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|  | David **De La Cerda**  Data Scientist | Aspiring Researcher   |  |  | | --- | --- | | **Address** Winston-Salem, NC, 27101  **Phone** (817) 800-6183  **E-mail** daviddlc09@gmail.com | LinkedIn https://www.linkedin.com/in/david-dlc-mph/  WWW https://ddelacer.github.io/ | |  |

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| Experienced researcher with over 5 years of experience in pre-clinical research. Excellent reputation for resolving problems and working collaboratively.     |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |  | **Education**   |  |  |  | | --- | --- | --- | |  | **Aug 2016 – Jan 2023** | Master of Science: Biomedical Sciences in Molecular Genomics  *Wake Forest School of Medicine - Winston-Salem, NC* |  |  |  |  | | --- | --- | --- | |  | **May 2014 - May 2016** | MPH: Epidemiology and Biostatistics  *Washington University - St. Louis, Louis, MO*   * Recipient of Dr. Clara Louise Myers Outstanding Practicum Student Award |  |  |  |  | | --- | --- | --- | |  | **Aug 2009 - Aug 2013** | BS: Biology  *University of North Texas - Denton, TX* | |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |  | **Skills**   |  |  | | --- | --- | |  | Statistical analysis |  |  |  | | --- | --- | |  | Data storyteller |  |  |  | | --- | --- | |  | In-depth genetics knowledge |  |  |  | | --- | --- | |  | Biomedical science background | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |  | **Software and Computing Languages**   |  |  | | --- | --- | |  | SAS |  |  |  | | --- | --- | |  | Stata |  |  |  | | --- | --- | |  | SPSS |  |  |  | | --- | --- | |  | R |  |  |  | | --- | --- | |  | Unix |  |  |  | | --- | --- | |  | Python |  |  |  | | --- | --- | |  | Shell scripting | |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | |  | **Work History**   |  |  |  | | --- | --- | --- | |  | **Aug 2017 - Current** | **Teaching Assistant**  *Wake Forest University, Winston-Salem, NC*  Courses taught: Intro Bio I, Intro Bio II, Genetics   * Participated in lesson planning and curriculum implementation to promote quicker rollout and delivery. * Implemented practice exercises and group assignments to assist students in information retention for nearly 30 students per semester. * Assessed student assignments to check quality and completeness before submission for grading |  |  |  |  | | --- | --- | --- | |  | **Jun 2016 - Current** | **Graduate Research Assistant**  *Wake Forest School of Medicine, Winston-Salem, NC*  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 evolutionary significance of gene expression of seven neotropical bird species. * Aided in statistical and software development of analysis toolset using Python and R now published under name PhyDGET.   Project: Uncovering the genomic regulatory role of Lsd2 in *S. pombe*   * Worked with collaborators to uncover functional role of 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. |  |  |  |  | | --- | --- | --- | |  | **May 2015 - Jun 2016** | **Graduate Research Assistant**  *Washington University School Of Medicine, St. Louis, MO*  Project: Play Across St. Louis   * Disseminated and analyzed community playground safety information to community meetings in St. Louis City for around 79 neighborhoods. * 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. |  |  |  |  | | --- | --- | --- | |  | **Jan 2014 - Jun 2014** | **Community Lab Assistant**  *Pathologists Biomedical, Lewisville, TX*   * 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 2013** | **Undergraduate Research Assistant Advisor**  *Howard Hughes Medical Institute, Denton, TX*  Project: Use of Genetic Markers in the Management of the Critically Endangered Attwater's Prairie-chicken   * 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** | **Undergraduate Research Assistant**  *Wake Forest Baptist Health, Winston-Salem, NC*  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. | |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | **Accomplishments**   |  |  | | --- | --- | |  | * Center for Molecular Signaling Graduate Fellow ($14,750) * University of Washington Summer Institute in Statistical Genetics Scholarship ($1,725) * University of Alabama Short Course on Statistical Gnetics Scholarship ($1,800) * Institute for Public Health at Washington University in St. Louis Public Health Cubed Seed Funding recipient ($15,000) | |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | **Affiliations**   |  |  | | --- | --- | |  | * Scientist Mentoring & Diversity Program Scholar * Society of Systematic Biologists * RNA Society * Genetics Society of America * The Society for Advancement of Chicanos/Hispanics and Native Americans in Science | |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | |  | **Certifications**   |  |  |  | | --- | --- | --- | |  | **Aug 2016** | Biomedical Responsible Conduct of Research (CITI) |  |  |  |  | | --- | --- | --- | |  | **Nov 2022** | Institutional Training Initiative Program (CITI) | |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | |  | **Publications**   |  |  | | --- | --- | |  | * Differential 3′ extension profiles enhance gene expression analysis in fission yeast (*Schizosaccharomyces pombe*). 2022. **D.A. de la Cerda**, J.B. Pease. In preparation. * Layered evolution of gene expression in ”superfast” muscles for courtship. 2022. 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. * The Catalytic-Dependent and -Independent Roles of Lsd1 and Lsd2 Lysine Demethylases in Heterochromatin Formation in *Schizosaccharomyces pombe*. 2020. B.F. Marayati, J. F. Tucker, **D. A. de la Cerda**, T. Hou, R. Chen, T. Sugiyama, J.B. Pease, K. Zhang. Cells. * A pedigree gone bad: increased offspring survival after using DNA-based relatedness to minimize inbreeding in a captive population. 2016. S.C. Hammerly, **D. A. de la Cerda**, H. Bailey, and J.A. Johnson. Animal Conservation. | |  | |