# César A. Lizárraga

e-mail: [calizarr@gmail.com](mailto:calizarr@gmail.com)  
github: <http://github.com/calizarr>  
LinkedIn: [http://linkedin.com/in/calizarr](http://www.linkedin.com/in/calizarr)

### Work Experience

* **December 2014 - Present:** [**Donald Danforth Plant Science Center**](https://www.danforthcenter.org/) **(St. Louis, MO)**
  + *Laboratory Technician (Bioinformatics/Statistics) in Mockler Lab*
  + Develop and document pipelines for analyzing high throughput sequencing and imaging data
  + Analytics and Data Management for the [Brachypodium ENCODE Project](http://genomicscience.energy.gov/research/DOEUSDA/abstracts/2014mockler_abstract.shtml)
  + Analytics and Data Management for the [EPSCoR Project](https://missouriepscor.org/)
  + Assist with data analysis whenever requested
* **July 2014 - Present:** [**Nanaya**](http://www.nanaya.co) **(St. Louis, MO)**
  + *Statistician/Back-end developer*
  + Develop, design, and test algorithm(s) from prototype
  + Verify that proper statistical procedures are being used within prototype algorithm(s)
  + Facilitate communication between developers and R&D Team members
  + Manage and update server depending on needs of team
* **December 2014 - September 2015:** [**Benson Hill Biosystems**](http://www.bensonhillbio.com/) **(St. Louis, MO)**
  + *Independent Contractor (Bioinformatics/Statistics)*
  + Developed high throughput imaging analysis pipeline for a custom in-house imaging system
  + Developed an RNA-seq pipeline to discover novel transcripts
  + Provided statistical consultation when necessary

### Education

**B.A. Mathematics, 2008**  
*Probability and Statistics*  
Department of Mathematics, Washington University in St. Louis

### Project Experience

* **General Lab Projects**
  + Develop, maintain, and test an RNA-seq pipeline for NGS data from Illumina sequencing platform
  + Develop, maintain, and test a SNP calling pipeline for NGS paired-end read data from Illumina sequencing platform
    - [Developed in Python and Bash wrapper script: PyPipe](https://github.com/calizarr/PyPipeline/)
  + Develop, maintain, and test a ChIP-seq pipeline for NGS data from Illumina sequencing platform
    - [Developed in Python: PyChIP](https://github.com/calizarr/PyChIP-seq)
  + Developed high throughput phenotyping pipeline using PlantCV and R for imaging analysis for internal use with LemnaTec HTP facility
* **Brachypodium ENCODE Project**
  + Mapped forward previous structural *Brachypodium distachyon* annotations to new genome assembly using MAKER
  + Mapped functional domains with InterProScan to the annotations and converted locations to genomic coordinates
  + Structural and functional annotations were placed as tracks in a genome browser
* **PheNode: Field canopy sensor system**
  + Develop code for Arduino to interface with sensors
  + Develop code to control Arduino from Raspberry Pi, read, and save results
  + Assess power requirements and setup batteries, relays, etc.
* **Benson Hill Biosystems**
  + Developed high throughput phenotyping pipeline using HTPheno, R, and Python for a custom in-house imaging system
  + Developed an RNA-seq pipeline to discover novel transcripts using structural annotations, a new genome assembly, and set intersections.

### Bioinformatics Skills

* NGS data analysis: *RNA-seq, ATAC-seq, ChIP-seq, variant calling*
* Biostatistics: *Regression, multiple test correction, modelling, heritability (broad-sense)*
* Clustering analysis data: *UPGMA, K-means, Agglomerative, hierarchical clustering*
* Databases and repositories: *Ensembl, Phytozome, NCBI Gene Expression Omnibus*

### Computer Skills

* Languages: *Python, R, Bash, Perl, Java, MATLAB*
* Operating systems and GNU/Linux: *AWK, sed, grep, Emacs, UNIX*

### Languages

* Spanish: *Fluent*
* Italian: *Intermediate*

### Publications

* Laura Rayhel, B.A., Copper Aitken-Palmer, D.V.M., Ph.D., Priscilla Joyner, B.Sc., B.V.M.S., Carolyn Cray, Ph.D., **César Andrés Lizárraga, B.A.**,  
  Betty Ackerman, M.T. (A.S.C.P.), and Chris Crowe, B.S. Hematology and biochemistry in captive white-naped cranes (*Grus VIPIO*). *Journal of Zoo and*  
  *Wildlife Medicine 46(4):747-754. http://dx.doi.org/10.1638/2015-0027.1 (2015)*

### Professional Presentations

* Skyler Mitchell, Stuart Marshall, Stephanie Turnipseed, Luke Burnham, **César Lizárraga**, Jared Streich, Rob Alba, and Todd C. Mockler (2015)  
  "Effect of drought treatments on transpiration rate and stomatal density in *Brachypodium distachyon*." Donald Danforth Plant Science Center  
  and Missouri Botanical Gardens Joint Fall Symposium, St. Louis, MO, October 2015
* **César A. Lizárraga**, Henry D. Priest, Noah Fahlgren, Rob Alba, and Todd C. Mockler. Bioinformatics Pipelines for Purple False Brome  
  (Brachypodium distachyon) Donald Danforth Plant Science Center, St. Louis, MO. (2015)
* **Cesar Lizarraga**, Stuart Marshall, Bradley Flynn, Nadia Shakoor1 and Todd C. Mockler. PhenoPiSight: Fixed Camera Greenhouse-based Phenotyping Platform. (2016)