Maulik Nariya, Ph.D.

Postdoctoral Fellow

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Experience

2022–present **Postdoctoral Fellow**
Institut de Génétique et de Biologie Moléculaire et Cellulaire, Strasbourg
Developmental Biology and Stem Cells
Advisor: Nacho Molina

2018–2022 **Postdoctoral Fellow**
Harvard Medical School, Boston
Department of Systems Biology &
Laboratory of Systems Pharmacology
Advisor: Peter Sorger

2009–2012 **Junior Research Fellow**
India-based Neutrino Observatory
Tata Institute of Fundamental Research
Advisor: S. Uma Sankar

Education

2012–2018 **Ph.D. in Physics**
University of Kansas, Lawrence
Dissertation: Mathematical Model of Length Control in the Type III Secretion System
Advisors: Eric Deeds and Jack Shi

2007–2010 **M.S. in Physics**
University of Pune, Pune
Thesis: Review of Neutrino Oscillations
Advisor: S. Uma Sankar

| 2004–2007 | **B.S. in Physics | Minor: Electronics**
St. Xavier's College, Mumbai |

Skills

Computational

Proficient with data mining and machine learning in Python

Experience with Fortran, C++

Proficient with Linux-based research computing (SLURM)

Software development

Deploying software development and version control using GitHub

Experience with containerizing software tools using Docker

Mathematics

Probability theory and advanced statistics

Linear algebra

Research projects

| 2022–present | **Biophysical modeling of binding in Ikaros family transcription factors**
Description |

| 2022–present | **Modeling gene regulation dynamics during the cell cycle in pluripotent stem cells**
We develop a deep learning approach that combines single cell measurements from gene expression (scRNA-seq), chromatin accessibility (ATAC-seq) and genome architecture mapping (GAM) to understand the dynamics of gene regulation during cell cycle in pluripotent stem cells. |

| 2019–2022 | **Improved estimate of machine learning predictor performance in presence of known confounders**
In this project, we highlight useful properties of the leave-pair-out cross-validation approach for bioinformatics data (RNA-seq data for breast cancer cells and Alzheimer's patient data), in particular we propose a method that helps improve the estimate of the predictor performance. |

| 2018–2022 | **Predicting drug response from baseline omics profiles of breast cancer cells**
NIH LINCS funded project at the Laboratory of Systems Pharmacology, Harvard Medical School. In this work we used baseline RNA-seq, proteomics, and phosphoproteomics data on breast cancer cells to build predictive models using a random forest regressor to predict drug response across a variety of cancer drugs. |

2014–2018 **Mathematical modeling for length control in type III secretion system**
Ph.D. dissertation at Department of Physics and Astronomy in collaboration with Center for Computational Biology, University of Kansas. This work involved developing mathematical models and performing stochastic simulations of biochemical reactions involved in the growth of the type III secretion injectisome.

2016–2018 **Comparative characterization and biosimilarity assessment of drug samples using data mining and machine learning techniques**
FDA-funded project at the Macromolecule and Vaccine Stabilization Center and Center for Computational Biology, University of Kansas. The goal of this project was to model the assessment of biosimilar drugs based on the data available from biological, chemical and physical assays.

Publications

1. **Nariya, M.K.**, Sorger, P.K., and Sokolov, A., Paired evaluation defines performance landscapes of machine learning models (manuscript in submission *Nature Machine Intelligence*)
2. Mills, C.E., **Nariya, M.K.**, Subramanian, K., Chen, C., Hafner, M., Sokolov, A., Boswell, S., Everley, R.A., Berberich, M.J., Kalocsay, M., Gaudio, B., Victor, C., Chung, M., Bradshaw, G., and Sorger, P.K., Predicting drivers of drug response from baseline omics data across breast cancer cells and models (manuscript in preparation)
3. Schapiro, D., Sokolov, A., Yapp, C., Muhlich, J.L., Hess, J., Lin, J.R., Chen, Y.A., **Nariya, M.K.**, Baker, G.J., Ruokonen, J., Maliga, Z., Jacobson, C.A., Farhi, S.L., Abbondanza, D., McKinley, E.T., Betts, C., Regev, A., Coffey, R.J., Lisa, M., Coussens, L.M., Santagata, S., and Sorger, P.K., MCMICRO: A scalable, modular image-processing pipeline for multiplexed tissue imaging *Nature Methods*
4. Kalocsay, M., Berberich, M.J., Everley, R.A., **Nariya, M.K.**, Chung, M., Gaudio, B., Victor, C., Bradshaw, G.A., Hafner, M., Sorger, P.K., Mills, C.E., and Subramanian, K., Data Descriptor: Proteomic profiling across breast cancer cells and models (in review with *Scientific Data*)
5. **Nariya, M.K.**, Shi, J.J., Mallela, A., and Deeds, E.J., Robustness and Evolution of Length Control Strategies in the Type III Secretion System and Flagellar Hook *Biophysical Journal*
6. Mallela, A., **Nariya, M.K.**, and Deeds, E.J., Crosstalk and Ultra-sensitivity in Protein Degradation Pathways, *PLoS Comp Biol* 16(12):e1008492.
7. **Nariya, M.K.**, Israeli, J., Shi, J.J., and Deeds, E.J., Mathematical Model for Length Control by the Timing of Substrate Switching in the Type III Secretion System, *PLoS Comp Biol* 12(4): e1004851.
8. **Nariya, M.K.**, Kim, J.H., Xiong, J., Kleindl, P.A., Hewarathna, A.N., Joshi, S.B., Schöneich C., Forrest, M.L., Middaugh, C.R., Volkin, D.B., and Deeds, E.J., Comparative

Characterization of Crofelemer Samples Using Data Mining and Machine Learning Approaches with Analytical Stability Data Sets, *J Pharm Sci*, 106(11): 3270–3279

9. Hewarathna, A., Mozziconacci, O., **Nariya, M.K.**, Kleindl, P.A., Xiong, J., Fisher, A., Joshi, S.B., Middaugh, C.R., Forrest, M.L., Volkin, D.B., and Deeds, E.J., Chemical Stability of the Botanical Drug Substance Crofelemer: A Model System for Comparative Characterization of Complex Mixture Drugs, *J Pharm Sci*, 106(11): 3257–3269

10. Kleindl, P.A., Xiong, J., Hewarathna, A., Mozziconacci, O., **Nariya, M.K.**, Fisher, A., Deeds, E.J., Joshi, S.B., Middaugh, R.C., Volkin, D.B., and Forrest, M.L., The Botanical Drug Substance as a Model System for Comparative Characterization of Complex Mixture Drug, *J Pharm Sci*, 106(11): 3242–325

Conference presentations

2018   Predicting drug response from baseline omics profile of breast cancer cells. Poster presentation at HiTS Annual Symposium, Boston, MA

2017   Mathematical Modeling of Ruler Mechanism for Length Control in Type III Secretion System. Poster presentation at 11th Annual q-bio Conference, Rutgers University, New Brunswick, NJ

2016   Mathematical Modeling for Type III Secretion System. Poster presentation at 10th Annual q-bio Conference, Vanderbilt University, Nashville, TN

Teaching Experience

Statistical Physics — University of Kansas
Led discussions, graded homework assignments, and designed exams for undergraduate level course on statistical physics

General Physics Laboratory — University of Kansas
Taught several general physics laboratory courses (including one honors course)

Awards

2018   NIH LINCS Fellowship — Harvard Medical School

2017   Graduate Scholarly Presentation Travel Fund — University of Kansas

2014   E. E. Slossen Award for Outstanding Graduate Teaching Assistants — University of Kansas