

Rahul Mehta

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Education

- 2013–2020 **Ph.D in Bioengineering**, *University of Illinois at Chicago, Chicago, IL*,
Dissertation: Patterns Among and Between Somatic Mutations and Medical Imaging in Human Cancers.
- 2005–2011 **Bs.C in Electrical Engineering**, *University of Illinois at Urbana Champaign, Urbana-Champaign, IL*.

Skills

- Computing Python, BASH, Git, AWS, Jupyter, Slurm, C++, Latex, PostgreSQL
- Machine Learning API and Methods PyTorch, openCV, Likelihood-free inference, Diffusion models, Sparse Neural Networks, Density Estimation Algorithms, 3D Point Clouds, Self-supervised learning, Recurrent Neural Networks, Transformers (LLM)
- Bioinformatics API SAMtools, PLINK, Hidden-Markov Models, SnakeMake, RFMix
- Analysis Multimodal datasets, latent-space/unsupervised analysis, genetic admixture, genetic risk scores, parallel computing
- Medical Imaging Magnetic Resonance Imaging, Computed Tomography, Positron Emitted Tomography, Fluorescence in situ hybridization, DICOM, PACS

Experience

- 2023– **Genomic Data Science Fellow**, *Ancestry*.
 - Developed a multimodal deep learning pipeline that integrates genomic data from more than 2 million people (800,000 genotyped markers) and 100 million family trees to reveal recent, fine-scale population histories of communities that share genetic ancestry.
- 2020–2023 **Postdoctoral Scholar**, *Department of Human Genetics, University of Chicago*.
 - Developed a novel deep learning generative method for likelihood free inference to analyze evolutionary parameters impacting nearly 150 million alleles that included very rare allele frequencies ($> .0001$) in GWAS from the UK Biobank.
- 2019–2020 **Graduate Research Assistant**, *Center for Magnetic Resonance Research, University of Illinois at Chicago*.
 - Generated Diffusion Weighted Magnetic Resonance images of breast cancer that offers richer information about the heterogeneity of a lesion.
 - Designed a machine learning model for predicting if a breast lesion in the diffusion weighted MRI image was malignant or benign showing superior performance than standard breast imaging techniques.

2014–2020 **Graduate Research Assistant**, *Laboratory of Computational Proteomics*, University of Illinois at Chicago.

- Developed a machine learning model and 3D computer vision algorithm to extract 3D features of medical images enabling accurate prediction of patient response to radiotherapy.
- Designed a state-of-the-art multi-modal deep generative model for the simultaneous analysis of medical images and somatic mutation data allowing the prediction of somatic mutations from medical images.
- Designed an innovative probabilistic model with efficient Bayesian inference to determine co-occurrence or mutual exclusivity of cancerous mutations.

Papers

Journal and Conference Papers

- 2023 Mehta, R., M. Karaman, Y. Bu, Z. Zhong, W. Shiwei, C. Zhou, H. Weihong, X. Maosheng, and Z. J. Xiaohong. "Characterization of breast lesions using multi-parametric diffusion MRI and machine learning." *In Physics in Medicine and Biology* (2023).
- 2020 Mehta, R. and M. Karaman. "Correlated Mixed Membership Modeling of Somatic Mutation Profiles". *In International Joint Conference on Neural Networks*. IEEE. 2020.
- Mehta, R., M. Karaman, and Y. Lu. "Mapping of Lesion Images to Somatic Mutations". *In Data and Text Mining in Biomedical Informatics*. ACM. 2020.
- 2017 Mehta, R., K. Cai, N. Kumar, M. G. Knuttinen, T. M. Anderson, H. Lu, and Y. Lu. "A lesion-based response prediction model using pretherapy PET/CT image features for Y90 radioembolization to hepatic malignancies". *In Technology in cancer research & treatment* 16.5 (2017), pp. 620–629.

Workshop Papers

- 2018 Mehta, R. and H. Lu. "Bayesian Power Law Models for Somatic Mutation Profiles". *In the ISMB workshop on Machine Learning in Computational and Systems Biology*. 2018.
- Mehta, R. and H. Lu. "Normalized Random Measure Mixture Models in Variational Autoencoders". *In the NeurIPS workshop on Advances in Approximate Bayesian Inference*. 2018. URL: <http://approximateinference.org/2018/accepted/MehtaLu2018.pdf>.
- Mehta, R. and H. Lu. "Power Law Models in Somatic Mutation Profiles". *In the IJCAI workshop on Biomedical Informatics with Optimization and Machine Learning*. 2018.

Manuscripts in Progress

- Mehta, R. and J. Berg J. *Deep Generative Modeling of Pleiotropy and Evolutionary Parameters using Genome Wide Association Summary Statistics*.
- Mehta, R., Y. Wang, and K. Noto. *Inference of (very) Recent Admixture*.

Presentations

- 2022 Deep Generative Modeling Pleiotropy and Natural Selection in Complex Traits. Probabilistic Modeling in Genomics, 2022. **Poster**

- 2020 Correlated Mixed Membership Modeling of Somatic Mutations.
International Joint Conference on Neural Networks, 2020. **Contributed Talk**
- 2020 Diffusion-Weighted MRI-Based Quantitative Markers for Characterizing Breast Cancer Lesions Using Machine Learning.
The International Society for Magnetic Resonance in Medicine, 2020. **Poster**
- 2019 Non-parametric Models of Somatic Mutation Profiles.
IEEE Biomedical Health Informatics Special Session on Nonparametric Statistics in Omics Applications, 2019. **Invited Talk**
- 2018 Power Law Models in Somatic Mutation Profiles.
IJCAI workshop on Biomedical Informatics with Optimization and Machine Learning, 2018. **Contributed Talk**
- 2018 Bayesian Power Law Models for Somatic Mutation Profiles.
Intelligent Systems for Molecular Biology, 2018. **Poster**
- 2018 Normalized Random Measure Mixture Models in Variational Autoencoders.
NeurIPS workshop on Advances in Approximate Bayesian Inference, 2018. **Poster**
- 2014 Computer Aided Response Prediction Based on Pre-therapy FDG PET/CT Imaging Biomarkers of Y90-SIRT Therapy in Patients with Primary and Metastatic Liver Cancers.
Radiological Society of North America, 2014. **Contributed Talk**