MATTHEW A. HIBBS, PH.D. ◆ ASSOCIATE PROFESSOR ◆ TRINITY UNIVERSITY

Computer Science Department ◆ One Trinity Place ◆ San Antonio, TX 78212 ◆ mhibbs@trinity.edu

EDUCATION

Princeton University, Ph.D. in Computer Science *Dissertation*: Analysis and Visualization of Large-Scale Gene Expression Microarray Compendia *Advisors*: Olga Troyanskaya, Kai Li	1/2008
University of Texas at Austin, B.S. in Computer Science, B.A. in Plan II (interdisciplinary honors major) *Honors*: Summa cum laude, Special honors in Plan II	5/2002

ACADEMIC APPOINTMENTS

Associate Professor, Trinity University, Department of Computer Science	since 2017
Assistant Professor, Trinity University, Department of Computer Science	2012-2017
Adjunct Professor, The Jackson Laboratory	since 2012
Assistant Professor, The Jackson Laboratory	2009-2012
Adjunct Professor, University of Maine, Graduate School of Biomedical Sciences (GSBS)	since 2009
Post-Doctoral Research Assistant, Princeton University	2008
Graduate Research Assistant, Princeton University	2004-2007

HONORS AND AWARDS

New Scholar in Aging Research, Ellison Medical Foundation	2011-2015
Princeton University Teaching Award for Excellence in Instruction	2005
Program in Integrative Information, Computer and Application Sciences (PICASso) Fellowship, Princeton University	2004-2006
Endowed Presidential Scholarship, University of Texas at Austin	2001-2002
Dean's List, University of Texas at Austin	1997-2002
National Merit Scholarship, University of Texas at Austin	1997-2001

TEACHING EXPERIENCE

CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2024
CSCI3353, Introduction to Computer Graphics, Trinity University	Spring 2024
CSCI1320, Principles of Computer Science I, Trinity University	Fall 2023
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Fall 2023
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2023
CSCI4312, Advanced Game Development, Trinity University	Spring 2023
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2022
CSCI1321, Principles of Computer Science II, Trinity University	Fall 2022
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2022
CSCI3353, Introduction to Computer Graphics, Trinity University	Spring 2022
CSCI2094, Computer Science Colloquium, Trinity University	Spring 2022
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2021

CSCI1321, Principles of Computer Science II, Trinity University	Fall 2021
CSCI2094, Computer Science Colloquium, Trinity University	Fall 2021
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2021
CSCI3353, Introduction to Computer Graphics, Trinity University	Spring 2021
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2020
CSCI3395, Adv CS Topics – Intro to Computational Biology, Trinity University	Fall 2020
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2020
CSCI1321, Principles of Computer Science II, Trinity University	Spring 2019
CSCI3353, Introduction to Computer Graphics, Trinity University (2 sections)	Spring 2019
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2018
CSCI3312, Introduction to Game Development, Trinity University	Fall 2018
Genetics of Aging and Cancer, Arkansas Governor's School	July 2018
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2018
CSCI4312, Advanced Game Development, Trinity University	Spring 2018
CSCI1320, Principles of Computer Science I, Trinity University	Fall 2017
CSCI3312, Introduction to Game Development, Trinity University (2 sections)	Fall 2017
CSCI3353, Introduction to Computer Graphics, Trinity University	Spring 2017
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2017
CSCI3312, Introduction to Game Development, Trinity University	Fall 2016
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2016
PRIME Summer School on Computational Immunology, Yale Medical School	June 2016
CSCI4312, Advanced Game Development, Trinity University	Spring 2016
CSCI1321, Principles of Computer Science II, Trinity University	Spring 2016
CSCI3353, Introduction to Computer Graphics, Trinity University	Fall 2015
CSCI3312, Introduction to Game Development, Trinity University	Fall 2015
CSCI1311, Introduction to Programming Logic, Trinity University	Fall 2015
CSCI4312, Advanced Game Development, Trinity University	Spring 2015
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2015
CSCI3395, Adv CS Topics – Intro to Computational Biology, Trinity University	Fall 2014
CSCI1320, Principles of Computer Science I, Trinity University	Fall 2014
CSCI1311, Introduction to Programming Logic, Trinity University	Fall 2014
CSCI3312, Introduction to Game Development, Trinity University	Spring 2014
CSCI1321, Principles of Computer Science II, Trinity University (2 sections)	Spring 2014
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2013
CSCI3353, Introduction to Computer Graphics, Trinity University	Fall 2013
CSCI1320, Principles of Computer Science I, Trinity University (3 sections)	Spring 2013

CSCI1311, Introduction to Programming Logic, Trinity University	Fall 2012
CSCI1320, Principles of Computer Science I, Trinity University (2 sections)	Fall 2012
BMB550, Functional Genomics, Univ of Maine, Guest Lecturer	Feb 2010-2012
BMS625, Signaling Pathways and Cancer, Univ of Maine, Guest Lecturer	Sept 2011
Genomic and Proteomic Approaches to Complex Heart, Lung, Blood & Sleep Disorders, The Jackson Laboratory, Lecturer	Sept 2011
Short Course on Experimental Models of Cancer, The Jackson Laboratory, Lecturer	Aug 2010-2011
PRIME Summer School in Immune Modeling, Yale Medical School, Instructor	June 2011
Short Course on Systems Genetics, The Jackson Laboratory, Lecturer	Sep 2009-2011
Intro to Microarray Analysis, Cold Spring Harbor Laboratory, Instructor	Oct 2006-2007
COS 116, Princeton University, Guest Lecturer	April 2007
Intro to Scientific Visualization, Princeton University, Lecturer	Nov 2006
CHM/COS/MOL/PHY 233-234, Integrated Science, Princeton University, TA	Spring 2005
COS 302, Artificial Intelligence, Princeton University, TA	Fall 2003
Tutor, University of Texas at Austin, UT Learning Center	2000-2002

Additional Academic Service

Editorial Board Member, *Scientific Data* (www.nature.com/sdata)	2016-present
Scientific Advisory Board Member, Gene Ontology Consortium	2013-2016

Conference program committee member: ACM BCB 2023, ACM BCB 2022, ACM BCB 2021, ISMB 2012, ISMB/ECCB 2011, ISMB 2010, ECCB 2010, CSB 2010, ISMB/ECCB 2009, CSB 2009

Additional conference service: BioViz 2012 Papers Co-Chair; VizBi 2012 Publicity Chair; VizBi 2011 Session Chair; BioViz 2011 Invited Session Co-Chair; BioViz 2011-2012 Steering Committee

Referee: *PLoS Computational Biology*, *Nature Protocols*, *Scientific Data*, *PLoS Genetics*, *Nucleic Acids Research*, *Genome Biology*, *Bioinformatics*, *Genomics*, *BMC Bioinformatics*, *PLoS ONE, Workshop on Algorithms in Bioinformatics* (*WABI*), *IEEE Gensips, RECOMB, FEBS Letters*

Study section member: NSF 2010; NIH Special Emphasis Panel (ENCODE) 2011; NSF 2016

Judge, National Siemens Competition in Math, Science & Technology	2009-2014
Co-organizer, Computation and Data Analysis in Biology and Information Sciences Seminar Series, Princeton University	2005-2006
Member, Genetics Society of America (GSA)	2006-present
Member, International Society for Computational Biology (ISCB)	2005-present

Publications

1. Rizzo HE, Escaname EN, Alana NB, Lavender E, Gelfond J, Fernandez R, **Hibbs MA**, King JM, Carr NR, Blanco CL. Maternal diabetes and obesity influence the fetal epigenome in a largely Hispanic population. *Clinical Epigenetics* (2020) 12(1):1-10.

2. Ball RL, Fujiwara Y, Sun F, Hu J, **Hibbs MA**, Handel MA, Carter GW. Regulatory complexity revealed by integrated cytological and RNA-seq analyses of meiotic substages in mouse spermatocytes. *BMC Genomics* (2016) 17(1):628.

3. Lewis KN, Soifer I, Melamud E, Roy M, McIsaac RS, **Hibbs MA**, Buffenstein R. Unraveling the message: insights into comparative genomics of the naked mole-rat. *Mammalian Genome* (2016) 27(7): 259-278.
4. Gelfond JA, Ibrahim JG, Chen M, Sun W, Lewis K, Kinahan S, **Hibbs MA**, Buffenstein R. Homology cluster differential expression analysis for interspecies mRNA-Seq experiments. *Statistical applications in genetics and molecular biology* (2015) 14(6): 507-516.
5. Zheng H, Forgetta V, Hsu Y, Estrada K, Rosello-Diez A, …, **Hibbs MA**, …, Ackert-Bicknell CL, Joyner AL, Duncan EL, Kiel DP, Rivadeneira F, Richards JB (>100 authors total). Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature* (2015) 526(7571): 112-117.
6. Walker M, Billings T, Baker CL, Powers N, Tian H, Saxl RL, Choi KB, **Hibbs MA**, Carter GW, Handel MA, Paigen K, Petkov PM. Affinity-seq detects genome-wide PRDM9 binding sites and reveals the impact of prior chromatin modifications on mammalian recombination hotspot usage. *Epigenetics & Chromatin* (2015) 8(1): 1-13.
7. Munger SC, Raghupathy N, Choi KB, Simons AK, Gatti DM, Hinerfeld DA, Svenson KL, Keller MP, Attie AD, **Hibbs MA**, Graber JH, Chesler EJ, Churchill GA. RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. *Genetics* (2014) 198:75-86.
8. Kemp JP, Medina-Gomez C, Estrada K, St Pourcain B, Heppe DHM, Warrington NM, Oei L, Ring SM, Kruithof CJ, Timpson NJ, Wolber LE, Reppe S, Gautvik K, Grundberg E, Ge B, van der Eerden B, van de Peppel J, **Hibbs MA**, Ackert-Bicknell CL, Choi KB, Koller DL, Econs MJ, Williams FMK, Foroud T, Zillikens MC, Ohlsson C, Hofman A, Uitterlinden AG, Smith GD, Jaddoe VWV, Tobias JH, Rivadeneira F, Evans DM. Phenotypic Dissection of Bone Mineral Density Reveals Skeletal Site Specificity and Facilitates the Identification of Novel Loci in the Genetic Regulation of Bone Mass Attainment. *PLoS Genetics* (2014) 10(6): e1004423. doi:10.1371/journal.pgen.1004423.
9. Dowell KG, Simons AK, Bai H, Kell B, Wang ZZ, Yun K, **Hibbs MA**. Novel Insights into Embryonic Stem Cell Self-Renewal Revealed Through Comparative Human and Mouse Systems Biology Networks. *Stem Cells* (2013) 32(5): 1161-1172.
10. Dowell KG, Simons AK, Wang ZZ, Yun K, **Hibbs MA**. Cell-Type-Specific Predictive Network Yields Novel Insights into Mouse Embryonic Stem Cell Self-Renewal and Cell Fate. *PLoS ONE* (2013) 8(2): e56810.
11. Gu T, Buaas FW, Simons AK, Ackert-Bicknell CL, Braun RE*, **Hibbs MA***. Canonical A-to-I and C-to-U RNA editing is enriched at 3'UTRs and microRNA target sites in multiple mouse tissues. *PLoS ONE* (2012) 7(3):e33720. (*Co-senior authors)
12. Guan Y, Gorenshteyn D, Burmeister M, Wong AK, Schimenti JC, Handel MA, Bult CJ*, **Hibbs MA***, Troyanskaya OG*. Tissue-specific functional networks for prioritizing disease genes. *PLoS Comp Biol* (2012) 8(9):e1002694. (*Co-senior authors)
13. Ackert-Bicknell CL and **Hibbs MA**. The need for mouse models in osteoporosis genetics research. *BoneKEY* (2012) 1:98.
14. Aljakna A, Choi S, Savage H, Hageman-Blair R, Gu T, Svenson K, Churchill GA, **Hibbs MA**, Korstanje R. Pla2g12b and Hpn are HDL-regulating Genes Identified by ENU Mutagenesis in the Mouse and HPN is Associated with HDL Cholesterol Levels in Human. *PLoS ONE* (2012) 7(8):e43139.
15. Li Y*, **Hibbs MA***, Gard AL*, Shylo NA, Yun K. Genome-wide analysis of N1ICD/RBPJ targets in vivo reveals direct transcriptional regulation of Wnt, SHH, and Hippo pathway effectors by Notch1. *Stem Cells* (2012) 30(4):741-752. (*Equal contribution)

16. GR Howell GR, Macalinao DG, Sousa GL, Walden M, Soto I, Kneeland SC, Barbay JM, King BL, Marchant JK, **Hibbs MA**, Stevens B, Barres BA, Clark AF, Libby RT, John SW. Molecular clustering identifies complement and endothelin induction as early events in a mouse model of glaucoma. *Journal of Clinical Investigation* (2011) 121(4):1429-1444.
17. Guan Y, Ackert-Bicknell CL, Kell B, Troyanskaya OG, **Hibbs MA**. Functional Genomics Complements Quantitative Genetics in Identifying Disease-Gene Associations. *PLoS Comp Biol* (2010) 6(11):e1000991.
18. Baryshnikova A, Costanzo M, Kim Y, Ding H, Koh J, Toufighi K, Youn JY, Ou J, San Luis BJ, Bandyopadhyay S, **Hibbs MA**, Hess D, Gingras AC, Bader GD, Troyanskaya OG, Brown GW, Andrews B, Boone C, Myers CL. Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. *Nat Methods* (2010) 7(12):1017-1024.
19. **Hibbs MA**. Advanced Bioinformatics Tools and Strategies, in *Principles and Practices of Plant Genomics: Volume 3: Advanced Genomics*, Eds. Kole C and Abbott AG. Science Publishers Inc: New Hampshire (2010).
20. Gehlenborg N, O'Donoghue SI, Baliga NS, Goesmann A, **Hibbs MA**, Kitano H, Kohlbacher O, Neuweger H, Schneider R, Tenenbaum D, Gavin A. Visualization of omics data for systems biology. *Nat Methods* (2010) 7(3):S56-S68.
21. Huttenhower C, Myers CL, **Hibbs MA**, Troyanskaya OG. Computational analysis of the yeast proteome: understanding and exploiting functional specificity in genomic data. *Methods Mol Biol* (2009) 548:273-93.
22. **Hibbs MA**. The Effects of Pre-processing and Parameter Choices on Searches Through Large Gene Expression Data Collections. *IEEE Int Conf on Genomic Signal Processing and Statistics* (2009).
23. Huttenhower C*, **Hibbs MA***, Myers CL*, Caudy AA, Hess DC, Troyanskaya OG. The impact of incomplete knowledge on evaluation: an experimental benchmark for protein function prediction. *Bioinformatics* (2009) doi10.1093. (*Equal contribution)
24. **Hibbs MA***, Myers CL*, Huttenhower C*, Hess DC, Caudy AA, Li K, Troyanskaya OG. Analysis of Computational Functional Genomic Approaches for Directing Experimental Biology: a Case Study in Mitochondrial Inheritance. *PLoS Computational Biology* (2009) 5(3):e1000322. (*Equal contribution)
25. Hess DC, Myers CL*, Huttenhower C*, **Hibbs MA***, Hayes A, Paw J, Clore J, Mendoza R, San Luis B, Costanzo M, Boone C, Caudy AA, Troyanskaya OG. Computationally driven, quantitative experiments discover genes required for mitochondrial biogenesis. *PLoS Genetics* (2009) 5(3):e1000407. (*Equal contribution)
26. Huttenhower C, Haley EM, **Hibbs MA**, Dumeaux V, Barrett DR, Coller HA, Troyanskaya OG. Exploring the human genome with functional maps. *Genome Res* (2009) 19(6):1093-106.
27. **Hibbs MA**, Hess DC, Myers CL, Huttenhower C, Li K, Troyanskaya OG. Exploring the functional landscape of gene expression: directed search of large microarray compendia. *Bioinformatics* (2007) 23(20):2692-9.
28. Huttenhower C, Flamholz A, Landis J, Sahi S, Myers CL, Olszewski K, **Hibbs MA**, Siemers NO, Troyanskaya OG, Coller HA. Nearest Neighbor Networks: Clustering Expression Data Based on Gene Neighborhoods. *BMC Bioinformatics* (2007) 8:250.
29. **Hibbs MA**, Wallace G, Dunham M, Li K, Troyanskaya OG. Viewing the Larger Context of Genomic Data through Horizontal Integration. *Proceedings of IEEE-CS 11th Int. Conf. on Information Visualization* (2007) pp326-334.

30. Wallace G, **Hibbs MA**, Dunham M, Sealfon RSG, Troyanskaya OG, Li K. Scalable, Dynamic Analysis and Visualization for Genomic Datasets. *Proceedings of IPDPS 2007 Workshop on Next Generation Software* (2007).
31. Haarer B, Viggiano S, **Hibbs MA**, Troyanskaya OG, Amberg DC. Modeling Complex Genetic Interactions in a Simple Eukaryotic Genome: Actin Displays a Rich Spectrum of Complex Haploinsufficiencies. *Genes & Development* (2006) 21(2):148-59.
32. Sealfon RSG, **Hibbs MA**, Huttenhower C, Myers CL, Troyanskaya OG. GOLEM: an interactive graph-based gene ontology navigation and analysis tool. *BMC Bioinformatics* (2006) 7:443.
33. Myers CL, Barrett D, **Hibbs MA**, Huttenhower C, Troyanskaya OG. Finding function: evaluation methods for functional genomic data. *BMC Genomics* (2006) 7:187.
34. Huttenhower C, **Hibbs MA**, Myers C, Troyanskaya OG. A scalable method for integration and functional analysis of multiple microarray data sets. *Bioinformatics* (2006) 22:2890.
35. Myers CL, Robson D, Wible A, **Hibbs MA**, Chiriac C, Theesfeld CL, Dolinski K, Troyanskaya OG. Discovery of biological networks from diverse functional genomic data. *Genome Biology* (2005) 6(13):R114.
36. **Hibbs MA**, Dirksen NC, Li K, Troyanskaya OG. Visualization Methods for Statistical Analysis of Microarray Clusters. *BMC Bioinformatics* (2005) 6:115.
37. Wallace G, Chen H, Chen Y, Liu Z, Samanta R, Bi P, Gupta A, **Hibbs MA**, Li K, Finkelstein A, Funkhouser T, Cook P, Sukthankar R, and Troyanskaya OG. Tools and Applications for Large Scale Display Walls. Special Issue on Large Format Displays, *IEEE Computer Graphics and Applications*, July/August 2005.
38. Li K, **Hibbs MA**, Wallace G, Troyanskaya OG. Dynamic Scalable Visualization for Collaborative Scientific Applications. *Proceedings of IPDPS 2005 Workshop on Next Generation Software* (2005).

INVITED PRESENTATIONS

1. *Computationally Dissecting Molecular Mechanisms of Aging.* Research Seminar, Calico Labs, San Francisco, CA, April 2015.
2. *Traversing the Transcriptome of the Naked Mole-rat*. with Shelley Buffenstein, Jonathan Gelfond, and Katie Lewis. The Barshop Institute for Longevity and Aging Studies Seminar Series, UT Health Science Center, San Antonio, TX, May 2013.
3. *Biases in High-throughput Sequencing Obscure RNA Editing Signals*. Biostatistics Seminar Series, American Statistical Association – San Antonio Chapter, San Antonio, TX, April 2013.
4. *Measuring RNA Editing*. Biology Department Seminar, Trinity University, San Antonio, TX, February 2013.
5. *Measuring Mammalian Somatic Mutation Rates.* The Barshop Institute for Longevity and Aging Studies Seminar Series, UT Health Science Center, San Antonio, TX, October 2012.
6. *Keynote Address: Biology is Complicated: Study Bias, Unknown Unknowns, and Data Analysis.* Intelligent Systems in Molecular Biology Student Council (ISMBSC) Symposium, Long Beach, CA, July 2012.
7. *Computationally Assessing Self-Renewal of Stem Cells*. Symposium on Genome Instability and Cancer, Dartmouth University, Hanover, NH, July 2011.
8. *Using Functional Genomics to Identify Genotype-Phenotype Associations.* Maine Medical Center Research Institute (MMCRI) Seminar Series. Scarborough, ME. December 2010.

9. *Systems Biology Data Visualization*. VisWeek 2010 Panel on Biomedical Data Visualization. Salt Lake City, UT. October 2010.
10. *Keynote Address: Translating from Raw Data to Concrete Biological Knowledge.* Maine Society of Eye Physicians and Surgeons Annual Meeting. Bar Harbor, ME. September 2010.
11. *Using Functional Genomics to Identify Genotype-Phenotype Associations*. JAX-MDIBL Joint Scientific Symposium. Bar Harbor, ME. September 2010.
12. *Visualization Methods for Gene Expression Data.* EMBO Workshop on Visualizing Biological Data (VizBi). Heidelberg, Germany. March 2010.
13. *The Effects of Pre-processing and Parameter Choices on Searches Through Large Gene Expression Data Collections*. IEEE Int Conf on Genomic Signal Processing and Statistics (Gensips). Minneapolis, MN. May 2009.
14. *Computationally Discovering Biology.* University of Maine Computer Science Colloquium. Orono, ME. May 2009.
15. *Computational Approaches for Directing Experimental Biology*. Maine Biological and Medical Sciences Symposium. Bar Harbor, ME. April 2009.
16. *Directed Search of Large Microarray Compendia.* Highlights Track at Intelligent Systems for Molecular Biology (ISMB). Toronto, Canada. August 2008.
17. *Viewing the Larger Context of Genomic Data through Horizontal Integration*. IEEE-CS Int Conf on Information Visualization (IV'07). Zurich, Switzerland. July 2007.
18. *Fishing for Function in a Sea of Expression Data*. Genetics Society of America Yeast Genetics and Molecular Biology Meeting, Workshop on Bioinformatics. Princeton, NJ. July 2006.
19. *How Computers Can Cure Cancer*. Arkansas Governor's School. Conway, AR. July 2006.
20. *Query-driven search methods for large microarray databases*. PICASso Computation and Data Analysis in Biology and Information Sciences Series. Princeton, NJ. April 2006.

STUDENT SENIOR THESES ADVISED

- Cole McGuire, Senior Thesis 2023-2024
- Nathaniel Kleffner, Senior Thesis 2022-2023
- Thuong (Lucy) Pham, Senior Thesis 2022-2023 (now in PhD program at UT-Arlington)
- Fan Lee, Senior Thesis 2021-2022
- Alex Walker, Senior Thesis 2020-2021
- Christine Kindrick, Senior Thesis 2020-2021
- Lechuan Li, Senior Thesis 2019-2020 (now in PhD program at Rice University)
- Morgan King, Senior Thesis 2018-2019
- Caleb Escobedo, Senior Thesis 2018-2019 (now in PhD program at Univ of Colorado – Boulder)
- Horst Evans, Senior Thesis 2018-2019
- Bowen (Eddie) Li, Senior Thesis 2018-2019
- Christopher (Shea) Luikart, Senior Thesis 2018-2019
- Kayako Yamakoshi, Senior Thesis 2018-2019 (now in MS program at Johns Hopkins University)
- Emily Herbert, Senior Thesis 2017-2018 (now in PhD program at Univ of Massachusetts)

- Mary Yang, Senior Thesis 2017-2018
- Nicholas Samoray, Senior Thesis 2017-2018
- Asa Turner, Senior Thesis 2017-2018
- Evan Cofer, Senior Thesis 2016-2017 (now in PhD program at Princeton University)
- Evan LeGros, Senior Thesis 2016-2017
- Subrat Mahaptra, Senior Thesis 2016-2017
- Isaac Thacker, Senior Thesis 2016-2017
- Jacob Luber, Senior Thesis 2015-2016 (now in PhD program at Harvard University)
- Rodney Kennedy, Senior Thesis 2015-2016
- Kat Fisher, Senior Thesis 2015-2016
- Irene Fan, Senior Thesis 2014-2015 (now in MS program at Princeton University)
- Rosemary Steup, Senior Thesis 2013-2014 (now in PhD program at Indiana University)

SUMMER RESEARCH AND INDEPENDENT STUDIES ADVISED

- Cole McGuire, Summer 2022-Summer 2024
- Gabriel Manners, Summer 2020, Summer 2021
- Samantha Ortiz, Fall 2018-Spring 2019
- Calvin Usiri, Spring 2018
- Robbie Andres, Fall 2017-Spring 2018
- Heather Rizzo (co-advised by Jonathan King), Summer 2017
- Sarah Fordin (co-advised by Jonathan King), Summer 2017
- Mohammed Mnete, Summer 2017
- Asa Turner, Summer 2017
- Mary Yang, Summer 2017
- Evan Cofer, Summer 2016
- Zachary Kurima-Blough, Summer 2016
- Jorgen Viltoft, Summer 2016
- Zackery Zimdars, Summer 2016
- Ali Mangalji, Summer 2015
- Isaac Thacker, Summer 2015
- Joshua Ward, Summer 2015
- Jacob Luber, Summer 2014
- Sean Kinahan, Summer 2014

Ongoing and Prior Research Support

MRI-ACI-1531594, Hibbs (PI) 8/1/15-7/31/18
NSF $547,076 (direct costs)
Acquisition of High Performance Scientific Computing Cluster at Trinity University
This proposal requests funds for the acquisition of a high-performance scientific computing cluster for use by undergraduate research students in a variety of departments at Trinity University.
Role: Principal Investigator

AG-NS-0773-11 Hibbs (PI) 8/1/11-7/31/15
Ellison Medical Foundation $370,372 (direct costs)
Mammalian Somatic Mutations and Aging
This project will use high-throughput sequencing and rigorous statistical methods to empirically measure the whole-genome somatic mutation rate in mice at multiple stages of adulthood and old age.
Role: Principal Investigator

2 P50 GM076468-06 Churchill (PI) 7/15/11-6/30/16
NIH/NIGMS $299,355 (direct costs to Project E)
Center for Genome Dynamics - Project E: Data Driven Systems Genetics Workflow for New Experimental Platforms
The goal of this project is the development and application of high throughput RNA sequencing technology (HTPS) as the sole source of transcription and polymorphism data for an expression QTL experiment.
Role: Co-PI for Project E

1 R21 AR060981-01 Hibbs (multi-PI) 3/15/11-2/28/13
NIH/NIAMS $275,000 (direct costs)
Genetics of Osteoblast Differentiation
The goal of this project is to determine the key regulators and modulators of osteoblastogenesis by thoroughly measuring the transcriptional dynamics and phenotypic properties of differentiating osteoblasts derived from five diverse genetic backgrounds of laboratory mouse.
Role: Principal Investigator