# Simon Lizarazo Chaparro

📞 217-819-8427  ✉ [simonl3@illinois.edu](mailto:simonl3@illinois.edu)  in slizarazo ⊙ slizarazo21.github.io

I am a highly motivated and detail-oriented PhD candidate with a strong background in genomics, data analysis, bioinformatics, and molecular biology. I am enthusiastic about leveraging my expertise to contribute to cutting-edge genomics projects. My goal is to integrate genomics and statistics dynamically via research that has far-reaching implications in both fields. Additionally, I am a quick learner, readily adapting to new challenges and technologies to enhance my research and contributions.

## SKILLS

- **Programming:** R, Unix-Linux, Bash, GitHub, Python
- **Research Methods:** Primary Cell (Neuronal) and Cell Line Culture, Confocal Microscopy, Western Blot, Multielectrode Array, PCR.
- **Data Analysis:** Next-generation sequencing (ATAC-Seq, CLIP-Seq, RNA-Seq, scRNA-Seq), Multielectrode Array Data, Advanced Data Analysis and Visualization, Machine-Learning.

## EDUCATION

| | |
|---|---|
| **PhD Molecular and Integrative Physiology** | **Expected May 2025** |
| *Molecular and Integrative Physiology, University of Illinois Urbana-Champaign* | **GPA 4.0/4.0** |
| **MS. Applied Statistics** | **Expected Dec 2024** |
| *Applied Statistics, University of Illinois Urbana-Champaign* | **GPA 3.96/4.0** |
| **BS. Pharmacy** | **2018** |
| *Pharmacy, Universidad Nacional de Colombia* | **GPA 4.4/5.0** |

## SELECTED WORK AND RESEARCH EXPERIENCE

**PhD Candidate in Bioinformatics**                                          **Sept 2022 – To Date**
*Van Bortle Lab, University of Illinois Urbana-Champaign, IL*

- Development of a genomic atlas for RNA-Polymerase III non-coding RNAs through the analysis of high throughput sequencing complex data such as ATAC-Seq, Chip-Seq, and WGSB-Seq. Data mining from TCGA, ENCODE, GEO, SRA, CHIP-Atlas and other public data
- Creation and leadership in the development of an R Package. *(github.com/VanBortleLab/ dominatR/)*
- Creation of a repository for Lamin Associated Domains Frequency Analysis. *(github.com/VanBortleLab/LADFreq)*
- Establishment and optimization of analysis pipelines for next-generation sequencing data.
- Development of codes capable of simultaneously analyzing hundreds of genomic datasets.
- Investigation and analysis of interaction profiles between proteins and RNAs using eCLIP data.
- Review of manuscripts submitted to peer-reviewed journals.
- Collaboration with interdisciplinary research teams and cross-functional groups.

**Selected Skills:** Next Generation Sequencing data analysis (ATAC-Seq, Chip-Seq, eCLIP-Seq, WGSB-Seq), Statistical Analysis, Data Visualization, Programming, Coding

**Computational Scientist Intern in Immunology – Rheumatoid Arthritis.**          **May 2024 – Aug 2024**
*Johnson & Johnson Research & Development, Spring House, PA*

- Development of an association framework between peripheral and tissue transcriptome data for Rheumatoid Arthritis.

- Identification of effective biomarkers useful for predicting treatment response and patient stratification across different ongoing clinical trials.

**Selected Skills:** Single-cell and bulk RNA sequencing analysis, Machine learning.

**PhD Candidate in Neurobiology**                                    **Sept 2019 – Sept 2022**
*Tsai Lab, University of Illinois Urbana-Champaign, IL*
- Exploration of the role of the Fragile X Mental Retardation protein in mRNA translation regulation within an Alzheimer's Disease model.
- Employment of mouse models and primary neuronal cultures for delving into molecular mechanisms associated with mRNA translation in Alzheimer's Disease.
- Guidance and mentorship to undergraduates and multiple rotation students in experimental research.

**Selected Skill**: Primary neuronal culture, PCR, Western Blot, Multielectrode Array, Behavioral experiments.

## COURSES (SELECTED)

- **University of Illinois at Urbana Champaign**

Statistics and Probability II, Statistical Learning I & II, Unsupervised Learning, Bioinformatics, Infectious Disease Modeling, Statistical Modeling, Applied Statistical Methods, Neuroimmunology.
- Selected Projects
  - *Investigating the function of the mouse hypothalamic preoptic region using scRNA-seq and MERFISH data produced by Moffit et all (2018)*
  - *Impacts of environmental conditions on airborne disease progression*
  - *A recommender movie shiny app: https://sleezch.shinyapps.io/movie_recommender/*

## SELECTED AWARDS AND HONORS

- David and Julie Mead Graduate Fellowship – School of Molecular Biology. UIUC       **2022**
- Travel fellowship. Alzheimer's Association International Conference                 **2022**
- Department travel fellowship – Department of Molecular and Integrative Physiology. UIUC   **2021**
- Merit Scholarship Admission – Department of Molecular and Integrative Physiology. UIUC   **2019**

## SELECTED PUBLICATIONS

**Peer Reviewed:**
- Zhou S, **Lizarazo S,** Mouli L, Chorghade S, Cheng R, KC R, Kalsotra A, Van Bortle K (2024). Cancer-associated snaR-A noncoding RNA interacts with core splicing machinery and disrupts processing of mRNA subpopulations. (Preprint) bioRxiv.
- KC R, Cheng R, Zhou S, **Lizarazo S**, Smith D, Van Bortle K (2024). Evidence of RNA Polymerase III recruitment and transcription at protein coding gene promoters. (Preprint) bioRxiv.
- Yook Y, Lee KY, Kim E, **Lizarazo S,** Yu X, Tsai NP (2024). Hyperfunction of post-synaptic density protein 95 promotes seizure response in early amyloid beta pathology. *EMBO reports, 25 (3), 1233 – 1255.*
- Cheng R, Zhou S, KC R, **Lizarazo S**, Mouli L, Jayanth A, Liu Q, VanBortle K (2023). A combinatorial regulatory platform determines expression of RNA polymerase III subunit RPC7$\alpha$ (POLR3G) in cancer. *Cancers, 15, 4995*
- **Lizarazo S**, Yook, Y, & Tsai, NP (2022). Amyloid beta inducesFmr1-dependent translational suppression and hyposynchrony of neural activity via phosphorylation of eIF2α and eEF2. *Journal of Cellular Physiology*,1–14.
- Liu DC, Lee KY, **Lizarazo S,** Cook JK and Tsai NP (2021) ER stress-induced modulation of neural activity and seizure susceptibility is impaired in a fragile X syndrome mouse model. Neurobiol Dis 158, 105450

**Abstracts Presented at Conferences:**

- **Lizarazo S,** KC R, Zhou S, Cheng R, Van Bortle K. 'A multi tissue and cancer atlas of Pol III activity uncovers context specific transcriptional expansion to genes implicated in disease progression'. Poster presentation. Biology of Genomes. Cold Spring Harbor, NY, USA
- **Lizarazo S,** Yook Y, Tsai, NP. 'Amyloid Beta induces Fmr1 dependent translational suppression and hyposynchrony of neural activity''. Poster Presentation. Alzheimer's Association International Conference. Chicago, IL, USA.