# CURRICULUM VITAE

## KELLIE J. ARCHER, PH.D.

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## 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: ordinal response modeling, genomic biostatistics, data mining, statistical learning, statistical computing, applications of statistical methods to high-throughput genomic data including next-generation sequencing data

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## EDUCATION

### GRADUATE

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

### UNDERGRADUATE

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

## CERTIFICATION AND LICENSURE

Not applicable.

## ACADEMIC APPOINTMENT HISTORY

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|---|---|
| 2016-present | Professor & Chair (with tenure), Division of Biostatistics, College of Public Health, The Ohio State University, Columbus, Ohio |
| 2016-present | 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

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|---|---|
| 1998-2002 | Research Specialist, Division of Hematology & Oncology, The Ohio State University, Columbus, Ohio<br>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

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## 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

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## SCIENTIFIC AND SCHOLARLY ACTIVITIES

### Expert services

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 Infaction, 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-present 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-present 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 is 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

R01DK109581 (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%

R01CA284595 (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 logitudinal twin study to assess the role of genetics and environment on their frequency and inter-relationships
Role: co-I (PI of subaward)
Effort: 10%

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%

R21 AI172077-01A1 (Valeria Mas & **Kellie J. Archer**, MPI)
NIH/NIAID
Dates: 03/16/2023 - 02/28/2025
Pre-transplant comprehensive scores to predict long term graft outcomes
Role: MPI
Effort: 10%

R01LM013879-01 (**Kellie J. Archer**, PI)
NIH/NLM
Dates: 01/01/2022 - 12/31/2025
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: 07/2022 – 06/2027
Chronic Respiratory Effect and Control of Occupational Exposure of Wildland Firefighters to Smoke
Role: co-I
Effort: 5%

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: 4%

## Grants and Contracts: Past

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
Total award: $434,586
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
Total award: $147,894
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
Percent 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
Percent 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)
Percent Effort: 5% cost share

1U01HD087198 (Charles Chalfant, PI)
National Institutes of Child Health & Human Development
Total Award: $4,183,480
Dates: 09/17/2015 - 08/31/2019 (effort ended 06/2016 left VCU)
The utilization of photonics technology to rapidly detect bioactive lipids associated with preeclampsia development
Role: co-Investigator
Percent Effort: 4%

1R01CA191002-01A1 (Zheng Fu, PI)
National Cancer Institute
Total Award: $228,750
Dates: 04/01/2016-03/31/2021 (effort ended 06/2016 left VCU)
The Role of PLK1 in Prostate Cancer
Role: co-Investigator
Percent Effort: 1%

1R01CA206028 (David Gewirtz, PI)
National Cancer Institute
Total Award: $259,883
Dates: 04/15/2016-03/31/2021 (effort ended 06/2016 left VCU)
(PQ9) Mitigation of chemotherapy induced peripheral neuropathy
Role: co-Investigator
Percent Effort: 5%

1R01DK080074-01 (Valeria R. Mas, PI)
National Institutes of Diabetes, Digestive & Kidney Diseases
Total Award: $2,168,647
Dates: 08/05/08 - 05/31/13
Molecular pathways leading to chronic allograft dysfunction
Role: co-Investigator
Percent Effort: 16%

U54 HL090516 (Wally Smith, PI)
Basic and Translational Research Program in Sickle Cell Disease
Project 4b (Joyce Lloyd, PI)
Effects of developmental stage and of KLF2 on mouse erythroid genetic profiles
Total Award: $120,331 per year
National Institutes of Health/NHLBI
Dates: 04/01/08 - 03/31/12
Role: co-Investigator
Percent effort: 5%

1R03LM009347-02 (**Kellie J. Archer**, PI)
NIH/National Institute of Library Medicine
Total Award: $149,000
Dates: 08/15/08 - 07/31/11
Recursive partitioning and ensemble methods for classifying an ordinal response
Role: PI
Percent Effort: 15%

U01DK062531-08 (Robert A. Fisher, PI)
NIH/NIDDK
Total Award: $1,218,335
Dates: 09/30/09-08/31/11
Adult to Adult Living Donor Liver Transplantation
Role: co-investigator
Percent Effort: 2%

R01 DK069859-02 (Robert Fisher, PI)
National Institutes of Health/NIDDK
Total Award: $3,570,708
Dates: 04/01/06 - 03/31/11
Genes related to HCC progression in living donor and deceased donor transplant liver recipients.
Role: Co-investigator

Percent Effort: 25%

3R03LM009347-02S1 (**Kellie J. Archer**, PI)
NIH/National Institute of Library Medicine
Total Award: $75,000
Dates: 09/30/09 - 09/29/10
American Reinvestment and Recovery Act of 2009: Competing Revision of Recursive partitioning and ensemble methods for classifying an ordinal response
Role: PI
Percent Effort: 13%

3R03LM009347-02S2 (**Kellie J. Archer**, PI)
NIH/National Institute of Library Medicine
Total Award: $5,742
Dates: 05/01/10 - 07/31/10
American Reinvestment and Recovery Act of 2009: Administrative Supplement for Students and Science Educators under the Recovery Act
Role: PI

Pharmion (John McCarty, PI)
Title: A Phase II Study of the Use of 5-Azacytidine as Pre-Transplant Cytoreduction Prior to Allogeneic Stem Cell Transplantation for High Risk Myelodysplastic Syndromes
Dates: 4/30/08-4/30/11 (effort ended 09/30/09)
Role: Biostatistician
Percent Effort: 2%

Genzyme (Amir Toor, PI)
Title: 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
Percent Effort: 2%

VR Mas & DG Maluf (PIs)
Roche Laboratories
Total Award: $133,000
Dates: 12/01/06 - 11/30/08
New strategies for non-invasive detection of chronic allograft nephropathy
Role: Biostatistician
Percent Effort: 5%

5F37LM008728-03 (**Kellie J. Archer**, Sponsor)
NIH/National Institute of Library Medicine
Individual Biomedical Informatics Fellowships, Richard E. Kennedy
Total Award: $159,689
Dates: 08/01/05 - 07/31/08
Mixed Effects Modeling of Microarrays Using the S-score
Role: Sponsor
Effort not funded

A.D. Williams Trust Fund (**Kellie J. Archer**, PI)
A.D. Williams Trust Fund
Total Award: $10,342
Dates: 01/01/07 - 12/31/07
Title: Extending the random forest methodology for predicting an ordinal response.
Role: PI
Effort not funded

Pfizer (**Kellie J. Archer**, subaward from R. Kightlinger (PI), UVA)
Pfizer International Health Initiative
Total Award: $7,500
Dates: 01/01/07 - 12/31/07
HIV, cervical cancer, HPV, and HPV genotypes among women in rural and urban regions of Guyana, South America
Role: Biostatistician
Percent Effort: 7.5%

Translational Research Award (Peter O'Connell, PI)
The V Foundation for Cancer Research
Total Award: $300,000
Dates: 10/31/04 - 10/30/07
Neoadjuvant chemotherapy for breast cancer: Gene expression and MTA1 protein isoform-based predictive factors.
Role: Biostatistician
Percent Effort: 10%

Pilot Project (**Kellie J. Archer** & Valeria R. Mas, Co-PIs)
Funding source: Massey Cancer Center
Total Award: $30,000
Dates: 08/01/05 - 07/31/06
Title: Predicting HCC progression using molecular markers in patients awaiting liver transplantation.
Role: co-PI
Percent Effort: 2%

MCC Pilot Project (C.I. Dumur & W. Broaddus, Co-PIs)
Massey Cancer Center
Total Award: $30,000
Dates: 12/31/04 - 12/30/05
Title: Role of necrosis in induction of the malignant phenotype in glioblastoma multiforme: gene expression and molecular analysis.
Role: Biostatistician
Percent Effort: 2%

Individual Allocation, ACS Institutional Research Grant (**Kellie J. Archer**, PI)
Funding source: American Cancer Society
Total Award: $2844
Dates: 09/01/03-08/31/04

Title: Exploration and identification of novel methodologies for image analysis and probe set expression summaries for oligonucleotide microarrays
Role: PI

MCC Pilot Project (Penberthy, Lynne, PI)
Massey Cancer Center
Total Award: $30,000
Dates: 01/01/03-12/31/03
Title: Pilot to evaluate Cancer and Genomics in Elderly versus Young Cancer Patients
Role: Biostatistician

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## EXTRAMURAL PRESENTATIONS

### Invited

(1) Denison University, Department of Mathematics, February 22, 2023: "The Role of Biostatistics in Public Health and Clinical Medicine."

(2) 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."

(3) Georgetown University Department of Biostatistics, Bioinformatics, and Biomathematics, October 25, 2019: "Algorithmic and statistical learning methods for high-dimensional variable selection."

(4) University of Minnesota Division of Biostatistics, September 18, 2019: "High-dimensional variable selection and prediction of ordinal pathological response data."

(5) National Library of Medicine, Bethesda, MD June 15, 2016: "Predicting an ordinal response using features from high-throughput genomic assays."

(6) 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."

(7) 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."

(8) Division of Biostatistics, The Ohio State University, Columbus, OH October 30, 2015: "Penalized ordinal response models for high-dimensional feature data."

(9) West Virginia University, Morgantown, WV April 1, 2015: "Identifying factors related to micronuclei frequency in women with breast cancer."

(10) 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."

(11) 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."

(12) 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.

(13) Virginia State University, Petersburg, VA, March 1, 2013: "Identifying Genes for Establishing a Multigenic Test for HCC Surveillance in HCV+ Cirrhotic Patients."

(14) Air Force Institute of Technology, Dayton, OH, May 24, 2012: "Classification and variable selection for high-dimenstional datasets using Random Forests."

(15) Cambridge Healthtech Institute's Advances in Gene Expression Profiling, Philadelphia, PA, November 18, 2010: "Evaluating Quality in a Multicenter Gene Expression Microarray Study."

(16) James Madison University Department of Mathematics & Statistics Colloquium, Harrisonburg, VA, November 10, 2008: "Statistics in medical and high-throughput genomic research."

(17) 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."

(18) National Institutes of Health Microarray Special Interest Group, Bethesda, MD, April 2, 2008: "An exploratory approach for assessing aberrant methylation using Affymetrix GeneChip data."

(19) George Mason University Bioinformatics Colloquium, Manassas, VA, March 25, 2008: "A combined statistical and bioinformatic approach for identifying hypermethylated genes in human hepatocellular carcinoma."

(20) 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."

(21) 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."

(22) College of William and Mary, Department of Mathematics Applied Mathematics Colloquim, March 24, 2003: “Expression summaries for oligonucleotide arrays: implications for multiple hypothesis testing,” Williamsburg, Virginia.

## Contributed

(1) **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.

(2) **Kellie Archer**, Han Fu, Krzysztof Mrózek, Deedra Nicolet, Jessica Kohlschmidt, Alice S. Mims, Geoffrey L. Uy, Wendy Stock, John C. Byrd, Ann-Kathrin Eisfeld. 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.

(3) **Kellie Archer**, Yiran Zhang, Sai Vineela Bontha, J Eason, Lorenzo Gallon, Enver Akalin, Daniel Maluf, Valeria Mas. 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.

(4) **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.

(5) **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.

(6) **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.

(7) **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.

(8) **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.

(9) **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.

(10) **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.

(11) **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.

(12) **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.*

(13) **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.

(14) **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.

(15) **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.

(16) **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.

(17) **Kellie J. Archer**. Joint Statistical Meetings, Seattle, Washington, August 9, 2006: "Ensemble methods for predicting an ordinal response." Oral presentation.

(18) **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.

(19) **Kellie J. Archer**. Joint Statistical Meetings, Toronto, Ontario, August 9, 2004: "Parallel Coordinate Plots of Gene Expression Data Differentiated by Phenotype." Oral presentation.

(20) **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

1. 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.
2. Guowei Li, **Kellie Archer**. Variable selection for competing risks in high-dimensional covariate spaces with missing data. Oral presentation, ENAR, March 20, 2023.
3. Guowei Li, **Kellie Archer**. Variable selection for high-dimensional competing risks data. Oral presentation, Joint Statistical Meetings, August 9, 2022.
4. Anna Eames Seffernick, **Kellie Archer**. Feature Selection in High-dimensional Genomic Data Using a Bayesian Stereotype Model. Oral presentation, ENAR, March, 2022.
5. Anna Eames Seffernick, **Kellie Archer**. Bayesian Stereotype Model for Feature Selection in High-Dimensional Genomic Data. Contributed Poster, ENAR, March 17, 2021.
6. 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.
7. 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.
8. Yiran Zhang, **Kellie J. Archer**. Bayesian variable selection for high-dimensional data with ordinal responses. Poster Presentation: Variable Subset Selection. ENAR, March 24, 2019.
9. 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.
10. 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.
11. 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.
12. 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.

(13) Qing Zhou, **Kellie J. Archer**. Penalized Bayesian cumulative logit model for high-dimensional datasets. ENAR, Poster Presentation: Machine Learning. Austin, TX, March 7, 2016.

(14) Amanda E. Gentry, **Kellie J. Archer**. Mixed models for ordinal outcomes in twin and sibling studies with high-dimesional covariate spaces. ENAR, Poster Presentation: Machine Learning. Austin, TX, March 7, 2016.

(15) 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.

(16) 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.

(17) 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.

(18) 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.

(19) 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.

(20) Andre Williams, **Kellie J. Archer**. Stereotype logit models for high-dimensional data. ENAR, New Orleans, LA, March 23, 2010.

(21) Andre Williams, **Kellie J. Archer**. Stereotype logit models for high-dimensional data. Bioinformatics - Contributed Papers. Joint Statistical Meetings, Seattle, WA, August 2, 2010.

(22) 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.

(23) 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.

(24) 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.

(25) 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.

(26) 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.

(27) 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

(1) OSU Department of Biomedical Informatics, Columbus, OH, October 29, 2021: “Identifying features associated with long-term outcome using penalized mixture cure models.”

(2) OSU CCTS BERD Secondary Data Analysis Workshop, Columbus, OH, August 19, 2021: “NIDDK Central Repository Data and Samples.”

(3) OSU Department of Statistics, Columbus, OH, November 14, 2017: “Modeling an Ordinal Response when Confronted with a High-Dimensional Feature Space.”

(4) OSUCCC Molecular Biology & Cancer Genetics Program, Columbus, OH, September 7, 2016: “Applications of statistical methods for establishing multigenic tests for polygenic traits & conditions.”

(5) 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.”

(6) 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.”

(7) 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. OSU Department of Biomedical Informatics.

Guy Brock, Ph.D. OSU Department of Biomedical Informatics.

## Postdoctoral students trained

Wenan Chen, Ph.D. *Machine learning methods for classifying an ordinal response*
Funded by Kellie Archer's R01 (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 Big Data to Knowledge (BD2K) Data Science Rotation for Advancing Discovery Trip (RoAD-TRIP)

Veronica Haywood , Ph.D. 2018 *Differential Glycosylation Related Gene Expression during Wound Healing*
Funded by NIH Big Data to Knowledge (BD2K) Data Science Rotation for Advancing Discovery Trip (RoAD-TRIP)

## Graduate students trained

### Thesis Advisor

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 Ph.D., Biostatistics *Variable selection for competing risks in high-dimensional covariate spaces without and with missing data*

Anna Eames Seffernick, 2022 Ph.D., Biostatistics *Penalized Bayesian ordinal response models with applications to discrete survival time and non-proportional odds models*

Han Fu, 2022 Ph.D., Biostatistics *Variable selection for high-dimensional data with error control*

Yiran Zhang, 2019 Ph.D., Biostatistics *Bayesian variable selection for high-dimensional data with an ordinal response*

Amanda Gentry, 2018 Ph.D., Biostatistics *Penalized mixed-effects ordinal response models for high-dimensional genomic data in twins and families*

Rebecca Lehman, 2017 Ph.D., Biostatistics *The generalized monotone incremental forward stagewise method for modeling longitudinal, clustered, and overdispersed count data: Application predicting nuclear bud and micronuclei frequencies*

Kyle Ferber, 2016 Ph.D., Biostatistics *Methods for predicting an ordinal response with high-throughput genomic data*

Qing Zhou, 2016 Ph.D., Biostatistics *An extension of penalized ordinal response models*

Umaporn Siangphoe, 2015 Ph.D., Biostatistics *Meta-analysis of gene expression studies*

Mateusz Makowski, 2015 Ph.D., Biostatistics *High-throughput data analysis: Application to micronuclei frequency and T-cell receptor sequencing*

Jiayi Hou, 2013 Ph.D., Biostatistics *Regularization methods for predicting an ordinal response using longitudinal high-dimensional genomic data*

Sarah E. Reese, 2013 Ph.D., Biostatistics *Detecting and correcting batch effects in high-throughput genomic experiments*

Maria I. Capparuccini, 2010 Ph.D., Biostatistics *Inferential methods for high-throughput methylation data*

André A.A. Williams, 2010 Ph.D., Biostatistics *Stereotype logit models for high-dimensional data*

Xueping Zhang, M.S., 2010 Clinical Research and Biostatistics *A Meta-analysis of microRNA microarray studies in prostate cancer*

Xiangrong Kong, Ph.D., 2008 Biostatistics *Variable selection in competing risks under the $L_1$-penalized Cox model*

Tobias Guennel, 2008 Diploma thesis, Technische Universität Chemnitz *Ordinal Classification Approach using Bagged Classification Trees and the Proportional Odds Model as Splitting Criteria*

Ryan V. Kimes, M.S. 2006 Biostatistics *Quantifying the Effects of Correlated Covariates on Variable Importance Estimates from Random Forests*

S. Brett Kliner, M.S. 2006 Bioinformatics *Empirical characterization of variability among Affymetrix probe set expression summaries by sequence fidelity*

**Candidacy Exam Committee Member**

Juan Xie 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**

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 chromatins 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 Diagnositic 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*

**Thesis Committee Member**

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 Influenze 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

| | |
|---|---|
| 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

Responsible for 100% of course unless indicated otherwise.

### Virginia Commonwealth University

| | | |
|---|---|---|
| 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) |
| 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 |
| Fall 2015 | BIOS 690 | Biostatistics Seminar |
| Spring 2016 | BIOS 690 | Biostatistics Seminar |

⋆: Redesigned existing course. ‡: Developed this course.

**The Ohio State University**

| | | |
|---|---|---|
| Spring 2017 | PUBHBIO 6211 | Design & Analysis of Health Studies II (50%) |
| Spring 2017 | PUBHBIO 7245 | Biostatistical Collaboration |
| Fall 2017 | PUBHBIO 8899 | Doctoral Seminar in Biostatistics |
| Spring 2018 | PUBHBIO 6211 Online | Design & Analysis of Health Studies II (33%) |
| Spring 2018 | PUBHBIO 7245 | Biostatistical Collaboration |
| Fall 2018 | PUBHBIO 2210 | Biostatistics for Public Health |
| Fall 2018 | PUBHBIO 8899 | Doctoral Seminar in Biostatistics |
| Spring 2019 | PUBHBIO 6211 | Design & Analysis of Health Studies II (50%) |
| Spring 2019 | PUBHBIO 7245 | Biostatistical Collaboration |
| Fall 2019 | PUBHBIO 8899 | Doctoral Seminar in Biostatistics |
| Spring 2020 | PUBHBIO 6211 | Design & Analysis of Health Studies II (50%) |
| Spring 2020 | PUBHBIO 7245 | Biostatistical Collaboration |
| Fall 2020 | PUBHBIO 7250 | Special Topics: Statistical Learning and Data Mining in Public Health |
| Fall 2020 | PUBHBIO 8899 | Doctoral Seminar in Biostatistics |
| Spring 2021 | PUBHBIO 7245 | Biostatistical Collaboration |
| Fall 2021 | PUBHBIO 6250 | Regression Methods for the Health Sciences |
| Fall 2021 | 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 |

### Other teaching responsibilities & awards

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.

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## SERVICE ACTIVITIES

### Service to the Profession

Member, Math Alliance Facilitated Graduate Application Program (F-GAP) Executive Committee, 2024–present.

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, 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 at 2023 Conference of the Eastern North American Region of the International Biometrics Society 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 Review Meeting, November 8-9, 2022.

Panelist, Career Panel on Statistics and Data Science, American Statistical Association Columbus Chapter, Columbus, Ohio, 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 for SBIR/STTR applications ZRG1 OTC-R (12) B, June 16-17, 2022.

Ad hoc reviewer, Pennsylvania Department of Health Formula Grants Final Performance Review 21-22 Cycle B, 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, American Statistical Association Statistical Learning and Data Science Section, 2022.

Member, DSMB, A Phase I/II, Randomized Pilot Study of Human Embryonic Stem Cell-Derived Cardiomyocytes (hESC-CMs) in PaTients with ChrOnic Ischemic Left VentRicular Dysfunction Secondary to Myocardial Infarction (HECTOR), Stanford, December 2021 - present.

Reviewer, Environmental Health Sciences Core Centers (EHSRC) Review Meeting (EHS K P), October 4-6, 2021.

Volunteer, ASA Committee on Career Development: Guided Networking Session, August 5, 2021.

Ad hoc reviewer, T15 Review Committee, Applications submitted in response to RFA-LM-21-001, July 23, 2021.

Ad hoc reviewer, ZDK1 GRB- S (O2) Review Committee, NIDDK Central Repositories Non-renewable Sample Access (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 (EHS (T) 1) Review Committee Meeting, November 19, 2020.

Panelist, Career Panel sponsored by Association for Women in Mathematics (AWM) chapter at University of California 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), "NIDDK Central Repositories Non-Renewable Sample Access (X01)," September 3, 2020.

Volunteer, ASA Committee on Career Development "Guided Virtual Networking Session," July 30, 2020.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1 GRB-S (O3), "PAR17-123: Biomarkers for Diabetes, Digestive, Kidney and Urologic Diseases Using Biosamples from the NIDDK Repository (R01)," June 3, 2020.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1 GRB-S (O1), "NIDDK Biorepository Non-Renewable Sample Access (X01)," May 28, 2020.

Ad hoc reviewer, Florida Breast Cancer Foundation, April, 2020.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1 GRB-S (M2) "NIDDK Central Repositories Non-renewable Sample Access(X01)," January 15, 2020.

Committee member, 2020-2023 Field of Dreams Agenda Committee.

Ad hoc reviewer, NIEHS R25 Special Emphasis Panel "Undergraduate Research Education Program (UP) to Enhance Diversity in the Environmental Health Sciences," November 20, 2019.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1 GRB-S (M1) "Biomarkers for Diabetes, Digestive, Kidney and Urologic Diseases using Biosamples from the NIDDK Repository (R01)," September 26, 2019.

Ad hoc reviewer, NIEHS Environmental Health Sciences Review Committee Meeting: P30 Core Center, August 14-15, 2019.

Invited Session Chair, 2019 Joint Statistical Meetings, “The Impacts of Measurement Error in Scientific Discoveries,” 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 Non-Renewable Sample Access (X01) for PAR-17-270, May 7, 2019.

Ad hoc reviewer, NCI Special Emphasis Panel ZCA1 TCRB-D (M1): Informatics Tools for Cancer Research and Surveillance, March 21-22, 2019.

Judge at 2019 Conference of the Eastern North American Region of the International Biometrics Society poster competition, March 2019.

Ad hoc reviewer, NIEHS Special Emphasis Panel ZES1 LKB K R: Maintain and Enrich Resource Infrastructure for 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: The Role of Anonymization. Social Solutions International, Inc., January 2019.

Statistical Editorial Board Member, *JNCI* and *JNCI Spectrum*, appointment term 2019-present.

Ad hoc reviewer, NIDDK Central Repositories Non-Renewable Sample Access (X01) for PAR-17-270, October 3, 2018.

Ad hoc reviewer, NCI Program Project (P01) III Review ZCA1 RPRB-J (J1), September 24-25, 2018.

Member, Chairs of Biostatistics Leadership Team, appointment term 2018-2020.

Member, NIH/NLM Biomedical Informatics Library and Data Science Review Committee (BILDS), June 14-15, 2018.

Ad hoc reviewer, NCI Program Project Review I (P01) ZCA1 RTRB-R (O1) April 17-18, 2018.

Ad hoc reviewer, NIEHS Special Emphasis Panel: Maintain and Enrich Resource Infrastructure for Existing Environmental Epidemiology Cohorts (R24), April 11, 2018.

Judge at 2018 Conference of the Eastern North American Region of the International Biometrics Society poster competition, March 2018.

Member, NIH/NLM Biomedical Informatics, Library and Data Sciences (BILDS), March 8-9, 2018.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1 GRB-S (O1) Central Biorepositories Non-Renewable Sample Access (X01), February 5, 2018.

Member, NIH/NLM Biomedical Informatics, Library and Data Sciences (BILDS), November 2-3, 2017.

Ad hoc reviewer, NIEHS Environmental Health Sciences Review Committee EHS P3, August 29-30, 2017.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), June 15-16, 2017.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1-GRB-S (01) NIDDK Central Repositories Non-renewable Sample Access(X01), May 11, 2017.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), March 9-10, 2017.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), November 3-4, 2016.

Ad hoc reviewer, Cancer, Heart, and Sleep Epidemiology Panel B review panel (CHSB), October 24-25, 2016.

Ad hoc reviewer, NIDDK Special Emphasis Panel ZDK1 GRB-S (J2) Biomarkers for Diabetes, Digestive, Kidney and Urologic Diseases Using Biosamples from the NIDDK Repository (R01), September 21, 2016.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), June 16-17, 2016.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), March 10-11, 2016.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), Nov 5-6, 2015.

Ad-hoc reviewer, NIEHS 2016/01 EHS (TK) Environmental Health Sciences Review Committee, Nov 4, 2015.

Ad-hoc reviewer, NIDDK Biomarkers for TID and Kidney Disease (R01) DK1 GRB-S (J2), October 1, 2015.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), June 4-5, 2015.

Ad-hoc reviewer, NIDDK's Chronic Kidney Disease Biomarkers Consortium (CKD BioCon) ZDK1 GRB-J M1, March 24, 2015.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), March 19-20, 2015.

Ad-hoc reviewer, NIDDK Central Repositories Non-Renewable Sample Access (X01) ZDK GRB-S (M1), January 9, 2015.

Member, NIH/NLM Biomedical Library and Informatics Review Committee (BLIRC), November 6-7, 2014.

Ad-hoc reviewer, NCI's Small Grants Program for Cancer Epidemiology (R03), October 30, 2014.

Ad-hoc reviewer, NIDDK's Biomarkers for Diabetes, Kidney Disease and Urology (R01) ZDK1 GRB-S (J2), September 25, 2014.

Lead guest editor, *Cancer Informatics* Computer simulation, bioinformatics, and statistical analysis of cancer data and processes supplement, 2014-2015.

Ad-hoc reviewer, NIDDK's 2014/10 ZDK1 GRB-N (O2) 1 PAR-14-065: Research Using Biosamples from Selected Type 1 Diabetes Clinical Studies (DP3), July 1, 2014.

Ad-hoc reviewer, NCI's 2014/10 ZCA1 RPRB-0 (O1) S Omnibus Special Emphasis Panel EP-4, June 24-25, 2014.

Ad-hoc reviewer, 2014/05 ZRG1 BST-Z (52) R RFA-HG-13-009: Big Data to Knowledge (BD2K) U54 Centers of Excellence April 10-11, 2014.

Statistical Consultant, *Nature* Publishing Group, 2013-present.

Session Chair, 2014 Eastern North American Region Spring Meeting of the International Biometric Society, "Prediction and Prognostic Modeling," Baltimore, MD, March 19, 2014.

Ad-hoc reviewer, NCI Special Emphasis Panel ZCA1 SRLB-Y (M3) Small Grants Program for Cancer Epidemiology, February 26, 2014.

Ad-hoc reviewer, ZDK1 GRB-S (M2) S PAR13-228: Biomarkers for Diabetes, Digestive,Kidney and Urologic Diseases using Repository Biosamples (Teleconference) February 20, 2014.

Ad-hoc reviewer, ZDK1 GRB-S (M1) S PAR11-306: NIDDK Central Repositories Non-Renewable Sample Access Review (X01): HCC, Urology and Hemodialysis (Teleconference) , January 24, 2014.

Ad-hoc reviewer, NCI Special Emphasis Panel ZCA1 SRLB-D (J1) Small Grants Program for Cancer Epidemiology, November 7, 2013.

Ad-hoc member, NCI Cancer Management, Epidemiology, and Health Behavior ZCA1 SRLB-B (J1) S Review Meeting, October 29-30, 2013.

Ad-hoc reviewer, ZDK1 GRB-S (O5) S PAR-13-013-Research Using Biosamples from TrialNet/DPT-1 Type Diabetes Clinical Studies, June 10, 2013.

Ad-hoc reviewer, ZDK1 GRB-S (M6) NIDDK Central Repositories Sample Access (X01): Hepatitis E and Advanced Chronic Hepatitis C, March 27, 2013.

Ad-hoc reviewer, NCI Special Emphasis Panel ZCA1 SRLB-D (M1) R03 Small Grants Program for Cancer Epidemiology, March 21-22, 2013.

Ad-hoc reviewer, NCI Special Emphasis Panel ZCA1 SRLB-4 (J2) R03 Small Grants Program for Cancer Epidemiology, October 16-17, 2012.

Ad-hoc reviewer, Special Emphasis Panel/Scientific Review Group for NIDDK Sample Repositories Non-Renewable Sample Access 2013/01 ZDK1 GRB-S (J1) S, September 4, 2012.

Ad-hoc reviewer, NCI Special Emphasis Panel ZCA1 SRLB-D(O1) R03 Small Grants Program for Cancer Epidemiology, June 21-22, 2012.

Organized and chaired the Statistical Methods for High-throughput Genomic Technologies at the Southern Regional Council On Statistics (SRCOS) Summer Research Conference, June 3-5, 2012, Jekyll Island, GA.

National Science Foundation Panel Review Member April 3-4, 2012.

Ad-hoc mail reviewer, NIH. NCI Provocative Questions March 27-29, 2012.

Ad-hoc Reviewer, NCI Special Emphasis Panel ZCA1 SRLB-Q (M1) R03 Small Grants Program for Cancer Epidemiology, March 22, 2012.

Ad-hoc reviewer, NIH Special Emphasis Panel/Scientific Review Group 2012/05 ZDK1 GRB-S (M2) S meeting, January 04, 2012.

Ad-hoc Reviewer, NCI Special Emphasis Panel ZCA1 SRLB-Q (J1) Small Grants Program for Cancer Epidemiology, November 17-18, 2011.

Ad-hoc Reviewer, NCI Special Emphasis Panel ZCA1 SRLB-D (O1) Small Grants Program for Cancer Epidemiology, July 21-22, 2011.

Ad-hoc Reviewer, NCI Special Emphasis Panel ZCA1 SRLB-3 (O1) 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, Special Emphasis Panel/Scientific Review Group 2011/10 ZRG1 OBT-N (02) M, April 27, 2011.

Session Chair, *Genomics.* Eastern North American Region of the International Biometrics Society, Miami, Florida, March 22, 2011.

Panel member, General and Plastic Surgery Devices Panel of the FDA Medical Devices Advisory Committee, November 18, 2010.

Ad-hoc Reviewer, NIH Cancer Genetics (CG) Study section, October 7-8, 2010.

Panel member, Radiological Devices Panel of the FDA Medical Devices Advisory Committee, September 24, 2010.

Ad-hoc Reviewer, Research Promotion Foundation of Cyprus, Health and Biological Sciences Programme/ Public Health Action of the Foundation's Framework Programme for Research, June 2010.

Ad-hoc Reviewer, NIH Genes, Computational Biology and Technology (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 of the Landesstifiung Baden-Wurttemberg, May 2010.

Ad-hoc Reviewer, NIH Genomics and Computational Biology ZRG1-GGG-M(91) Special Emphasis Panel, March 25-26, 2010.

Ad-hoc Reviewer, NIH/NIAID. RFA-AI-09-015 Study Section ZAI1-MFH-I-J2 "Coordinating Center for Organ Transplant Clinical Trials" October 23, 2009.

Ad-hoc Reviewer, NIH Genes, Computational Biology and Technology (GCAT) Study section, October 14-15, 2009.

Stage 1 Reviewer, NIH Challenge Grant applications. ZRG1 PSE-J and ZRG1 PSE-C, June, 2009.

Session Chair, *Methods in Statistical Genomics.* Joint Statistical Meetings, Denver, Colorado, August 3, 2008.

Editorial Board Member, *Progress in Transplantation.* June, 2008 - December, 2016.

Member, Radiological Devices Advisory Committee to the FDA. May, 2008 - January, 2011.

Member, Clinical Laboratory and Standards Institute (CLSI, formerly NCCLS) "MM12-A Diagnostic Nucleic Acid Arrays - Approved Guideline" (ISBN 1-56238-608-5). CLSI is a global, nonprofit, standards-developing organization that promotes the development and use of voluntary consensus standards and guidelines within the healthcare community.

**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*
*BMC Genomics*
*BMC Bioinformatics*
*Briefings in Bioinformatics*
*Cancer, Epidemiology, Biomarkers and Prevention*
*Communications in Statistics - Simulation and Computation*
*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*
*Methods of Information in Medicine*
*Nature Cancer*
*Nature Medicine*
*Nature Biotechnology*
*Nature Communications*
*Nature Immunology*
*PLoS One*
*Radiology*
*Radiology: Artificial Intelligence*
*Radiology: Cardiothoracic Imaging*
*Radiology: Imaging Cancer*
*Reproductive Sciences*
*Sankhya B*
*Science*
*Scientific Reports*
*Statistical Modeling*
*Statistics in Medicine*
*Statistical Methodology*
*Statistics in Biopharmaceutical Research*
*STATS*
*The American Statistician*
*Thailand Statistician*

## Service to the University

Member, Foods for Health Advisory Board Member, The Ohio State University, 2022 - present.

Chair, Health Sciences Library Advisory Board, The Ohio State University, 2022 - present.

Member, University Fellowship Review Committee, The Ohio State University, 2022.

Member, ENGIE-Axium Graduate Fellowship Review Committee, The Ohio State University, 2022.

Grant reviewer, CCTR KL2 applications, The Ohio State University, January 2020.

Grant reviewer, CCTS Secondary Data Analysis pilot grant applications, The

Ohio State University, 2019.

Denman Undergraduate Research Forum judge, The Ohio State University, 2018.

Member, Health Sciences Library Advisory Board, The Ohio State University, 2017 - 2022.

Judge, The Ohio State University Denman Undergraduate Research Forum, March 2017.

Ad-hoc Reviewer, A.D. Williams Multi-school Grant Application, Fall 2007.

Member, VCU High Performance Computing Committee, 2006-2007.

Ad-hoc Reviewer, Center for Teaching Excellence Small Grants Program, Fall 2004.

Member, Bioinformatics Admissions Committee, Center for the Study of Biological Complexity, 2004-2006.

Member, Bioinformatics Program Committee, Center for the Study of Biological Complexity, 2004-2006.

Member, Commonwealth Technology Trust Fund (CTRF) Cancer Genomics Committee, 2002-2005.

## Service to the School of Medicine/College of Public Health

Chair, College of Public Health Blue Sky Squad Workgroup, 2020-2021.

co-Chair, College of Public Health Incentive Plan Committee, 2020-2021.

Member, College of Public Health Executive Committee, The Ohio State University, 2016 - present.

Chair, Search Committee for Health Science Management & Policy Division Chair, 2018 - 2019.

Co-Chair, DT Metabolomics Search Committee 2016-2017.

Member, Promotion & Tenure Committee for Bassam Dahman, Department of Healthcare Policy & Research, 2015.

Member, Promotion & Tenure Committee for Derek Chapman, Department of Epidemiology & Community Health, 2013.

Member, Promotion & Tenure Committee for Dr. Zhibing Zhang, from Assistant to Associate Professor in the Department of Obstetrics/Gynecology, 2010.

Participant, School of Medicine Faculty Focus Group - LCME Accreditation Self Study, April 2007.

Member, Ad-hoc Infrastructure Wish List Committee, School of Public Health, 2006.

Member, Ad-hoc School of Public Health website design committee, 2005.

Member, Protocol Review & Monitoring System, Massey Cancer Center, 2002-2016.

## Service to the Department/Division

Member, Graduate Studies Committee, Interdisciplinary PhD Biostatistics, 2018-2021.

Member, Admissions Committee, Interdisciplinary PhD Biostatistics, 2016-2022.

Member, College of Public Health Executive Committee, 2016-present.

Chair, Search Committee: Department of Biostatistics open-rank faculty position, 2014-2015.

Chair, Search Committee: Department of Biostatistics open-rank genomic biostatistics faculty position, 2014-2015.

Chair, Seminar Committee, Department of Biostatistics, 2014-2016.

Member, Seminar Committee, Department of Biostatistics, 2013-2014.

Search Committee Member: Department of Biostatistics, CCTR faculty position with David Fenstermacher, 2013-2014.

Member, Promotion & Tenure Committee for Roy Sabo, Department of Biostatistics, 2013.

Member, Promotion & Tenure Committee for Nitai Mukhopadhyay, Department of Biostatistics, 2012.

Member, Self-assessment study ad-hoc committee, Department of Biostatistics, 2012.

Chair, Search Committee: Open-rank tenure track position, Department of Biostatistics, 2012-2013.

Member, Search Committee: Tenure track Assistant Professor, Department of Biostatistics, 2012.

Member, Executive Committee, Department of Biostatistics, 2011-2016.

Chair, Search Committee: Open-rank tenure track positions, Department of Biostatistics, 2010-2011.

Member, Search Committee: Non-tenure track Assistant Professor, Department of Biostatistics, 2009.

Chair, Search Committee: Joint faculty candidate in Biostatistics & Social & Behavioral Health, 2008.

Member, Biostatistics Curriculum committee, 2009-2011.

Chair, Biostatistics Curriculum committee, 2007-2009; co-chair V. Ramakrishnan.

Member, Department of Biostatistics Promotion & Tenure Guidelines Development Committee, 2008.

Member, Search Committee: Radiation Oncology/Biostatistics joint appointment, Department of Biostatistics, 2006-2007.

Member, Search Committee: Department of Biostatistics Chair, Department of Biostatistics, 2006-2007.

Chair, Search Committee: Genomic Biostatistics Faculty candidate, Department of Biostatistics, 2006.

Chair, Genomic Biostatistics Curriculum Committee, Department of Biostatistics, 2005-2007.

Member, Biostatistics Admissions Committee, 2005-2007.

Representative, Biostatistics departmental representative for Virginia Institute of Psychiatric and Behavioral Genetics (VIPBG) training grant, 2003-2008.

Coordinator, Department of Biostatistics S-Plus and Insightful Miner user licenses, 2003-2006. Member, Biostatistics Curriculum committee, 2002-2005.

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## PUBLICATIONS

### Papers published in peer reviewed journals

Note: Names of students I 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, Kolitz 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, Maghraby 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, Maghraby 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.

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(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 soluable 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.

(40) Prom-Wormley EC, Eaves LJ, Foley DL, Gardener CO, **Archer KJ**, Wormley BK, Maes HH, Riley BP, Silberg JL. Monoamine oxidase A and childhood adversity as risk factors for conduct disorder in females. *Psychological Medicine*, 39(4):579-90, 2009.

(41) Mas VR, Maluf DG, **Archer KJ**, Yanek K, Kong X, Kulik L, Freise CE, Olthoff KM, Ghobrial RM, McIver P, Fisher R. Genes involved in viral carcinogenesis and tumor initiation in Hepatitis C Virus-induced Hepatocellular Carcinoma. *Molecular Medicine*, 15(3-4):85-94, 2009.

(42) Brophy DF, Bukaveckas BL, Ferreira-Gonzalez A, **Archer KJ**, Martin EJ, Gehr TWB. A Pilot Study of Genetic Polymorphisms and Hemodialysis Vascular Access Thrombosis. *Hemodialysis International*, 13:19-26, 2009.

(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.

(51) Kightlinger RS, Irvin WP, **Archer KJ**, Huang NW, Wilson RA, Doran JR, Quigley NB, Pinkerton JV. Prevalence of cervical cancer and human papillomavirus in indigenous Guyanese women. *American Journal of Obstetrics and Gynecology*, Jun;202(6):626.e1-7, 2010.

(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 mechansims 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 Hapatol.* 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 incurrent and former smokers. *Biomarkers*, 15(8):715-30, 2010.

(59) Mas VR, **Archer KJ**, Suh L, Scian M, Posner MP, Maluf DG. Distinctive Gene Expression Profiles Characterize Donor Biopsies From HCV-Positive Kidney Donors. *Transplantation*, 90(11):1172-9, 2010.

(60) Scian MJ, Maluf DG, **Archer KJ**, Suh JL, Massey D, Fassnacht RC, Whitehill B, Sharma A, King A, Gehr T, Cotterell A, Posner MM, Mas V. Gene expression changes are associated with loss of kidney graft function and interstitial fibrosis and tubular atrophy: diagnosis versus prediction. *Transplantation* Mar 27;91(6):657-65, 2011.

(61) Mas VR, Mueller TF, **Archer KJ**, Maluf DG. Identifying biomarkers as diagnostic tools in kidney transplantation. *Expert Rev Mol Diagn.* Mar;11(2):183-96, 2011.

(62) Redmond LC, Dumur CI, **Archer KJ**, Grayson DR, Haar JL, Lloyd JA. Kruppel-like factor 2 regulated gene expression in mouse embryonic yolk sac erythroid cells. *Blood Cells, Molecules, and Diseases*, 47(1):1-11, 2011.

(63) Mas V, Maluf D, **Archer KJ**, Potter A, Suh J, Gehrau R, Descaizi V, Villamil. Transcriptome at the time of Hepatitic C Virus recurrence may predict the severity of fibrosis progression after liver transplantation. *Liver Transplantation*, 17(7):824-35, 2011.

(64) Gehrau R, Maluf D, **Archer K**, Stravitz R, Suh J, Le N, Mas V. Molecular pathways differentiate HCV recurrence from acute cellular rejection in HCV liver recipients. *Molecular Medicine*, 17(7-8):824-33, 2011.

(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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