Aritra Bose

IBM T.J. Watson Research Center
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Research Interests

Statistical Genetics, Quantum Computing, Foundation Models, Spatial Transcriptomics, Multi-omics Integration, Artificial Intelligence, Data Mining, Topological Data Analysis, Randomized Numerical Linear Algebra, Human Genomics, Biomedical Informatics

Education

Purdue University — West Lafayette, IN, USA
Ph.D. in *Computer Science* — Aug 2016 - Aug 2019
Advisor: Prof. Petros Drineas
Thesis: Computational Methods for Population Genetics

Rensselaer Polytechnic Institute — Troy, NY, USA
M.S. in *Computer Science* — Aug 2014 - Jul 2016

West Bengal University of Technology — Kolkata, WB, India
B.Tech in *Information Technology* — Aug 2009 - Jun 2013

Experience

IBM T.J. Watson Research Center — Yorktown Heights, NY, USA
Staff Research Scientist — Feb 2021 - Present

- Leading a team of 10+ scientists in an external collaboration with clinicians from the Cleveland Clinic to develop quantum algorithms for biomedical imaging, multi-omics, and spatial transcriptomics.
- Leading a team of eight scientists across four global IBM Research locations to model cellular environment with quantum computing.
- Led development of a multimodal foundation model for learning genetic associations from brain imaging phenotypes.
- Contributed to the development and validation of a biomedical foundation model for biologics for antibody discovery with free-energy perturbations.
- Filed multiple patents on multi-omics integration, generative models, and patient stratifications using AI, quantum computing, and applied mathematics.
- Led development of various pipelines for genotype-phenotype association studies and defining phenotypes in large-scale biobanks.
- Mentored junior team members and tracked progress for multiple internal and external projects.
- Presented research in various conferences such as ASHG, ISMB, RECOMB, etc.

Postdoctoral Researcher — Sep 2019 - Feb 2021

- Led the development of a causal machine learning framework based on invariant risk minimization to improve generalization of polygenic risk score across diverse populations.

- Developed tools for higher-order interaction in multi-omics data.
- Developed machine learning and statistical genetics methods for large biobanks.

Research Intern May 2018 - Jul 2018
Research Intern May 2017 - Aug 2017
Research Intern May 2016 - Aug 2016

- Developed an ancestral recombination graph simulator for population genetics with selection and epistasis.

IBM India Research Lab Gurgaon, India
Research Scientist Sep 2022 - Sep 2023

- Developed quantum algorithms for systems biology and modeling the interactome.

Broad Institute of MIT and Harvard Cambridge, MA, USA
Visiting Scientist Jun 2021 - Jan 2023

- Led the development of a DNA language model based on long range interactions in the sequence to predict cardiovascular phenotypes such as Atrial Fibrillation and LDL cholesterol.

Purdue University West Lafayette, IN, USA
Research Assistant Aug 2016 - Aug 2019

- Developed machine learning and randomized algorithms for cost-effective computations of PCA and GWAS on large-scale biobanks with genomics and clinical records.
- Led the development of mathematical models to integrate social, linguistics, and environmental factors which contribute to the genetic sub-structure of India.
- Led the study of population genetic structure of the Peloponnese, which settled a historical debate persisting over 200 years.

Rensselaer Polytechnic Institute Troy, NY, USA

- Built population genetic netowrks based on Identity by descent and identified genetic sub-structure using graph partitioning algorithms.

Teaching Assistant Aug 2014 - May 2015

- Teaching Assistant of approximately 200 students in Data Structures for Fall 2014, 2015, and Spring 2015.

Teradata Corporation Hyderabad, India
Analyst Oct 2013 - Apr 2014

- Wrote software patches for Teradata data warehouse and designed SQL queries, ensuring proper functioning of the database.

Bose Institute Kolkata, India
Research Trainee Sep 2012 - Oct 2013

- Worked on developing a temporal statistical algorithm analysing pathways in multi-omics cancer datasets.

Indian Institute of Technology Guwahati, India
Summer Intern May 2012 - Jul 2012

- Worked on transcription factor networks from ChIP-Seq data.

Indian Statistical Institute Kolkata, India
Winter Intern Dec 2011 - Mar 2012

- Worked on a mathematical genomics algorithm using fractals in human olfactory receptors.

Publications

Journals

1. **A. Bose**†, K. Rhrissorrakrai†, F. Utro, L. Parida, Quantum for Healthcare Life Sciences Consortium, *Advancing single-cell omics and cell-based therapeutics with quantum computation*, Accepted, Nature Reviews Molecular Cell Biology, 2025.
2. D. Machado Reyes, M.C. Burch, L. Parida, **A. Bose**, *A Foundation Model for Learning Genetic Associations from Brain Imaging Phenotypes*, Bioinformatics Advances, 2025; `https://doi.org/10.1093/bioadv/vbaf196`
3. D. Gurnari, A. Guzmán-Sáenz, F. Utro, **A. Bose**, S. Basu, L. Parida, *Probing omics data via harmonic persistent homology*, Accepted, Scientific Reports, 2025.
4. H. Doga†, **A.Bose**†, M. Emre Sahin, J. Bettencourt-Silva, A. Pham, E. Kim, A. Andress, S. Saxena, L. Parida, J. L. Robertus, H. Kawaguchi, R. Soliman, D. Blankenberg, *How can quantum computing be applied in clinical trial design and optimization?*, Trends in Pharmacological Sciences, 2024; `https://doi.org/10.1016/j.tips.2024.08.005.`
5. M.C. Burch†, **A. Bose**†, L. Parida, G. Dexter, P. Drineas, *Matrix sketching framework for linear mixed models in association studies*, Genome Research, gr-279230, 2024; `https://doi.org/10.1101/gr.279230.124`
6. D.E. Platt, **A. Bose**, C. Levovitz, K. Rhrissorrakrai, L. Parida, *Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions*, Bioinformatics, Volume 40, Issue Supplement_1, July 2024, Pages i199i207; `https://doi.org/10.1093/bioinformatics/btae235`
7. D.E. Platt, A. Guzmán-Sáenz, **A. Bose**, S. Saha, F. Utro, L. Parida, *AI-enabled evaluation of genome-wide association relevance and polygenic risk score prediction in Alzheimer's disease*, iScience, 2024; `https://doi.org/10.1016/j.isci.2024.109209`
8. **A. Bose**, M.C. Burch, A. Chowdhury, P. Paschou, P. Drineas, *Structure-informed clustering for population stratification in association studies.* BMC Bioinformatics 24, no. 1, 2023: 411; `https://doi.org/10.1186/s12859-023-05511-w`
9. **A. Bose**, F. Utro, D.E. Platt, L. Parida, *Multiple Loci Selection with Multiway Epistasis in Coalescence with Recombination*, Algorithms 14 (5), 136, 2021; `https://doi.org/10.3390/a14050136`

10. **A. Bose**, D.E. Platt, L. Parida, P. Paschou, P. Drineas, *Integrating linguistics, social structure, and geography to model genetic diversity within India*, Molecular Biology and Evolution 38 (5), 1809-1819, 2021; `https://doi.org/10.1093/molbev/msaa321`

11. **A. Bose**, V. Kalantzis, E. Kontopoulou, M. Elkady, P. Paschou, P. Drineas, *TeraPCA: a fast and scalable software package to study genetic variation in tera-scale genotypes*, Bioinformatics, Volume 35, Issue 19, 1 October 2019, Pages 36793683. `https://doi.org/10.1093/bioinformatics/btz157`

12. G. Stamatoyannopoulos, **A. Bose**, A. Teodasiadis, F. Tsetsos, A. Plantiga, N. Psatha, N. Zogas, E. Yannaki, P. Zalloua, K.K. Kidd, B.L. Browning, J. Stamatoyannopoulos, P. Paschou, P. Drineas, *Genetics of the Peloponnesean populations and the theory of the extinction of the medieval Peloponnesean Greeks*, European Journal of Human Genetics, 25(5), pp. 637-645, 2017; `https://doi.org/10.1038/ejhg.2017.18`

Conferences

13. D. Gurnari, A. Guzmán-Sáenz, F. Utro, **A. Bose**, S. Basu, L. Parida, (2023). *Probing omics data via harmonic persistent homology.* Accepted, RECOMB-CCB, 2024.

14. D.E. Platt, **A. Bose**, C. Levovitz, K. Rhrissorrakrai, L. Parida, *Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions*, In Intelligent Systems for Molecular Biology (ISMB) 2024.

15. M.C. Burch, **A. Bose**, L. Parida, G. Dexter, P. Drineas, *MaSk-LMM: A Matrix Sketching Framework for Linear Mixed Models in Association Studies*, Accepted, RECOMB 2024.

16. D.E. Platt, A. Guzmán-Sáenz, **A. Bose**, S. Saha, F. Utro, L. Parida, *Characterizing Single Nucleotide Polymorphism Relevance by Significance and Predictivity in Alzheimer's Disease using Machine Learning and Polygenic Risk Score Analysis*, RECOMB Genetics, 2023.

17. D. Machado Reyes[†], **A. Bose**[†], E. Karavani, L. Parida, *FairPRS: adjusting for admixed populations in polygenic risk scores using invariant risk minimization* , In PACIFIC SYMPOSIUM ON BIOCOMPUTING 2023: Kohala Coast, Hawaii, USA, 37 January 2023, pp. 198-208. ([†] Equal Contributors)

18. D.E. Platt, **A. Bose**, C. Levovitz, K. Rhrissorrakrai, L. Parida, *Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions*, In AMIA Annual Symposium 2022. American Medical Informatics Association.

19. A. Chowdhury[†], **A. Bose**[†], S. Zhou, D. P. Woodruff, P. Drineas, *A Fast, Provably Accurate Approximation Algorithm for Sparse Principal Component Analysis Reveals Human Genetic Variation Across the World*, In Research in Computational Molecular Biology: 26th Annual International Conference, RECOMB 2022, San Diego, CA, USA, May 2225, 2022, Proceedings, pp. 86-106. Cham: Springer International Publishing, 2022. [1]

20. S. Dey[†], **A. Bose**[†], S. Saha, P. Chakraborty, M. Ghalwash, A.G. Sáenz, F. Utro, K. Ng, J. Hu, L. Parida, D. Sow, *Impact of Clinical and Genomic Factors on COVID-19 Severity*, In AMIA Annual Symposium Proceedings (Vol. 2021, p. 378). American Medical Informatics Association.

[1] [†] Equal Contributors

21. **A. Bose**, M.C. Burch, A. Chowdhury, P. Paschou, P. Drineas, *CluStrat: a structure informed clustering strategy for population stratification*, In Research in Computational Molecular Biology: 24th Annual International Conference, RECOMB 2020, Padua, Italy, May 1013, 2020, Proceedings 24 (pp. 234-236). Springer International Publishing.

Under Submission

22. M. Burch, J. Zhang, G. Idumah, H. Doga, R. Lartey, L. Yehia, M. Yang, M. Yildirim, M. Karaayvaz, O. Shehab, W. Guo, Y. Ni, L. Parida, X. Li, and **A. Bose**, *Towards Quantum Tensor Decomposition in Biomedical Applications*, Under Review in Nature Methods, 2025.
23. L. Yehia, G. Idumah, T.W. Frazier, V. Makarov, **A. Bose**, L. Parida, A. Hardan, J.A. Martinez-Agosto, D.M. Ritter, M. Sahin, C. Eng, Y. Ni, on behalf of the Developmental Synaptopathies Consortium. *Genomic modifiers of malignant and neurodevelopmental phenotypes in individuals with PTEN hamartoma tumor syndrome*, Under Review in Genetics in Medicine, 2025.
24. **A. Bose**, D.E. Platt, A. Guzmán-Sáenz, K. Rhrissorrakrai, N. Haiminen, L. Parida, *Remics: A Redesription-based Framework for Multi-Omics analysis*, Under Review, Frontiers in Cell and Developmental Biology, 2025.

Preprints

25. V. Dubovitskii†, **A. Bose**†, F. Utro, L. Parida, *On Quantum Random Walks in Biomolecular Networks*, arXiv, 2025.
26. Burch, M., Zhang, J., Idumah, G., Doga, H., Lartey, R., Yehia, L., Yang, M., Yildirim, M., Karaayvaz, M., Shehab, O., Guo, W., Ni, Y., L. Parida, Li, X. and **A. Bose**, *Towards Quantum Tensor Decomposition in Biomedical Applications*, arXiv, 2024.
27. H. Doga, M. Emre Sahin, J. Bettencourt-Silva, A. Pham, E. Kim, A. Andress, S. Saxena, **A. Bose**, L. Parida, J. L. Robertus, H. Kawaguchi, R. Soliman, D. Blankenberg, *Towards quantum computing for clinical trial design and optimization: A perspective on new opportunities and challenges*, arXiv, 2024.
28. D.E. Platt, A.G. Sáenz, **A. Bose**, O. Shehab, F. Utro, H. Doga, K. Rhrissorrakrai, S. Basu, K. Najafi, L. Parida, *Quantum Computation of Cumulants with Error Propagation using Lee-Yang Zeros of the Ising Model*, In preparation, 2024.
29. S. Rabinovici-Cohen, D.E. Platt, T. Iwamori, I. Guez, S. Dey, **A. Bose**, M. Kudo, L. Cosmai, C. Porta, A. Koseki, P. Meyer, *Multimodal predictions of End Stage Chronic Kidney Disease from asymptomatic and prodromal individuals*, medRxiv, 2024-10.
30. D. Machado Reyes, M.C. Burch, L. Parida, **A. Bose**, *A Multimodal Foundation Model for Discovering Genetic Associations with Brain Imaging Phenotypes*, medRxiv, 2024.
31. D. Gurnari, A. Guzmán-Sáenz, F. Utro, **A. Bose**, S. Basu, L. Parida, (2023). *Probing omics data via harmonic persistent homology.* arXiv preprint arXiv:2311.06357.
32. S. Basu, J. Born, **A. Bose**, S. Capponi, D. Chalkia, T. A. Chan, H. Doga, et al., *Towards quantum-enabled cell-centric therapeutics.*, arXiv, 2023.
33. **A. Bose**†, D.E. Platt†, K. Ng, L. Parida, *Role of genetics in capturing racial disparities in cardiovascular disease*, medRxiv, 2023.

34. D. Machado Reyes†, **A. Bose**†, E. Karavani, L. Parida, *FairPRS: a fairness framework for polygenic risk scores*, medRxiv, 2022.

35. D.E. Platt, **A. Bose**, C. Levovitz, K. Rhrissorrakrai, L. Parida, *Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions*, medRxiv, 2022.

36. **A. Bose**, D.E. Platt, N. Haiminen , L. Parida, *CuNA: Cumulant-based genotype-phenotype interaction networks in Parkinson's Disease*, medRxiv, 2021.

37. S. Dey, **A. Bose**, P. Chakraborty, M. Ghalwash, A.G. Saenz, F. Utro, K. Ng, J. Hu, L. Parida, D. Sow, *Impact of Clinical and Genomic Factors on SARS-CoV2 Disease Severity*, medRxiv, 2021.

38. S. Saha †, A.G Sáenz †, **A. Bose** †, F. Utro, D.E. Platt, L. Parida, *RubricOE: a learning framework for genetic epidemiology*, medRxiv, 2021.

39. **A. Bose**, M.C. Burch, A. Chowdhury, P. Paschou, P. Drineas, *Structure informed clustering adjusts for population stratification in association studies*, BioRxiv, 2020.

40. **A. Bose**, D.E. Platt, L. Parida, P. Paschou, P. Drineas, *Dissecting Population Substructure in India via Correlation Optimization of Genetics and Geodemographics*, BioRxiv, 2017.

41. S. Hassan, P. Pal Choudhury and **A. Bose**, (2011), *A Quantitative model for Human Olfactory Receptors*, Nature Precedings, npre20126967-2, 2012.

Abstracts (peer reviewed only)

42. V. Dubovitskii†, **A. Bose**†, F. Utro, L. Parida, *On Quantum Random Walks in Biomolecular Networks*, Intelligent Systems for Molecular Biology (ISMB), 2025. **Selected for Platform presentation.**

43. B. Raubenolt, A. Mohan, K. K. Rhrissorrakrai, **A. Bose**, F. Utro, E. Plow, D. Blankenberg, L. Parida, *Guiding Quantum and Classical Machine Learning Model Selection for Multi-omics via Data Complexity*, Intelligent Systems for Molecular Biology (ISMB), 2025.

44. Burch, M., Zhang, J., Idumah, G., Doga, H., Lartey, R., Yehia, L., Yang, M., Yildirim, M., Karaayvaz, M., Shehab, O., Guo, W., Ni, Y., L. Parida, Li, X. and **A. Bose**, *Advancing Quantum Tensor Decomposition in Biomedical Data Analysis*, Intelligent Systems for Molecular Biology (ISMB), 2025.

45. **A. Bose**, H. Doga, O. Shehab, *Polynomial Quantum Speedup for Black-box Feature Selection*, Quantum Techniques in Machine Learning (QTML) 2024.

46. M. Burch, **A. Bose**, L. Parida, P. Drineas, *MaSk-LMM: a matrix sketching-based fast and scalable linear mixed model for association studies in large biobanks*, Annual meeting of the American Society for Human Genetics (ASHG), 2022.

47. D.E. Platt†, **A. Bose**†, K. Ng, L. Parida, *Race versus Genetics in clinical decision-making: a perspective from cardiovascular disease*, Intelligent Systems for Molecular Biology (ISMB), 2022. [2]

48. M. Burch, P. Jain, Z. Yang, A. Topaloudi, P. Paschou, **A. Bose**, P. Drineas, *Predicting Complex Disorders by Combining Comorbidity Data and Polygenic Risk Scores*, ISMB, 2022.

49. A. Guzmán-Sáenz, D.E. Platt, F. Utro, **A. Bose**, S. Saha, L. Parida, *RubricOE: what Machine Learning can say about Alzheimers Disease*, ISMB, 2022.

[2] † Equal Contributors

50. **A. Bose**, M.C. Burch, A. Chowdhury, P. Paschou, P. Drineas, *Structure informed clustering for population stratification and genetic risk prediction*, ASHG, 2019.
51. **A. Bose**, F. Utro, D.E. Platt, L. Parida, *Algorithms to modulate ARG by Selection*, RECOMB-Genetics, 2018. **Selected for Platform presentation.**
52. **A. Bose**, V. Kalantzis, E. Kontopoulou, M. Elkady, P. Paschou, P. Drineas, *TeraPCA: a fast and scalable software package to study genetic variation in terascale genotypes*, ASHG, 2017.
53. **A. Bose**, D.E. Platt, L. Parida, P. Paschou, P. Drineas, *Correlation Optimization of Genetics and Geodemographics*, ASHG, 2016. **Selected for Platform presentation.**

Dissertation

54. **A.Bose**, *Computational Methods for Population Genetics*, `https://doi.org/10.25394/PGS.9752924.v1`, Purdue University, 2019.

Patents

1. Data Complexity-based Model Selection
   A. Bose, K. Rhrissorrakrai, F. Utro, L. Parida
   To be Filed, 2025.
2. IsoLat: subgraph Isomorphisms for Lattices
   F. Utro, L. Parida, **A. Bose**
   Filed, 2024.
3. Cumulant-enabled muti-omics neural network embeddings
   A. Bose, A. Guzmán-Sáenz, K. Rhrissorrakrai, L. Parida
   Filed, 2024.
4. Multi-omics Tensor Regression for Complex Diseases
   A. Bose, M.C. Burch, L. Parida
   Filed, 2024.
5. Pharmacogenomics induced protein function of therapeutic targets
   A. Bose, F.Utro, L. Parida
   Filed, 2023.
6. Contrastive multi-omics association learning for complex diseases.
   A. Bose, D. Machado Reyes, M.C. Burch, L. Parida
   Filed, 2023.
7. Complex disease marker discovery using cumulants and Ising Hamiltonians
   A. Guzmán-Sáenz, **A. Bose**, D. E. Platt, F. Utro, K. Rhrissorrakrai, L. Parida
   U.S. Patent Application No. 18/621,167, 2025.
8. Cross-disorder multi-omics feature ranking.
   A. Bose, F. Utro, M.C. Burch, L. Parida
   U.S. Patent Application No. 18/616,298, 2025.
9. A multi-modal Cumulant-based Risk Score for complex diseases.
   A. Bose, L. Parida
   U.S. Patent Application No. 18/323,640, 2023.
10. Interactive network for multi-modal biomarker discovery for complex diseases.
    A. Guzmán-Sáenz, **A. Bose**, D. E. Platt, L. Parida, N. Haiminen
    U.S. Patent Application No. 18/115,295, 2024.

11. Multivariate Gaussian GAN for generation of synthetic patient multi-view data for modal incompleteness.
D.E. Platt, **A. Bose**, K. Rhrissorrakrai, A. Guzmán-Sáenz, N. Haiminen and L. Parida
U.S. Patent Application No. 17/930,477, 2024.

12. Discovering biomarkers via higher-order genotype-phenotype interactions in complex diseases.
A. Bose, D.E. Platt, N. Haiminen and L. Parida
U.S. Patent Application No. 17/453,221, 2023.

Google Scholar

- Citations: 208
- h-index: 7
- i10-index: 5

Teaching

- Mentored 7 students in Purdue University, CS490: Data Science Capstone Project in Spring 2024.
- Teaching Assistant for Rensselaer Polytechnic Institute, CSCI 1200: Data Structures in Fall 2014 and Spring 2015. Taught one section with 40 students.

Research Collaborations

- Algorithmiq, Helsinki, Finland.
- Department of Mathematics, Case Western Reserve University, Cleveland, OH.
- Lerner Research Institute, Cleveland Clinic, Cleveland, OH.
- Biotherapeutics Discovery, Boehringer Ingelheim, Ridgefield, CT
- Cardiovascular Disease Initiative at Broad Institute, Cambridge, MA.
- Biomedical Engineering Department , Rensselaer Polytechnic Institute, Troy, NY.
- Computer Science Department, Purdue University, West Lafayette, IN.

Professional Activities

- Member of the SIAM Imaging Science 2026 Program Committee.
- Editorial Board Member of BMC Genomics.
- Member of the RECOMB 2025 Program Committee.
- Member of IBM Healthcare Invention Disclosure Team.
- Reviewer for the following (> 70 papers):
  - Journals:
    - Nature Communications; Communications Medicine; PLoS Computational Biology; Frontiers in Genetics; Frontiers in Psychiatry; Human Genomics; Patterns; Genome Research; Annals of Epidemiology; American Journal of Human Genetics; Patterns; Circulation Genomics and Precision Medicine; Pattern Recognition; Nucleic Acids Research; Computers in Biology and Medicine; iScience; Journal of the American Heart Association; IEEE Transactions on Computational Biology and Bioinformatics; Bioinformatics; BMC Bioinformatics; Bioinformatics Advances; Computational Biology and Chemistry; Scientific Reports; American Journal of Medical Genetics
  - Conferences:
    - IEEE Quantum Week 2025; RECOMB; PSB; AMIA; Clinical Informatics; ISMB; NeurIPs; KDD; WABI

- Member: American Society of Human Genetics, International Society for Computational Biology.
- Served on the committee of the following PhD students:
  - Diego Machado Reyes, Rensselaer Polytechnic Institute
  - Myson Burch, Purdue University, Graduated, 2023.
- Mentoring a group of seven students from Purdue University in CS490, Spring 2024 on the project *Predictive power of lower-dimensional embeddings of single-cell RNA-seq data*.
- Challenge lead in IBM Research projects and external partnerships in 2022 and 2023. Leading a team of over 10 people across global IBM Research labs.
- Organized science summer camps in IBM Research for middle school students.
- Peer Adviser to incoming graduate students in the Computer Science Department in Rensselaer Polytechnic Institute and in Purdue University.
- Co-Founder of the Robotics club of Meghnad Saha Institute of Technology which has over 400 students now.

News Articles

1. *Cleveland Clinic Advances in 1st NIH Quantum Computing Challenge*
   https://www.hpcwire.com/off-the-wire/cleveland-clinic-advances-in-1st-nih-quantum-computing-challenge/
2. *Researchers Say Quantum Machine Learning, Quantum Optimization Could Enhance The Design And Efficiency of Clinical Trials*
   https://thequantuminsider.com/2024/10/05/researchers-say-quantum-machine-learning-quantum-optimization-could-enhance-the-design-and-efficiency-of-clinical-trials/
3. *Quantum Computing Revolutionizes Clinical Trials*
   https://www.azoquantum.com/News.aspx?newsID=10525
4. *Severe COVID linked to RAAS and hyperlipidemia associated metabolic syndrome conditions*
   https://www.news-medical.net/news/20220406/Severe-COVID-linked-to-RAAS-and-hyperlipidemia-associated-metabolic-syndrome-conditions.aspx
5. *Combined clinical and genomic data better predicts COVID-19 severity*
   https://www.news-medical.net/news/20210328/Combined-clinical-and-genomic-data-better-predicts-COVID-19-severity.aspx
6. *Language (not geography) major force behind Indias gene flow.*
   https://bigthink.com/culture-religion/indian-genetics
7. *In India, People Who Speak the Same Language Have Similar DNA: Study*
   https://theswaddle.com/in-india-people-who-speak-the-same-language-have-similar-dna-study/
8. *New study ties Indias genetic diversity to language, not geography.*
   https://www.newsbug.info/lafayette_leader/news/local/new-study-ties-india-s-genetic-diversity-to-language-not-geography/article_52415487-9f63-5ce8-87d4-8edaba12aa0e.html
9. *New study ties Indias genetic diversity to language, not geography.*
   https://www.purdue.edu/newsroom/releases/2021/Q1/new-study-ties-indias-genetic-diversity-to-language,-not-geography.html

10. *In India, People Who Speak the Same Language Have Similar DNA.* https://theswaddle.com/in-india-people-who-speak-the-same-language-have-similar-dna-study/
11. *Genetic testing has a data problem. New software can help.* https://www.nsf.gov/discoveries/disc_summ.jsp?cntn_id=298521&org=NSF.
12. *Genetic testing has a data problem. New software can help.* https://www.purdue.edu/newsroom/releases/2019/Q2/genetic-testing-has-a-data-problem.-new-software-can-help..html.

Invited Presentations

- **Invited** presentation on *Quantum Algorithms for Biomedical and Translational Applications* in the NIH/ODSS Technical Implementation Working Group meeting in Sep 2025.
- **Platform** presentation on *On Quantum Random Walks in Biomolecular Networks* in Intelligent Systems for Molecular Biology (ISMB) held in Liverpool, UK in July 2025.
- **Tutorial** organizer with 50 participants on *Quantum machine learning for multi-omics analysis* in ISMB held in Liverpool, UK in July 2025.
- **Tutorial** organizer with 40 participants on *Quantum machine learning in healthcare: Bring Your Own Data* in Cleveland Clinic, held in Cleveland, OH in May 2025.
- **Platform** presentation on *Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions* in ISMB held in Montreal, Quebec, Canada in July 2024.
- **Tutorial** organizer with 50 participants on *Quantum-enabled multi-omics analysis* in ISMB held in Montreal, Quebec, Canada in July 2024.
- **Platform** presentation on *Probing omics data via harmonic persistent homology* in Research in Computational Molecular Biology (RECOMB) Computational Cancer Biology meeting held in Cambridge, MA in Apr 2024.
- **Platform** presentation on *Quantum machine learning for multi-omics data: Insights from the HCLS Quantum working group*, at the Cleveland Clinic, Cleveland, OH, April, 2024.
- Discussion chair on *Quantum Computing: Where It Is Differentiated, What Has Been Demonstrated, and When It Reaches "Maturity"*, at the IBM Innovation Studio, NYC, April, 2024.
- **Platform** presentation on *Race versus Genetics in clinical decision-making: a perspective from cardiovascular disease* in ISMB held in Madison, WI in July 2022.
- **Platform** presentation on *A Fast, Provably Accurate Approximation Algorithm for Sparse Principal Component Analysis Reveals Human Genetic Variation Across the World* in RECOMB held in San Diego, CA in May 2022.
- Impact of Clinical and Genomic Factors on COVID-19 Severity
  - IBM Got Science! 2021 Seminar series.
- *Machine Learning framework in Genetic Epidemiology*
  - Broad Institute of MIT and Harvard, Cambridge, MA, Jun 2021.
- *Computational methods in Population Genomics*
  - Regeneron Genetics Center, Tarrytown, NY, Dec 2020.
  - Inari Agriculture Inc., Cambridge, MA, Nov 2020.
  - Allen Institute of Brain Science, Seattle, WA, Nov 2020.

- *CluStrat: a structure informed clustering strategy for population stratification*
  - **Platform** presentation in Research in Computational Molecular Biology (RECOMB), held virtually in June 2020.
  - Poster presentation in American Society of Human Genetics (ASHG) meeting 2019, Houston, TX.
- **Platform** presentation on *Algorithms to modulate ARG by Selection* at the RECOMB-Genetics meeting, Paris, April, 2018. (This talk is given by Dr. Laxmi Parida)
- *TeraPCA: A fast and scalable method to study genetic variation in tera-scale genotypes*
  - Poster presentation in Conference of Scientific Computing and Approximation, Purdue University, West Lafayette, IN.
  - Poster presentation in ASHG 2017 meeting, Orlando, FL.
- *Integrating Linguistics, Social Structure and Geography to model genetic diversity within India.*
  - Poster presentation in Summer Intern Showcase 2017, IBM T.J Watson Research Center, NY.
  - Poster presentation in Biology of Genomes (BOG) 2017 meeting, Cold Spring Harbor Labs, NY.
  - **Platform** presentation in ASHG 2016 meeting, Vancouver, BC, Canada. (Abstract selected in top 8% of over 6000 submissions)
  - Poster presentation at Student Research Showcase in Computer Science Department, Purdue University, West Lafayette, IN.
  - Poster presentation in BOG 2016 meeting, Cold Spring Harbor Labs, NY.
  - Poster presentation in Student Research Symposium 2016 in Computer Science Department, Rensselaer Polytechnic Institute.
- Summer school on "Mathematics of Data", organized by Park City Mathematics Institute (PCMI) and the Institute for Advanced Study (IAS), held in, Midway, Utah, USA.
- ASHG 2015, Annual Meeting in Baltimore, MD, USA as a trainee researcher.
- Gene Golub SIAM Summer School 2015, held in, Delphi, Greece.

Mentoring

- PhD students
  - Diego Machado Reyes (4^{th} year, Rensselaer Polytechnic Institute)
  - Myson Burch (Graduated, 2023, Purdue University)
- High School students
  - Inaara Tuan, Mustafa Khan, Justin Gingrich, Romit Ghosh, Srihan Balaji

Grants/Funding

- (**PI X. Li, co-PI A. Bose**) "*Quantum Tensor Decomposition for Medical Image Analysis*", NIH Quantum Computing Challenge Stage I, $10,000, 2025-2026.

Awards of Merit

- Outstanding technical contribution awards from IBM in 2024 and 2023.
- Plateau from IBM for inventors showcasing creativity and technical knowledge.
- IBM First Patent Application Invention Achievement Award.
- ISCB (International Society for Computational Biology) Travel Fellowship for RECOMB 2020 in Padua, Italy.
- NSF Travel Grants to the following conferences:
  - Biology of Genomes: 2016 and 2017.
  - American Society of Human Genetics (ASHG), 2015 - 2019.
  - International Conference for Distributed Computing and Internet Technologies (ICDCIT) 2017 meeting held at Bhubaneswar, Odisha, India.
- Received a 4 year fellowship from Ministry of Human Resource Development (M.H.R.D), Government of India for significant achievement in Higher Secondary Examination

Computer Skills

- ***Languages:*** Qiskit, PyTorch, Tensorflow, Python, R, C, C++, MATLAB, Java, postgreSQL, Scripting(AWK, bash,etc), Perl, HTML, LaTeX
- ***Operating Systems:*** GNU/Linux, Unix, Windows
- ***Computational Biology:*** SAIGE, REGENIE, BOLT-LMM, SKAT, PLINK, GATK, GCTA, Beagle, bcftools, Cytoscape and other computational biology and population genetic tools and workflows.
- ***Cloud Platforms:*** IBM, Google Cloud, AWS
- ***Databases:*** MySQL, TERADATA, Oracle, DB2

Graduate Coursework (selected)

Machine Learning, Computational Linear Algebra, Parallel Computing, Foundations of Data Science, Algorithms Design, Frontiers of Network Science, Distributed Systems, Randomized Algorithms, Theory of Computation

Independent Coursework

Coursera.org: Deep Learning Specialization; Python for Genomic Data Science; Algorithms: Design and Analysis; Bioinformatics I and II
IBM: Machine Learning Essentials, Qiskit Global Summer School 2023, Qiskit Global Summer School: Path to utility 2024

References

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Additional Information

- *Date of Birth*: August 8, 1990
- *Marital Status*: Married
- *Citizenship*: Indian