

Catherine E. Welsh

Rhodes College
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Education

- December 2014 **Ph.D., Computer Science**, *University of North Carolina*, Chapel Hill, NC.
Dissertation Title: *Computational Tools to Aid in the Design and Development of a Genetic Reference Population*
Advisor: Dr. Leonard McMillan
- May 2007 **M.S., Computer Science**, *Lehigh University*, Bethlehem, PA.
- May 2004 **B.S., Computer Science**, *Ursinus College*, Collegeville, PA.
Graduated magna cum laude with minors in mathematics and business administration

Academic Positions

- 2013-Present **Assistant Professor**, *Department of Mathematics and Computer Science*, Rhodes College, Memphis, TN.
- 2015-Present **Visiting Scientist**, *Department of Computational Biology*, St. Jude Children's Research Hospital, Memphis, TN.
- 2015-Present **Affiliate**, *Bioinformatics Masters Program*, University of Memphis, Memphis, TN.

Research and Professional Experience

- 2007-2013 **Research Assistant**, *Computational Genetics Group (UNC)*, Chapel Hill, NC.
Research in the areas of bioinformatics and developing efficient algorithms to work with large datasets, such as genotyping and sequencing data.
- 2006-2007 **Research Assistant**, *Semantic Web Group (Lehigh University)*, Bethlehem, PA.
Adapted an existing knowledge base system to support functions related to routing, forwarding, storage management, progressive name resolution, policy processing, and content-based retrieval of information, and modified this system to be efficient and reliable for use with disruption tolerant networks.
- 2004-2006 **Software Engineer**, *ICANON Associates*, Hatfield, PA.
Developed software in Java using the JBoss environment set up as described during internship. Also worked as a sub-contractor on an IRS project team, converting an existing application to a web application using an Oracle Application Server and Oracle Database.
- 2002-2004 **Intern/Web Site Developer**, *ICANON Associates*, Hatfield, PA.
Converted web pages from ASP to JSP, created Java applications to access remote databases and aid in data conversion, and wrote a new company website in JSP, that incorporated JavaBeans, SQL, HTML, and Javascript. Set up an IDE to work with a JBoss server, Ant scripts, XDoclet, and XJavadoc to create Enterprise JavaBeans.

Peer-Reviewed Publications

Refereed Journal Articles

- J8. Andrew P. Morgan, Chen-Ping Fu, Chia-Yu Kao, **Catherine E. Welsh**, John P. Didion, Liran Yadgary, Leeanna Hyacinth, Martin T. Ferris, Timothy A. Bell, Darla R. Miller, Paola Giusti-Rodriguez, Randal J. Nonneman, Kevin D. Cook, Jason K. Whitmire, Lisa E. Gralinski, Mark Keller, Alan D. Attie, Gary A. Churchill, Petko Petkov, Patrick F. Sullivan, Jennifer R. Brennan, Leonard McMillan, and Fernando Pardo-Manuel de Villena. The mouse universal genotyping array: From substrains to subspecies. *G3: Genes, Genomes, Genetics*, February 2016.
- J7. Andrew P. Morgan and **Catherine E. Welsh**. Informatics resources for the Collaborative Cross and related mouse populations. *Mammalian Genome*, July 2015.
- J6. James J. Crowley, Vasyl Zhabotynsky, Wei Sun, Shunping Huang, Isa Kemal Pakatci, Yunjung Kim, Jeremy R. Wang, Andrew P. Morgan, John D. Calaway, David L. Aylor, Zaining Yun, Timothy A. Bell, Ryan J. Buus, Mark E. Calaway, John P. Didion, Terry J. Gooch, Stephanie D. Hansen, Nashiya N. Robinson, Ginger D. Shaw, Jason S. Spence, Corey R. Quackenbush, Cordelia J. Barrick, Randal J. Nonneman, Kyungsu Kim, James Xenakis, Yuying Xie, William Valdar, Alan B. Lenarcic, Wei Wang, **Catherine E. Welsh**, Chen-Ping Fu, Zhaojun Zhang, James Holt, Zhishan Guo, David W. Threadgill, Lisa M. Tarantino, Darla R. Miller, Fei Zou, Leonard McMillan, Patrick F. Sullivan, and Fernando Pardo-Manuel de Villena. Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. *Nature Genetics*, May 2015.
- J5. **Catherine E. Welsh**, Darla R. Miller, Kenneth F. Manly, Jeremy Wang, Leonard McMillan, Grant Morahan, Richard Mott, Fuad A. Iraqi, David W. Threadgill, and Fernando Pardo-Manuel de Villena. Status and access to the Collaborative Cross population. *Mammalian Genome*, July 2012.
- J4. Karen L. Svenson, Daniel M. Gatti, William Valdar, **Catherine E. Welsh**, Riyan Cheng, Elissa J. Chesler, Abraham A. Palmer, Leonard McMillan, and Gary A. Churchill. High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. *Genetics*, 190(2):437–447, July 2012.
- J3. **Catherine E. Welsh** and Leonard McMillan. Accelerating the inbreeding of multi-parental recombinant inbred lines generated by sibling matings. *G3: Genes, Genomes, Genetics*, 2(2):191–8, February 2012.
- J2. Collaborative Cross Consortium **Catherine E. Welsh**. The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. *Genetics*, 190(2):389–402, February 2012.
- J1. Hyuna Yang, Jeremy R. Wang, John P. Didion, Ryan J. Buus, Timothy A. Bell, **Catherine E. Welsh**, François Bonhomme, Alex Hon-Tsen Yu, Michael W. Nachman, Jaroslav Pialek, Priscilla Tucker, Pierre Boursot, Leonard McMillan, Gary A. Churchill, and Fernando Pardo-Manuel de Villena. Subspecific origin and haplotype diversity in the laboratory mouse. *Nature Genetics*, 43(7):648–55, July 2011.

Papers Published in Conference Proceedings with Acceptance Based on Peer Reviews

Note: Undergraduate students that I advised at Rhodes are underlined.

- C3. C. Shane Elder and **Catherine E. Welsh**. MitoMut: An Efficient Approach to Detecting Mitochondrial DNA Deletions from Paired-end Next-generation Sequencing Data. *Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Health Informatics*, 2019.
- C2. **Catherine E. Welsh**, Chen-Ping Fu, Fernando Pardo-Manuel de Villena, and Leonard McMillan. Fine-Scale Recombination Mapping of High-Throughput Sequence Data. *Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine Informatics*, 2013.
- C1. Chen-Ping Fu, **Catherine E. Welsh**, Fernando Pardo-Manuel de Villena, and Leonard McMillan. Ancestry Inference of Admixed Populations with Microarray Probe Intensities. *Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, 2012.

In Preparation/Submitted to Journals and in Review

* *Denotes co-first authors*

- S2. Kelly McCastlain*, **Catherine E. Welsh***, Ti-Cheng Chang, Wenan Chen, Liang-Ding, Yiping Fan, Patrick Schreiner, Sasi Arunachalam, Veronica Gonzalez-Pena, Samuel Brady, Huiyun Wu, Jinghui Zhang, Charles Gawad, Stanley Pounds, Jiyang Yu, Gang Wu, Mondira Kundu. Somatic mtDNA mutations promote reactivation of silenced T-cell specific pathways in B-cell lymphoblastic leukemias. *In preparation*.
- S1. Kelly McCastlain, **Catherine E. Welsh**, Zhaoming Wang, Carmen L. Wilson, Heather Mulder, John Easton, Ann C. Mertens, Jinghui Zhang, Yutaka Yasui, Melissa M. Hudson, Leslie L. Robison, Kirsten K. Ness, and Mondira Kundu. The Association of Mitochondrial Copy Number with Sarcopenia in Adult Survivors of Childhood Cancer. Submitted and under review at *Lancet Oncology*

Presentations and Posters (acceptance based on peer-reviewed abstract)

- P8. **Catherine E. Welsh**, Kelly McCastlain, and Mondira Kundu. *An automated pipeline for detecting and annotating mitochondrial variants from paired tumor-normal samples*. Poster presentation at Intelligent Systems for Molecular Biology/European Conference on Computational Biology. 2019.
- P7. C. Shane Elder and **Catherine E. Welsh**. *MitoMut: an efficient approach to detecting mitochondrial DNA deletions from paired-end next-generation sequencing data*. Poster presentation at Great Lakes Bioinformatics Conference. 2019.
- P6. Madeline P. Griffin and **Catherine E. Welsh**. *Comparative Analysis of Tools for Predicting the Functional Impact of mtDNA Variants*. Poster presentation at ACM-BCB: Conference on Bioinformatics and Computational Biology. 2018.
- P5. **Catherine E. Welsh**, Darla R. Miller, Kenneth F. Manly, Jeremy Wang, Leonard McMillan, David W. Threadgill, and Fernando Pardo-Manuel de Villena. *In silico predictions of the genomic structure for extant CC lines*. Oral and poster presentations at International Mammalian Genome Conference. 2012.
- P4. Chen-Ping Fu, **Catherine E. Welsh**, John P. Didion, John D. Calaway, Fernando Pardo-Manuel de Villena, and Leonard McMillan. *MegaMUGA: A versatile medium density mouse genotyping platform*. Poster presentation at International Mammalian Genome Conference. 2012.

- P3. **Catherine E. Welsh**, Darla R. Miller, Kenneth F. Manly, Jeremy Wang, Leonard McMillan, Grant Morahan, Richard Mott, Fuad A. Iraqi, David W. Threadgill, and Fernando Pardo-Manuel de Villena. *An update on the distribution center for the Collaborative Cross population at UNC-Chapel Hill*. Poster presentation at International Mammalian Genome Conference. 2012.
- P2. **Catherine Welsh**, Ryan Buus, Fernando Pardo-Manuel de Villena, and Leonard McMillan. *A Low-density Mouse Universal Genotyping Array (MUGA)*. Poster presentation at Mouse Genetics. 2011.
- P1. **Catherine E. Welsh**, Ryan J. Buus, Jennifer Shockley, Stephanie Hansen, Darla Miller, Fernando Pardo-Manuel de Villena, and Leonard McMillan. *Techniques for Accelerating the Inbreeding in the Collaborative Cross*. Oral presentation at the annual meeting of the Complex Trait Community. 2010.

Invited Talks

- T1. **Catherine E. Welsh** *Whole Genome Sequencing: Fine-Scale Recombination Mapping and Mitochondrial Analysis*. University of Tennessee Health Science Center, Biostatistics Departments Seminar, 2016.

External Grant Awards

- NSF IIS-1433589 **ACM BCB 2014: Conference on Bioinformatics and Computational Biology, 5/1/2014 - 4/30/2015**, Role: PI, Direct Annual: \$24,800.
Goal: Participant support for conference held in September 2014 in Newport Beach, CA

Internal Research Grant Awards

- 2019 **Rhodes College Faculty Development Endowment Grant**, *Detection of mitochondrial DNA insertions from next-generation sequencing data*.
- 2019 **Rhodes College Fellowship Fund**, *Bioinformatics Fellowship*, This fund supported two Rhodes undergraduates, Madeline Griffin and Zoe Brookover, during the summer.
- 2018 **Rhodes College Faculty Development Endowment Grant**, *Determining the Functional Impact of mtDNA Mutations in Pediatric High-grade Gliomas*.
- 2018 **Rhodes College Fellowship Fund**, *Bioinformatics Fellowship*, This fund supported two Rhodes undergraduates, Madeline Griffin and Shane Elder, during the summer.
- 2016 **Rhodes College Faculty Development Endowment Grant**, *Determining the Frequency and Functional Impact of mtDNA Mutations in Adult Survivors of Childhood Cancers*.

National and International Service

- 2019 Selection Committee Member for Travel Award Recipients for ACM-BCB Conference, Niagara Falls (NY)
- 2019 Session chair at ACM-BCB Conference, Niagara Falls (NY)
- 2019 Session chair at Great Lakes Bioinformatics Conference, Madison (WI)
- 2015-present NCWIT Aspirations in Computing Award Coordinator, West-Tennessee Affiliate
- 2015 Poster Judge, Grace Hopper Women in Computing Conference, Houston (TX)

- 2014 Student Travel Award Chair, ACM-BCB Conference, Newport Beach (CA)
- 2013 Poster Judge, Southeast Women in Computing Conference, Guntersville (AL)
- 2013 Panelist for Women in Bioinformatics Panel, ACM-BCB Conference, Bethesda (MD)

Conferences and Workshops Attended

- 2011, 2013, 2014, 2018, 2019 ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)
- 2019 Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB)
- 2019 Great Lakes Bioinformatics Conference
- 2019 NCWIT Summit on Women and IT
- 2018 AAC&U Institute on General Education and Assessment
- 2016, 2018 Consortium for Computing Sciences in Colleges Mid-South Conference
- 2015 Grace Hopper Women in Computing Conference
- 2014 CUR Institute: Beginning a Research Program in the Natural Sciences at a PUI
- 2014, 2018 ACM Special Interest Group on Computer Science Education Technical Symposium (SIGCSE)
- 2013, 2015 Southeast Women in Computing Conference
- 2012 International Mammalian Genome Conference
- 2011 Mouse Genetics Conference
- 2010 Complex Trait Community annual meeting
- 2009 Google Workshop for Women Engineers
- 2008, 2009 CRA-W Grad Cohort Workshop

Institutional Service

Rhodes College

- 2019 Member of Provost and Vice President of Academic Affairs Search Committee
- 2018 Reviewed internal Fullbright Scholarship Applications
- 2017-present Member of Foundations Curriculum Committee
- 2015, 2018 Reviewed internal Goldwater Scholarship Applications
- 2014-present St. Jude Partnership Committee

Rhodes College Department of Mathematics and Computer Science

- Spring 2019 Member of Search Committee for Visiting Assistant Professor of Biology
- 2018-2019 Member of Search Committee for Tenure-Track Assistant Professor of Computer Science
- Spring 2017 Member of Search Committee for Visiting Assistant Professor of Computer Science
- 2014-2015 Member of Search Committee for Tenure-Track Assistant Professor of Computer Science
- Spring 2014 Member of Search Committee for Visiting Assistant Professor of Mathematics (2 positions)

2014-present Rhodes College ACM-W Student Chapter: Faculty advisor to this student computer science organization

Teaching Experience

- 2013-Present **Assistant Professor**, *Rhodes College*.
Computer Science 141: Programming Fundamentals (F13 [26 students], S14[55], F14 [26], S16[56], F16[58], F17[54], S18[28], S19[48])
Computer Science 142: Object-Oriented Programming (F14[26], S15[32])
Computer Science 231: Introduction to Computer Organization (S15[29], S18[23])
Computer Science 345: Data Mining (S15[32], F18[42])
Computer Science 355: Advanced Algorithms (S14[16], S16[28], F17[25])
Computer Science 465: Special Topics: Bioinformatics (F13[11], F16[9])
Computer Science: Directed Inquiry (S14[2], F16[1], S18[1], F18[1], S19[2])
Computer Science 451/452: Research (F17[1], S18[4], F18[3], S19[2])
Computer Science 486: Senior Seminar (S19[21])
FYS: First-Year Seminar (AY19-20 [21])
- Fall 2018 **Module Leader**, *Computational Biology Workshop*, Carleton College.
- Spring 2012 **Guest Lecturer**, *Data Mining*, UNC-Chapel Hill.
- Spring 2012 **Teaching Assistant**, *Practical Computing for Biologists*, NEScent Academy.
Assisted with software installation, classroom assignments, and taught database design section of course.
- Spring 2011 **Instructor**, *COMP 110 - Introduction to Programming*, UNC-Chapel Hill.
Topics Included: Algorithm Design, Control Statements, Loops, Arrays, Inheritance.
Designed (and graded): Syllabus, Slides, Lectures, Projects, Assignments and Exams.
Class consisted of 35 undergraduates.
- 2011-2012 **Tutor**, *COMP 110 - Introduction to Programming*, UNC-Chapel Hill.
Held weekly tutoring sessions throughout the summer semester for 3 different students.
- Spring 2009 **Teaching Assistant**, *Professor Wei Wang's Data Mining*, UNC-Chapel Hill.
Met with students upon request and graded all written work, including final projects.