David de la Cerda
Curriculum Vitae

📱 *(817) 800-6183*
✉ *daviddlc09@gmail.com*
in *david-dlc-mph*
⚙ *ddelacer*

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

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, LaTeX

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.