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| CONTACT INFORMATION     | Department of Biostatistics and Computational Biology<br>Dana-Farber Cancer Institute<br>450 Brookline Avenue<br>Boston, MA 02215 USA   |  | twitter: @stephaniehicks<br>email: shicks@jimmy.harvard.edu<br>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 pre-processing, normalizing and analyzing gene expression and DNA methylation data based on microarray and next-generation sequencing platform technologies.   |  |  |
| CURRENT APPOINTMENT     | Postdoctoral Research Fellow, Boston MA<br>Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute<br>Department of Biostatistics, Harvard School of Public Health<br>Mentor: Rafael Irizarry   |  | 2013 - Present   |
| EDUCATION               | 2007 - 2013   | PhD. & M.A., Statistics, Rice University, Houston, TX USA<br>Thesis Advisors: Marek Kimmel, Ph.D. (Rice, Statistics) and Sharon Plon, M.D., Ph.D. (Baylor College of Medicine)<br>Thesis Title: Probabilistic Models for Genetic and Genomic Data with Missing Information |  |
|                         | 2003 - 2007   | B.S., Mathematics, Louisiana State University, Baton Rouge, LA USA<br>magna cum laude, Phi Beta Kappa  |  |
| PROFESSIONAL EXPERIENCE | 2013 -  | Postdoctoral Research Fellow, DFCI and HSPH, Boston, MA<br>Mentor: Rafael Irizarry   |  |
|                         | 2007 - 2013   | Graduate Student Researcher, Rice University, Houston, TX<br>Advisors: Marek Kimmel and Sharon Plon (Baylor College of Medicine)   |  |
|                         | 2006  | Undergraduate Researcher (REU), Statistics, University of Wisconsin, Madison, WI<br>Mentors: Murray Clayton and Jo Handelsman  |  |
|                         | 2005  | Undergraduate Researcher (REU), Statistics, Rice University, Houston, TX<br>Mentor: Javier Rojo  |  |
|                         | 2005 - 2007   | Undergraduate Researcher, Psychology, LSU, Baton Rouge, LA<br>Mentor: Robert Mathews   |  |
|                         | 2005 - 2007   | Undergraduate Tutor, Roadmap 2 Redesign Program, LSU, Baton Rouge, LA<br>Tutored college algebra, trigonometry and pre-calculus students.  |  |
|                         | 2003 - 2004   | Undergraduate Tutor, LSU, Baton Rouge, LA<br>Tutored students at Scotlandville Magnet High School in algebra for 3hrs/week.  |  |
| RESEARCH                | Pre-prints<br>[1] Hicks SC, Irizarry RA. (2014). When to use Quantile Normalization? <i>bioRxiv</i><br>doi: <a href="http://dx.doi.org/10.1101/012203">http://dx.doi.org/10.1101/012203</a> .<br><br>Journal Articles<br>[1] Hicks SC. (2014). When Women in Statistics Come to Know Their Power. <i>Chance</i> 27. |  |  |

- [2] 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
- [3] 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
- [4] 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
- [5] 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
- [6] 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
- [7] Li LT, Jafrani RJ, Becker NS, Berger RL, **Hicks SC**, Davila JA, Liang MK. (2014). Outcomes of acute versus elective primary ventral hernia repair. *J Trauma Acute Care Surg* **76**: 523-528. PMID: 24458061
- [8] 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.
- [9] 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.
- [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] 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.
- [15] 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.
- [16] 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
- [17] Neskey DM, Klein JD, **Hicks S**, Garden AS, Bell DM, El-Naggar Ak, Kies MS, Weber RS, Kupferman ME. (2013). Prognostic Factors Associated With Decreased Survival in Patients With Acinic Cell Carcinoma. *JAMA Otolaryngol Head Neck Surg* **139**: 1195-1202. PMID: 24076756

- [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 HC<sup>1</sup>, 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**<sup>2</sup>, 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.

### Contributed Talks

- [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.

### Conference Proceedings

- [1] Saliba J, Trevino LR, Meng Q, Zabriskie R, Powell B, **Hicks S**, Kimmel M, Cheung H, Muzny DM, Reid JG, Wheeler D, Gibbs RA, and Plon SE. Abstract 5113: Functional analysis of genomic variants identified through whole exome sequencing for susceptibility to lymphocytic leukemia. *AACR 103rd Annual Meeting*. 2012 Mar 31-Apr 4. Chicago, IL.
- [2] Saliba J, Zabriskie R, Powell B, **Hicks S**, Kimmel M, Cheung H, Ritter D, Muzny DM, Reid JG, Wheeler DA, Gibbs RA, Plon SE. Abstract A8: Functional analysis of genomic variants identified through whole exome sequencing of pediatric lymphocytic leukemia kindreds. *AACR Special Conference: Pediatric Cancer at the Crossroads: Translating Discovery into Improved Outcomes*. 2013 Nov 3-6. San Diego, CA.

### 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.

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<sup>1</sup> 'Highly Accessed' on BioMed Central

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

- [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.
- [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.

## 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](#)]

TEACHING  
EXPERIENCE

- 2014      **Lead Teaching Fellow**, Data Science (Harvard - CS109)  
*Held weekly lab sections. Developed course material, homework and solutions.  
 Coordinated and directed 25 teaching fellows. All material available on: [Github](#)  
 Course taught by Rafael Irizarry and Verena Kaynig-Fittkau.*
- 2014      **Discussion Leader**, Data Analysis for Genomics (HarvardX - PH525x)  
*Course taught by Rafael Irizarry with Teaching Assistant Mike Love.*
- 2010, 2011      **Teaching Assistant**, Probability in Bioinformatics and Genetics (Rice - STAT 423/623)  
*Grade homeworks, provide solutions, hold office hours and gave several guest lectures.*
- 2010      **Teaching Assistant**, Applied Stochastic Processes (Rice - STAT 552)  
*Grade homeworks, provide solutions, hold office hours and gave several guest lectures.*
- 2008, 2009      **Lab Instructor**, Introduction to Statistics for the Biosciences (Rice - STAT 305)  
*Hold labs 3hr/week to teach students to use R.*
- 2007, 2008      **Teaching Assistant**, Probability and Statistics (Rice - STAT 310)  
*Grade homeworks, provide solutions, hold office hours and gave several guest lectures.*

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, Git, Perl, LaTeX, SAS, Matlab, Shell scripting  
**Operating Systems:** Mac OS X, Unix, Windows

JOURNAL  
REFEREE /  
REVIEWER

*Bioinformatics, BMC Medical Genetics, Human Mutation*

PROFESSIONAL  
MEMBERSHIPS

Member, American Statistical Association (ASA)  
 Member, American Mathematical Society (AMS)  
 Member, American Society of Human Genetics (ASHG)