Stephanie C. Hicks **Updated November 5, 2015**

CONTACT INFORMATION

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RESEARCH INTERESTS

My research interests are focused on developing statistical methods, tools and software for the analysis of genomics data. Specifically, my research addresses statistical challenges in epigenomics and functional genomics such as the pre-processing, normalization, analysis of raw high-throughput data (microarray and next-generation sequencing) leading to an improved quantification and understanding of biological variability.

CURRENT APPOINTMENT

Postdoctoral Research Fellow, Boston MA 2013 - Present
Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute
Department of Biostatistics, Harvard T.H. Chan School of Public Health
Mentor: Rafael Irizarry

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

08/2013 - **Postdoctoral Research Fellow**, DFCI and HSPH, Boston, MA
Mentor: Rafael Irizarry

06/2013 **Research Staff**, Rice University, Houston, TX

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

Pre-prints

[1] **Hicks SC**, Teng M, Irizarry RA. (2015). On the widespread and critical impact of systematic bias and batch effects in single-cell RNA-Seq data. *bioRxiv*. doi: http://dx.doi.org/10.

1101/025528.

Peer-reviewed Journal Articles

[1] **Hicks SC**[1], Irizarry RA. (2015). quantro: a data-driven approach to guide the choice of an appropriate normalization method. *Genome Biol* **16**:117. PMID: 26040460.

[2] Osman AA, Neskey DM, Katsonis P, Patel AA, Ward AM, Hsu TK, **Hicks SC**, McDonald TO, Ow TJ, Alves MO, Pickering CR, Skinner HD, Zhao M, Sturgis EM, Kies MS, El-Naggar A, Perrone F, Licitra L, Bossi P, Kimmel M, Frederick MJ, Lichtarge O, Myers JN. (2015). Evolutionary Action Score of TP53 Coding Variants Is Predictive of Platinum Response in Head and Neck Cancer Patients. *Cancer Res* **75**: 1-11. PMID: 25691460

[3] Neskey DM, Osman AA, Ow TJ, Katsonis P, McDonald T, **Hicks SC**, Hsu TK, Pickering CR, Ward A, Patel A, Yordy JS, Skinner HD, Giri U, Sano D, Story MD, Beadle BM, El-Naggar AK, Kies MS, William WN, Caulin C, Frederick M, Kimmel M, Myers JN, Lichtarge O. (2015). Evolutionary Action score of TP53 (EAp53) identifies high risk mutations associated with decreased survival and increased distant metastases in head and neck cancer. *Cancer Res* **75**: 1527-1536. PMID: 25634208.

[4] 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

[5] 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

[6] 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

[7] **Hicks SC**. (2014). When Women in Statistics Come to Know Their Power. *Chance* **27**.

[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] 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

[11] 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.

[12] 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.

[13] 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

[14] 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

[1] 'Highly Accessed' on BioMed Central

[15] 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

[16] 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.

[17] 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.

[18] 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.

[19] 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

[20] 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

[21] 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

[22] 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.

[23] **Hicks S**, Plon SE, Kimmel M. (2013). Statistical Analysis of Missense Mutation Classifiers. *Hum Mut* **34**: 405-406. PMID: 23086893.

[24] Cheung HC[2], 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.

[25] **Hicks S**[3], 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] Why Statistics Matters in the Analysis of Genomics Data. Computational Biology Seminar, Department of Biology, Louisiana State University. 2015 Feb 11. Baton Rouge, LA.

[2] 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 S**[4], Teng M, Irizarry R. On the widespread and critical impact of batch effects and systematic bias in single-cell RNA-Seq data. 2015 PQG Conference: *Single-cell Genomics: Technology, Analysis, and Applications.* 2015 Nov 5-6. Boston, MA.

[2] 'Highly Accessed' on BioMed Central

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

[4] Selected for a Stellar Abstract Award

[2] **Hicks SC**, Irizarry R. quantro: When should you use quantile normalization? Flashlight talk at *Bioconductor Conference*. 2014 Jul 30-Aug 1. Boston, MA.

[3] **Hicks S**, Plon SE, Kimmel M. Modeling Discovery Of Functional SNPs From Genome Scale Data. *Joint Statistical Meetings*. 2011 Aug 5. Miami, FL.

[4] **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**, Teng M, Irizarry R. On the widespread and critical impact of batch effects and systematic bias in single-cell RNA-Seq data. Poster presented at 2015 Genome Informatics. 2015 Oct 28-31. Cold Spring Harbor Laboratories.

[2] **Hicks S**, Irizarry R. When to use Quantile Normalization? Poster presented at: *2014 Women in Statistics Conference*. 2014 May 15-17. Cary, NC.

[3] **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.

[4] **Hicks S**, Plon SE, Kimmel M. postMUT: A Statistical Tool for Combining Predictions of Missense Mutation Functionality using Capture-Recapture Methods. Poster presented at: *63nd Annual Meeting of The American Society of Human Genetics*. 2013. Oct 22-26. Boston, MA.

[5] 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: *63nd Annual Meeting of The American Society of Human Genetics*. 2013. Oct 22-26. Boston, MA.

[6] **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.

[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: *Beyond The Genome*. 2012 Sept 27-29. Boston, MA.

[8] **Hicks S**, Plon SE, Kimmel M. Bernoulli Mixture Models in Application of the Evaulation of Algorithms Estimating Functionality of Missense Mutations. Poster presented at: *International Conference in Stochastic Processes*. 2012. Aug 21-25. Houston, TX.

[9] **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.

[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: *60th Annual Meeting of the American Society of Human Genetics*. 2010 Nov 2-6. Washington, D.C.

[11] **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.

[12] 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.

[13] **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.

[14] **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.

Teaching Experience

2015 **Teaching Assistant**, Statistical Methods for Functional Genomics (CSHL)
Contributed course material, gave a lecture, answered questions.

2015 **Contributor and Discussion Leader**
(1) Statistics and R for the Life Sciences (Harvard edX - PH525.1x)
(2) Case study: DNA methylation data analysis (Harvard edX - PH525.8x)
Contributed course material, created screencasts, developed assessments, answered questions.
Courses taught by Rafael Irizarry with Teaching Assistant Mike Love.

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 (Harvard edX - 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.

Hacking Experience

Sept 2015 **Mozilla Open Science Leadership Summit** (website), Mozilla, Toronto, Canada
Invited to work with community leaders furthering open practice and open science through creating community events, tools for collaboration and learning resources.

Mar 2015 **ROpenSci Unconference** (website), GitHub, San Francisco, CA
Invited to work with over 40 R enthusiasts from industry, academia, non-profits and government on projects supporting open data, open science and data visualization in R.

Software

Bioconductor and Github

[1] *explainr*: An R-package to translate S3 objects into text using standard templates in a simple and convenient way. Developed at ROpenSci Unconference with Hilary Parker, David Robinson and Roger Peng. [Available on GitHub]

[2] *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]

[3] *quantroSim*: A supporting data simulation R-package for the *quantro* R-package to simulate gene expression and DNA methylation data [Available on GitHub]

[4] *postMUT*: A tool implemented in Perl and R to predict the functionality of missense mutations [Available on GitHub]

Grants and Awards

2015	Stellar Abstract Award for the 2015 PQG Conference
2015	Travel award for the Genome Informatics Meeting 2015 at CSHL
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	HMMI 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, Biometrics, BMC Medical Genetics, Human Mutation, PLoS Computational Biology

Professional Memberships

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