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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 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 Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute Department of Biostatistics, Harvard School of Public Health <i>Mentor: Rafael Irizarry</i> | 2013 - Present |
| EDUCATION | 2007 - 2013 PhD. & M.A., Statistics , Rice University, Houston, TX USA <i>Thesis Advisors: Marek Kimmel, Ph.D. (Rice, Statistics) and Sharon Plon, M.D., Ph.D. (Baylor College of Medicine)</i> <i>Thesis Title: Probabilistic Models for Genetic and Genomic Data with Missing Information</i> 2003 - 2007 B.S., Mathematics , Louisiana State University, Baton Rouge, LA USA <i>magna cum laude, Phi Beta Kappa</i> | |
| PROFESSIONAL EXPERIENCE | 2013 - Postdoctoral Research Fellow , DFCI and HSPH, Boston, MA <i>Mentor: Rafael Irizarry</i> 2007 - 2013 Graduate Student Researcher , Rice University, Houston, TX <i>Advisors: Marek Kimmel and Sharon Plon (Baylor College of Medicine)</i> 2006 Student Researcher (REU) , Dept. of Statistics, University of Wisconsin, Madison, WI <i>Mentors: Murray Clayton and Jo Handelsman</i> 2005 Student Researcher (REU) , Dept. of Statistics, Rice University, Houston, TX <i>Mentor: Javier Rojo</i> 2005 - 2007 Student Researcher , Dept of Psychology, LSU, Baton Rouge, LA <i>Mentor: Robert Mathews</i> 2005 - 2007 Undergraduate Tutor , Roadmap 2 Redesign Program, LSU, Baton Rouge, LA <i>Tutored college algebra, trigonometry and pre-calculus students.</i> 2003 - 2004 Undergraduate Tutor , LSU, Baton Rouge, LA <i>Tutored students at Scotlandville Magnet High School in algebra for 3hrs/week.</i> | |
| RESEARCH | Manuscripts in Preparation Hicks SC , Plon SE, Kimmel M. postMUT: A Statistical Tool Combining Predictions of Missense Mutation Functionality using Capture-Recapture Methods. Hicks SC , Plon SE, Kimmel M. Improved Detection of Regions of Identity-By-Descent in Whole-Exome Sequencing Data using Hidden Markov Models with Conditional Emission Probabilities. | |

Journal Articles

- 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* [Epub ahead of print].
- Carter SA, **Hicks SC**, Brahmabhatt R, Liang MK. (2014). Recurrence and Pseudorecurrence after Laparoscopic Ventral Hernia Repair: Predictors and Patient-focused Outcomes. *Am Surg* **80**: 138-148. PMID: 24480213
- 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
- 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
- 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
- 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.
- 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.
- 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.
- 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
- 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.
- Hicks S**, Plon SE, Kimmel M. (2012). Statistical Analysis of Missense Mutation Classifiers. *Hum Mut.* e-pub 10/2012. PMID: 23086893.
- Cheung HC^a, 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.
- Hicks S**^b, 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.

^a 'Highly Accessed' on BioMed Central

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

Conference Oral Presentations

- 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.
- 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

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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.

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

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

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| GRANTS AND AWARDS | 2014 | Travel award for the inaugural <i>Women in Statistics</i> Conference |
| | 2011 | Travel and tuition award for the <i>16th Annual Summer Institute in Statistical Genetics</i> 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 | 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> |
| SERVICE | 2008 - 2012 | Coordinator of the Computational Biology Seminar , Rice University <i>Responsible for maintaining the website, scheduling and announcing the speakers.</i> |
| | 2008 - 2009 | VP of Graduate Mathematics, Applied and Computational Mathematicians and Statisticians , Rice University <i>To foster an environment of growth and enthusiasm for math among the students through intellectual and social events.</i> |
| | 2005 - 2007 | Treasurer of LSU Habitat for Humanity |
| SOFTWARE | <i>quantro</i> : An R-package that can be used to test for differences between groups of distributions to guide the choice of an appropriate normalization approach <i>postMUT</i> : A tool implemented in Perl and R to predict the functionality of missense mutations <i>IBD2cond</i> : A tool implemented in Perl and R to predict regions of IBD in siblings | |
| STATISTICAL EXPERTISE | Statistical Genetics, Stochastic Processes, Survival Analysis, Bayesian Data Analysis, Multivariate Analysis, Biostatistics, Probabilistic Models in Bioinformatics, General Linear Models, Statistical Sampling, Statistical Learning | |
| TECHNICAL SKILLS | Programming: R, Perl, Python, LaTeX, SAS, Matlab Operating Systems: Mac OS X, Unix, Windows | |
| PROFESSIONAL MEMBERSHIPS | Member, American Statistical Association (ASA) Member, American Mathematical Society (AMS) Member, American Society of Human Genetics (ASHG) | |