

David de la Cerda

Curriculum Vitae

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Education

- 2022 **Wake Forest School of Medicine**, *MS, Biomedical Sciences in Molecular Genetics and Genomics, Winston-Salem, NC*
- 2016 **Washington University in St. Louis**, *MPH, Epidemiology and Biostatistics, St. Louis, MO*
- 2013 **University of North Texas**, *BS, Biology, Minor in Chemistry, Denton, TX*

Employment

2016–Present Wake Forest School of Medicine, Winston-Salem, NC

Graduate Research Assistant

Advisor: James Pease, Ph.D.

Current Project: Multivariate statistical profiling of *S. pombe*

- Developed bioinformatic pipeline using next-gen sequencing tools, Bash scripts, and R to detect fine-scale variation in gene expression
- Designed statistical method that leverages multivariate modeling using RNA-Seq data to better understand regulatory stress response
- Awarded semester of Research Fellowship funding to design and implement statistical analyses

Project: Evolution of Gene Expression in Neotropical Bird Species

- Collaborated with Brown University and East Carolina University to examine the evolutionary significance of gene expression of seven neotropical bird species
- Aided in the statistical and software development of the analysis toolset using Python and R now published under the name PhyDGET

Project: Uncovering the genomic regulatory role of Lsd2 in *S. pombe*

- Worked with collaborators to uncover the functional role of the essential gene: *lsd2*, which is involved with gene silencing
- Designed and performed statistical analyses and data visualization involving differential gene expression using next-gen sequencing tools, Bash scripts, R, and has code hosted on my Git repository

- 2017–Present Wake Forest University, Winston-Salem, NC
Teaching Assistant
Courses taught: Intro Bio I, Intro Bio II, Genetics
- Facilitate lab oversight in the classroom to facilitate weekly in-class activities
 - Assist in reagent prep and implementation
 - Meet with lab supervisor and instructor of record regarding student learning and lab activities
- 2015–2016 Washington University in St. Louis, St. Louis, MO
Graduate Research Assistant
Advisor: Cassandra Arroyo, Ph.D.
Project: Play Across St. Louis
- Disseminated and analyzed community playground safety information to neighborhood meetings in St. Louis City
 - Aggregated, maintained, and compared playground survey data using SAS software
- Project: Fatal Encounters with Police
- Attained seed funding with Harvard and St. Louis University to collect nationally crowdsourced data regarding fatal encounters of private citizens with police officers
 - Designed and implemented statistical models using SAS to understand current trends pertaining to deaths of individuals involving law enforcement
- 2015 Pathologists Biomedical, Lewisville, TX
Community Lab Assistant
Supervisor: Anthony Born
- Provided client and product services to clinicians about medical supply and specimen deliveries to Dallas/Ft. Worth metro hospitals
 - Filed and organized pathology samples processed by pathologists and lab technicians
- 2012–2014 Howard Hughes Medical Institute, Denton, TX
Undergraduate Research Assistant
Advisor: Jeff Johnson, Ph.D.
Project: Use of Genetic Markers in the Management of the Critically Endangered Attwater's Prairie-chicken to Reduce Inbreeding Depression
- Completed genotyping and sequencing experiments on hundreds of blood, eggshell, and feather samples using ABI 3100 sequencing machine
 - Optimized PCR temperatures for microsatellite molecular markers
 - Performed genotype calling of microsatellite markers

- 2012 Excellence in Cardiovascular Science, Winston-Salem, NC
Summer Undergraduate Research Assistant
 Advisor: Nicholette Allred, Ph.D.
 Project: Evaluation of Positional Candidate Loci from Admixture Mapping of Coronary Artery Calcified Plaque: The African American Diabetes Heart Study
- Designed SNP primers and genotyped human blood samples using multiplexed candidate markers from previous research using Sequenom protocols
 - Performed SNP identification of genetic loci of interest
 - Analyzed genetic frequencies of samples using admixture mapping analyses in PLINK

Computing Software

Statistics JMP, SAS, SPSS, STATA, R

NGS Tools **Quality Control**
 fastQC, RSeQC
Read Mapping
 bwa, STAR
Sequencing
 bcftools, bedtools, deepTools, IGV, Salmon,
 SAMTOOLS, SRA-toolkit, Trimmomatic
Quantification
 featureCounts, GATK
Analysis
 adonis, DESeq2, edgeR, MACS2, PLINK

Office MS WORD, MS EXCEL, MS POWERPOINT

Languages UNIX, PYTHON, L^AT_EX

Misc. ARCGIS, BIOCONDA, BIOCONDUCTOR

Certifications

Aug 2016 **Biomedical Investigators - Human Research**, COLLABORATIVE
 INSTITUTIONAL TRAINING INITIATIVE PROGRAM, (Renewed Nov 2022)

Nov 2022 **Biomedical Responsible Conduct of Research**, COLLABORATIVE
 INSTITUTIONAL TRAINING INITIATIVE PROGRAM

Invited Talks

2020 Multivariate quantification of 3' UTRs expands differential expression analyses in fission yeast (*Schizosaccharomyces pombe*). **East Carolina University**.

Awards and Scholarships

2016-Current **Wake Forest School of Medicine**

- Fall 2019 **Center for Molecular Signaling**
Graduate Fellow (\$14,750)
- Summer 2019 **University of Washington**
Summer Institute in Statistical Genetics Scholarship (\$1,725)
Modules: Bayesian Statistics for Genetics, Statistical Genetics, Advanced Quantitative Genetics
- Spring 2016 **University of Alabama**
Short Course on Statistical Genetics Travel Grant
- Spring 2015 **Institute for Public Health - Washington University in St. Louis**
Public Health Cubed Seed Funding (\$15,000)
- Spring 2016 **Washington University in St. Louis**
Dr. Clara Louise Myers Outstanding Practicum Student Award
- 2014-2016 George Warren Brown School of Social Work Scholarship

Memberships and Affiliations

- 2021-Present Scientist Mentoring & Diversity Program Scholar
- 2021-Present Society of Systematic Biologists
- 2019-Present Wake Forest School of Medicine Honor Council
- 2019-Present RNA Society
- 2019-Present Genetics Society of America
- 2018-Present The Society for Advancement of Chicanos/Hispanics and Native Americans in Science

Attendance of Scientific Meetings

- 2022 BIO International Convention - San Diego, CA
- 2021 Evolution - Virtual Meeting
- 2019 RNA Society Symposium - Durham, NC
SACNAS - Honolulu, HI

Publications

- 2022 Differential 3' extension profiles enhance gene expression analysis in fission yeast (*Schizosaccharomyces pombe*). **D.A. de la Cerda**, J.B. Pease. *In preparation*.
Layered evolution of gene expression in "superfast" muscles for courtship. J.B. Pease, R.J. Driver, **D. A. de la Cerda**, E. R. Schuppe, W.R. Lindsay, L.B. Day, C.N. Balakrishnan, M.J. Fuxjager. Proceedings of the National Academy of Sciences of the United States of America.

- 2020 The Catalytic-Dependent and -Independent Roles of Lsd1 and Lsd2 Lysine Demethylases in Heterochromatin Formation in *Schizosaccharomyces pombe*. B.F. Marayati, J. F. Tucker, **D. A. de la Cerda**, T. Hou, R. Chen, T. Sugiyama, J.B. Pease, K. Zhang. *Cells*.
- 2016 A pedigree gone bad: increased offspring survival after using DNA-based relatedness to minimize inbreeding in a captive population. S.C. Hammerly, **D. A. de la Cerda**, H. Bailey, and J.A. Johnson. *Animal Conservation*.