Statistics, Brigham Young University
Faculty Advisor, BYU Analytics Club (2013-present)
Member, Rank & Status Committee (2013-present)
Chair, Program & Students Subcommittee: B.S. in Actuarial Science (2012-present)
Chair, Teaching and Learning Subcommittee on Actuarial Science (2011-present)
Member, BYU Actuarial Advisory Board (2011-present)

Faculty Advisor, BYU Actuarial Club (2012-2013)
Member, Strategic Plan Subcommittee (2012-2013)
Member, Recruiting Majors from Intro Stat Committee (2007-2013)
Chair, Teaching and Learning Subcommittee on Statistical Theory (2009-2010)
Coordinator, Department Seminar (2008–2009)
Member, Search Committee (2007–2009)

Student Advising and Mentoring, Department of Statistics, Brigham Young University

M.S. Committee Member, Ryan Roundy (2015)
M.S. Committee Member, Arthur Lui (2015)
M.S. Committee Member, Devyn Woodfield (2014-2015)
M.S. Committee Member, Mickey Warner (2014-2015)
Undergraduate Advisor, Shaun Goh Wenjun (2014)
Undergraduate Advisor, Justin Barnes (2013-2014)
Undergraduate Advisor, Nelson Walker (2013)
M.S. Committee Member, Brittany Spencer (2013)
M.S. Advisor, Chace McNeil (2012-2013)
M.S. Advisor, Madeline Meng (2012-2013)
M.S. Advisor, Ariana Hedges (2012-2013)
M.S. Advisor, Emily Wilson (2012-2013)
Undergraduate Advisor, Xin Xu (2012)
M.S. Advisor, Wei Zhou (2011-2012)
Undergraduate Advisor, Jordan Johns (2011-2012)
M.S. Committee Member, Douglas VanDerwerken (2010-2011)
M.S. Advisor, Mark Nielsen (2010-2011)
M.S. Committee Member, Michelle Withers (2010-2011)
M.S. Advisor, Serena Baker (2009-2010)
M.S. Committee Member, Ryan Eliason (2009-2010)
M.S. Committee Member, Michelle Allan (2008-2009)
M.S. Committee Member, Brenda Ginos (2008-2009)

PROFESSIONAL ACTIVITIES

Journal Editorial Board:

International Journal of Computational Mathematics

Journal Referee:

Annals of Applied Statistics
Bioinformatics
Biometrical Journal
Biometrics
Cancer Genetics
Computational Statistics and Data Analysis
Genomics
Journal of Neurology, Neurosurgery & Psychiatry
Statistical Applications in Genetics and Molecular Biology
Statistics in Medicine
Trials Journal

American Statistical Association, Utah Chapter, Second Vice President (2007–2009)