

# 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
- 2014–2016 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

## 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.