Stephanie C. Hicks

CONTACT INFORMATION	Department of Biostatistics Johns Hopkins Bloomberg School of Public Health 615 North Wolfe Street Baltimore, MD 21205-2179 USA	email: shicks19@jhu.edu twitter: @stephaniehicks github: stephaniehicks website: stephaniehicks.com

RESEARCH INTERESTS

I develop statistical methods, tools and software for the analysis of genomics data. Specifically, my research addresses statistical challenges in epigenomics, functional genomics and single-cell genomics such as the pre-processing, normalization, analysis of raw, noisy high-throughput data (microarray and next-generation sequencing) leading to an improved quantification and understanding of biological variability. This work resulted in a K99/R00 grant from the National Human Genome Research Institute (NHGRI).

EDUCATION

2013   **PhD., Statistics**, Rice University, Houston, TX USA
Ph.D. Advisors: Marek Kimmel, Ph.D. (Statistics - Rice) and Sharon Plon, M.D., Ph.D. (Baylor College of Medicine, TX Children's)
Dissertation: Probabilistic Models for Genetic and Genomic Data with Missing Information

2012   **M.A., Statistics**, Rice University, Houston, TX USA

2007   **B.S., Mathematics**, Louisiana State University, Baton Rouge, LA USA
magna cum laude, Phi Beta Kappa

PROFESSIONAL POSITIONS

2018 -   **Assistant Professor**, Baltimore, MD
Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health

2013 - 2018   **Postdoctoral Research Fellow**, Boston, MA
Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute
Department of Biostatistics, Harvard T.H. Chan School of Public Health
Mentor: Rafael Irizarry, Ph.D.
K99/R00 Co-mentors: Franziska Michor, Ph.D. and Bradley Bernstein, M.D, Ph.D

2007 - 2013   **Graduate Student Researcher**, Houston, TX
Rice University
Ph.D. Advisors: Marek Kimmel and Sharon Plon

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 Tutor**, Roadmap 2 Redesign Program, LSU, Baton Rouge, LA
Tutored college algebra, trigonometry and pre-calculus students

Additional Professional Appointments

2018 - Present   Faculty member, Johns Hopkins Data Science Lab

Professional Societies

2017 - Present   Member, Caucus for Women in Statistics (CWS)

2007 - Present   Member, American Statistical Association (ASA)

2007 - Present   Member, American Mathematical Society (AMS)

2007 - 2013   Member, American Society of Human Genetics (ASHG)

2017	Travel award from the Caucus for Women in Statistics (CWS) to attend the 2017 Joint Statistical Meetings in Baltimore, MD, USA
2017	Travel award for the Ascona Workshop 2017 on Statistical Challenges in Single-Cell Biology in Ascona, Switzerland
2016	Travel award for the Women in Statistics and Data Science Conference 2016 in NC, USA
2015	Stellar Abstract Award for the 2015 PQG Conference in Boston, MA, USA
2015	Travel award for the Genome Informatics Meeting 2015 at CSHL
2014	Travel award for the Women in Statistics Conference 2014 in NC, USA
2011	Travel and tuition award for the 16th Annual Summer Institute in Statistical Genetics at University of Washington (Population Genetics, Coalescent Theory modules)
2007	Phi Beta Kappa Society
2007	LSU Austin Chapter Scholarship Award
2003 - 2007	TOPS Tuition Award, LSU

PUBLICATIONS

Pre-prints

[1] **Hicks SC**, Irizarry RA. (2017). Technology-independent estimation of cell type composition using differentially methylated regions. *bioRxiv*. doi: https://doi.org/10.1101/213769.

[2] Townes FW, **Hicks SC**, Ayree MJ Irizarry RA. (2017). Varying-Censoring Aware Matrix Factorization for Single Cell RNA-Sequencing. *bioRxiv*. doi: https://doi.org/10.1101/166736.

[3] Kumar MS, Slud EV, Okrah K, **Hicks SC**, Hannenhalli S, Corrada Bravo H. (2017). Analysis And Correction Of Compositional Bias In Sparse Sequencing Count Data. *bioRxiv*. doi: https://doi.org/10.1101/142851.

Peer-reviewed Journal Articles

[1] **Hicks SC**, Townes FW, Teng M, Irizarry RA. (2017). Missing Data and Technical Variability in Single-Cell RNA-Sequencing Experiments. In press at *Biostatistics*. doi: http://dx.doi.org/10.1101/025528.

[2] **Hicks SC**, Irizarry RA. (2017). A Guide to Teaching Data Science. In press at *The American Statistician*. http://dx.doi.org/10.1080/00031305.2017.1356747.

[3] **Hicks SC**, Okrah K, Paulson JN, Quackenbush J, Irizarry RA, Corrada Bravo H. (2017). Smooth Quantile Normalization. In press at *Biostatistics*. doi: http://dx.doi.org/10.1101/085175

[4] Saliba J, Zabriskie R, Ghosh R, Powell BC, **Hicks S**, Kimmel M, Meng Q, Ritter DI, Wheeler DA, Gibbs RA, Tsai FTF, Plon SE. (2016). Pharmacogenetic characterization of naturally occurring germline NT5C1A variants to chemotherapeutic nucleoside analogs. *Pharmacogenetics and Genomics* **26**: 271-279. PMID: 26906009. PMCID: PMC4853247.

[5] **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. PMCID: PMC4495646.

[6] 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

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[1] 'Highly Accessed' on BioMed Central

[7] 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.

[8] 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

[9] 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

[10] 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

[11] 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

[12] 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

[13] 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

[14] 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.

[15] 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.

[16] 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

[17] 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

[18] 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

[19] 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.

[20] 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.

[21] 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.

[22] 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

[23] 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

[24] 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

[25] 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.

[26] 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.

[27] **Hicks S**[3], Wheeler DE, Plon SE, Kimmel M. (2011). Prediction of Missense Mutation Functionality Depends on both the Algorithm and Sequence Alignment Employed. *Human Mutation.* **32**: 661-668. PMID: 21480434.

Invited Editorials

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

Letters

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

Ph.D. Dissertation

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

PRESENTATIONS

Invited Talks

[1] CONTRA Innovative Training Network Workshop: Handling Single Cell data. 2018 Sept 9-15. Hotel Sobieski, Warsaw, Poland.

[2] Single Cell Data Science: Making Sense of Data from Billions of Single Cells. 2018 Jun 4-8. Lorentz Center, Leiden University, Netherlands.

[3] Technology-independent estimation of cell type composition using differentially methylated regions. 2018 Apr 24. Office of Biostatistics Research at NHLBI/NIH. Bethesda, MD. USA.

[4] Estimating cell type composition in whole blood using differentially methylated regions. *Bioconductor Conference.* 2017 Jul 26-28. Boston, MA, USA.

[5] Setting the Stage for Reproducibility and Replicability in Science. 2017 Mar 22. Brandeis University, Waltham, MA, USA.

[6] Batch effects and technical biases in scRNA-Seq data. HSCI Single-Cell Workshop. 2016 Nov 29-30. Harvard Medical School, Boston, MA, USA.

[7] Towards progress in batch effects and biases in single-cell RNA-seq data. *Single-Cell Genomics Conference.* 2016 Sept 14-16. Wellcome Genome Campus, Hinxton, Cambridge, UK.

[8] On the widespread and critical impact of systemic bias and batch effects in single-cell RNA-seq data. *Joint Statistical Meetings.* 2016 July 31-Aug 4. Chicago, IL, USA.

[9] On the widespread and critical impact of systemic bias and batch effects in single-cell RNA-seq data. *Boston Single-Cell Network Meeting.* 2016 March 15. Boston, MA, USA.

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[2] 'Highly Accessed' on BioMed Central
[3] Cited and Discussed in Nature **482**: 257-262. 09 Feb 2012. PMID: 22318607

[10] Why Statistics Matters in the Analysis of Genomics Data. Computational Biology Seminar, Department of Biology, Louisiana State University. 2015 Feb 11. Baton Rouge, LA, USA.

[11] 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, USA.

Contributed Talks

[1] **Hicks SC**. Missing Data and Technical Variability in Single-Cell RNA-Sequencing Experiments. *Joint Statistical Meetings*. 2017 Jul 29-Aug 3. Baltimore, MD, USA.

[2] **Hicks SC**. Missing Data and Technical Variability in Single Cell RNA-Sequencing Experiments. Ascona Workshop 2017: Statistical Challenges in Single Cell Biology. 2017 Apr 30-May 5. Ascona, Switzerland.

[3] **Hicks SC**. Transforming the Classroom to Teach Statistics and Data Science with Active Learning. *Women in Statistics and Data Science Conference*. 2016 Oct 20-22. Charlotte, NC, USA.

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

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

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

[7] **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., USA.

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 SC**, Townes WF, Teng M, Irizarry RA. Missing Data and Technical Variability in Single Cell RNA-Sequencing Experiments. Poster presented at *2018 NHGRI Annual Meeting*. 2018 Mar 18-21. UCLA.

[2] **Hicks SC**, 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.

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

[4] **Hicks SC**, 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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[4]Selected for a Stellar Abstract Award

[5] **Hicks SC**, 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.

[6] Kimmel M, **Hicks SC**, 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.

[7] **Hicks SC**, 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.

[8] **Hicks SC**, 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.

[9] **Hicks SC**, 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.

[10] **Hicks SC**, 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.

[11] **Hicks SC**, 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.

[12] **Hicks SC**, 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.

[13] 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.

[14] **Hicks SC**, 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.

[15] **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.

FELLOWSHIPS

2017 - 2021 NIH/NHGRI K99/R00 Pathway to Independence Award – Statistical Methods for the Normalization and Quantification of Single-Cell RNA-Sequencing Data

2009 - 2011 NIH/NCI T32 Predoctoral Training Program in Biostatistics, Rice University

2005 - 2007 LA-STEM Research Scholars, LSU

2004 - 2005 HMMI Professors Program, LSU

EDITORIAL
ACTIVITIES **Editorial Board Membership**

2018 - Present   Associate Editor, *biOverlay*

Peer Review Activities

Journal Referee for Annals of Statistics, Bioinformatics, Biometrics, BMC Medical Genetics, F1000, Genome Biology, Human Mutation, Nature Communications, Nature Structural & Molecular Biology, Nature Scientific Reports, PLoS Computational Biology, PLoS One, R Journal,

Book reviewer for Chapman & Hall/CRC

SERVICE

International and National

2018 - Present   Co-founder of R-Ladies Baltimore
                   An organization to promote gender diversity in the R community

2017 - 2019   Member of ASA Committee on Women in Statistics

2015 - Present   Board Member of Cards Against Humanities Science Ambassador Scholarship

SOFTWARE

Bioconductor and Github

[1]   *methylCC*: An R-package to estimate the cell composition of whole blood in DNA methylation samples in microarray or sequencing platforms [Available on GitHub]

[2]   *qsmooth*: An R-package that implements a generalization of quantile normalization, referred to as smooth quantile normalization (**qsmooth**), which is based on the assumption that the statistical distribution of each sample should be the same (or have the same distributional shape) within biological groups or conditions [Available on GitHub]

[3]   *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]

[4]   *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]

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

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

GRANTS

Current Grant Support

Chan Zuckerberg Institute   03/01/2018 – 02/28/2019
Davide Risso, PI   (5%)
Statistical Analysis and Comprehension of the Human Cell Atlas in R / Bioconductor: Access and Scalable Infrastructure
Provide R / Bioconductor software (A) to provide coherent programmatic interface to the HCA, and (B) to enable scalable interactive statistical analysis of single-cell data.
Role: Co-Investigator

NIH/NHGRI (K99) R00HG009007   12/23/2016 – 02/28/2019
Stephanie Hicks, PI   (75%)
Statistical Methods for the Normalization and Quantification of Single-Cell RNA-Sequencing Data
To develop novel statistical methods that will 1) remove systematic errors in single-cell RNA-sequencing data by accounting for variability visible only at the single-cell level and 2) quantify biological variability such as transcriptional heterogeneity within and between populations of cells.
Role: Principal Investigator

Previous Grant Support

NIH T32 CA096520   08/01/2009 – 12/31/2011
Marina Vannucci, PI
Predoctoral Training Program in Biostatistics, Rice University
Prepare a new generation of biostatisticians who will work side-by-side with biomedical investigators in modern cancer research.
Role: Predoctoral Trainee

EDUCATIONAL
ACTIVITIES   **Doctoral Thesis Committees**

2018   Tom Luechtefeld, Environmental Health and Engineering
            Alternate committee member

TEACHING
            Classroom Instruction

2016   **Co-instructor**, Introduction to Data Science (HSPH - BIO 260).
            Co-taught lectures with Rafael Irizarry. Developed course material.

2015   **Teaching Assistant**, Statistical Methods for Functional Genomics (CSHL).
            Developed course material, gave one 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 Michael 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 and Michael 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.

            Other teaching

2017   Instructor, Introduction to R, RStudio and the "Tidyverse". How It's Done Seminar in the
            Biostatistics and Computational Biology Department, DFCI. 2017 Sept 20. Boston, MA, USA.

2016   Instructor, Introduction to R and R Package Demonstration. Department of Biostatistics and
            Computational Biology Training Sessions. DFCI. 2016 March 9. Boston, MA, USA.

COMMUNITY
CODING
            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.
Contributed to R-packages including explainr and catsplainr.