Francisco Huizar

Data-driven drug discovery scientist

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Skills

Innovative problem solver

Excellent

Collaborate cross-functionally

Excellent

Project management

Excellent

Information and data management

Excellent

S.M.A.R.T. goals and objectives

Very Good

Leadership and initiative

Very Good

Professional self-awareness

Very Good

Communicate effectively

Very Good

Biostatistics and data analysis

Excellent

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.
- Helping, guiding, leading, lifting, and loving others fills my heart, gives me motivation, and creates unbounding feelings of significance.
- To achieve **my mission** of service, I aim to utilize **my talents** of communication, execution, and discernment to perform **my passion** of planning, solving, and analyzing by using data-driven approaches to discover novel therapeutics for patients.

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, genomics, computational biology, and clinical therapeutic development.
- Inspiring leader with experience to foster listening, patience, encouragement, collaborative environments, and achieving success together as evidenced by participation in 2 lead mentoring training workshops, mentoring 8 undergraduate and 9 graduate students.
- Risk management expertise with proficiency in analytical reasoning, prioritization, time appropriation, organization, and executive decision making to solve problems resulting in 4 optimized high throughput methodologies.
- 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.
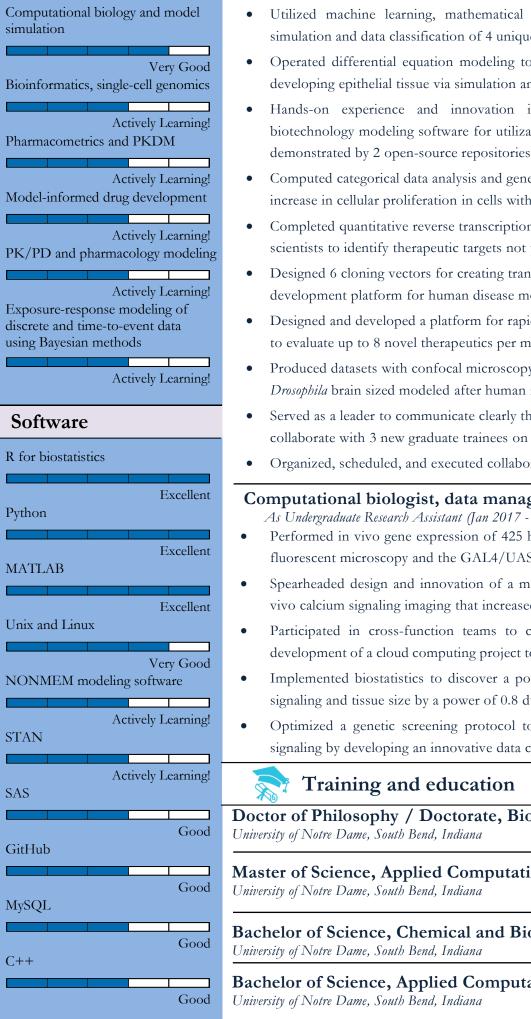
Professional experience

Quantitative systems biologist, model simulation and drug discovery

As Graduate Research Assistant (Jul 2018 - 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 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 phenotypic 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.

Skills

Computational biology and model simulation

Very Good

Bioinformatics, single-cell genomics

Actively Learning!

Pharmacometrics and PKDM

Actively Learning!

Model-informed drug development

Actively Learning!

PK/PD and pharmacology modeling

Actively Learning!

Exposure-response modeling of discrete and time-to-event data using Bayesian methods

Actively Learning!

Software

R for biostatistics

Excellent

Python

Excellent

MATLAB

Excellent

Unix and Linux

Very Good

NONMEM modeling software

Actively Learning!

STAN

Actively Learning!

SAS

Good

GitHub

Good

MySQL

Good

C++

Good

- 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.
- 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.
- Computed categorical data analysis and generalized linear regression to discover a 2 fold increase in cellular proliferation in cells with upregulated Gαq protein.
- Completed quantitative reverse transcription PCR of 21 genes to collaborate with other scientists to identify therapeutic targets not yet recorded in literature.
- Designed 6 cloning vectors for creating transgenic model organisms to optimize a drug development platform for human disease models of cancer.
- Designed and developed a platform for rapid in vivo *Drosophila* drug development assay to evaluate up to 8 novel therapeutics per month.
- Produced datasets with confocal microscopy to discover an 11 percent increase in *Drosophila* brain sized modeled after human neurodegenerative disease.
- Served as a leader to communicate clearly the standard operating procedures and collaborate with 3 new graduate trainees on laboratory operations.
- Organized, scheduled, and executed collaborative weekly group meetings for 7 colleagues.

Computational biologist, data management and data science
As Undergraduate Research Assistant (Jan 2017 - May 2018)   University of Notre Dame, Indiana

- Performed in vivo gene expression of 425 human disease related genes in *Drosophila* with fluorescent microscopy and the GAL4/UAS system.
- 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.
- 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.
- Implemented biostatistics to discover a power-law scaling relationship between calcium signaling and tissue size by a power of 0.8 during using a Box-Cox transformation.
- Optimized a genetic screening protocol to identify 4 key regulatory genes of calcium signaling by developing an innovative data collection procedure.

🎓 Training and education

Doctor of Philosophy / Doctorate, Bioengineering
University of Notre Dame, South Bend, Indiana   *Jul 2018 – Current*

Master of Science, Applied Computational Mathematics and Statistics
University of Notre Dame, South Bend, Indiana   *Jul 2018 – Current*

Bachelor of Science, Chemical and Biomolecular Engineering
University of Notre Dame, South Bend, Indiana   *Aug 2013 – May 2018*

Bachelor of Science, Applied Computational Mathematics and Statistics
University of Notre Dame, South Bend, Indiana   *Aug 2013 – May 2018*