PRAMOD SHINDE

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EDUCATION

La Jolla Institute for Immunology, San Diego, USA , Postdoctoral Fellow in Computational Immunology. *Postdoc Mentor*: Professor Bjoern Peters 2020 – present

- Research focus: Systems immunology multi-omics investigations on infection and vaccine responses.

Indian Institute of Technology (IIT) Indore, India, Ph.D in Bioinformatics and Computational Biology. *PhD Advisor*: Professor Sarika Jalan 2014 – 2019

University of Mumbai, Mumbai, India 2008 – 2013

- M. Sc Bioinformatics, University Gold Medal
- B. Sc Microbiology, Best Student of the Year

GRANTS AND AWARDS

- **HIPC IOF Grant (USD45000) NIH/NIAID Human Immunology Project Consortium, USA, Aug 2022/2023.** To carry out research on Immune signatures related to vaccines and infections project at La Jolla Institute of Immunology
- **EMBL travel grant (Euro 1000), European Molecular Biology Lab, Heidelberg, Germany, Feb 2019**. To attend symposium on “Reconstructing human past using ancient and modern genomics” at Heidelberg, Germany
- **INSPIRE PhD fellowship, Department of Science and Technology, Government of India, 2015-2019.** Prestigious fellowships are awarded to meritorious students from Indian universities who are pursuing Ph.D.
- **Received research grant for Short Term Training Internship Program, Haffkine Institute, Mumbai, 2011** Every year, 10 projects have been selected to conduct own research in labs at Haffkine Institute of Research and training, Mumbai.
- **Best Student of the Year and Best Science Student of the Year awards, Sathaye College, University of Mumbai, 2011.** The annual award is given to the best academic & extra-curricular performers among 1200 students and 400 students from the science faculty.

PHD THESIS

Title: Analysis of genomic and proteomic networks, Advisor: Prof. Sarika Jalan, IIT Indore 2014 – 2020

The thesis focuses on the applications of Network Science tools on the mitochondrial genomic data. It provides novel methodology to view epistatic interactions but also identifies important genomic regions which are over-represented in providing evolution in human mitochondria (mt). Our major results are:

- Evidence that mutation biases at codon positions and RNA genes were critical to producing continental, tribal and disease-level heterogeneity among human subpopulations.
- Demonstration of dense sub-graph structures particularly hierarchical modularity as a crucial agent for a nucleotide co-occurrence network make-up. More profoundly, our ancestry-based nucleotide module analyses showed that nucleotide co-changes cluster preferentially in mt-haplogroups.
- Contemporary human mt-genome nucleotides most closely resemble the ancestral state and very few of them were ancestral-variants.

Overall, these results demonstrated that subpopulation-based factors such as intra-species evolution do exert selection on mitochondrial genes by favoring specific epistatic genetic variants.

TEACHING EXPERIENCE

Department of Bioinformatics, Guru Nanak Khalsa College, Mumbai, India. 2013 – 2014

- Courses taught: Application of Bioinformatics, Bioinformatics Perspectives on Human Diseases, Molecular modeling & Drug designing, Concepts in computing with Java, Perl, SQL

Published CourseSource, an open-access and peer-reviewed, teaching resource: Jason H., Shinde P., Willemsen L., Kojima M., Reyna J., Peters B., and Grant B. Exploring Pertussis Vaccination Through Systems Vaccinology. CourseSource, 2024

ACADEMIC SERVICE (JOURNAL EDITORIAL AND REVIEWER ROLES)

- **Editorial Experience**: PLoS Computational Biology (2024-present)
- **Journals Reviewed for**: Journal of Clinical Medicine, BMC Infectious Diseases, BMC Genomics, Biology, Microorganisms, Genes, Cell, Cells, Journal of Computational Science

ACADEMIC EXPERIENCE

Workshop organization

- Global Initiative of Academic Network (GIAN) course on "Biomathematics: from Gene Expression to Bone Mechanics" by Prof. Alexey Zaikin (University College London, London, UK) during Aug 15 - 20, 2016, at IIT Indore
- GIAN course on "Statistics in Systems Biology and Programming in R" by Dr. Oleg Blyuss (University College London, London, UK) during Aug 22 - 27, 2016, at IIT Indore
- GIAN course on "Network science – from structure to dynamics" by Dr. Baruch Barzel (Bar-Ilan University, Israel) during Aug 6-10, 2018, at IIT Indore

RESEARCH PUBLICATIONS (PEER-REVIEWED):

Google Scholar: https://scholar.google.com/citations?user=2GeAO4IAAAAJhl=enoi=ao

21. **Shinde, P.**, Willemsen, L., Anderson, M., Aoki, M., Basu, S., Burel, J.G., Cheng, P., Dastidar, S.G., Dunleavy, A., Einav, T., . . . and Peters, B. (2025). Putting computational models of immunity to the test—an invited challenge to predict *B.pertussis* vaccination outcomes. *PLoS Computational Biology* DOI: `https://doi.org/10.1371/journal.pcbi.1012927`.

20. Willemsen, L., Lee, J., **Shinde, P.**, Soldevila, F., Aoki, M., Orfield, S., Kojima, M., Antunes, R.D.S., Sette, A., & Peters, B. (2025). Th1 polarization in *Bordetella pertussis* vaccine responses is maintained through a positive feedback loop. *Nature Communications*. DOI: `https://doi.org/10.1038/s41467-025-58460-8`. IF: 15

19. Richardson, E., Willemsen, L., **Shinde, P.**, Nielsen, M., Peters, B. (2025). Is the vaccination-induced B cell receptor repertoire predictable? *ImmunoInformatics*, 100057. DOI: https://doi.org/10.1016/j.immuno.2025.100057

18. **Shinde, P.**, Soldevila, F.C., Reyna, J., Kojima, M., Overton, J.A., Ha, B., Greenbaum, J., Ay, F., Grant, B.J., Kleinstein, S.H., & Peters, B. (2024). A multi-omics systems vaccinology resource to develop and test computational models of immunity. *Cell Reports Methods*, 4(3). (Featured on the cover page of the journal issue). DOI: `https://doi.org/10.1016/j.crmeth.2024.100731`.

17. Gygi, J., Maguire, C., Patel, R., **Shinde, P.**, Konstorum, A., Shannon, C., Xu, L., Hoch, A., Jayavelu, N., IMPACC Network, Peters, B., Kleinstein, S.H., & Guan, L. (2024). Integrated longitudinal multi-omics study identifies immune programs of COVID-19 severity and mortality in 1152 hospitalized participants. *Journal of Clinical Investigation*. DOI: `https://doi.org/10.1172/JCI176640`. IF: 13.1

16. Jason H., **Shinde, P.**, Willemsen L., Kojima M., Reyna J., Peters B., and Grant B. Exploring Pertussis Vaccination Through Systems Vaccinology. CourseSource, 2024

15. Verma, R. K., **Shinde, P.**, Mishra, A., & Jalan, S. (2023). Higher-order co-mutation interactions in mitochondrial genomes. *New Journal of Physics*, 25(9), 093021. DOI: `https://doi.org/10.1088/1367-2630/acf51a`.
14. Verma, R.K., **Shinde, P.**, & Jalan, S. (2022). Nucleotide-based genetic networks: Methods and applications. *Journal of Biosciences*, 47(4), 63. DOI: `10.1007/s12038-022-00290-7`.
13. **Shinde, P.**, Whitwell, H.J., Verma, R.K., Zaikin, A., & Jalan, S. (2022). Impact of mitochondrial epistatic interactions on evolution of different human subpopulations. *Mitochondrion*, 505818. DOI: `https://doi.org/10.1016/j.mito.2021.02.004`.
12. Verma, R.K., Kalyakulina, A., Giuliani, C., **Shinde, P.**, Kachhvah, A.D., Ivanchenko, M., & Jalan, S. (2021). Analysis of human mitochondrial genome co-occurrence networks of Asian population at varying altitudes. *Scientific Reports*, 11(1), 133. DOI: `https://doi.org/10.1038/s41598-020-80271-8`.
11. **Shinde, P.**, Marrec, L., Rai, A., Yadav, A., Kumar, R., Ivanchenko, M., Zaikin, A., & Jalan, S. (2019). Symmetry in cancer networks identified: Proposal for multicancer biomarkers. *Network Science*, 7(4), 541-555. DOI: `https://doi.org/10.1017/nws.2019.55`.
10. Rai, A., **Shinde, P.**, & Jalan, S. (2018). Network spectra for drug-target identification in complex diseases: New guns against old foes. *Applied Network Science*, 3, 1-18. DOI: `10.1007/s41109-018-0107-y`.
9. **Shinde, P.**, Sarkar, C., & Jalan, S. (2018). Codon based co-occurrence network motifs in human mitochondria. *Scientific Reports*, 8(1), 3060. DOI: `https://doi.org/10.1038/s41598-018-21454-2`.
8. Gohil, D., Kothari, S., **Shinde, P.**, Meharunkar, R., Warke, R., Chowdhary, A., & Deshmukh, R. (2017). Genetic characterization of Influenza A (H1N1) pandemic 2009 virus isolates from Mumbai. *Current Microbiology*, 74, 899-907. DOI: `10.1007/s00284-017-1262-6`.
7. Chavan, R.D., **Shinde, P.**, Girkar, K., Madage, R., & Chowdhary, A. (2016). Assessment of anti-influenza activity and hemagglutination inhibition of *Plumbago indica* and *Allium sativum* extracts. *Pharmacognosy Research*, 8(2), 105. DOI: `10.4103/0974-8490.172562`.
6. **Shinde, P.**, & Jalan, S. (2015). A multilayer protein-protein interaction network analysis of different life stages in *Caenorhabditis elegans*. *Europhysics Letters*, 112(5), 58001. DOI: `10.1209/0295-5075/112/58001`.
5. Gohil, D.J., Kothari, S.T., **Shinde, P.**, Chintakrindi, A.S., Meharunkar, R., Warke, R.V., Kanyalkar, M.A., Chowdhary, A.S., & Deshmukh, R.A. (2015). Drug susceptibility of Influenza A/H3N2 strains co-circulating during 2009 influenza pandemic: First report from Mumbai. *Infection, Genetics and Evolution*, 29, 75-81. DOI: `10.1016/j.meegid.2014.11.005`.
4. **Shinde, P.**, Yadav, A., Rai, A., & Jalan, S. (2015). Dissortativity and duplications in oral cancer. *The European Physical Journal B*, 88, 1-7. DOI: `10.1140/epjb/e2015-60426-5`.
3. Kulkarni, A., **Shinde, P.**, Kothari, S., Warke, R., Chowdhary, A., & Deshmukh, R.A. (2015). A novel tetravalent recombinant envelope domain III vaccine against Dengue: An in silico approach. *International Journal of Pharmaceutical Sciences and Research*, 6(6), 2441-2450. DOI: `10.13040/IJPSR.0975-8232.6(6).2441-50`
2. Gohil, D., Kothari, S., **Shinde, P.**, Krindi, A.C., Meharunkar, R., Warke, R., Kanyalkar, M., Chowdhary, A., & Deshmukh, R. (2015). Genetic characterization of oseltamivir-resistant seasonal Influenza A (H1N1) virus circulating during 2009 pandemic influenza in Mumbai. *International Journal of Advanced Research*, 3(3), 252-261. DOI: `10.1016/j.meegid.2010.07.019`
1. Gohil, D., Kothari, S., **Shinde, P.**, Krindi, A.C., Meharunkar, R., Warke, R., Kanyalkar, M., Chowdhary, A., & Deshmukh, R. (2015). Oseltamivir-resistant Influenza A (H1N1) virus infection in Mumbai, India. *Journal of Antivirals & Antiretrovirals*, 7, 108-114. DOI: `10.4172/jaa.1000126`.

RESEARCH PUBLICATIONS (UNDER REVIEW/PREPARATION):

4. Yadav, P., **Shinde, P.**, & Singh, A. (2024). Brain rewiring during developmental transitions: A Comparative Analysis of Larva and Adult Drosophila melanogaster. bioRxiv, 2024-05. (Accepted in Network Neuroscience)
3. Richardson, E., Willemsen, L., **Shinde, P.**, Nielsen, M., & Peters, B. (2025). Is the vaccination-induced B cell receptor repertoire predictable? (Under review)
2. **Shinde, P.**, Willemsen, L., Kojima, M., Reyna, J., Gygi, J., Orfield, S., Rasmussen, M., Soldevila, F., Greenbaum, J., Guan, L., Grant, B., Ay, F., Kleinstein, S. H., Peters, B. Validating computational models of immunity: Insights from a community-driven challenge on predicting vaccination outcomes.

1. **Shinde, P.**, Gygi, J. P., Xing, J., Burel, J., Gabernet, G., McDougal, R., Guan, L., Peters, B., and Kleinstein, S. H. Development of a data-driven multi-omics module repertoire for data analysis and interpretation.

KEY CONFERENCE PRESENTATIONS

- International Conference on Intelligent Systems for Molecular Biology (ISMB) 2024, Montreal, Quebec, Canada. Title: Development of a data-driven multi-omics module repertoire for data analysis and interpretation
- American Association of Immunologists Immunology 2024, Chicago, Illinois, USA. Poster title: A series of formal contests to predict B. pertussis vaccination outcomes - Join us for round 3!
- Human Immunology Project Consortium (HIPC) Annual Meeting, Match 2024, NIH, Rockville, MD, USA. Talk title: Comparison of infection response transcriptional signatures with vaccine responses using SARS-CoV-2 infection data.
- Symposium on "Reconstructing human past using ancient and modern genomics" during March 31 to April 3, 2019 at European Molecular Biology Lab, Heidelberg, Germany (Received travel grant). Poster title: Impact of epistatic interaction on evolution of human mitochondrial DNA
- Symposium on "Advances in Biosciences and Bioengineering" on Feb 24, 2019, at Indian Institute of Technology Indore, India (Received Best Oral Presentation Award). Poster title: Impact of epistatic interaction on evolution of human mitochondrial DNA
- Nextgen Genomics, Biology, Bioinformatics and Technologies (NGBT) Conference during ,2017 at Kalinga University, Bhubaneshwar, India (Received travel grant). Poster title: Codon based epistatic in interactions in human mitochondrial genome
- NGBT 2015, CCMB Hyderabad, India (Received travel grant). Poster title: A multilayer protein-protein interaction network analysis of different life stages in Caenorhabditis elegans
- Carcinogenesis 2015 conference at Tata Memorial Centre Advanced Centre for Treatment, Research and Education in Cancer (ACTREC) Mumbai. Poster title: Randomness and preserved patterns in Breast Cancer network
- International Symposium on Infectious Disease and Cancer, Indian Chemical Technology, Mumbai. Poster title: In silico drug docking of phyto inhibitors against Triosephosphate Isomerase in Plasmodium falciparum

SCIENTIFIC EXPERTISE

Languages: R, Python, SQL, C, C++, Java

Systems Immunology: Multi-omics integration (MCIA, MOFA), predictive modeling (Caret, WGCNA, DESeq, BTMs)

Technologies: Git, VS Code, RStudio, WebDev (Django, CMS, SQLAlchemy), Postgres

Technical writing: LaTeX, Microsoft Office, Inkscape, GIMP

SUMMARY

I lead interdisciplinary efforts in systems immunology and computational biology, with a focus on modeling immune responses to infections and vaccination. My research centers on integrating diverse multi-omics datasets to uncover immune signatures, identify biomarkers, and understand host immune responses. I develop and apply statistical and machine learning frameworks to study immune variation, combining insights from genomics, transcriptomics, proteomics, and metabolomics. Our work is informed by prior experience in evolutionary biology, mitochondrial genomics, and gene interactions, and is increasingly oriented toward predictive modeling and network-based analyses in computational biology.