

Narmada Sambaturu

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Current Position	Director's Postdoctoral Fellow, Theoretical Biology and Biophysics, Los Alamos National Laboratory, Los Alamos, USA. Mentors: Dr. Thomas Leitner, Prof. Carmen Molina-París.	Oct 2021 - Present
Education	PhD, Interdisciplinary Mathematical Sciences, Mathematical and Computational Biology Stream, IISc Mathematics Initiative, Indian Institute of Science, Bangalore, India. Supervisors: Prof. Nagasuma Chandra, Prof. N. Srinivasan. Thesis: <i>Multi-scale Modelling of Immune Response and Disease Spread: Methods and Applications.</i>	2015 - 2021
	Master of Science, School of Computing, National University of Singapore, Singapore. Supervisor: Prof. Wing-Kin Sung. Thesis: <i>Towards Handling Repeats in Genome Assembly.</i>	2012 - 2015
	Bachelor of Engineering, Computer Science and Engineering, M.S.Ramaiah Institute of Technology, Bangalore, India. Visvesvaraya Technological University.	2005 - 2009
Awards	<ul style="list-style-type: none">• Director's Postdoctoral Fellow, Los Alamos National Laboratory (2021).• Best Student Paper Award, 2015 IEEE International Conference on Bioinformatics and Biomedicine (BIBM).• One of 50 students selected from all over India for participation in a summer camp in Biotechnology at M.S.Swaminathan Research Foundation, Chennai, India (2003).• All India Rank 25 in Secondary School Certificate Examination (Grade 10) (2003).	
Research Experience	<ul style="list-style-type: none">• Director's Postdoctoral Fellow, Theoretical Biology and Biophysics, Los Alamos National Laboratory. Mentors: Dr. Thomas Leitner, Prof. Carmen Molina-París. Within and between host scale integration to model HIV transmission.• Senior Research Scientist, HealSeq Precision Medicine. Analyzing immune response to vaccinations.• PhD Fellow, Interdisciplinary Mathematical Sciences, IISc Mathematics Initiative, Indian Institute of Science, Bangalore, India. Supervisors: Prof. Nagasuma Chandra, Prof. N. Srinivasan. Developing algorithms for multi-scale modeling of immune response and disease spread, including methods for mining omics-integrated biological networks to identify dysregulated paths and influential nodes, incorporating genetic heterogeneity into epidemic models, and designing vaccine candidates maximising population coverage.	<div>Oct 2021 - Present</div> <div>Summer 2021</div> <div>2015 - 2021</div>

	<ul style="list-style-type: none"> • Visitor, Winter 2016 Department of Applied Mathematics, University of Leeds, Leeds, UK Supervisors: Prof. Carmen Molina-París, Prof. Grant Lythe. Developing method to study the role of genetic heterogeneity in epidemiological spread of H1N1 influenza, as well as modeling tumour immune surveillance. • Junior Research Fellow, Summer 2015 Indian Institute of Science, Bangalore, India. Supervisor: Prof. Nagasuma Chandra. Introduction to Systems Biology and graph-theoretical analysis of biological networks. • MSc Student, 2012 - 2015 School of Computing, National University of Singapore, Singapore. Supervisor: Prof. Wing-Kin Sung. Developing 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. • Intern, 2006 Bioinformatics Centre, Indian Institute of Science, Bangalore, India. Supervisor: Prof. K. Sekar. Contributed towards development of a method to identify intergenic sRNAs in completely sequenced bacterial genomes.
Teaching Experience	<ul style="list-style-type: none"> • Guest Lecturer for course <i>Molecular Biology</i>. Winter 2021 Pre-Medical Program leading to Doctor of Medicine (MD). International Medical School (St. George's University) Bangalore campus, Karnataka, India. Topics: <i>Molecular Biology Tools and Concepts of OMICS, Bioinformatics, Transgenic Plants, Transgenic Animals, Molecular Medicine, Gene Therapy</i>. • Teaching Assistant for course <i>Current trends in drug discovery</i>. Summer 2018 Indian Institute of Science, Bangalore, Karnataka, India. • Learning Enabler, Tata Consultancy Services. 2010 Common Initial Learning Program. Bidadi, Karnataka, India.
Work Experience	<ul style="list-style-type: none"> • Senior Research Scientist, HealSeq Precision Medicine. Summer 2021 Bangalore, India. • Developer, Tata Consultancy Services. 2009 - 2011 Technology Excellence Group, Bangalore, India.
Publications	<ol style="list-style-type: none"> 1. 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." <i>Research Square</i>, 2022. 2. Vishal N. Rao, Ushashi Banerjee, Narmada Sambaturu, Sneha Chunchanur, R. Ambica, and Nagasuma Chandra. "Predicted CTL responses from pressured epitopes in SARS-CoV-2 correlate with COVID-19 severity." <i>medRxiv</i>, 2021. 3. Narmada Sambaturu. "Multi-scale Modelling of Immune Response and Disease Spread: Methods and Applications." <i>PhD dissertation, Indian Institute of Science</i>, 2021.

4. **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.
6. **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.
7. **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).
8. **Narmada Sambaturu**. "Towards handling repeats in genome assembly." *MSc dissertation, National University of Singapore*, 2014.
9. Sridhar, Jayavel, **Narmada Sambaturu**, Radhakrishnan Sabarinathan, Hong-Yu Ou, Zixin Deng, Kanagaraj Sekar, Ziauddin Ahamed Rafi, and Kumar Rajakumar. "sR-NAScanner: a computational tool for intergenic small RNA detection in bacterial genomes." *PLOS ONE* 5, no. 8, 2010: e11970.
10. Annapurna P. Patil, **Narmada Sambaturu**, and Krittaya Chunhaviyakul. "Convergence time evaluation of algorithms in MANETs." *International Journal of Computer Science and Information Security*, Vol. 5, No. 1, pp. 144-149, September 2009.

Workshop and Conference Presentations

- **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.
- **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.
- **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.
- **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.
- **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.
- **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.

Invited Talks	<ul style="list-style-type: none"> • Data Science in Bioinformatics. Women in Data Science (WiDS) Mysuru, India, Sep 2020. • Network Algorithms and their Applications in Biology. Sanjay Ghodawat University, Kolhapur, India, Dec 2018. • Statistical Thinking in Biomedical Research. KLE College of Pharmacy, Bangalore, India, Apr 2018. 												
Professional Service	<ul style="list-style-type: none"> • Review Editor: Frontiers in Systems Biology, Journal of Theoretical Biology. 												
Graduate Coursework	<ul style="list-style-type: none"> • PhD (IISc): Current Trends in Drug Discovery, Special Topics in Theoretical Biology. • MSc (NUS): Advanced Combinatorial Methods in Bioinformatics, Advanced Algorithms, Knowledge Discovery and Data Mining, Modeling and Analysis Techniques in Systems Biology, Advanced Topics in Data Mining. 												
Skills	<table> <tr> <td>Programming languages:</td><td>Python, R, MATLAB, C, C++, Java, Perl, HTML.</td></tr> <tr> <td>Database management:</td><td>SQL.</td></tr> <tr> <td>Machine learning packages:</td><td>scikit-learn, scipy, Weka.</td></tr> <tr> <td>Bioinformatics tools:</td><td>IEDB tools, Cytoscape, STRING, BLAST, CLUSTALW, SAMtools, BWA.</td></tr> <tr> <td>Version control:</td><td>SVN, Git.</td></tr> <tr> <td>Writing and typesetting:</td><td>LaTeX, MS Office, Google Docs.</td></tr> </table>	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.
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Outreach	<ul style="list-style-type: none"> • Tutoring underprivileged children in local community in topics ranging from arithmetic and English, to Engineering Mathematics and Programming. Helped a student pass Engineering Mathematics course after two prior unsuccessful attempts. • Presenting talks in workshops and undergraduate colleges, aimed at encouraging students to pursue a career in science. <ul style="list-style-type: none"> – Women in Data Science (WiDS) Mysuru, India, Sep 2020. – Sanjay Ghodawat University, Kolhapur, India, Dec 2018. – KLE College of Pharmacy, Bangalore, India, Apr 2018. 												
Community Service	<ul style="list-style-type: none"> • Volunteer with STEM Santa Fe. • Volunteer with Habitat for Humanity. • Participated in tree planting initiatives. • Participated in initiatives to clean up hiking trails. 												