

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,
Binghamton University, 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**
- 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.

Teaching

- **Instructor** for course 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** for course *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** for course *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**
- 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.
- Professional Activities & Affiliations**
- Review Editor: *Frontiers in Systems Biology*, *Frontiers in Immunology*, *Frontiers in Genetics*, *Journal of Theoretical Biology*, *NPJ Systems Biology and Applications*.
 - Lifetime Member, *Society for Mathematical Biology*.
- Skills**
- | | |
|----------------------------|-------------------------------------------------------------------------------------------------------------|
| Modeling: | Agent Based Modeling, Deterministic (Ordinary 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. |
- 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 5 talks in workshops and undergraduate colleges aimed at encouraging students to pursue a career in science.
- Community Service**
- 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 Publications**
11. 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.
 10. 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.
 9. 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.

8. 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.
7. 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)
6. **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.
5. **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)
4. **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.
3. **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).
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.

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**, Emily J Fray, Fengting Wu, Vivek Hariharan, 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. “Last in first out: SIV proviruses seeded later in infection are harbored in short-lived CD4⁺ T cells.”, *bioRxiv* 2023.11.03.565539.
3. Macauley Locke, **Narmada Sambaturu**, Carmen Molina-París, and Thomas Leitner. “Within-host parameters regulate HIV epidemiological outcomes.” (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.” (Ongoing work).

- Invited Talks**
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**
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.