

# 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.  
Project: Multivariate quantification of 3' UTRs expands differential expression analyses in fission yeast (*Schizosaccharomyces pombe*)  
*My current research detects downstream regions of genes that are extended under environmental stress conditions.*
- 2017–Present Wake Forest University, Winston-Salem, NC  
**Teaching Assistant**  
Courses taught: Intro Bio I, Intro Bio II, Genetics
- 2014–2016 Washington University in St. Louis, St. Louis, MO  
**Graduate Research Assistant**  
Advisor: Cassandra Arroyo, Ph.D.  
Projects: Play Across St. Louis:  
*This project was in conjunction with the City of St. Louis to assess the safety of the playgrounds in several neighborhoods across the city using quantitative methods outlined from national safety standards.*  
Fatal Encounters with Police  
*This project required the data collection and analysis of fatalities involving police officers across the United States.*
- 2014–2016 Washington University in St. Louis, St. Louis, MO  
**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.

- 2012–2013 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  
*This research examined the genomic regions of an endangered avian species from several captive breeding programs and allowed our Lab to make breeding recommendations based upon their genetic relatedness.*
- 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  
*This summer research project examined the genetic variants associated with cardiovascular disease in a population of African Americans with Type 2 diabetes.*

## 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

## 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

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## 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<sup>A</sup>T<sub>E</sub>X

Misc. ARCGIS, BIOCONDA, BIOCONDUCTOR

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## 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.