

Curriculum Vitae

Kellie J. Archer, Ph.D.

PERSONAL INFORMATION

Kellie J. Archer
Professor & Chair
Division of Biostatistics
College of Public Health
The Ohio State University
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PROFESSIONAL SUMMARY

Primary Area: Biostatistics

Specific areas of expertise: mixture cure modeling, ordinal response modeling, genomic biostatistics, statistical learning, statistical computing, data mining, applications of statistical methods to high-throughput genomic data including next-generation sequencing data

EDUCATION

GRADUATE

- **1996-2001** Ph.D., The Ohio State University School of Public Health, Columbus, Ohio
Public Health with specialization in Biometrics
Thesis: *Goodness-of-fit tests for logistic regression models developed using data collected from a complex sampling design*
Advisor: Dr. Stanley Lemeshow.
- **1992-1993** M.A.S. from the Department of Statistics, The Ohio State University, Columbus, Ohio

UNDERGRADUATE

- **1987-1991** B.A. in Mathematics & Philosophy at Franklin College, Franklin, Indiana
Graduated *summa cum laude*.

CERTIFICATION AND LICENSURE

Not applicable.

ACADEMIC APPOINTMENT HISTORY

- **2016-present** Professor & Chair (with tenure), Division of Biostatistics, College of Public Health, The Ohio State University, Columbus, Ohio
- **2016-2023** Affiliate Professor, Department of Biostatistics, Virginia Commonwealth University, Richmond, Virginia
- **2015-2016** Professor (with tenure), Department of Biostatistics, Virginia Commonwealth University, Richmond, Virginia
- **2011-2016** Director, VCU Massey Cancer Center Biostatistics Shared Resource, Richmond, Virginia
- **2009-2015** Associate Professor (with tenure), Department of Biostatistics, Virginia Commonwealth University, Richmond, Virginia
- **2002-2009** Assistant Professor, Department of Biostatistics, Virginia Commonwealth University, Richmond, Virginia
- **2002-2016** Fellow, Center for the Study of Biological Complexity, Virginia Commonwealth University, Richmond, Virginia

EMPLOYMENT HISTORY

- **1998-2002** Research Specialist, Division of Hematology & Oncology, The Ohio State University, Columbus, Ohio. Promoted to Research Scientist in 2002
- **1996-1998** Biostatistician, Grant Medical Center, Columbus, OH
- **1995-1996** Biostatistician, Pharmacia, Dublin, OH
- **1993-1995** Data and Statistical Analyst, Grant Medical Center, Columbus, OH

SPECIAL AWARDS AND HONORS

- Elected Fellow, The American Statistical Association, 2021
- 2006 Outstanding Teaching Award, Department of Biostatistics, Virginia Commonwealth University
- Phi Kappa Phi, inducted 2002 at The Ohio State University

MEMBERSHIPS IN SCIENTIFIC OR PROFESSIONAL SOCIETIES

- Eastern North American Region Biometrics Society, 2007-present
- International Association for Statistical Computing, section of the International Statistical Association, 2007-present
- American Statistical Association, 1996-present
- Member, Cancer and Leukemia Group B, 1998-2002

SCIENTIFIC AND SCHOLARLY ACTIVITIES

Expert services

- **Deputy Editorial Board Member, 2026-present** *Radiology*.

- **Member, 2025 - 2027** Fonds Wetenschappelijk Onderzoek (FWO), Fund for Scientific Research, Research Foundation Flanders Review College.
- **Special Government Employee, 2023-2027** Radiological Devices Panel, Medical Devices Advisory Committee, Center for Devices & Radiological Health of the Food & Drug Administration.
- **DSMB Member, 2021-present** A Phase I/II Randomized Pilot Study of hESC-CMs in Patients with Chronic Ischemic Left Ventricular Dysfunction Secondary to Myocardial Infarction, Stanford Cardiovascular Institute, Stanford University.
- **Member, 2019-2023** Environmental Health Sciences Review Committee, National Institute of Environmental Health Sciences.
- **Statistical Editorial Board Member, 2021-present** *JNCI Spectrum*.
- **Statistical Editorial Board Member, 2019-present** *Journal of the National Cancer Institute*.
- **BrainBox Solutions, 2019-2024** Consultant for BrainBox Solutions: Biomarkers for traumatic brain injury.
- **ImmunArray, 2015** Consultant for ImmunArray: identifying biomarkers for traumatic brain injury.
- **Member, 2014-2018** Biomedical Informatics Library and Data Sciences (BILDS) Review Committee, National Library of Medicine.
- **Cancer Informatics, 2014** Lead guest editor for supplement: Computer simulation, bioinformatics, and statistical analysis of cancer data and processes.
- **Merz North America, 2014** Consultant for Mock General Plastic Surgery Device Panel meeting.
- **University of Virginia, 2013-2017** Consultant to provide statistical analysis of high-throughput genomic assay data.
- **Nature Publishing Group, 2013-2018** Statistical consultant for the *Nature* journals.
- **algorithmRx, LLC 2012** Consultant for the development of a clinical decision support tool.
- **Editorial Board Member, 2008-2016** *Progress in Transplantation*.
- **Special Government Employee, 2008-2011** Radiological Devices Advisory Committee to the Food & Drug Administration.
- **Capital One, 2007** Provide a three-day statistical computing workshop.
- **KPIT Infosystems, 2007** Collaborate in the submission of an RFP in response to solicitation NIH-NIDDK-07-07 NIDDK Data Repository.
- **Statistical Editorial Board Member, 2006-present** *Radiology*.
- **StatSolvers, LLC 2006-2009** Provide statistical expertise in the design and analysis of a high-throughput methylation study in Chronic Obstructive Pulmonary Disease.
- **Riverside Regional Medical Center, 2006** Provide statistical expertise in the design of a clinical trial titled, "A Phase I-II trial of an altered GOG 172-type schedule: Intraperitoneal Paclitaxel, followed by Intravenous Paclitaxel and Intraperitoneal Cisplatin for Stage III Ovarian Cancer."

Grants and Contracts: Active

- **T32 TR005761** (Lang Li, Mitch Phelps, **Kellie J. Archer**, MPIs)
NIH/NCATS
Dates: 09/17/2025 - 07/31/2030
Clinical and Translational Data Science Training Program
Role: MPI
Effort: 7.5% cost share
- **R01 DK109581** (Valeria R. Mas, **Kellie J. Archer**, MPIs)

NIH/NIDDK

Dates: 03/15/2024 - 01/31/2028

Assessment of Donor Quality for Improving Kidney Transplant Outcomes

Role: MPI

Effort: 15%

- **R01 CA284595** (AK Eisfeld, HL Grimes, ER Mardis MPIs)

NIH/NCI

Dates: 09/18/2023 - 07/31/2028

Towards an inclusive genomic risk classification for acute myeloid leukemia (AML)

Role: co-I

Effort: 5%

- **R01 AG082811-01** (Colleen Jackson-Cook, PI)

NIH/NIA

Dates: 09/15/2023 - 05/31/2028

Cytosolic DNA, telomeres/subtelomeres, and epigenetics: A longitudinal twin study to assess the role of genetics and environment on their frequency and inter-relationships

Role: co-I (PI of subaward)

Effort: 8%

- **R01 HD111943-01** (Colleen Jackson-Cook, PI)

NIH/NICHD

Dates: 05/01/2023 - 04/30/2026

A mosaic Down syndrome model system comparing isogenic trisomic/disomic cells to unmask trisomy 21 related genomic, epigenomic, and senescence changes acquired across the lifespan

Role: co-I (PI of subaward)

Effort: 10%

- **R01LM013879-01** (Kellie J. Archer, PI)

NIH/NLM

Dates: 01/01/2022 - 12/31/2026

Penalized mixture cure models for identifying genomic features associated with outcome in acute myeloid leukemia

Role: PI

Effort: 30%

- **1R01OH012224-01A1** (Olorunfemi Adetona & Luke Naeher, PI)

NIOSH

Dates: 09/2022 – 08/2026

Chronic Respiratory Effect and Control of Occupational Exposure of Wildland Firefighters to Smoke

Role: co-I

Effort: 5%

Grants and Contracts: Past

- **R21 AI172077-01A1** (Valeria Mas & Kellie J. Archer, MPI)

NIH/NIAID

Dates: 03/16/2023 - 02/28/2026 (No cost extension)

Pre-transplant comprehensive scores to predict long term graft outcomes

Role: MPI

- **R01GM137578** (Charles Chalfant, PI)

NIH/NIGMS

Dates: 09/20/2020 - 06/30/2024

- The role of ceramide kinase in mitophagy
 Role: co-I (PI of sub-award from Univ of Virginia)
 Effort: 5%
- **Origin Editorial LLC (PCORI)** (John Bridges, PI)
 Dates: 02/01/2022 - 12/31/2023
 Peer review management services of PCORI-funded research results: A response from Origin
 Editorial Role: Biostatistician
 Effort: 20%
 - **R21NR018936** (Debra Lyon, PI)
 NIH/NINR
 Dates: 03/20/2020 - 02/28/2023
 Metabolomic Signature of PN Symptoms in Breast Cancer Over the First Year of Treatment and Survivorship
 Role: co-I (PI of sub-award from Univ of Florida)
 Effort: 10%
 - **R03CA245771 (Kellie J. Archer, PI)**
 NIH/NCI
 Dates: 12/13/2019 - 11/30/2022
 High-dimensional variable selection and prediction of ordinal pathological response data
 Role: PI
 Effort: 10%
 - **R01DK109581-01** (Valeria Mas & **Kellie J Archer**, MPI)
 NIH/National Institute of Diabetes Digestive and Kidney Diseases
 Total award: \$2,008,527
 Dates: 02/01/2017 - 11/30/2022
 Assessment of donor quality for improving post-kidney transplant outcomes
 Role: MPI
 Effort: 15%
 - **3U01CA164973-09S1** (Le Marchand, Haiman, Wilkens, MPI)
 University of Hawaii (Prime: NIH)
 Dates: 07/01/2020 – 06/30/2021
 Understanding Ethnic Differences in Cancer: The Multiethnic Cohort Study
 Role: co-Investigator
 Effort: 5%
 - **UG1CA233338** (John Byrd, PI)
 NIH
 Total award: \$1,237,334
 Dates: 03/01/2019 - 06/30/2021
 ITSC for Leukemia: Novel Molecular Strategies for NCTN: "Individualized" Therapies
 Role: Co-investigator
 Effort: 5%
 - **1UL1TR002733-01** (Rebecca D Jackson, PI)
 NIH/National Center for Advancing Translational Sciences
 Total award (direct): \$3,055,975
 Dates: 06/29/2018 - 10/31/2021
 The OSU Center for Clinical and Translational Science: Advancing today's discoveries to improve health
 Role: Biostatistician
 Effort: 5%
 - **4P50CA180908-04** (ME Wewers & P Shields, MPI)

National Institutes of Health/National Cancer Institute
Total Award: \$18M
Dates: 09/01/16 (effort started) - 08/31/18
Understanding Adolescent Trajectories, Exposures and Susceptibilities
Role: co-Investigator
Effort: 10%

- **R01LM011169 (Kellie J. Archer, PI)**
National Institutes of Health/National Library of Medicine
Total Award: \$957,815
Dates: 09/01/2012 - 08/31/2017
Informatic tools for predicting an ordinal response for high-dimensional data Role: PI
Effort: 35%
- **5P30CA16059-29 (Gordon Ginder, PI)**
National Institutes of Health/NCI
Total Award: \$7,972,299
Dates: 07/08/02 (effort started) - 04/30/17 (effort ended 06/2016 left VCU) Massey
Cancer Center Core Support - Biostatistics Core.
Role: Director, Biostatistics Shared Resource
Effort: 10%
- **5T32ES007334 (Kellie J. Archer, PI)**
National Institutes of Environmental Health Science
Annual Award: \$88,405
Dates: 07/01/07 - 06/30/17 (effort ended 06/2016 left VCU)
Integration of mixtures toxicology, toxicogenomics, and statistics
Role: PI (as of 09/01/2014; previously Associate Director)
Effort: 5% cost share
- **1U01HD087198 (PI: Charles Chalfant)**
NIH/NICHD
Total Award: \$4,183,480
Dates: 09/17/2015 – 08/31/2019 (effort ended 06/2016)
The utilization of photonics technology to rapidly detect bioactive lipids associated with
preeclampsia development
Role: co-Investigator
Effort: 4%
- **1R01 CA191002-01A1(PI: Zheng Fu)**
NCI
Total Award: \$228,750
Dates: 04/01/2016 – 03/31/2021 (effort ended 06/2016)
The Role of PLK1 in Prostate Cancer
Role: co-Investigator
Effort: 1%
- **1R01CA206028 (PI: David Gewirtz)**
NCI
Mitigation of chemotherapy induced peripheral neuropathy
Total Award: \$259,883
Dates: 04/15/2016 – 03/31/2021 (effort ended 06/2016)
Role: co-Investigator
Effort: 5%
- **1R01DK080074-01(PI: Valeria R. Mas)**
NIH/NIDDK
Molecular pathways leading to chronic allograft dysfunction

Total Award: \$2,168,647
Dates: 08/05/08 – 05/31/13
Role: co-Investigator
Effort: 16%

- **U54 HL090516 (Project 4b)** (PI: Joyce Lloyd)
NIH/NHLBI
Effects of developmental stage and of KLF2 on mouse erythroid genetic profiles
Total Award: \$120,331 per year
Dates: 04/01/08 – 03/31/12
Role: co-Investigator
Percent effort: 5%
- **1R03LM009347-02** (PI: Kellie J. Archer)
NIH/NLM
Recursive partitioning and ensemble methods for classifying an ordinal response
Total Award: \$149,000
Dates: 08/15/08 – 07/31/11
Role: PI
Effort: 15%
- **U01DK062531-08** (PI: Robert A. Fisher)
NIH/NIDDK
Adult to Adult Living Donor Liver Transplantation
Total Award: \$1,218,335
Dates: 09/30/09 – 08/31/11
Role: co-investigator
Effort: 2%
- **R01 DK069859-02** (PI: Robert Fisher)
NIH/NIDDK
Genes related to HCC progression in living donor and deceased donor transplant liver recipients
Total Award: \$3,570,708
Dates: 04/01/06 – 03/31/11
Role: Co-investigator
Effort: 25%
- **3R03LM009347-02S1** (PI: Kellie J. Archer)
NIH/NLM
American Reinvestment and Recovery Act of 2009: Competing Revision of Recursive partitioning and ensemble methods for classifying an ordinal response
Total Award: \$75,000
Dates: 09/30/09 – 09/29/10
Role: PI
Percent Effort: 13%
- **3R03LM009347-02S2** (PI: Kellie J. Archer)
NIH/NLM
Administrative Supplement for Students and Science Educators under the Recovery Act
Total Award: \$5,742
Dates: 05/01/10 – 07/31/10
Role: PI
- **Pharmion** (PI: John McCarty)
Pharmion

A Phase II Study of the Use of 5-Azacytidine as Pre-Transplant Cytoreduction Prior to Allogeneic Stem Cell Transplantation

Dates: 4/30/08 – 4/30/11 (effort ended 09/30/09)

Role: Biostatistician

Effort: 2%

- **Genzyme** (PI: Amir Toor)

Genzyme

Reduced Intensity Myeloablative Total Body Irradiation and Thymoglobulin Followed by Allogeneic Peripheral Blood Stem Cell Transplantation

Dates: 4/30/08 – 4/30/11 (effort ended 09/30/09)

Role: Biostatistician

Effort: 2%

- **Roche Laboratories** (PIs: VR Mas & DG Maluf)

Roche Laboratories

New strategies for non-invasive detection of chronic allograft nephropathy

Total Award: \$133,000

Dates: 12/01/06 – 11/30/08

Role: Biostatistician

Effort: 5%

- **5F37LM008728-03** (Fellow: Richard E. Kennedy)

NIH/NLM

Mixed Effects Modeling of Microarrays Using the S-score

Total Award: \$159,689

Dates: 08/01/05 – 07/31/08

Role: Sponsor

- **A.D. Williams Trust Fund** (PI: Kellie J. Archer)

A.D. Williams Trust Fund

Extending the random forest methodology for predicting an ordinal response

Total Award: \$10,342

Dates: 01/01/07 – 12/31/07

Role: PI

- **Pfizer** (PI: R. Kightlinger)

Pfizer International Health Initiative

HIV, cervical cancer, HPV, and HPV genotypes among women in rural and urban regions of Guyana

Total Award: \$7,500

Dates: 01/01/07 – 12/31/07

Role: Biostatistician

Effort: 7.5%

- **The V Foundation for Cancer Research** (PI: Peter O'Connell)

The V Foundation

Neoadjuvant chemotherapy for breast cancer

Total Award: \$300,000

Dates: 10/31/04 – 10/30/07

Role: Biostatistician

Effort: 10%

- **Massey Cancer Center Pilot** (Co-PIs: Kellie J. Archer & Valeria R. Mas)

Massey Cancer Center

Predicting HCC progression using molecular markers in patients awaiting liver transplantation

Total Award: \$30,000
Dates: 08/01/05 – 07/31/06
Role: co-PI
Effort: 2%

- **Massey Cancer Center Pilot** (Co-PIs: C.I. Dumur & W. Broaddus)
Massey Cancer Center
Role of necrosis in glioblastoma multiforme
Total Award: \$30,000
Dates: 12/31/04 – 12/30/05
Role: Biostatistician
Effort: 2%
- **ACS Institutional Research Grant** (PI: Kellie J. Archer)
American Cancer Society
Image analysis and probe set expression summaries for oligonucleotide microarrays
Total Award: \$2,844
Dates: 09/01/03 – 08/31/04
Role: PI
- **Massey Cancer Center Pilot** (PI: Lynne Penberthy)
Massey Cancer Center
Evaluate Cancer and Genomics in Elderly versus Young Cancer Patients
Total Award: \$30,000
Dates: 01/01/03 – 12/31/03
Role: Biostatistician

EXTRAMURAL PRESENTATIONS

Invited Presentations

- **Conference of the American Statistical Association Statistical Learning and Data Science section**, Newport Beach, CA, November 7, 2024: “Penalized mixture cure models for identifying latent subgroups to improve risk stratification systems in cancer.”
- **Denison University**, Department of Mathematics, February 22, 2023: “The Role of Biostatistics in Public Health and Clinical Medicine.”
- **University of Cincinnati**, Division of Biostatistics and Bioinformatics, Department of Environmental and Public Health Sciences, October 7, 2022: “Regularized Mixture Cure Models for Identifying a Gene Signature to Improve Risk Stratification in Acute Myeloid Leukemia Patients.”
- **Georgetown University** Department of Biostatistics, Bioinformatics, and Biomathematics, October 25, 2019: “Algorithmic and statistical learning methods for high-dimensional variable selection.”
- **University of Minnesota** Division of Biostatistics, September 18, 2019: “High-dimensional variable selection and prediction of ordinal pathological response data.”
- **National Library of Medicine**, Bethesda, MD June 15, 2016: “Predicting an ordinal response using features from high-throughput genomic assays.”
- **National Institute of Environmental Health Sciences**, Biostatistics and Computational Biology Branch, Research Triangle Park, NC, May 3, 2016: “Statistical models for elucidating molecular features associated with exposure-induced chromosomal aberrations.”

- **Franklin College**, Franklin, Indiana, Scholar-in-Residence, March 16-18, 2016: “The Role of Biostatistics in Public Health and Clinical Medicine” and “An Overview of Statistical Methods for Analyzing Data from High-Throughput Genomic Experiments.”
- **Division of Biostatistics, The Ohio State University**, Columbus, OH October 30, 2015: “Penalized ordinal response models for high-dimensional feature data.”
- **West Virginia University**, Morgantown, WV April 1, 2015: “Identifying factors related to micronuclei frequency in women with breast cancer.”
- **Institute of Applied Statistics Sri Lanka (IASSL) 2014 Conference**, Colombo, Sri Lanka, December 30, 2014: “Extending the Generalized Monotone Incremental Forward Stagewise Method for Modeling Longitudinal High-Dimensional Genomic Feature Data.”
- **Mathematical Biosciences Institute CTW: Molecular to Systems Physiology**, Ohio State University, Columbus, OH, May 7, 2014: “Ordinal Response Models for Modeling Longitudinal High-Dimensional Genomic Feature Data.”
- **Sixth Annual Math Awareness Society for Industrial and Applied Mathematics (SIAM) Conference**, Old Dominion University, Norfolk, VA, April 13, 2013: “Penalized ordinal response models for high-dimensional datasets.” Keynote plenary speaker.
- **Virginia State University**, Petersburg, VA, March 1, 2013: “Identifying Genes for Establishing a Multigenic Test for HCC Surveillance in HCV+ Cirrhotic Patients.”
- **Air Force Institute of Technology**, Dayton, OH, May 24, 2012: “Classification and variable selection for high-dimensional datasets using Random Forests.”
- **Cambridge Healthtech Institute’s Advances in Gene Expression Profiling**, Philadelphia, PA, November 18, 2010: “Evaluating Quality in a Multicenter Gene Expression Microarray Study.”
- **James Madison University** Department of Mathematics & Statistics Colloquium, Harrisonburg, VA, November 10, 2008: “Statistics in medical and high-throughput genomic research.”
- **Institute for Operations Research and the Management Sciences (INFORMS)** Annual Meeting, Washington, D.C., October 13, 2008: “Variable Selection in High-dimensional Ordinal Class Prediction Problems with Genomics Applications.”
- **National Institutes of Health Microarray Special Interest Group**, Bethesda, MD, April 2, 2008: “An exploratory approach for assessing aberrant methylation using Affymetrix GeneChip data.”
- **George Mason University** Bioinformatics Colloquium, Manassas, VA, March 25, 2008: “A combined statistical and bioinformatic approach for identifying hypermethylated genes in human hepatocellular carcinoma.”
- **Longwood University** Mathematics Department Colloquium, Farmville, VA, November 1, 2007: “The importance of integrating knowledge of biology, statistics, and computer science in high-throughput genomic research.”
- **Presentation to NIH funded Adult to Adult Living Liver Transplant (A2ALL) Steering Committee Meeting**, Washington D.C., June 13, 2006: “Study Design and Statistical Analysis Plan for A2ALL Ancillary Study: Genes related to HCC progression in living donor and deceased donor transplant liver recipients.”
- **College of William and Mary**, Department of Mathematics Applied Mathematics Colloquium, March 24, 2003: “Expression summaries for oligonucleotide arrays: implications for multiple hypothesis testing,” Williamsburg, Virginia.

Contributed Presentations

- **Kellie J. Archer**, 2025 Joint Statistical Meetings, Nashville, TN, August 6, 2025: “Regularized mixture cure models for improving cancer risk stratification systems by identifying latent subgroups.” Topic contributed talk.
- **Kellie J. Archer**, R/Medicine Conference, June 13, 2024: “Identifying latent subgroups using regularized mixture cure models to develop risk stratification systems in cancer: Illustration using the `hdcuremodels` R package.” Regular talk.
- **Kellie J. Archer**, Han Fu. 64th ISI World Statistics Congress, Ottawa, Canada, July 18, 2023: “Penalized Mixture Cure Models For Modeling A Time-To-Event Outcome With Long-Term Survivors In A High-Dimensional Covariate Space.” Oral presentation in High-dimensional statistics session.
- **Kellie Archer**, Han Fu, et al., 2022 American Society of Hematology, New Orleans, LA, December 12, 2022: “Regularized Mixture Cure Models Identify a Gene Signature That Improves Risk Stratification within the Favorable-Risk Group in 2017 European Leukemianet (ELN) Classification of Acute Myeloid Leukemia (Alliance 152010).” Oral presentation.
- **Kellie Archer**, Yiran Zhang, et al., 2019 American Transplant Congress, Boston, MA, June 1, 2019: “Predicting Post-Transplant Graft Function in Deceased Donor Kidney Transplant Recipients.” Poster presentation (Awarded Poster of Distinction).
- **Kellie J. Archer**, Yiran Zhang, Qing Zhou. 2018 Eastern North American Region of the International Biometric Society Meeting, Atlanta, GA, March 27, 2018: “Bayesian Ordinal Response Models for Identifying Molecular Mechanisms in the Progression of Cervical Cancer.” Oral presentation.
- **Kellie J. Archer** and Jiayi Hou. 2014 Eastern North American Region of the International Biometric Society Meeting, Orlando, FL, March 10, 2014: “Generalized incremental forward stagewise ordinal models: Application predicting stage of Alzheimer’s disease.” Poster presentation.
- **Kellie J. Archer** and André A.A. Williams. 2013 Eastern North American Region of the International Biometric Society Meeting, Orlando, FL, March 10, 2013: “Feature selection among ordinal classes for high-throughput genomic data.” Poster presentation.
- **Kellie J. Archer** and André A.A. Williams. 2011 Eastern North American Region of the International Biometric Society Meeting, Miami, FL, March 22, 2011: “A Comparison of Frequentist and Bayesian Penalized Continuation Ratio Models for Predicting an Ordinal Response in High-Dimensional Datasets.” Oral presentation.
- **Kellie J. Archer**, 2010 Eastern North American Region of the International Biometric Society Meeting, New Orleans, LA, March 23, 2010: “Penalized models for ordinal response prediction: Application discriminating patients with early stage Parkinson’s disease.” Oral presentation.
- **Kellie J. Archer**, Joint Statistical Meetings, Washington, D.C., August 2-6, 2009: “Identifying Important Predictors Using L1 Penalized Models and Random Forests.” Poster presentation.
- **Kellie J. Archer**, 2009 American Transplant Congress, Boston, MA, June 1, 2009: “Identifying genes for establishing a multigenic test for HCC surveillance in HCV+ cirrhotic patients.” Oral presentation.
- **Kellie J. Archer**, 2009 American Transplant Congress, Boston, MA, June 1, 2009: “Identifying microRNAs involved in the regulation of gene expression in HCV-induced HCC progression: Preliminary results.” Oral presentation.
- **Kellie J. Archer**, 2009 American Transplant Congress, Boston, MA, June 1, 2009: “Genome wide hypermethylation and its association with gene expression in the

molecular pathogenesis of HCV-induced hepatocellular carcinoma.” Poster presentation (Awarded Poster of Distinction).

- **Kellie J. Archer**, 2009 Eastern North American Region of the International Biometric Society Meeting, San Antonio, Texas, March 18, 2009: “Variable selection for ordinal response models with applications to high dimensional data.” Oral presentation.
- **Kellie J. Archer**, 2008 American Transplant Congress, Toronto, Canada, June 2, 2008: “High-throughput assessment of CpG site methylation in HCV-infected hepatocellular carcinoma patients.” Oral presentation.
- **Kellie J. Archer**, 2008 Eastern North American Region of the International Biometric Society Conference, Washington, D.C., March 16, 2008: “Bootstrap aggregation for ordinal response prediction in high-throughput genomic datasets.” Poster presentation.
- **Kellie J. Archer**, “An ordinal impurity function for classification trees when predicting an ordinal response.” Meeting of the Classification Society of North America, June 7-11, 2007, Urbana, Illinois. Oral presentation.
- **Kellie J. Archer**, Joint Statistical Meetings, Seattle, Washington, August 9, 2006: “Ensemble methods for predicting an ordinal response.” Oral presentation.
- **Kellie J. Archer**, Joint Statistical Meetings, Minneapolis, Minnesota, August 11, 2005: “Measurement error models for estimating cross-platform correlations and gene-specific reliabilities.” Oral presentation.
- **Kellie J. Archer**, Joint Statistical Meetings, Toronto, Ontario, August 9, 2004: “Parallel Coordinate Plots of Gene Expression Data Differentiated by Phenotype.” Oral presentation.
- **Kellie J. Archer**, 36th Symposium on the Interface (Interface 2004): Computational Biology and Bioinformatics, Baltimore, MD, May 27, 2004: “Mixed effects model for assessing RNA degradation in Affymetrix GeneChip experiments.” Oral presentation.

Student Contributed Presentations

- Justice Ameyi, **Kellie J. Archer**. Penalized Excess Hazards Mixture Cure Model for High-dimensional Survival Data. Oral presentation, 2026 Eastern North American Meeting of the International Biometric Society, Indianapolis, IN, March 15, 2026.
- Wei-Ting Chen, **Kellie J. Archer**. Comparative Evaluation of Nonparametric, Parametric, and Semiparametric Approaches for Incidence and Latency in Mixture Cure Models under Misspecification. Poster presentation, 2026 Eastern North American Meeting of the International Biometric Society, Indianapolis, IN, March 15, 2026.
- Yihao Zhao, **Kellie J. Archer**. Diagnostic Goodness-of-Fit Tests for Incidence and Latency Components in Mixture Cure Models with Application to Pediatric Acute Myeloid Leukemia. Poster presentation, 2026 Eastern North American Meeting of the International Biometric Society, Indianapolis, IN, March 15, 2026.
- Christilene Tumsiah, **Kellie J. Archer**. Evaluating Sufficient Follow-Up in Mixture Cure Models: Simulation and Application to Pediatric Acute Myeloid Leukemia. Poster presentation, 2026 Eastern North American Meeting of the International Biometric Society, Indianapolis, IN, March 15, 2026.
- Justice Ameyi, Deedra Nicolet, Michael Walker, Krzysztof Mrozek, A-K Einfeld, **Kellie Archer**. Accounting for long-term survivors and population-expected survival improves survival outcomes estimation and prediction in older patients with core-binding factor (CBF) acute myeloid leukemia. Poster presentation, 2025 67th Annual Meeting of the American Society of Hematology, Orlando, FL, December 2025. ASH Abstract Achievement Award.

- Shuai Sun, **Kellie Archer**. Controlled variable selection in generalized odds rate mixture cure models for high-dimensional data. Oral presentation, 2025 Joint Statistical Meetings, August 5, 2025.
- Shuai Sun, **Kellie Archer**. Extending the Ordinal Cumulative Probability Model to High-throughput Genomic Settings to Model a Continuous Outcome or a Discrete Ordinal Outcome With Large Number of Levels. Oral presentation, ENAR, March 11, 2024.
- Anna Eames Seffernick, **Kellie Archer**. Penalized Bayesian forward continuation ratio model with application to high-dimensional data with a discrete survival outcome. Oral presentation, ENAR, March 20, 2023.
- Guowei Li, **Kellie Archer**. Variable selection for competing risks in high-dimensional covariate spaces with missing data. Oral presentation, ENAR, March 20, 2023.
- Guowei Li, **Kellie Archer**. Variable selection for high-dimensional competing risks data. Oral presentation, Joint Statistical Meetings, August 9, 2022.
- Anna Eames Seffernick, **Kellie Archer**. Feature Selection in High-dimensional Genomic Data Using a Bayesian Stereotype Model. Oral presentation, ENAR, March, 2022.
- Anna Eames Seffernick, **Kellie Archer**. Bayesian Stereotype Model for Feature Selection in High-Dimensional Genomic Data. Contributed Poster, ENAR, March 17, 2021.
- Han Fu, **Kellie Archer**. Penalized Weibull mixture cure models with high-dimensional predictors. Variable Selection and Computationally Intensive Methods - Contributed Papers, Joint Statistical Meetings, August 5, 2020.
- Han Fu, **Kellie Archer**. High-dimensional controlled variable selection for ordinal outcomes. Bayesian Modeling and Variable Selection Methods - Contributed Papers, Joint Statistical Meetings, Denver, CO, July 30, 2019.
- Yiran Zhang, **Kellie J. Archer**. Bayesian variable selection for high-dimensional data with ordinal responses. Poster Presentation: Variable Subset Selection. ENAR, March 24, 2019.
- Rebecca Lehman, Colleen Jackson-Cook, **Kellie J. Archer**. Modeling longitudinal count data using the generalized monotone incremental forward stagewise method. ENAR, Poster Presentation: Cancer Applications. Washington, DC, March 12, 2017.
- Rebecca Lehman, Colleen Jackson-Cook, **Kellie J. Archer**. Modeling micronuclei count data using the generalized monotone incremental forward stagewise method: Application in women with breast cancer. Statistical Methods for High-dimensional Data - Contributed Papers, Joint Statistical Meetings, Chicago, IL, August 1, 2016.
- Rebecca Lehman, Colleen Jackson-Cook, **Kellie J. Archer**. Modeling overdispersed nuclear bud count data using the generalized monotone incremental forward stagewise method. ENAR, Poster Presentation: Classification, Testing, and Networks. Austin, TX, March 6, 2016.
- Kyle L. Ferber, **Kellie J. Archer**. Extending the method, feature augmentation via nonparametrics and selection, to the ordinal response setting. ENAR, Poster Presentation: Machine Learning. Austin, TX, March 7, 2016.
- Qing Zhou, **Kellie J. Archer**. Penalized Bayesian cumulative logit model for high-dimensional datasets. ENAR, Poster Presentation: Machine Learning. Austin, TX, March 7, 2016.
- Amanda E. Gentry, **Kellie J. Archer**. Mixed models for ordinal outcomes in twin and sibling studies with high-dimensional covariate spaces. ENAR, Poster Presentation: Machine Learning. Austin, TX, March 7, 2016.
- Amanda E. Gentry, **Kellie J. Archer**. Mixed models for ordinal outcomes in twin studies with high-dimensional covariate spaces. Behavior Genetics Association Annual Conference, Brisbane, Australia, June 2016.

- Kyle Ferber, **Kellie J. Archer**. Modeling an ordinal outcome in high dimensions with nonparametric feature augmentation and proportional odds boosting. Statistical Learning with Censored Data and Systematic Sampling - Contributed Papers. Joint Statistical Meetings, Chicago, IL, August 3, 2016.
- Uma Siangphoe, **Kellie J. Archer**. Estimation of random effects in meta-analysis of gene expression studies. Methodological Developments in Meta-Analysis - Contributed Papers. Joint Statistical Meetings, Seattle, WA, August 10, 2015.
- Jiayi Hou, **Kellie J. Archer**. Regularization methods for predicting an ordinal response using longitudinal high-dimensional genomic data. Biodata Methods - Contributed Papers. Joint Statistical Meetings, Boston, MA, August 6, 2014.
- Sarah E. Reese, Terry M. Therneau, Elizabeth J. Atkinson, **Kellie J. Archer**, Jeanette E. Eckel-Passow. Statistical methods for identifying batch effects in copy number data. ENAR, Poster Presentation: Statistical Genetics/Genomics. Washington, DC, April 1, 2012.
- Andre Williams, **Kellie J. Archer**. Stereotype logit models for high-dimensional data. ENAR, New Orleans, LA, March 23, 2010.
- Andre Williams, **Kellie J. Archer**. Stereotype logit models for high-dimensional data. Bioinformatics - Contributed Papers. Joint Statistical Meetings, Seattle, WA, August 2, 2010.
- Sarah Reese, **Kellie Archer**. Detection call algorithms for high-throughput gene expression microarray data. Contributed Oral Poster Presentations - Biometrics Section. Joint Statistical Meetings, Seattle, WA, August 3, 2010.
- Andre A.A. Williams, **Kellie J. Archer**. Analysis of microRNA data. Microarray Data - Topic Contributed - Poster Presentations. Joint Statistical Meetings, Washington, DC, August 4, 2009.
- Xiangrong Kong, **Kellie J. Archer**. Variable selection in competing risks using the L1 penalized Cox Model. Contributed Oral Poster Presentations - Section on Risk Analysis. Joint Statistical Meetings, Washington, DC, August 4, 2009.
- Xiangrong Kong, **Kellie J. Archer**. A non-parametric meta-analysis approach for combining independent microarray datasets pertaining to chronic allograft nephropathy. ENAR, Arlington, VA, March 19, 2008.
- Xiangrong Kong, **Kellie J. Archer**. Application of discrimination method on combining gene expression data of kidney transplant patients. Recent Advances in Microarray Data Analysis II - Contributed Papers. Joint Statistical Meetings, Salt Lake City, Utah, July 30, 2007.
- Richard E. Kennedy, **Kellie J. Archer**. A mixed effects model implementation of the S-score algorithm. Poster Presentation. ENAR, Atlanta, GA, March 11, 2007.

Invited local oral presentations

- **OSU Division of Computational Biology and Bioinformatics**, Columbus, OH, April 18, 2025: "The chicken or the egg and what geocentrism and the space shuttle Challenger have in common with the somatic mutation theory of cancer."
- **OSU Cancer Biology Program**, Columbus, OH, March 6, 2024: "Identifying latent risk groups with distinct survival profiles from RNA-Seq data: Applications in acute myeloid leukemia."
- **OSU Department of Biomedical Informatics**, Columbus, OH, February 9, 2024: "Identifying transcriptionally defined subgroups using regularized mixture cure models to improve risk stratification in acute myeloid leukemia patients."

- **OSU Department of Biomedical Informatics**, Columbus, OH, October 29, 2021: "Identifying features associated with long-term outcome using penalized mixture cure models."
- **OSU CCTS BERD Secondary Data Analysis Workshop**, Columbus, OH, August 19, 2021: "NIDDK Central Repository Data and Samples."
- **OSU Department of Statistics**, Columbus, OH, November 14, 2017: "Modeling an Ordinal Response when Confronted with a High-Dimensional Feature Space."
- **OSUCCC Molecular Biology & Cancer Genetics Program**, Columbus, OH, September 7, 2016: "Applications of statistical methods for establishing multigenic tests for polygenic traits & conditions."
- **Center for the Advancement of Research Methods and Analysis**, Virginia Commonwealth University, Richmond, VA, April 30, 2004: "Robust and exploratory statistics: Applications using microarray data."
- **Center for the Study of Biological Complexity Annual Research Review**, Virginia Commonwealth University, Richmond, VA, December 16, 2003: "Graphical techniques for identifying a monotonic variance stabilizing transformation for absolute gene intensities."
- **NIH CaBIG Site Visit Review Panel**, Massey Cancer Center, Richmond, VA, September 8, 2003: "Biostatistics Program Resources."

TEACHING, ADVISING, AND MENTORING

Faculty Mentor

- David Kline, Ph.D. (2019-2021) – OSU Department of Biomedical Informatics
- Guy Brock, Ph.D. (2019-2021) – OSU Department of Biomedical Informatics

Postdoctoral Students Trained

- Wenan Chen, Ph.D. – *Machine learning methods for classifying an ordinal response*; Funded by NIH R01LM011169 (11/2012-09/2013)
- Richard E. Kennedy, M.D., Ph.D. (2008 Biostatistics) – *Mixed Effects Modeling of Microarrays Using the S-score*; Funded by Individual Biomedical Informatics Fellowships 1F37LM008728-01
- Allison Bradley, Ph.D. (2017) – *Predicting Childhood Listening Difficulties*; Funded by NIH BD2K Data Science RoAD-TRIP
- Veronica Haywood, Ph.D. (2018) – *Differential Glycosylation Related Gene Expression during Wound Healing*; Funded by NIH BD2K Data Science RoAD-TRIP

PhD Dissertation Advisor

- Xinyu Li (in progress) – *Machine learning based mixture cure models for modeling long-term survival in high-dimensions*
- Justice Ameyi (in progress) – *Causal inference for high-dimensional survival models with a cured subset*
- Shuai Sun (in progress) – *Extending generalized odds rates models to high-dimensional covariate spaces*
- Guowei Li (2023) – *Variable selection for competing risks in high-dimensional covariate spaces without and with missing data*
- Anna Eames Seffernick (2022) – *Penalized Bayesian ordinal response models with applications to discrete survival time and non-proportional odds models*

- Han Fu (2022) – *Variable selection for high-dimensional data with error control*
- Yiran Zhang (2019) – *Bayesian variable selection for high-dimensional data with an ordinal response*
- Amanda Gentry (2018) – *Penalized mixed-effects ordinal response models for high-dimensional genomic data in twins and families*
- Rebecca Lehman (2017) – *The generalized monotone incremental forward stagewise method for modeling longitudinal, clustered, and overdispersed count data*
- Kyle Ferber (2016) – *Methods for predicting an ordinal response with high-throughput genomic data*
- Qing Zhou (2016) – *An extension of penalized ordinal response models*
- Umaporn Siangphoe (2015) – *Meta-analysis of gene expression studies*
- Mateusz Makowski (2015) – *High-throughput data analysis: Application to micronuclei frequency and T-cell receptor sequencing*
- Jiayi Hou (2013) – *Regularization methods for predicting an ordinal response using longitudinal high-dimensional genomic data*
- Sarah E. Reese (2013) – *Detecting and correcting batch effects in high-throughput genomic experiments*
- Maria I. Capparuccini (2010) – *Inferential methods for high-throughput methylation data*
- Andr'e A.A. Williams (2010) – *Stereotype logit models for high-dimensional data*
- Xiangrong Kong (2008) – *Variable selection in competing risks under the -penalized Cox model*

MS Thesis Advisor

- Yihao Zhao (in progress) – *Goodness-of-fit tests for the incidence and latency components of mixture cure models*
- Eric Chen (in progress) – *Non-parametric covariate tests in mixture cure models*
- Xueping Zhang (2010) – *A Meta-analysis of microRNA microarray studies in prostate cancer*
- Tobias Guennel (2008) – *Ordinal Classification Approach using Bagged Classification Trees and the Proportional Odds Model as Splitting Criteria*
- Ryan V. Kimes (2006) – *Quantifying the Effects of Correlated Covariates on Variable Importance Estimates from Random Forests*
- S. Brett Kliner (2006) – *Empirical characterization of variability among Affymetrix probe set expression summaries by sequence fidelity*

MPH Integrated Learning Experience Advisor

- Claudia R. Kelly (2025–present) Evaluating the impact of cytogenetics and gene mutations on cure fraction estimates in pediatric acute myeloid leukemia

Candidacy Exam Committee Member

- Arkobrato Gupta 2025 Biostatistics
- Anthony Akande 2025 Environmental Health
- Yameng Wu 2024 Biomedical Informatics
- Juan Xie 2024 Biostatistics
- Qingyu Chen 2023 Biostatistics
- David Angeles 2023 Biostatistics
- Rejuan Haque 2022 Biostatistics
- Qiaolan Deng 2021 Biostatistics
- Zihan Lin 2021 Biostatistics

- Yiwen Wang 2021 Epidemiology
- Shuyuan Lou 2019 Biostatistics
- Xiao Zang 2019 Biostatistics
- Xiaoyu Cai 2018 Biostatistics
- Yihan Sui 2017 Biostatistics

Dissertation Committee Member

- Juan Xie, Ph.D. 2025 Biostatistics *Statistical methods for design and analysis of single-cell and spatial omics experiments*
- David Angeles, Ph.D. 2024 Biostatistics *Algorithmic estimation for partially observed functions and shapes*
- Qingyu Chen, Ph.D. 2023 Biostatistics *Association test and variable selection in microbiome analysis with phylogeny*
- Rejuan Haque, Ph.D. 2023 Biostatistics *Testing global hypotheses using combination tests, with application to phylogenetic inference*
- Qiaolan Deng, Ph.D. 2022 Biostatistics *Multi-trait analysis of genome-wide association studies using adaptive Fisher's method*
- Yiwen Wang, Ph.D. 2022 Epidemiology *The role of genetic variants and genomic features in outcomes following transplantation*
- Xiaoyu Cai, Ph.D. 2021 Statistics *Detecting dense and sparse signals in genetic and genomic studies*
- Shuyuan Lou, Ph.D. 2021 Biostatistics *Bayesian analysis for significant interactions of chromatin and simulation algorithm*
- Xiao Zang, Ph.D. 2021 Biostatistics *Clustering functional data based on amplitude phase separation*
- Ezgi Karaesmen, Ph.D. 2020 Pharmaceutical Sciences *Genetic associations with survival outcomes after matched unrelated donor allogeneic hematopoietic stem cell transplantation*
- Kelly Rafferty, Ph.D. 2017 Human Genetics *Comparisons of Isogenic Trisomic and Disomic Cells from People with Mosaicism for Down Syndrome Unmask Cellular Differences Related to Trisomy 21*
- Bhavi Modi, Ph.D. 2016 Human Genetics *Genetic and epigenetic mechanisms of complex reproductive disorders*
- Maren Smith, Ph.D. 2016 Human Genetics *System genetic analysis of mechanisms underlying excessive alcohol consumption*
- Jenna Czarnota, Ph.D. 2016 Biostatistics *Modeling spatially varying effects of chemical mixtures*
- David Brohawn, Ph.D. 2016 Human Genetics *Investigating the molecular etiologies of sporadic ALS (sALS) using RNA-Sequencing*
- Paul Manser, Ph.D., 2014 Biostatistics *Methods for integrative analysis of genomic data*
- Mba Uzoma Udo Mba, Ph.D., 2014 Physiology & Biophysics *Pursuing the roles of non-invasive biomarkers in chronic renal allograft dysfunction*
- Paul Hope Bailey, Ph.D., 2012 Chemistry *Chemometric analysis of comprehensive two-dimensional liquid chromatographic-diode array detection data: Peak resolution, quantification and rapid screening*
- David Nagarkatti-Gude, Ph.D., 2012 Biochemistry *SPAG16 is a bifunctional gene regulating male fertility*
- Latasha Redmond, Ph.D. 2008 Human Genetics *Differential gene expression during mouse embryonic yolk sac erythropoiesis*

- Elizabeth Prom, Ph.D. 2007 Life Sciences *Addressing issues in the detection of gene-environment interaction through the study of conduct disorder*
- G. Scott Taylor, Ph.D. 2006 Engineering *Design and Development of Oligonucleotide Microarrays and their Application in Diagnostic and Prognostic Estimation of Human Gliomas*
- Rong Liu, Ph.D. 2006 Biostatistics *A comparison for longitudinal data missing due to truncation*
- Heather Hoffman, Ph.D. 2005 Biostatistics *Maximum likelihood estimation of multivariate normal parameters in the presence of left censored and missing values*
- Eric Harvey, Ph.D. 2003 Biostatistics *Normal mixture models for gene cluster identification in two dimensional microarray data*

MS Thesis Committee Member

- Alex Ning, M.S. 2024 Biostatistics *Variable Selection Methods in Threshold Regression Models for Survival Data*
- Carly Middleton, M.S. 2022 Biostatistics *A comparison of two maximum likelihood selection identification methods applied to protein-coding regions of the SARS-CoV-2 variant genomes*
- Ashley Keiter, M.S. 2020 Biostatistics *Linear Regression Analysis Using Survey Sample Data: An Evaluation of Diagnostic Tests for the Use of Weights*
- Lindsey Nicely, M.S., 2012 Mathematical Sciences *Applications of Sure Independence Screening Analysis for Supersaturated Designs*
- Alexander Philip, M.S., 2011 Physiology *Association between T cells-related gene expression and fibrosis progression in HCV recurrence disease*
- Huong Nguyen, M.S., 2011 Physiology *Molecular pathways involved in calcineurin inhibitor nephrotoxicity in kidney allograft transplants*
- Ryan Fassnacht, M.S., 2010 Physiology *Molecular mechanisms involved in the interaction effects of HCV and ethanol on liver cirrhosis*
- Jihee Lacey Suh, M.S., 2009 Physiology *Evaluation of association of microRNA 122 with histological severity of recurrent HCV infection in liver transplant recipients*
- Yue Zhao, M.Bioinf 2006 Bioinformatics *Methods for detecting horizontal gene transfer*
- Leslie Filicky, M.S. 2003 Biostatistics *Statistical assessment of the quality control processes for oligonucleotide microarrays*

MPH Culminating Projects/Integrated Learning Experience

- 2nd Reader, 2023 Anat Saka, *Role of treatment modality and race in survival outcomes among early-stage cervical cancer patients*
- 2nd Reader, 2022 Eric Brooks, *AutoGateR: An Intuitive R Shiny App for the Automatic Compensation and Gating of Flow Cytometry Data*
- 2nd Reader, 2021 Trae Gulgin, *Impacts of Surveillance-Based Insecticide Application on Insecticide Resistance in Culex pipiens*
- 2nd Reader, 2020 Julia Dionne, *Evaluating stimulant misuse via the College Prescription Drug Study*
- 3rd Reader, 2020 Tara Hill, *Perceptions of Risk of Swine-Lineage Influenza A viruses Among Veterinary Professionals*
- 2nd Reader, 2019 Hoi Ting (Ina) Yeung, *Improving Health by Reducing Healthcare-Associated Infections*

- 2nd Reader, 2018 Becky Legenza, *An Evaluation of Past Clients Participating in the Wellness Coaching Program at the University of Louisville*
- 2nd Reader, 2018 Grace Ferguson, *Are Adults 65 and Older Receiving their Vaccines? Influenza and Pneumococcal Vaccination Rates in Older Adults*

Other Students

- Undergraduate research Sana Sukhija, Public Health, Fall 2024-Spring 2025.
- Summer reading Pin-Hsun Mao, PhD Biostatistics student, Summer 2023.
- Ohio-5 SURE Linh Nguyen, Denison University, Ohio-5 SURE, Summer 2023.
- CREATES Thomas Gill, OSUCCC Cancer Research Experience for the Advancement and Training of Emerging Scientists, Summer 2023.
- F-GAP Mentor Sana Gupta, University of Connecticut, Spring-Fall 2023.
- F-GAP Mentor Odalys Garcia-Lopez, The College of New Jersey, Summer-Fall 2022.
- Mentor Seth Adarkwah Yiadom, Fall 2021 - Spring 2022
- F-GAP Mentor Katie Baines, California State University - Chico, Math Alliance, Summer - Fall 2021
- Mentor Micaela Richter, Fall 2020 - Spring 2021
- Supervisor Mariah Eisner, Graduate student worker, Fall 2019 – Spring 2020
- F-GAP Mentor Kristen Garcia, Boise State University, Math Alliance, Summer- Fall 2019
- Mentor Calvin Barber, Liberty High School/Olentangy Academy, Fall 2018
- Mentor Mrugank Deodhar, Liberty High School/Olentangy Academy, Fall 2018
- F-GAP Mentor Cinthia Calvo Martinez, University of Texas Rio Grande Valley, Math Alliance, Summer - Fall 2018
- Mentor Paula Kuhn, Circleville High School, Spring 2018
- Mentor Sheila Colbert, Liberty High School/Olentangy Academy, Spring 2017
- Supervised summer intern Julia Gallini, Summer 2014
- Mentor VCU Post-baccalaureate Research Education Program (PREP) scholar Nancy Asomaning, Fall 2010 - Spring 2011
- Mentor, Young Epidemiology Scholars Semi-finalist Ridge Archer, A Beka Academy, Pensacola, FL “Cross-sectional Gene Expression Study of Type II Diabetes” (Received \$1,000 scholarship) Fall 2010- Spring 2011
- Supervised ARRA summer intern Ridge L. Archer, Summer 2010
- Supervised summer intern Tobias Guennel, B.S. Summer 2006 & Spring 2007
- Supervised Student Technology Expert Program student Suresh E. Joel, Spring 2004

MAJOR TEACHING ASSIGNMENTS

Virginia Commonwealth University

Semester	Course Number	Course Title
Fall 2002	BIOS 513	Mathematical Statistics I
Spring 2003	BIOS 514	Mathematical Statistics II
Fall 2003	BIOL 591	Introduction to Bioinformatics: Microarray Data Analysis (2 lectures)
Spring 2004	BIOS 691	Special Topics: Statistical Methods for Microarray Data
	MICR 653	Advanced Molecular Genetics Bioinformatics & Computational Genomics: Supervised learning methods (1 three hour lecture)

Semester	Course Number	Course Title
Fall 2004	BIOS 667*	Advanced Data Analysis
	BNFO 601	Integrated Bioinformatics: Statistical analysis of microarray data (2 lectures)
Spring 2005	BIOS 691	Special Topics: Statistical Methods for Microarray Data
	MICR 653	Advanced Molecular Genetics Bioinformatics & Computational Genomics: Supervised learning methods (1 three hour lecture)
Fall 2005	BIOS 667	Advanced Data Analysis
	BNFO 650	Sequence Analysis in Biological Systems: Hidden Markov Models (1 three hour lecture)
	BNFO 601	Integrated Bioinformatics: Statistical analysis of microarray data (2 lectures)
Spring 2006	BIOS 567†	Statistical Methods for Microarray Data
	MICR 653	Advanced Molecular Genetics Bioinformatics & Computational Genomics: Supervised learning methods (1 lecture)
Fall 2006	BIOS 667	Advanced Data Analysis
	BNFO 650	Sequence Analysis in Biological Systems: Hidden Markov Models (1 three hour lecture)
Spring 2007	BIOS 567	Statistical Methods for Microarray Data
Fall 2007	BIOS 667	Advanced Data Analysis
Spring 2008	BIOS 567	Statistical Methods for Microarray Data
Fall 2008	BIOS 667	Advanced Data Analysis
Spring 2009	BIOS 567	Statistical Methods for Microarray Data
Spring 2010	BIOS 667	Advanced Data Analysis
Fall 2011	BIOS 553	Linear Regression
Spring 2012	BIOS 554	Analysis of Variance
Fall 2012	BIOS 567	Statistical Methods for High-Throughput Genomic Data I
Spring 2013	BIOS 667	Statistical Learning & Data Mining
Spring 2014	BIOS 668†	Statistical Methods for High-throughput Genomic Data II
Fall 2014	BIOS 667	Statistical Learning & Data Mining
Spring 2015	BIOS 690	Biostatistics Seminar
Fall 2015	BIOS 567	Statistical Methods for High-Throughput Genomic Data I
	BIOS 690	Biostatistics Seminar
Spring 2016	BIOS 690	Biostatistics Seminar

*Redesigned existing course.

†Developed this course.

The Ohio State University

Semester	Course Number	Course Title
Spring 2017	PUBHBIO 6211	Design & Analysis of Health Studies II (50%)
	PUBHBIO 7245	Biostatistical Collaboration
Fall 2017	PUBHBIO 8899	Doctoral Seminar in Biostatistics
Spring 2018	PUBHBIO 6211	Online Design & Analysis of Health Studies II (33%)

Semester	Course Number	Course Title
	PUBHBIO 7245	Biostatistical Collaboration
Fall 2018	PUBHBIO 2210	Biostatistics for Public Health
	PUBHBIO 8899	Doctoral Seminar in Biostatistics
Spring 2019	PUBHBIO 6211	Design & Analysis of Health Studies II (50%)
	PUBHBIO 7245	Biostatistical Collaboration
Fall 2019	PUBHBIO 8899	Doctoral Seminar in Biostatistics
Spring 2020	PUBHBIO 6211	Design & Analysis of Health Studies II (50%)
	PUBHBIO 7245	Biostatistical Collaboration
Fall 2020	PUBHBIO 7250	Special Topics: Statistical Learning and Data Mining in Public Health
	PUBHBIO 8899	Doctoral Seminar in Biostatistics
Spring 2021	PUBHBIO 7245	Biostatistical Collaboration
Fall 2021	PUBHBIO 6250	Regression Methods for the Health Sciences
	PUBHBIO 8899	Doctoral Seminar in Biostatistics
Spring 2022	PUBHBIO 7245	Biostatistical Collaboration
Spring 2023	PUBHBIO 5280	Introduction to Genomic Data Analysis
Spring 2024	PUBHBIO 5280	Introduction to Genomic Data Analysis
Fall 2024	PUBHBIO 5280	Introduction to Genomic Data Analysis
Fall 2025	PUBHBIO 5280	Introduction to Genomic Data Analysis

Other teaching responsibilities & awards

- MPI, NCATS T32 Training Grant, Clinical and Translational Science Training Program.
- PI, NIEHS T32 Training Grant, Integration of Chemical Mixtures Toxicology, Toxicogenomics and Statistics.
- 2006 Outstanding Teaching Award, Department of Biostatistics, Virginia Commonwealth University
- Developed VCU's Department of Biostatistics Genomic Biostatistics concentration, approved 2012.

SERVICE ACTIVITIES

Service to the Profession

- **Ad hoc reviewer**, NIH Analytics and Statistics for Population Research Panel A (ASPA) Review Panel, March 13, 2026.
- **Deputy Editorial Board Member**, *Radiology*, 2026–present.
- **Ad hoc reviewer**, ZRG1 EPH-V(56) R, NIEHS P30 Core Center Program Review Panel, December 16–17, 2025.
- **Member of Expert Panel**, Fonds Wetenschappelijk Onderzoek (FWO) W&T Projects - Mathematical Sciences, Brussels, Belgium, October 23, 2025.
- **Ad hoc reviewer**, NCI Special Emphasis Panel ZRG1 CTH-W (45) Program Project: Cancer Research, June 26–27, 2025.
- **Ad hoc reviewer**, Interdisciplinary approaches in oncogenic processes and therapeutic perspectives: Contributions to oncology of mathematics and informatics, Inserm (French National Institute for Biomedical Research), March 2025.

- **Ad hoc reviewer**, NIAID SBIR/STTR and SB1 Grant Application Peer Review Meeting SEP ZAI1 ZL-Z M1, April 30 – May 1, 2025.
- **Ad hoc reviewer**, NIAID Special Emphasis Panel ZAI1 SB-I (C1) Software or Web Services to Assess Quality and Reproducibility of Data and Information about Therapeutics and Vaccines (N01), February 5, 2025.
- **Reviewer**, 2025 Regular Fondecyt National Projects Competition, National Agency for Research and Development (ANID) of Chile, January 2025.
- **Program Committee co-Chair**, American Statistical Association Statistical Learning and Data Science Conference, 2024.
- **Member**, Math Alliance Facilitated Graduate Application Program (F-GAP) Executive Committee, 2024–2025.
- **Member**, 2024 ENAR Educational Advisory Committee.
- **Past-Chair (elected)**, American Statistical Association Statistical Learning and Data Science Section, 2024.
- **Member**, Math Alliance Doctoral Faculty Council, 2023–2024.
- **Reviewer**, Florida Breast Cancer Foundation, March 2024.
- **Reviewer**, Pennsylvania Department of Health Peer Review – Pediatric Cancer, November 2023.
- **Panelist**, "Preparing for your first professional position," Field of Dreams Conference, Atlanta, Georgia, November 4, 2023.
- **Ad-hoc reviewer**, European Science Foundation Grant Evaluation, August 2023.
- **Judge**, 2023 ENAR poster competition, March 2023.
- **Chair (elected)**, American Statistical Association Statistical Learning and Data Science Section, 2023.
- **Reviewer**, NIEHS Environmental Health Sciences Review Committee Meeting (T32 NRSA Training Grant), November 8–9, 2022.
- **Panelist**, Career Panel on Statistics and Data Science, ASA Columbus Chapter, October 25, 2022.
- **Reviewer**, NIEHS Environmental Health Sciences Review Committee Meeting (P30 Core Center Program), October 5–6, 2022.
- **Session chair**, 2022 Joint Statistical Meetings, "Life Science Applications of Data Science," Washington, D.C., August 11, 2022.
- **Ad hoc reviewer**, Cancer Biotherapeutics Development (CBD) Study Section (SBIR/STTR), June 16–17, 2022.
- **Ad hoc reviewer**, Pennsylvania Department of Health Formula Grants Final Performance Review, June 2022.
- **Ad hoc reviewer**, Florida Breast Cancer Foundation, Spring 2022.
- **Ad hoc reviewer**, NCI Transition Career Development Award and Institutional Training and Education (NCI-F), January 18, 2022.
- **Chair-Elect**, ASA Statistical Learning and Data Science Section, 2022.
- **Member, DSMB**, HECTOR Study (hESC-CMs in Chronic Ischemic Left Ventricular Dysfunction), Stanford, December 2021–present.
- **Reviewer**, Environmental Health Sciences Core Centers (EHSRC) Review Meeting, October 4–6, 2021.
- **Volunteer**, ASA Committee on Career Development: Guided Networking Session, August 5, 2021.
- **Ad hoc reviewer**, T15 Review Committee (RFA-LM-21-001), July 23, 2021.
- **Ad hoc reviewer**, ZDK1 GRB-S (O2) Review Committee, NIDDK Central Repositories (X01), May 28, 2021.
- **Ad hoc reviewer**, ZCA1 RTRB-R M3 S, NCI Information Technology in Cancer Research, March 30–31, 2021.

- **Reviewer**, NIEHS Environmental Health Sciences Review Committee Meeting, November 19, 2020.
- **Panelist**, Association for Women in Mathematics (AWM) Career Panel, UC Riverside, November 10, 2020.
- **Reviewer**, NIEHS Environmental Health Sciences Core Centers (EHSCC) Review Meeting, October 19–21, 2020.
- **Panelist**, Math Alliance workshop “Taking our Place in Graduate School,” October 17, 2020.
- **Ad hoc reviewer**, ZRG1 GGG-D (30) Shared Instrumentation for Genomics studies, November 9, 2020.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel ZDK1-GRB-S (J3) (X01), September 3, 2020.
- **Volunteer**, ASA Committee on Career Development “Guided Virtual Networking Session,” July 30, 2020.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel (PAR17-123 Biomarkers), June 3, 2020.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel (Biorepository X01), May 28, 2020.
- **Ad hoc reviewer**, Florida Breast Cancer Foundation, April 2020.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel ZDK1 GRB-S (M2) (X01), January 15, 2020.
- **Committee member**, 2020–2023 Field of Dreams Agenda Committee.
- **Ad hoc reviewer**, NIEHS R25 Special Emphasis Panel (Diversity in Environmental Health Sciences), November 20, 2019.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel (Biomarkers R01), September 26, 2019.
- **Ad hoc reviewer**, NIEHS Environmental Health Sciences Review Committee (P30 Core Center), August 14–15, 2019.
- **Invited Session Chair**, 2019 Joint Statistical Meetings, Denver, CO, August 1, 2019.
- **Ad hoc reviewer**, ZCA1 SRB-5 O1 NCI Program Project IV (P01), June 6–7, 2019.
- **Ad hoc reviewer**, NIDDK Central Repositories (X01 for PAR-17-270), May 7, 2019.
- **Ad hoc reviewer**, NCI Special Emphasis Panel (Informatics Tools), March 21–22, 2019.
- **Judge**, 2019 ENAR poster competition, March 2019.
- **Ad hoc reviewer**, NIEHS Special Emphasis Panel (Existing Environmental Epidemiology Cohorts), March 6, 2019.
- **Ad hoc reviewer**, Biostatistical Methods and Research Design Study Section (BMRD), February 14–15, 2019.
- **Peer reviewer**, Program Evaluation of NIH Peer Review Processes, Social Solutions International, Inc., January 2019.
- **Statistical Editorial Board Member**, *JNCI* and *JNCI Spectrum*, 2019–present.
- **Ad hoc reviewer**, NIDDK Central Repositories (X01), October 3, 2018.
- **Ad hoc reviewer**, NCI Program Project (P01) III Review, September 24–25, 2018.
- **Member**, Chairs of Biostatistics Leadership Team, 2018–2020.
- **Member**, NIH/NLM Biomedical Informatics Library and Data Science Review Committee (BILDS), 2014–2018.
- **Ad hoc reviewer**, NCI Program Project Review I (P01), April 17–18, 2018.
- **Ad hoc reviewer**, NIEHS Special Emphasis Panel (Existing Environmental Epidemiology Cohorts R24), April 11, 2018.
- **Judge**, 2018 ENAR poster competition, March 2018.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel (Central Biorepositories X01), February 5, 2018.

- **Member**, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), 2014–2017.
- **Ad hoc reviewer**, NIEHS Environmental Health Sciences Review Committee EHS P3, August 29–30, 2017.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel (X01), May 11, 2017.
- **Ad hoc reviewer**, Cancer, Heart, and Sleep Epidemiology Panel B (CHSB), October 24–25, 2016.
- **Ad hoc reviewer**, NIDDK Special Emphasis Panel (Biomarkers R01), September 21, 2016.
- **Ad-hoc reviewer**, NIEHS 2016/01 EHS Review Committee, November 4, 2015.
- **Ad-hoc reviewer**, NIDDK Biomarkers for T1D and Kidney Disease (R01), October 1, 2015.
- **Ad-hoc reviewer**, NIDDK's Chronic Kidney Disease Biomarkers Consortium (CKD BioCon), March 24, 2015.
- **Ad-hoc reviewer**, NIDDK Central Repositories (X01), January 9, 2015.
- **Ad-hoc reviewer**, NCI's Small Grants Program for Cancer Epidemiology (R03), October 30, 2014.
- **Ad-hoc reviewer**, NIDDK's Biomarkers (R01), September 25, 2014.
- **Lead guest editor**, *Cancer Informatics* supplement, 2014–2015.
- **Ad-hoc reviewer**, NIDDK's Research Using Biosamples from Selected T1D Clinical Studies (DP3), July 1, 2014.
- **Ad-hoc reviewer**, NCI's Omnibus Special Emphasis Panel EP-4, June 24–25, 2014.
- **Ad-hoc reviewer**, BD2K U54 Centers of Excellence, April 10–11, 2014.
- **Statistical Consultant**, Nature Publishing Group, 2013–2018.
- **Session Chair**, 2014 ENAR Meeting, Baltimore, MD, March 19, 2014.
- **Ad-hoc reviewer**, NCI Small Grants Program for Cancer Epidemiology, February 26, 2014.
- **Ad-hoc reviewer**, NIDDK Central Repositories Sample Access (X01), January 24, 2014.
- **Ad-hoc reviewer**, NCI Small Grants Program for Cancer Epidemiology, November 7, 2013.
- **Ad-hoc member**, NCI Cancer Management, Epidemiology, and Health Behavior Review Meeting, October 29–30, 2013.
- **Ad-hoc reviewer**, Research Using Biosamples from TrialNet/DPT-1 Type Diabetes Clinical Studies, June 10, 2013.
- **Ad-hoc reviewer**, NIDDK Central Repositories (X01) Hepatitis E/C, March 27, 2013.
- **Ad-hoc reviewer**, NCI Small Grants Program for Cancer Epidemiology, March 21–22, 2013 & October 16–17, 2012.
- **Ad-hoc reviewer**, NIDDK Sample Repositories (X01), September 4, 2012.
- **Ad-hoc reviewer**, NCI Small Grants Program for Cancer Epidemiology, June 21–22, 2012.
- **Organizer/Chair**, SRCOS Summer Research Conference, Jekyll Island, GA, June 3–5, 2012.
- **Panel Review Member**, National Science Foundation, April 3–4, 2012.
- **Ad-hoc mail reviewer**, NIH NCI Provocative Questions, March 27–29, 2012.
- **Ad-hoc Reviewer**, NCI Small Grants Program for Cancer Epidemiology, March 22, 2012.
- **Ad-hoc Reviewer**, NIH Special Emphasis Panel (ZDK1), January 4, 2012.
- **Ad-hoc Reviewer**, NCI Small Grants Program for Cancer Epidemiology, November 17–18, 2011 & July 21–22, 2011.
- **Ad-hoc Reviewer**, NCI Tumor Microenvironment (TMEN), June 29–July 1, 2011.

- **Ad-hoc Reviewer**, Genes, Computational Biology and Technology (GCAT) Study section, June 2–3, 2011.
- **Ad-hoc Reviewer**, NIH Special Emphasis Panel (ZRG1), April 27, 2011.
- **Session Chair**, Genomics, ENAR, Miami, FL, March 22, 2011.
- **Panel member**, FDA General and Plastic Surgery Devices Panel, November 18, 2010.
- **Ad-hoc Reviewer**, NIH Cancer Genetics (CG) Study section, October 7–8, 2010.
- **Panel member**, FDA Radiological Devices Panel, September 24, 2010 & 2008–2011.
- **Ad-hoc Reviewer**, Research Promotion Foundation of Cyprus, June 2010.
- **Ad-hoc Reviewer**, NIH GCAT Study section, June 2–3, 2010.
- **Ad-hoc Reviewer**, NCI Discovery and Development SEP, May 25–27, 2010.
- **Ad-hoc Reviewer**, Internationale Spitzenforschung II/2, Germany, May 2010.
- **Ad-hoc Reviewer**, NIH Genomics and Computational Biology Special Emphasis Panel, March 25–26, 2010.
- **Ad-hoc Reviewer**, Organ Transplant Clinical Trials Study Section, October 23, 2009.
- **Ad-hoc Reviewer**, NIH GCAT Study section, October 14–15, 2009.
- **Stage 1 Reviewer**, NIH Challenge Grant applications, June 2009.
- **Session Chair**, Methods in Statistical Genomics, JSM, Denver, CO, August 3, 2008.
- **Editorial Board Member**, *Progress in Transplantation*, 2008–2016.
- **Member**, Clinical Laboratory and Standards Institute (CLSI) MM12-A Diagnostic Nucleic Acid Arrays guideline.

Service to the University

- **Judge**, Denman Undergraduate Research Forum, The Ohio State University (OSU), 2026, 2025, 2018, 2017.
- **Member**, Health Sciences Library Advisory Board, OSU, 2017–2025.
- **Member**, Foods for Health Advisory Board, OSU, 2022–2025.
- **Chair**, Health Sciences Library Advisory Board, OSU, 2022–2024.
- **Member**, University Fellowship Review Committee, OSU, 2022.
- **Member**, ENGIE-Axium Graduate Fellowship Review Committee, OSU, 2022.
- **Grant reviewer**, CCTR KL2 applications, OSU, January 2020.
- **Grant reviewer**, CCTS Secondary Data Analysis pilot grant applications, OSU, 2019.
- **Ad-hoc Reviewer**, A.D. Williams Multi-school Grant Application, Fall 2007.
- **Member**, VCU High Performance Computing Committee, 2006–2007.
- **Ad-hoc Reviewer**, VCU Center for Teaching Excellence Small Grants Program, Fall 2004.
- **Member**, Bioinformatics Admissions Committee, VCU Center for the Study of Biological Complexity, 2004–2006.
- **Member**, Bioinformatics Program Committee, VCU Center for the Study of Biological Complexity, 2004–2006.
- **Member**, VCU Commonwealth Technology Trust Fund (CTRF) Cancer Genomics Committee, 2002–2005.

Service to the School of Medicine / College of Public Health

- **Member**, OSU College of Public Health (CPH) Awards Committee, 2024–present.
- **Chair**, OSU CPH Blue Sky Squad Workgroup, 2020–2021.
- **co-Chair**, OSU CPH Incentive Plan Committee, 2020–2021.
- **Member**, OSU CPH Executive Committee, 2016–present.

- **Chair**, Search Committee for OSU CPH Health Science Management & Policy Division Chair, 2018–2019.
- **Co-Chair**, OSU DT Metabolomics Search Committee, 2016–2017.
- **Member**, Promotion & Tenure Committee (multiple departments), VCU, 2010–2015.
- **Participant**, VCU School of Medicine Faculty Focus Group (LCME Accreditation), April 2007.
- **Member**, Ad-hoc Infrastructure Wish List Committee, VCU School of Public Health, 2006.
- **Member**, Ad-hoc VCU School of Public Health website design committee, 2005.
- **Member**, Protocol Review & Monitoring System, VCU Massey Cancer Center, 2002–2016.

Service to the Department / Division

- **Member**, Graduate Studies Committee, OSU Interdisciplinary PhD Biostatistics, 2018–2021.
- **Member**, Admissions Committee, OSU Interdisciplinary PhD Biostatistics, 2016–2022.
- **Chair**, Search Committee (various rank faculty positions), VCU Dept. of Biostatistics, 2010–2015.
- **Chair**, Seminar Committee, VCU Department of Biostatistics, 2014–2016.
- **Member**, Seminar Committee, VCU Department of Biostatistics, 2013–2014.
- **Member**, Promotion & Tenure Committee (multiple candidates), VCU Biostatistics, 2012–2013.
- **Member**, Executive Committee, VCU Department of Biostatistics, 2011–2016.
- **Chair**, VCU Biostatistics Curriculum Committee, 2007–2009 & member 2002–2011.
- **Chair**, Genomic Biostatistics Curriculum Committee, VCU Biostatistics, 2005–2007.
- **Member**, VCU Biostatistics Admissions Committee, 2005–2007.
- **Coordinator**, VCU Department of Biostatistics S-Plus and Insightful Miner user licenses,

Statistical Editorial Board Member:

- *Journal of the National Cancer Institute*
- *JNCI Spectrum*
- *Radiology*

Peer review activities:

- *American Journal of Transplantation*
- *Bioinformatics*
- *Biostatistics*
- *Biometrical Journal*
- *Biometrics*
- *Blood Cancer Discovery*
- *BMC Genomics*
- *BMC Bioinformatics*
- *Briefings in Bioinformatics*
- *Cancer, Epidemiology, Biomarkers and Prevention*
- *Communications in Statistics - Simulation and Computation*
- *Communications in Statistics - Theory and Methods*
- *Communications in Statistics - Case Studies and Data Analysis*
- *Computational Statistics*

- *Computational Statistics and Data Analysis*
- *Computer Methods and Programs in Biomedicine*
- *Genome Research*
- *Genomics*
- *Journal of the American Statistical Association*
- *Journal of Computational and Graphical Statistics*
- *Journal of Clinical and Translational Science*
- *Journal of Statistical Software*
- *Journal of the National Cancer Institute*
- *Journal of Personalized Medicine*
- *JNCI Cancer Spectrum*
- *Leukemia*
- *Methods of Information in Medicine*
- *Nature Cancer*
- *Nature Communications*
- *Nature Medicine*
- *Nature Biotechnology*
- *Nature Communications*
- *Nature Immunology*
- *Pharmaceutical Statistics*
- *PLoS One*
- *Radiology*
- *Radiology Advances*
- *Radiology: Artificial Intelligence*
- *Radiology: Cardiothoracic Imaging*
- *Radiology: Imaging Cancer*
- *Reproductive Sciences*
- *Sankhya B*
- *Science*
- *Scientific Reports*
- *Statistical Modeling*
- *Statistics in Medicine*
- *Statistical Methods in Medical Research*
- *Statistical Methodology*
- *Statistics in Biopharmaceutical Research*
- *STATS*
- *The American Statistician*
- *Thailand Statistician*

PUBLICATIONS

Papers published in peer reviewed journals

Note: Names of students directly supervised are underlined.

1. Mrózek K, Prior TW, Edwards C, Marcucci G, Carroll AJ, Snyder PJ, Koduru PRK, Theil KS, Pettenati MJ, Archer KJ, Caligiuri MA, Vardiman JW, Koltz JE, Larson RA and Bloomfield CD. Comparison of cytogenetic and molecular genetic detection of t(8;21) and inv(16) in a prospective series of adults with de novo acute myeloid leukemia: A

- Cancer and Leukemia Group B study. *Journal of Clinical Oncology*, 19(9):2482-2492, 2001.
2. Marcucci G, Caligiuri MA, Döhner H, **Archer KJ**, Schlenk RF, Döhner K, Maghaby EA and Bloomfield CD. Quantification of CBF /MYH11 fusion transcript by Real Time RT-PCR in patients with inv(16) acute myeloid leukemia (AML). *Leukemia*, 15(7):1072-1080, 2001.
 3. Whitman SP, **Archer KJ**, Feng L, Baldus C, Becknell B, Carlson BD, Carroll AJ, Mrózek K, Vardiman JW, George SL, Kolitz JE, Larson RA, Bloomfield CD and Caligiuri MA. Absence of the wild type allele predicts poor prognosis in adult de novo acute myeloid leukemia with normal cytogenetics and the internal tandem duplication of FLT3: A Cancer and Leukemia Group B study. *Cancer Research*, 61(19):7233-7239, 2001.
 4. Tanner, SM, Austin JL, Leone G, Rush LJ, Plass C, Heinonen K, Mrózek K, Sill H, Knuutila S, Kolitz JE, **Archer KJ**, Caligiuri MA, Bloomfield CD and de la Chapelle A. BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia. *Proc Natl Acad Sci U S A*, 98(24):13901-13906, 2001.
 5. Karrison T, **Archer KJ**, Espinosa R, Wen M and Huo D. Data management and statistical methods used in the analysis of balanced chromosome abnormalities in therapy-related myelodysplastic syndromes and therapy-related acute leukemia: Report from an international workshop. *Genes, Chromosomes and Cancer*, 33(4):346-361, 2002.
 6. Bloomfield CD, **Archer KJ**, Mrózek K, Lillington DM, Kaneko Y, Head DR, Dal Cin P and Raimondi SC. 11q23 balanced chromosome aberrations in treatment-related myelodysplastic syndromes and acute leukemia: Report from an international workshop. *Genes, Chromosomes and Cancer*, 33(4):362-378, 2002.
 7. Farag SS, **Archer KJ**, Mrózek K, Vardiman JW, Carroll AJ, Pettenati MJ, Moore JO, Kolitz JE, Mayer RJ, Stone RM, Larson RA, Bloomfield CD. Isolated Trisomy of Chromosomes 8, 11, 13 and 21 is an adverse prognostic factor in adults with de novo acute myeloid leukemia: Results from Cancer and Leukemia Group B 8461. *International Journal of Oncology* 21(5):1041-1051, 2002.
 8. Klisovic MI, Maghaby EA, Parthun MR, Guimond M, Sklenar AR, Whitman SP, Chan KK, Murphy T, Anon J, **Archer KJ**, Rush LJ, Plass C, Grever MR, Byrd JC, Marcucci G. Depsipeptide (FR 901228) promotes histone acetylation, gene transcription, apoptosis and its activity is enhanced by DNA methyltransferase inhibitors in AML1/ETO-positive leukemic cells. *Leukemia* 17(2): 350-358, 2003.
 9. Baldus CD, Tanner SM, Ruppert A, Whitman SP, **Archer KJ**, Marcucci G, Caligiuri MA, Carroll AJ, Vardiman JW, Powell B, Allen SL, Moore JO, Larson RA, Kolitz JE, de la Chapelle A, Bloomfield CD. BAALC expression predicts clinical outcome of de novo acute myeloid leukemia patients with normal cytogenetics: A Cancer and Leukemia Group B Study. *Blood* 102(5):1613-1618, 2003.
 10. Arthur DW, Koo D, Zwicker RD, Tong S, Bear HD, Kaplan BJ, Kavanagh BD, Warwicke LA, Holdford D, Amir C, **Archer KJ**, Schmidt-Ullrich RK. Partial breast brachytherapy following lumpectomy: a low dose rate and high dose rate experience. *International Journal of Radiation Oncology, Biology, Physics* 56(3):681-689, 2003.
 11. Mas VR, Fisher RA, Maluf DG, **Archer KJ**, Contos MJ, Mills SA, Shiffman ML, Wilkinson DS, Oliveros L, Garrett CT, Ferreira-Gonzalez A. Polymorphisms in cytokines and growth factor genes and their association with acute rejection and recurrence of hepatitis C virus disease in liver transplantation. *Clinical Genetics* 65(3):191-201, 2004.
 12. **Archer KJ**, Dumur CI, Ramakrishnan V. Graphical technique for identifying a monotonic variance stabilizing transformation for absolute gene intensity signals. *BMC Bioinformatics* 5(1):60, 2004.

13. Marcucci G, Mrózek K, Ruppert AS, **Archer KJ**, Pettenati MJ, Heerema NA, Carroll AJ, Koduru PR, Kolitz JE, Sterling LJ, Edwards CG, Anastasi J, Larson RA, Bloomfield CD. Abnormal cytogenetics at date of morphologic complete remission predicts short overall and disease-free survival, and higher relapse rate in adult acute myeloid leukemia: Results from Cancer and Leukemia Group B Study 8461. *Journal of Clinical Oncology* 22(12):2410-2418, 2004.
14. Dumur CI, Garrett CT, **Archer KJ**, Nasim S, Wilkinson DS, Ferreira-Gonzalez A. Evaluation of a linear amplification method for small samples used on high density oligonucleotide microarray analysis. *Analytical Biochemistry* 331(2):314-321, 2004.
15. Dumur CI, Nasim S, Best AM, **Archer KJ**, Ladd AC, Mas VR, Wilkinson DS, Garrett CT, Ferreira-Gonzalez A. Evaluation of quality control criteria for microarray gene expression analysis. *Clinical Chemistry* 50(11): 1994-2002, 2004.
16. Mas VR, Maluf DG, **Archer KJ**, Yanek K, King A, Cotterell A, Ferreira-Gonzalez A, Rodgers C, Fisher RA, Posner M. Study of mRNA growth factors in urinary cells of kidney transplant recipients as predictors of chronic allograft nephropathy. *Transplantation* 80(12):1686-1691, 2005.
17. Maluf DG, Mas VR, **Archer KJ**, Yanek K, King A, Ferreira-Gonzalez A, Fisher RA, Posner M. Apolipoprotein E genotypes as predictors of high-risk groups for developing hyperlipidemia in kidney transplant recipients undergoing sirolimus treatment. *Transplantation* 80(12):1705-1711, 2005.
18. **Archer KJ**, Dumur CI, Joel SE, Ramakrishnan V. Assessing quality of hybridized RNA in Affymetrix GeneChip experiments using mixed effects models. *Biostatistics* 7(2):198-212, 2006.
19. **Archer KJ** and Lemeshow S. Goodness-of-fit test for a logistic regression model estimated using survey sample data. *The Stata Journal*, 6(1): 97-105, 2006.
20. Farag SS, **Archer KJ**, Mrózek K, Ruppert AS, Carroll AJ, Vardiman, JW, Pettenati MJ, Baer MR, Qumsiyeh MB, Koduru PR, Stamberg J, Mayer RJ, Stone RM, Larson RA, Bloomfield CD. Pretreatment Cytogenetics add to Other Prognostic Factors Predicting Complete Remission and Long-Term Outcome in Patients 60 Years of Age or Older with Acute Myeloid Leukemia: Results from Cancer and Leukemia Group B 8461. *Blood*, 108(1):63-73, 2006.
21. Kennedy RE, **Archer KJ**, Miles MF. Empirical validation of the S-score algorithm in the analysis of gene expression data. *BMC Bioinformatics*, Mar 17; 7(1):154, 2006.
22. Kennedy RE, Kerns RT, Kong X, **Archer KJ**, Miles MF. An R package for detecting differential gene expression without gene expression summaries. *Bioinformatics*, 22(10):1272-1274, 2006.
23. Mas VR, Maluf DG, Dumur CI, **Archer KJ**, Yanek K, Jackson-Cook C, Fisher RA. Molecular techniques for identifying HCC origin and biology after orthotopic liver transplantation. *Diagnostic Molecular Pathology*, 15(2):90-94, 2006.
24. Mas VR, Maluf DG, **Archer KJ**, Yanek KC, Williams B, Fisher RA. Differentially expressed genes between early and advanced Hepatocellular Carcinoma (HCC) as a potential tool for selecting liver transplant recipients. *Molecular Medicine*, 12(4-6):97-104, 2006.
25. **Archer KJ** and Guennel T. An application for assessing quality of RNA hybridized to Affymetrix GeneChips, *Bioinformatics* 22: 2699-2701, 2006.
26. **Archer KJ**, Lemeshow S, Hosmer DW. Goodness-of-fit tests for logistic regression models when data are collected using a complex sampling design. *Computational Statistics and Data Analysis*, 51: 4450-4464, 2007.
27. Mas V, Maluf D, **Archer K**, Yanek K, Mas L, King A, Gibney E, Massey D, Cotterell A, Fisher R, Posner M. Establishing the molecular pathways involved in chronic allograft

- nephropathy (CAN) for testing new non-invasive diagnostic markers. *Transplantation*, 83(4):448-457, 2007.
28. Mas VR, Fisher RA, **Archer KJ**, Yanek KC, Williams B, Dumur CI, Maluf DG. Genes associated with progression and recurrence of Hepatocellular Carcinoma in Hepatitis C Patients Waiting and Undergoing Liver Transplantation: Preliminary results. *Transplantation*, 83(7):973-81, 2007.
 29. Kennedy RE, Yeatts SD, **Archer KJ**, Gennings C, Ramakrishnan V. Opportunities for biostatisticians: Training and fellowship grants from the National Institutes of Health. *The American Statistician*, 61(2):120-126, 2007.
 30. **Archer KJ**, Dumur CI, Taylor GS, Chaplin MD, Guiseppi-Elie A, Buck G, Grant GM, Ferreira-Gonzalez A, Garrett CT, A disattenuated correlation estimate when variables are measured with error: Illustration estimating cross-platform correlations. *Statistics in Medicine*, 27(7):1026-1039, 2008.
 31. Mas VR, Mas LA, **Archer K**, Yanek K, King A, Gibney E, Cotterell A, Fisher R, Posner M, Maluf D. Evaluation of a Gene Panel mRNAs in Urine Samples of Kidney Transplant Recipients as Non-invasive Indicator of Graft Function. *Molecular Medicine*, 13(5-6):315-324, 2007.
 32. Mas VR, Maluf DG, **Archer KJ**, Yanek KC, Fisher RA. Angiogenesis soluble factors as HCC non-invasive markers for monitoring HCV cirrhotic patients. *Transplantation*, 84(10):1262-71, 2007.
 33. **Archer KJ**, Dumur CI, Taylor GS, Chaplin MD, Guiseppi-Elie A, Grant G, Ferreira-Gonzalez A and Garrett CT. Application of a correlation correction factor in a microarray cross-platform reproducibility study. *BMC Bioinformatics*, 8:447, 2007.
 34. **Archer KJ** and Kimes RV. Empirical characterization of random forest variable importance estimates. *Computational Statistics and Data Analysis*, 52(4): 2249-2260, 2008.
 35. Redmond LC, Dumur CI, **Archer KJ**, Haar JL, Lloyd JA. Identification of Erythroid-Enriched Gene Expression in the Mouse Embryonic Yolk Sac using Microdissected Cells. *Developmental Dynamics*, 237(2):436-446, 2008.
 36. Mas VR, **Archer KJ**, Yanek K, Dumur CI, Capparuccini MI, Mangino MJ, King A, Gibney EM, Fisher R, Posner M, Maluf D. Gene expression patterns in donor kidneys developing delayed graft functions. *Transplantation*, 85(4):626-635, 2008.
 37. Kong X, Mas VR, **Archer KJ**. A non-parametric meta-analysis approach for combining independent microarray datasets: application using two microarray datasets pertaining to chronic allograft nephropathy. *BMC Genomics*, 9:98, 2008.
 38. Maluf DM, Mas VR, **Archer KJ**, Yanek K, Gibney EM, King AL, Cotterell A, Fisher RA, Posner MP. Molecular pathways involved in loss of kidney graft function with tubular atrophy and interstitial fibrosis. *Molecular Medicine*, May-Jun;14(5-6):276-85, 2008.
 39. Mas VR, Maluf DG, **Archer KJ**, Yanek K, Bornstein K, Fisher RA. Proteomic analysis of HCV cirrhosis and HCV-induced HCC: Identifying biomarkers for monitoring HCV-cirrhotic patients awaiting liver transplantation. *Transplantation*, Jan 15;87(1):143-152, 2009.
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43. **Archer KJ**, Mas VR, O'Brien TR, Pfeiffer R, Lum NL, Fisher RA. Quality assessment of microarray data in a multi-center study. *Diagnostic Molecular Pathology*, 18(1):34-43, 2009.
44. Mas VR, Fisher RA, **Archer KJ**, Maluf DG. Proteomics and Liver Fibrosis: identifying markers of fibrogenesis. *Expert Reviews of Proteomics*, Aug;6(4):421-31, 2009.
45. **Archer KJ**, Mas VR. Ordinal response prediction using bootstrap aggregation, with application to a high-throughput methylation dataset. *Statistics in Medicine*, Dec 20;28(29):3597-610, 2009.
46. **Archer KJ**, Mas VR, David K, Maluf DG, Bornstein K, Fisher RA. Identifying genes for establishing a multigenic test for HCC surveillance in HCV+ cirrhotic patients. *Cancer, Epidemiology, Biomarkers & Prevention*, 18(11):2929-32, 2009.
47. **Archer KJ**, Reese SE. Detection Call Algorithms for High-throughput Gene Expression Microarray Data. *Briefings in Bioinformatics*, 11(2):244-52, 2010.
48. **Archer KJ**, Mas VR, Maluf DG, Fisher RA. High-throughput assessment of CpG site methylation for distinguishing between HCV-cirrhosis and HCV-associated hepatocellular carcinoma. *Molecular Genetics and Genomics*, 283(4):341-9, 2010.
49. Mas VR, **Archer KJ**, Scian M, Maluf DG. Molecular pathways involved in loss of kidney graft function with tubular atrophy and interstitial fibrosis in kidney transplant recipients. *Expert Reviews in Molecular Diagnostics*, 10(3):269-84, 2010.
50. **Archer KJ**. rpartOrdinal: An R package for deriving a Classification Tree for Predicting an Ordinal Response. *Journal of Statistical Software*, 34(7): 1-17, 2010.
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52. Kong X, **Archer KJ**, Moulton LH, Gray RH, Wang M. Parametric Frailty Models for Clustered Data with Arbitrary Censoring: Application to Effect of Male Circumcision on HPV Clearance. *BMC Medical Research Methodology*, May 6;10:40, 2010.
53. **Archer KJ**, Lemeshow S, Litchner MI. st0099_1: Goodness-of-fit test for logistic regression fitted using survey sample data. *The Stata Journal*, 10(2):313, 2010.
54. **Archer KJ**, Zhao Z, Guennel T, Maluf DG, Fisher RA, Mas VR. Identifying genes progressively silenced in preneoplastic and neoplastic liver tissues. *International Journal of Computational Biology and Drug Design*, 3(1), 52-67, 2010.
55. Mas VR, Fassnacht R, **Archer KJ**, Posner M, Maluf D. Molecular mechanisms involved in the interaction effects of alcohol and HCV in liver cirrhosis. *Molecular Medicine*, 16(7-8):287-297, 2010.
56. Maluf DG, **Archer KJ**, Villamil F, Stravitz RT, Mas V. Hepatitis C virus recurrence after liver transplantation: Biomarkers of disease and fibrosis progression. *Expert Rev Gastroenterol Hepatol*. 4(4): 445-458, 2010.
57. Maluf DG, **Archer KJ**, Mas VR. Kidney Grafts From HCV-Positive Donors: Advantages and Disadvantages. *Transplantation Proceedings*, 42(7):2436-46.
58. Edmiston JS, **Archer KJ**, Scian MJ, Joyce AR, Zedler BK, Murrelle EL. Gene expression profiling of peripheral blood leukocytes identifies potential novel biomarkers of chronic obstructive pulmonary disease in current and former smokers. *Biomarkers*, 15(8):715-30, 2010.
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65. Wolstenholme JT, Warner JA, Capparuccini MI, **Archer KJ**, Shelton KL, Miles MF. Genomic analysis of individual differences in ethanol drinking: evidence for non-genetic factors in C57BL/6 mice. *PLoS One* 6(6):e21100, 2011.
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68. Kopec A, D'Souza M, Mets B, Burgoon L, Reese S, **Archer K**, Potter D, Tashiro C, Sharratt B, Harkema J, Zacharewski T. Non-additive hepatic gene expression elicited by 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) and 2,2',4,4',5,5'-hexachlorobiphenyl (PCB153) co-treatment in C57BL/6 mice. *Toxicology and Applied Pharmacology*, 256(2):154-67, 2011.
69. Mas VR, Scian MJ, **Archer KJ**, Suh JL, David KG, Ren Q, Gehr TW, King AL, Posner MP, Mueller TF, Maluf DG. Pretransplant transcriptome profiles identify among kidneys with delayed graft function those with poorer quality and outcome. *Molecular Medicine*, 17(11-12):1311-22, 2011.
70. Simon SD, Reig AS, **Archer KJ**, Mericle RA. Biomechanical attributes of microcatheters used in liquid embolization of intracranial aneurysms. *J Neurointerv Surg.*, 4(3):211-4, 2012.
71. Gao G, Kang G, Wang J, Chen W, Qin H, Jiang B, Li Q, Sun C, Liu N, **Archer KJ**, Allison DB. A generalized sequential Bonferroni procedure using smoothed weights for genome-wide association studies incorporating information on Hardy-Weinberg disequilibrium among cases. *Human Heredity*, 73(1):1-13, 2012.
72. Asomaning N, **Archer KJ**. High-throughput DNA methylation datasets for evaluating false discovery rate methodologies. *Computational Statistics and Data Analysis*, 56(6):1748-1756, 2012.
73. Mas VR, **Archer KJ**, Dumur CI, Scian MJ, Suh JL, King AL, Wardius ME, Straub JA, Posner MP, Brayman K, Maluf DG. Reduced expression of inflammatory genes in deceased donor kidneys undergoing pulsatile pump preservation. *PLoS One*, 7(4):e35526, 2012.
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