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| CONTACT INFORMATION | Department of Biostatistics and Computational Biology Dana-Farber Cancer Institute 450 Brookline Avenue Boston, MA 02215 USA | | twitter: @stephaniehicks email: shicks@jimmy.harvard.edu website: stephaniehicks.com |
| RESEARCH INTERESTS | My research interests focus around developing statistical methods and tools in application for genomics data. Currently, I am focused on methods for processing and analyzing DNA methylation and gene expression using microarrays and next-generation sequencing. | | |
| CURRENT APPOINTMENT | Postdoctoral Research Fellow, Boston MA Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute Department of Biostatistics, Harvard School of Public Health Mentor: Rafael Irizarry | | 2013 - Present |
| EDUCATION | 2007 - 2013 | PhD. & M.A., Statistics, Rice University, Houston, TX USA Thesis Advisors: Marek Kimmel, Ph.D. (Rice, Statistics) and Sharon Plon, M.D., Ph.D. (Baylor College of Medicine) Thesis Title: Probabilistic Models for Genetic and Genomic Data with Missing Information | |
| | 2003 - 2007 | B.S., Mathematics, Louisiana State University, Baton Rouge, LA USA magna cum laude, Phi Beta Kappa | |
| PROFESSIONAL EXPERIENCE | 2013 - | Postdoctoral Research Fellow, DFCI and HSPH, Boston, MA Mentor: Rafael Irizarry | |
| | 2007 - 2013 | Graduate Student Researcher, Rice University, Houston, TX Advisors: Marek Kimmel and Sharon Plon (Baylor College of Medicine) | |
| | 2006 | Undergraduate Researcher (REU), Statistics, University of Wisconsin, Madison, WI Mentors: Murray Clayton and Jo Handelsman | |
| | 2005 | Undergraduate Researcher (REU), Statistics, Rice University, Houston, TX Mentor: Javier Rojo | |
| | 2005 - 2007 | Undergraduate Researcher, Psychology, LSU, Baton Rouge, LA Mentor: Robert Mathews | |
| | 2005 - 2007 | Undergraduate Tutor, Roadmap 2 Redesign Program, LSU, Baton Rouge, LA Tutored college algebra, trigonometry and pre-calculus students. | |
| | 2003 - 2004 | Undergraduate Tutor, LSU, Baton Rouge, LA Tutored students at Scotlandville Magnet High School in algebra for 3hrs/week. | |
| RESEARCH | Journal Articles | | |
| | [1] Hicks SC, Irizarry RA. (2014). When to use Quantile Normalization? bioRxiv doi: http://dx.doi.org/10.1101/012203. | | |
| | [2] Hicks SC. (2014). When Women in Statistics Come to Know Their Power. Chance 27. | | |
| | [3] Liang MK, Li LT, Nguyen MT, Berger RL, Hicks SC, Kao LS. (2014). Abdominal reoperation | | |

and mesh explantation following open ventral hernia repair with mesh. *Am J Surg* **204**: 670-676. PMID: 25241955.

- [4] Liang MK, Berger RL, Nguyen MT, **Hicks SC**, Li LT, Leong M. (2014). Outcomes with Porcine Acellular Dermal Matrix versus Synthetic Mesh and Suture in Complicated Open Ventral Hernia Repair. *Surg Infect* **15**: 506-512. PMID: 25215466.
- [5] Berger RL, Li LT, **Hicks SC**, Liang MK. (2014). Suture versus preperitoneal polypropylene mesh for elective umbilical hernia repairs. *J Surg Res* **192**: 426-431. PMID: 24980854
- [6] Brahmbhatt R, Carter SA, **Hicks SC**, Berger DH, Liang MK. (2014). Identifying Risk Factors for Surgical Site Complications after Laparoscopic Ventral Hernia Repair: Evaluation of the Ventral Hernia Working Group Grading System. *Surg Infect (Larchmt)* **15**: 187-193. PMID: 24773169
- [7] Carter SA, **Hicks SC**, Brahmbhatt R, Liang MK. (2014). Recurrence and Pseudorecurrence after Laparoscopic Ventral Hernia Repair: Predictors and Patient-focused Outcomes. *Am Surg* **80**: 138-148. PMID: 24480213
- [8] Li LT, **Hicks SC**, Davila JA, Kao LS, Berger RL, Arita NA, Liang MK. (2014). Circular Closure is Associated with the Lowest Rate of Surgical Site Infection Following Stoma Reversal: A Systematic Review and Multiple Treatment Meta-analysis. *Colorectal Dis* **16**: 406-416. PMID: 24422861
- [9] Li LT, Brahmbhatt R, **Hicks SC**, Davila JA, Berger DH, Liang MK. (2014). Prevalence of Surgical Site Infection at the Stoma Site following Four Skin Closure Techniques: A Retrospective Cohort Study. *Dig Surg* **31**: 73-78. PMID: 24776653
- [10] Nguyen MT, Berger RL, **Hicks SC**, Davila JA, Li LT, Kao LS, Liang MK. (2014). Comparison of Outcomes of Synthetic Mesh vs Suture Repair of Elective Primary Ventral Herniorrhaphy: A Systematic Review and Meta-analysis. *JAMA Surg* **31**: 73-78. PMID: 24554114
- [11] Nguyen MT, Phatak UR, Li LT, **Hicks SC**, Moffett JM, Arita NA, Berger RL, Kao LS, Liang MK. (2014). Review of stoma site and midline incisional hernias after stoma reversal. *J Surg Res* **190**: 504-509. PMID: 24560428
- [12] Berger RL, Li LT, **Hicks SC**, Davila JA, Kao LS, Liang MK. (2013). Development and validation of a risk-stratification score for surgical site occurrence and surgical site infection after open ventral hernia repair. *J Am Coll Surg*. **217**: 974-982. PMID: 24051068
- [13] Clapp ML, **Hicks SC**, Awad SS, Liang MK. (2013). Trans-cutaneous Closure of Central Defects (TCCD) in Laparoscopic Ventral Hernia Repairs (LVHR). *World J Surg*. **37**: 42-51. PMID: 23052806.
- [14] Li LT, Jafrani RJ, Becker NS, Berger RL, **Hicks SC**, Davila JA, Liang MK. (2013). Outcomes of acute versus elective primary ventral hernia repair. *J Trauma Acute Care Surg* **76**: 523-528. PMID: 24458061
- [15] Liang MK, Clapp M, Li LT, Berger RL, **Hicks SC**, Awad S. (2013). Patient Satisfaction, Chronic Pain, and Functional Status following Laparoscopic Ventral Hernia Repair. *World J Surg*. **37**: 530-537. PMID: 23212794.
- [16] Liang MK, Li LT, Avellaneda A, Moffett JM, **Hicks SC**, Awad SS. (2013). Outcomes and Predictors of Incisional Surgical Site Infection in Stoma Reversal. *JAMA Surg* **148**: 183-189. PMID: 23426597.
- [17] Liang MK, Berger RL, Li LT, Davila JA, **Hicks SC**, Kao LS. (2013). Outcomes of laparoscopic vs open repair of primary ventral hernias. *JAMA Surg* **148**: 1043-1048. PMID: 24005537
- [18] Nguyen MT, Li LT, **Hicks SC**, Davila JA, Suliburk JW, Leong M, Kao LS, Berger DH, Liang MK. (2013). Readmission following open ventral hernia repair: incidence, indications, and predictors. *Am J Surg* **206**: 942-948. PMID: 24296099

- [19] Subramanian A, Clapp ML, **Hicks SC**, Awad SS, Liang MK. (2013). Laparoscopic ventral hernia repair: Primary versus secondary hernias. *J Surg Res* **181**: e1-5. PMID: 22795342.
- [20] **Hicks S**, Plon SE, Kimmel M. (2013). Statistical Analysis of Missense Mutation Classifiers. *Hum Mut* **34**: 405-406. PMID: 23086893.
- [21] Cheung HC¹, San Lucas FA, **Hicks S**, Chang K, Bertuch AA, Ribes-Zamora A. (2012). An S/T-Q cluster domain census unveils new putative targets under Tel1/Mec1 control. *BMC Genomics* **13**: 664. PMID: 23176708.
- [22] **Hicks S**², Wheeler DE, Plon SE, Kimmel M. (2011). Prediction of Missense Mutation Functionality Depends on both the Algorithm and Sequence Alignment Employed. *Hum Mut.* **32**: 661-668. PMID: 21480434.

Invited Talks

- [1] Normalization of DNA methylation and Gene Expression Data in the Context of Global Variation. Bioinformatics Meeting, Division of Immunology, Harvard Medical School. 2014 Sept 18. Boston, MA.

Conference Oral Presentations

- [1] **Hicks SC**, Irizarry R. quantro: When should you use quantile normalization? Flashlight talk at *Bioconductor Conference*. 2014 July 30-August 1. Boston, MA.
- [2] **Hicks S**, Plon SE, Kimmel M. Modeling Discovery Of Functional SNPs From Genome Scale Data. *Joint Statistical Meetings*. 2011 Aug 5. Miami, FL.
- [3] **Hicks S**, Plon SE, Wheeler DE, Kimmel M. Prediction of Missense Mutation Functionality Depends on both the Algorithm and Sequence Alignment Employed. *Human Genome Variation Society's Exploring the Functional Consequences of Genomic Variation Meeting*. 2010 Nov 1. Washington, D.C.

Selected Poster Presentations

- [1] **Hicks S**, Irizarry R. When to use Quantile Normalization? Poster presented at: *2014 Women in Statistics Conference*. 2014 May 15-17. Cary, NC.
- [2] **Hicks S**, Irizarry R. Estimating cell composition of whole blood using differentially methylated regions. Poster presented at: *2013 PQG Conference*. 2013. Nov 14-15. Boston, MA.
- [3] **Hicks S**, Plon SE, Kimmel M. postMUT: A Statistical Tool for Combining Predictions of Missense Mutation Functionality using Capture-Recapture Methods. Poster presented at: *63rd Annual Meeting of The American Society of Human Genetics*. 2013. Oct 22-26. Boston, MA.
- [4] Kimmel M, **Hicks S**, Plon SE. Applications of Hidden Markov Models with Conditional Emission Probabilities to Identify Regions of Identity-By-Descent in Whole-Exome Sequencing Data. Poster presented at: *63rd Annual Meeting of The American Society of Human Genetics*. 2013. Oct 22-26. Boston, MA.
- [5] **Hicks S**, Plon SE, Kimmel M. Capture-Recapture Models for Evaluation of Algorithms Estimating Functionality of Missense Mutations. Poster presented at: *62nd Annual Meeting of The American Society of Human Genetics*. 2012 Nov 6-12. San Francisco, CA.
- [6] **Hicks S**, Plon SE, Kimmel M. Bernoulli mixture models in application of the evaluation of algorithms estimating functionality of missense mutations. Poster presented at: *Beyond The Genome*. 2012 Sept 27-29. Boston, MA.

¹ 'Highly Accessed' on BioMed Central

² Cited and Discussed in Nature **482**: 257-262. 09 Feb 2012. PMID: 22318607

- [7] **Hicks S**, Plon SE, Kimmel M. Bernoulli Mixture Models in Application of the Evaluation of Algorithms Estimating Functionality of Missense Mutations. Poster presented at: *International Conference in Stochastic Processes*. 2012. Aug 21-25. Houston, TX.
- [8] **Hicks S**, Plon SE, Kimmel M. Using a Second-order Hidden Markov Model to Identify Regions of Identity-By-Descent in Exome Sequencing Data. Poster presented at: *12th International Congress of Human Genetics/61st Annual Meeting of The American Society of Human Genetics*. 2011 Nov 12-15. Montreal, Canada.
- [9] **Hicks S**, Plon SE, Wheeler DE, Kimmel, M. Prediction of Missense Mutation Functionality Depends on both the Algorithm and Sequence Alignment Employed. Poster presented at: *60th Annual Meeting of the American Society of Human Genetics*. 2010 Nov 2-6. Washington, D.C.
- [10] **Hicks S**, Plon SE, Wheeler DE, Kimmel, M. Prediction of Missense Mutation Functionality Depends on both the Algorithm and Sequence Alignment Employed. Poster presented at: *4th Annual Meeting of the Genomics of Common Diseases*. 2010 Oct 6-9. Houston, TX.
- [11] Cheung HC, San Lucas F, **Hicks S**, Chang K, Plon SE, Bertuch AA, Ribes-Zamora A. S/T-Q Cluster Domains in *Saccharomyces cerevisiae*: a bioinformatic census and analysis. Poster presented at: *BioScience Research Collaborative Grand Opening*. 2010 Apr 1. Houston, TX.
- [12] **Hicks S**, Plon SE, Wheeler DE, Kimmel, M. Predicting Functionality of Missense Mutations with Varying Levels of Evolutionary Depth. Poster presented at: *Computational & Theoretical Biology Symposium*. 2009 Dec 4-6. Houston, TX.
- [13] **Hicks S**, Plon SE, Wheeler DE, Kimmel, M. Predicting Functionality of Missense Mutations with Varying Levels of Evolutionary Depth. Poster presented at: *59th Annual Meeting of the American Society of Human Genetics*. 2009 Oct 20-24. Honolulu, HI.

Ph.D. Dissertation

- [1] **Hicks SC**. Probabilistic Models for Genetic and Genomic Data with Missing Information, Ph.D. Thesis, Rice University, 2013.

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| TEACHING EXPERIENCE | 2014 | Lead Teaching Fellow , Data Science (Harvard - CS109) <i>Held weekly lab sections. Developed course material, homework and solutions.</i> <i>All material available on: Github</i> <i>Course taught by Rafael Irizarry and Verena Kaynig-Fittkau</i> |
| | 2014 | Discussion Leader , Data Analysis for Genomics (HarvardX - PH525x) <i>Course taught by Rafael Irizarry with Teaching Assistant Mike Love</i> |
| | 2010, 2011 | Teaching Assistant , Probability in Bioinformatics and Genetics (Rice - STAT 423/623) <i>Grade homeworks, provide solutions, hold office hours and gave several guest lectures.</i> |
| | 2010 | Teaching Assistant , Applied Stochastic Processes (Rice - STAT 552) <i>Grade homeworks, provide solutions, hold office hours and gave several guest lectures.</i> |
| | 2008, 2009 | Lab Instructor , Introduction to Statistics for the Biosciences (Rice - STAT 305) <i>Hold labs 3hr/week to teach students to use R.</i> |
| | 2007, 2008 | Teaching Assistant , Probability and Statistics (Rice - STAT 310) <i>Grade homeworks, provide solutions, hold office hours and gave several guest lectures.</i> |

SOFTWARE **Bioconductor and Github**

- [1] *quantro*: An R-package that can be used to test for differences between groups of distributions to guide the choice if quantile normalization should be used [[Available on Bioconductor](#)]
- [2] *quantroSim*: A supporting data simulation R-package for the *quantro* R-package to simulate gene expression and DNA methylation data [[Available on Github](#)]
- [3] *postMUT*: A tool implemented in Perl and R to predict the functionality of missense mutations [[Available on Github](#)]

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| GRANTS AND AWARDS | 2014 | Travel award for the Women in Statistics Conference 2014 |
| | 2011 | Travel and tuition award for the 16th Annual Summer Institute in Statistical Genetics at University of Washington (Population Genetics, Coalescent Theory modules) |
| | 2008 - 2011 | NIH T32 Training Grant Fellow, Rice University |
| | 2007 | Inducted into Phi Beta Kappa |
| | 2007 | LSU Austin Chapter Scholarship Award |
| | 2005 - 2007 | LA-STEM Research Scholars, LSU |
| | 2004 - 2005 | HMM Professors Program, LSU |
| | 2003 - 2007 | TOPS Tuition Award, LSU |
| TECHNICAL SKILLS | Programming: R, Python, Perl LaTeX, SAS, Matlab Operating Systems: Mac OS X, Unix, Windows | |
| JOURNAL REFEREE / REVIEWER | <i>Bioinformatics, BMC Medical Genetics, Human Mutation</i> | |
| STATISTICAL EXPERTISE | Statistical Learning, Statistical Genetics, Stochastic Processes, Survival Analysis, Bayesian Data Analysis, Multivariate Analysis, Biostatistics, Probabilistic Models in Bioinformatics, General Linear Models, Statistical Sampling | |
| PROFESSIONAL MEMBERSHIPS | Member, American Statistical Association (ASA) Member, American Mathematical Society (AMS) Member, American Society of Human Genetics (ASHG) | |