Narmada Sambaturu

Binghamton, New York,
USA

Email: nsambaturu@binghamton.edu
Website: https://narmadasambaturu.github.io/

Current Position	**Assistant Professor,**	Aug 2024 - Present
	School of Systems Science and Industrial Engineering (SSIE),	
	Binghamton University (BU), State University of New York,	
	New York, USA.	

Education	**PhD, Interdisciplinary Mathematical Sciences,**	2015 - 2021
	Mathematical and Computational Biology Stream,	
	National Mathematics Initiative,	
	Indian Institute of Science (IISc), Bangalore, India.	
	Thesis: *Multi-scale Modelling of Immune Response and Disease Spread: Methods and Applications.*	
	MSc, School of Computing,	2012 - 2015
	National University of Singapore, Singapore.	
	Thesis: *Towards Handling Repeats in Genome Assembly.*	
	BE, Computer Science and Engineering,	2005 - 2009
	M.S.Ramaiah Institute of Technology, Bangalore, India.	
	Visvesvaraya Technological University.	

Awards

- Best Student Paper Award, 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM).
- Travel awards: BIBM (2015); RECOMB/ISCB Conference on Regulatory and Systems Genomics (2017); Lakshmi & Aravamudan Student Travel Fund, Office of Development and Alumni Affairs, IISc (2018).

Research Funding

- Binghamton University Projects for New Undergraduate Researchers (BUPNUR), Binghamton, New York, USA (Spring 2025).
- Director's Postdoctoral Fellowship, Laboratory Directed Research & Development, Los Alamos National Laboratory, New Mexico, USA (2021).

Professional Experience

- **Director's Postdoctoral Fellow,**   Oct 2021 - Aug 2024
  Theoretical Biology and Biophysics Group, Los Alamos National Laboratory.
  Modeled HIV evolution by integrating within and between host scales.
  Proposed resolution to seemingly contradictory findings in literature about timing of reservoir establishment.
  Revealed that within–host evolution has a greater impact on epidemiological outcomes than transmission.

- **Senior Research Scientist,**   Summer 2021
  HealSeq Precision Medicine.
  Developed methods to analyze immune response to vaccinations.

- **PhD Fellow,**   2015 - 2021
  Interdisciplinary Mathematical Sciences, IISc Mathematics Initiative,
  Indian Institute of Science, Bangalore, India.

Developed novel algorithms for multi–scale modeling of immune response and disease spread, including methods for mining omics–integrated biological networks, and incorporating genetic heterogeneity into epidemic models.

Applied algorithms in translational work to develop a biomarker for tuberculosis, suggest novel drug targets for SARS–CoV–2, and improve predictions of epidemic size.

- **Visitor,**   Winter 2016
  Department of Applied Mathematics,
  University of Leeds, Leeds, UK
  Developed first-ever method to study the role of genetic heterogeneity in the epidemiological spread of H1N1 influenza.

- **Junior Research Fellow,**   Summer 2015
  Indian Institute of Science, Bangalore, India.
  Developed graph-theoretical methods for the analysis of biological networks.

- **MSc Student,**   2012 - 2015
  School of Computing, National University of Singapore, Singapore.
  Developed method to improve handling of repeat regions in genome assembly by exploiting an overhang between adjacent genomic fragments caused by using certain transposons for library preparation.

- **Developer, Tata Consultancy Services.**   2009 - 2011
  Technology Excellence Group,
  Bangalore, India.
  Full stack developer for internal website to accept, track, and respond to requests for technical assistance.

- **Intern,**   2006
  Bioinformatics Centre,
  Indian Institute of Science, Bangalore, India.
  Wrote the code for a novel method to identify intergenic sRNAs in completely sequenced bacterial genomes.

Professional Service

- Review Editor: PLOS Computational Biology, Frontiers in Systems Biology, Frontiers in Immunology, Frontiers in Genetics, Journal of Theoretical Biology, NPJ Systems Biology and Applications.

- Organizing Committee: International Conference on Complex Networks and their Applications (2025), Conference on Complex Systems (2026).

Professional Societies

- Lifetime Member, Society for Mathematical Biology.

Skills

Modeling:	Agent Based Modeling, Deterministic (Oridnary Differential Equations) and Stochastic Mathematical Modeling.
Programming languages:	Python, R, MATLAB, C, C++, Java, Perl, HTML.
Database management:	SQL.
Machine learning packages:	scikit-learn, scipy, Weka.
Bioinformatics tools:	IEDB tools, Cytoscape, STRING, BLAST, CLUSTALW, SAMtools, BWA.
Version control:	SVN, Git.
Writing and typesetting:	LaTeX, MS Office, Google Docs.

Teaching	

- **Instructor:** ISE448/SSIE548, *Healthcare Data Science and Analytics.* Spring 2025
  School of Systems Science and Industrial Engineering,
  Binghamton University, State University of New York, USA.
  Topics: *Advanced data analytics with applications in healthcare systems engineering. Specifically descriptive, predictive, and prescriptive analytics.*

- **Co-instructor:** ISE314, *Computer Programming for Engineers.* Fall 2024
  School of Systems Science and Industrial Engineering,
  Binghamton University, State University of New York, USA.
  Topics: *Fundamental concepts and applications of computer programming, software engineering, database management, computational problem solving, and statistical techniques for data mining.*

- **Guest Lecturer:** *Molecular Biology.* Winter 2021
  Pre-Medical Program leading to Doctor of Medicine (MD).
  International Medical School (St. George's University) Bangalore campus,
  Karnataka, India.
  Topics: *Molecular Biology Tools and Concepts of OMICS, Bioinformatics, Transgenic Plants, Transgenic Animals, Molecular Medicine, Gene Therapy.*

- **Teaching Assistant:** *Current Trends in Drug Discovery.* Summer 2018
  IISc, Bangalore, Karnataka, India.
  Responsibilities: Managing logistics such as booking classrooms, communicating announcements, homework and assignments, solving doubts, and helping with seminars.

- **Learning Enabler:** Tata Consultancy Services. 2010
  Common Initial Learning Program. Bidadi, Karnataka, India.
  Training non–computer–science graduates to work as developers.
  Topics: *Algorithms, Data Structures, Introduction to Programming, Documentation.*

Mentorship

- Shriya Madhwani, Graduate student, SSIE, BU. Summer 2025
  Summer volunteer.

- Zachary Chen, Undergraduate, BU. Spring 2025
  Binghamton University Projects for New Undergraduate Researchers (BUPNUR).

- Yara Suleiman, Graduate Assistant, SSIE, BU. Jan 2025 - present

- Raksha Padaki, Intern, IISc. 2020 - 2021
  Publication in *Journal of Chemical Information and Modeling*, 2023.

- Vishal Rao, Undergraduate, IISc. 2020 - 2021
  Publication in journal *HLA*, 2023.

- Vaidehi Pusadkar, Intern, IISc. 2019 - 2020
  Publication in journal *Bioinformatics*, 2021.

- Sarthak Sahoo, Undergraduate, IISc. 2018 - 2019
  Poster in workshop *Mathematical and Statistical Explorations in Disease Modelling and Public Health*, 2019.

- Shamit Salim, MSc student, IISc. 2017 - 2018
  Dissertation on identifying correlates of protection in BCG strains.

Outreach

- Tutored underprivileged children in local community in India. Helped a student pass Engineering Mathematics course after two prior unsuccessful attempts.
  Topics: English, Arithmetic, Engineering Mathematics, Programming.

- Presented talks in workshops and undergraduate colleges aimed at encouraging students to pursue a career in science.

Community Service

- Active participant with Binghamton 2 Degrees, Binghamton, New York, USA.
- Volunteer with STEM Santa Fe, New Mexico, USA.
- Volunteer with Habitat for Humanity, USA.
- Participated in tree-planting initiatives.
- Participated in initiatives to clean up hiking trails.

Peer-reviewed Journal Publications

11. **Narmada Sambaturu**, Emily J. Fray, Vivek Hariharan, Fengting Wu, Carolin Zitzmann, Francesco R. Simonetti, Dan H. Barouch, Janet D. Siliciano, Robert F. Siliciano, Ruy M. Ribeiro, Alan S. Perelson, Carmen Molina-París and Thomas Leitner "SIV proviruses seeded later in infection are harbored in short-lived CD4+ T cells." *Cell Reports*, 44, no. 5, 2025.

10. Tin Phan, Jessica M. Conway, Nicole Pagane, Jasmine Kreig, **Narmada Sambaturu**, Sarafa Iyaniwura, Jonathan Z. Li, Ruy M. Ribeiro, Ruian Ke, and Alan S. Perelson. "Understanding early HIV-1 rebound dynamics following antiretroviral therapy interruption: The importance of effector cell expansion". *PLOS Pathogens*, 2024 20(7): e1012236.

9. Ushashi Banerjee, Adithya Chedere, Raksha Padaki, Abhilash Mohan, **Narmada Sambaturu**, Amit Singh, and Nagasuma Chandra. "Pathtracer comprehensively identifies hypoxia-induced dormancy adaptations in Mycobacterium tuberculosis". *Journal of Chemical Information and Modeling*, 2023.

8. Vishal Rao, Ushashi Banerjee, **Narmada Sambaturu**, Sneha Chunchanur, R. Ambica, and Nagasuma Chandra. "Pressured cytotoxic T cell epitope strength among SARS-CoV-2 variants correlates with COVID-19 severity." *HLA*, 2023.

7. Emily J. Fray, Fengting Wu, Francesco R. Simonetti, Carolin Zitzmann, **Narmada Sambaturu**, Carmen Molina-París, Alexandra M. Bender et al. "Antiretroviral therapy reveals triphasic decay of intact SIV genomes and persistence of ancestral variants." *Cell Host & Microbe* 31, no. 3 2023: 356-372.

6. Piyush Agrawal*, **Narmada Sambaturu***, Gulden Olgun, and Sridhar Hannenhalli. "A path-based analysis of infected cell line and COVID-19 patient transcriptome reveals novel potential targets and drugs against SARS-CoV-2." *Frontiers in immunology* 13 2022. (*equal contribution)

5. **Narmada Sambaturu**, Vaidehi Pusadkar, Sridhar Hannenhalli, and Nagasuma Chandra, "PathExt: a general framework for path-based mining of omics-integrated biological networks." *Bioinformatics* 37, no. 9 2021: 1254-1262.

4. **Narmada Sambaturu***, Sumanta Mukherjee*, Martín López-García, Carmen Molina-París, Gautam I. Menon, and Nagasuma Chandra. "Role of genetic heterogeneity in determining the epidemiological severity of H1N1 influenza." *PLoS Computational Biology* 14, no. 3, 2018: e1006069. (*equal contribution)

3. **Narmada Sambaturu**, Madhulika Mishra, and Nagasuma Chandra. "EpiTracer - an algorithm for identifying epicenters in condition-specific biological networks." *BMC genomics* 17, no. 4, 2016: 543.

2. Sridhar, Jayavel, **Narmada Sambaturu**, Radhakrishnan Sabarinathan, Hong-Yu Ou, Zixin Deng, Kanagaraj Sekar, Ziauddin Ahamed Rafi, and Kumar Rajakumar. "sRNAscanner: a computational tool for intergenic small RNA detection in bacterial genomes." *PLOS ONE* 5, no. 8, 2010: e11970.

1. Annapurna P. Patil, **Narmada Sambaturu**, and Krittaya Chunhaviriyakul. "Convergence time evaluation of algorithms in MANETs." *International Journal of Computer Science and Information Security*, Vol. 5, No. 1, pp. 144-149, September 2009.

Peer-reviewed Conference Publications

1. **Narmada Sambaturu**, Madhulika Mishra, and Nagasuma Chandra. "EpiTracer - an algorithm for identifying epicenters in condition-specific biological networks." *Proceedings of the 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*. IEEE Computer Society, 2015. (Best Student Paper Award).

Dissertations

2. **Narmada Sambaturu**. "Towards handling repeats in genome assembly." *MSc dissertation, National University of Singapore*, 2014.

1. **Narmada Sambaturu**. "Multi-scale Modelling of Immune Response and Disease Spread: Methods and Applications." *PhD dissertation, Indian Institute of Science*, 2021.

Work in Progress

4. **Narmada Sambaturu***, Zena Lapp*, Fernando D. K. Tria, Ethan Romero-Severson, Carmen Molina-París, and Thomas Leitner, "wavess: An R package for agent-based simulation of within-host virus sequence evolution." (*equal contribution) (Submitted).

3. Macauley Locke, **Narmada Sambaturu**, Zena Lapp, Carmen Molina-París, and Thomas Leitner. "Within- and between-host parameters regulate HIV epidemiological outcomes when two sub-types circulate in a population." (Manuscript in preparation).

2. Fernando D Tria, Zena Lapp, **Narmada Sambaturu**, Carmen Molina-París, and Thomas Leitner, "Replicative fitness and immune escape dominate at different times in HIV infection." (Manuscript in preparation).

1. Yara A. Suleiman, Congyu Wu, Sujoy Sikdar, and **Narmada Sambaturu**. "Analyzing empirically measured social connectivity patterns among university students: a case study with UT Austin." (Ongoing work).

Invited Talks

9. **Multi-scale Modeling of Infectious Diseases.** SSIE - Vellore Institute of Technology SHINE (India) Seminar series, Binghamton University, New York, USA, July 2025 (scheduled).

8. **Multi-scale Modeling of Infectious Diseases.** 2025 Ticks & Tick-borne Diseases Symposium, Binghamton University, New York, USA, May 2025.

7. **Stochastic Systems in Practice.** Guest lecture in SSIE 660, Stochastic Systems, Binghamton University, New York, USA, Oct 2024.

6. **Multi-scale Modeling of Infectious Diseases.** Center of Complex Systems (CoCo) seminar series, Binghamton University, New York, USA, Dec 2024.

5. **Pathways to STEM, Evolution of Human Immunodeficiency Virus.** STEM Santa Fe, New Mexico, USA, Jul 2023.

4. **Careers in Computer Science, Modeling Disease Spread.** STEM Santa Fe, New Mexico, USA, Jun 2022.

3. **Data Science in Bioinformatics.** Women in Data Science (WiDS) Mysuru, India, Sep 2020.

2. **Network Algorithms and their Applications in Biology.** Sanjay Ghodawat University, Kolhapur, India, Dec 2018.

1. **Statistical Thinking in Biomedical Research.** KLE College of Pharmacy, Bangalore, India, Apr 2018.

Workshop and Conference Presentations

9. Yara A. Suleiman, Congyu Wu, Sujoy Sikdar, **Narmada Sambaturu**. **(Poster)** *Analyzing empirically measured social connectivity patterns among university students: a case study with UT Austin.* North Eastern Regional Conference on Complex Systems (NERCCS), April 9-11 2025. **Presented by Yara A. Suleiman**.

8. **Narmada Sambaturu**, Macauley Locke, Zena Lapp, Carmen Molina-París, and Thomas Leitner. **(Talk)** *Within- and between-host parameters regulate HIV-1 epidemiological outcomes.* 31st International Dynamics & Evolution of Human Viruses Conference, June 19-22 2024.

7. **Narmada Sambaturu**, Emily J. Fray, Fengting Wu, Carolin Zitzmann, Francesco R. Simonetti, Dan H. Barouch, Janet D. Siliciano, Robert F. Siliciano, Ruy M. Ribeiro, Alan S. Perelson, Carmen Molina-París, and Thomas Leitner. **(Talk)** *Longitudinal dynamics of SIV and HIV divergence during antiretroviral therapy is determined by the decay of short- and long-lived cells.* 30th International Dynamics & Evolution of Human Viruses Conference, April 19-22 2023.

6. **Narmada Sambaturu**, Sumanta Mukherjee, Martín López-García, Carmen Molina-París, Gautam I Menon, and Nagasuma Chandra. **(Talk)** *Role of genetic heterogeneity in determining the epidemiological severity of H1N1 influenza.* Epidemiology meets Immunology and Vice Versa - Linking Math Epidemiology to Math Immunology, SMB Math-Epidemiology/Math-Immunology Subgroups Mid-Year Mini Virtual Conference, February 27-28 2022.

5. **Narmada Sambaturu**, Sumanta Mukherjee, Martín López-García, Carmen Molina-París, Gautam I Menon, and Nagasuma Chandra. **(Talk)** *Incorporating genetic heterogeneity into epidemic models for H1N1 influenza.* Mathematical and Statistical Explorations in Disease Modelling and Public Health, International Centre for Theoretical Sciences (ICTS), Bangalore, India, Jul 1 - 11 2019.

4. **Narmada Sambaturu**, Madhulika Mishra, Rahul Metri and Nagasuma Chandra. *An Algorithm for Identifying Druggable Targets Among Influential Mutations in Individual Cancer Patients.* **(Poster)** Indo-US Conference on Sculpting the future of medicine - Gateway to the post-proteogenome era, at Advanced Centre For Treatment, Research And Education In Cancer (ACTREC), Mumbai, India, Dec 10 - 11 2018.

3. **Narmada Sambaturu** and Nagasuma Chandra. *OptiNeo – an algorithm to optimise the number of neo-antigenic peptides for cancer immunotherapy.* **(Poster)** Nature Big Data and Cancer Precision Medicine, Boston, Massachusetts, Oct 1 - 2 2018.

2. **Narmada Sambaturu**, Sridhar Hannenhalli, and Nagasuma Chandra. **(Poster)** *Cutting through the complexity of genomic data: A general method to identify candidate genes.* RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges, New York, NY, Nov 19 - 21 2017.

1. **Narmada Sambaturu**, Sumanta Mukherjee, Martín López-García, Carmen Molina-París, Gautam I. Menon, and Nagasuma Chandra. **(Talk)** *Role of genetic heterogeneity in determining the epidemiological severity of H1N1 influenza.* Discussion meeting on Mathematical Models of Infection, Immunity and Inflammation, Indian Institute of Science, Bangalore. April 2017.