David de la Cerda
Curriculum Vitae

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

Education

2023 **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

Jan 2024– Current Texas Children's Hospital, Houston, TX
Bioinformatic Analyst II

➤ Provide bioinformatic support for Principal Investigators regarding study design and analysis of bulk RNA-Seq projects in CAR T or CAR NKT cells. This involves developing analytic pipelines with next-gen sequencing tools with custom shell and R scripts for QC, alignment, quantification, differential expression, and enrichment analyses.

➤ Analyze 10X Genomics scRNA-Seq data of clinical pediatric oncology samples in product or peripheral blood samples using CELLRANGER and downstream analyses of gene expression and VDJ-T libraries with SEURAT.

➤ Develop bioinformatic pipeline regarding custom-built transcription factor library using 2,796 ORFs with variable numbers of barcodes in CAR T cells. NGS tools like Cutadapt were used to clip barcodes and customized R scripts were used for quantification and differential expression analyses using DESeq2 and MAGECK used for CRISPR/Cas9 screening.

Aug 2016– Jan 2023	**Wake Forest School of Medicine**, Winston-Salem, NC **Bioinformatic Analyst** 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 across 42 RNA-Seq libraries.

➤ Aided in the Bayesian statistical model development and custom software development of the analysis toolset using Python and R now published under the name PhyDGET to discover 178 genes involved with rapid wing movement using high-performance cluster computers

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

➤ Worked with collaborators to uncover the functional role of essential gene: *lsd2*, which is involved with silencing in 68 high-confidence genes involved with HMG-box domain proteins responsible for repressing centromeric and telomeric regions of chromosomes

➤ Designed and performed statistical analyses and data visualization involving RNA-Seq, WGS, and ChIP-Seq analyses using next-gen sequencing tools, and custom-built R scripts

May 2015– Jun 2016	**Washington University in St. Louis**, St. Louis, MO **Statistical Research Assistant** Project: Play Across St. Louis Project: Fatal Encounters with Police

➤ Attained seed funding with Harvard and St. Louis University to collect, aggregate, and maintain, 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

Jan 2014– Jun 2014	**Pathologists Biomedical**, Lewisville, TX **Community Lab Assistant**

➤ Assisted with ordering supplies and equipment, calibrating instruments and preventive maintenance for 3 major hospitals and 5 clinics

➤ Managed specimen sample handling, receiving, storage and inventory.

➤ Maintained lab by calibrating equipment and cleaning surfaces and items used

Aug 2012– Dec 2014	Howard Hughes Medical Institute, Denton, TX **Undergraduate Research Assistant** Project: Use of Genetic Markers in the Management of the Critically Endangered Attwater's Prairie-chicken to Reduce Inbreeding Depression

➤ Performed sequencing experiments on 135 of blood, eggshell, and feather samples

➤ Optimized PCR temperatures for microsatellite molecular markers

➤ Recorded microsatellite genotyping data and maintained source documentation following good documentation practices

May 2012– Jul 2012	Excellence in Cardiovascular Science, Winston-Salem, NC **Summer Undergraduate Research Assistant** Project: Evaluation of Positional Candidate Loci from Admixture Mapping of Coronary Artery Calcified Plaque: The African American Diabetes Heart Study

➤ Conducted research pertaining to cardiovascular disease to generate 369 genotype markers for GWAS analysis for 985 individuals

➤ Generated statistical models and performed analysis to produce reports outlining results

➤ Collaborated with others in team-based environment to identify key findings from GWAS analysis using PLINK

Computing Software

Statistics	JMP, SAS, SPSS, STATA, R
NGS Tools	**Quality Control** fastQC, RSeQC **Read Mapping** bwa, STAR, RSEM, CellRanger **Sequencing** bcftools, bedtools, deepTools, IGV, Salmon, samtools, SRA-toolkit, Trimmomatic, Cutadapt **Quantification** featureCounts, GATK **Analysis** adonis, DESeq2, edgeR, MACS2, PLINK, Seurat
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 Jan 2024)
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

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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

2024   Human scFv based, ALPPL2-specific CAR expressing T cells induce potent antitumor activity in an IL15-dependent manner. D. Cunningham, J. Liu **D. A. de la Cerda**, N. Gatwai, A. Courtney, L. Guo, P. Rathi, Y. Q. Cathy, N. Zhang, Z. An, A. Heczey. Nature Communications. *In submission.*

Hyperleukocytosis in a neuroblastoma patient after treatment with natural killer T cells expressing a GD2-specific chimeric antigen receptor and IL15. G. Tian, A. Courtney, H. Yu, X. Xu, G. Barragan, C. Martinez Amador, N. Ghatwai, D. Schady, A. Montalbano, **D. A. de la Cerda**, D. Williams Parsons, E. J. Di Pierro, A. Heczey, L. S. Metelitsa. Journal for the Immunotherapy of Cancer.

The Cross-Regulation Between Histone H3 lysine 4 and 9 Methyltransferases and Demethylases in *Schizosaccharomyces pombe*. H. Liu, B. F. Marayati, **D. A. de la Cerda**, B. M. Lemezis, J. Gao, Q. Song, M. Chen, and K. Zhang Reid. PLOS Genetics .

2022   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.

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