

Francisco Huizar

Data-driven drug discovery scientist

Contact

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Skills

Transferrable and Professional

- Innovative problem solver
- Collaborate cross-functionally
- Project management
- Information, data management

Excellent

- S.M.A.R.T. goals and objectives
- Leadership and initiative
- Professional self-awareness
- Communicate effectively

Very Good

Technical and Software

- Biostatistics and data analysis
- R for biostatistics
- Python, Pandas, Matplotlib
- MATLAB and SimBiology

Excellent

- Computational biology
- Model simulation and development
- Unix, Linux, Cloud Computing
- PyTorch, Keras, TensorFlow

Very Good

- SAS analytics software
- GitHub, Git, GitLFS
- MySQL, SQL, Tableau
- Mathematica
- Bayesian modeling software
- STAN, RStan, MCMC
- C++, OOP

Experienced

- Bioinformatics, single-cell genomics
- Seurat, ScanPy, STAR for scRNA
- AWS, Azure, GCP
- Pharmacometrics and PKDM
- Model-informed drug development
- PK/PD, pharmacology modeling
- NONMEM, Monolix, Phoenix
- NLME, WinNonLin
- Exposure-response modeling of discrete and time-to-event data
- Quantitative systems pharmacology

Actively Learning!

Mission statement

- I am a collaborative cross-functional scientist with expertise in computational biology, mathematical modeling, science-based decision making, and interdisciplinary communication.
- **The core mission of my professional endeavors is to serve patients** afflicted by genetic-related disease with therapeutic approaches and innovative biotechnology in a clinical setting.
- To achieve **my mission** of service, I aim to utilize **my talents** of communication and execution to perform **my passion** of planning and analyzing by using data-driven approaches for drug discovery.

Summary of qualifications

- Articulate communicator with expertise in data visualization and scientific presentation resulting in 1 [academic journal front cover](#), 14 conference and 5 seminar presentations.
- Self-motivated project manager with excellent written communication, strategic planning, innovation, and problem solving abilities resulting in 3 first-author publications, 1 first-author review, and 5 fellowships totaling in \$96,000 in funding.
- Flexible, adaptive, and versatile learner committed to professional development as evidenced by participation in 3 training workshops specific to computational modeling, pharmacometrics, single-cell genomics, computational biology, and clinical therapeutic development.
- Inspiring leader with experience to foster listening, patience, encouragement, collaborative environments, and collective success as evidenced by engagement in 2 lead mentoring training workshops, mentoring 8 undergraduate and 9 graduate students.
- Dedicated, dependable, and ethical scientist committed to integrity, reproducibility, responsibility, and accountability resulting in 3 unique discoveries in relation to drug discovery research for oncology and neurodegenerative preclinical disease modeling.

Professional experience

Quantitative systems biologist, model simulation and drug discovery

As Graduate Research Assistant (Dec 2019 - Current)

University of Notre Dame, Indiana

- Responsible for collaborative relationship building by leading 4 cross-functional teams spanning simulation techniques, drug discovery, and machine learning for application to computational biology, biostatistics, simulation, and mathematical modeling.
- Developed a Gaussian process surrogate model (PyTorch) for prediction and simulation of therapeutic viability of 1,498 compounds to 172 kinase targets for cancer research.
- Deployed bioinformatics, data processing, and data science methods for analysis of phenomic datasets to identify 4 lead therapeutic candidates using Python and MATLAB.
- Implemented 2 machine learning approaches for de novo therapeutic design as a scientific approach for identification and simulation of new therapeutics using generative models.
- Utilized machine learning, mathematical modeling, and cloud computing for rapid simulation and data classification of 4 unique calcium signatures in developmental biology.
- Operated differential equation modeling tools to discover 2 distinct cell populations in developing epithelial tissue via simulation and analytic techniques.
- Designed and developed a platform for rapid in vivo *Drosophila* drug development assay to evaluate up to 8 novel therapeutics per month.

Computational biologist, data management and data science

As Graduate Research Assistant (Jul 2018 - Dec 2019)

University of Notre Dame, Indiana

- Participated in cross-function teams to collaborate with other scientists that led to development of a cloud computing project to manage datasets consisting of 13,324 images.
- Performed in vivo gene expression of 425 human disease related genes in *Drosophila Melanogaster*
- Spearheaded design and innovation of a more efficient coverslip plating protocol for in vivo calcium signaling imaging that increased throughput by a factor of 2.
- Hands-on experience and innovation in data democratization by generating biotechnology modeling software for utilization of packages by non-technical users as demonstrated by 2 open-source repositories for biological simulation and biostatistics.
- Optimized a genetic screening protocol to identify 4 key regulatory genes of calcium signaling by developing an innovative data collection procedure.

Training and education

Ph.D., Bioengineering *University of Notre Dame*

Jul 2018 – Current

M.S., Computational Statistics *University of Notre Dame*

Jul 2018 – Current

B.S., Chemical and Biomolecular Engineering *University of Notre Dame*

Aug 2013 – May 2018

B.S., Computational Statistics *University of Notre Dame*

Aug 2013 – May 2018