Stephanie C. Hicks   Updated September 26, 2014

CONTACT
INFORMATION

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RESEARCH
INTERESTS

My research interests focus around developing statistical methods and tools in application for genomics and epigenomics 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   2013 - Present
Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute
Department of Biostatistics, Harvard 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

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] 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* [Epub ahead of print] PMID: 25241955.

[2] 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* [Epub ahead of print] PMID: 25215466.

[3] Berger RL, Li LT, **Hicks SC**, Liang MK. (2014). Suture versus preperitoneal polypropylene mesh for elective umbilical hernia repairs. *J Surg Res* [Epub ahead of print] PMID: 24980854

[4] 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

[5] 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

[6] 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

[7] 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

[8] 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

[9] 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

[10] 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

[11] 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.

[12] 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

[13] 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.

[14] 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.

[15] 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

[16] 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

[17] 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.

[18] Cheung HC[1], 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.

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[1] 'Highly Accessed' on BioMed Central

[19] **Hicks S**, Plon SE, Kimmel M. (2012). Statistical Analysis of Missense Mutation Classifiers. *Hum Mut.* e-pub 10/2012. PMID: 23086893.

[20] **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. Oral presentation: *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. Oral presentation: *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: *63nd 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: *63nd 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 Evaulation 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.

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

[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.

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

TEACHING EXPERIENCE

2014   **Lead Teaching Fellow**, Data Science (Harvard - CS109)
Held weekly lab sections. Developed course material, homework and solutions.
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 and 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.

SOFTWARE	*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]
	epigenomeSim: An R-package to simulate data from the epigenome including gene expression and DNA methylation data
	postMUT: A tool implemented in Perl and R to predict the functionality of missense mutations
	IBD2cond: A tool implemented in Perl and R to predict regions of IBD in siblings

TECHNICAL SKILLS

Programming: R, Python, Perl LaTeX, SAS, Matlab
Operating Systems: Mac OS X, Unix, Windows

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)