

PRANAV KHADE

Ph.D. Bioinformatics

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JOB EXPERIENCE

Research Associate

Iowa State University

August 2017 – Ongoing Ames, IA

- Aided in research input into four grants from which \$1M NSF (1856477) was awarded in 2019 and several others under review
- Served on Bioinformatics and Computational Biology Graduate Student Organization committee at Iowa State University (2019)

EDUCATION

Ph.D Bioinformatics

Iowa State University

August 2017 – Ongoing Ames, IA

M.Sc. Bioinformatics

Savitribai Phule Pune University, India

2014 – 2016 Pune, India

- GPA: 5.34 out of 6
- Thesis Project: Systematic Conformer Generation (Cheminformatics)
- Training: Cell Biology, Immunology, Structural Biology, Genetics, Omics, Evolution, Cheminformatics, Data Mining, and Biostatistics. Overall, my Masters degree included a detailed overview of Bioinformatics. I learned everything from predicting epitomes given viral protein sequences to relating Single Nucleotide Polymorphism to phenotypes.

B.Sc. Biotechnology

Savitribai Phule Pune University, India

2014 – 2016 Pune, India

- Grade: First-Class
- Training: All the wetlab techniques that generate data for the Bioinformaticians.

PROJECTS

- Characterizing and Predicting Protein Hinges for Mechanistic Insight
- hdANM: Novel Comprehensive Elastic Network Model
- Structural Compliance - A New Metric for Protein Flexibility
- GOFindBias: An analysis tool for finding bias in the GAF files
- Graphically Accelerated CUDA based Systematic Conformer Generation Method
- Model for Identification of Antimicrobial Peptides
- Fast and Simple Protein Entropy Calculation Using Voronoi Diagrams

LIFE PHILOSOPHY

“Any problem is solvable as long as it can be broken down into smaller and manageable pieces.”

HONORS AND AWARDS



IGIB-GNR Scholarship

Institute of Genomics and Integrative Biology, Delhi, India

- Issued for Excellent performance in the entrance and academics at the Bioinformatics Centre, University of Pune.



DBT Fellowship

Department of Biotechnology, Government of India

- For each semester of M. Sc., top-performing students are awarded a monthly fellowship.



NSF Travel Grant

National Science Foundation, United States Government

- Support to attend “International Conference on Mathematical Multiscale Modeling in Biology”- Guanacaste, Costa Rica.



BCB Travel Fund

BCB Program, Iowa State University

- Based on my performance and work presentation

STRENGTHS

Innovative

Quick Learner

Persistent

Parallel Programming

API Development

Statistical Models

Machine Learning

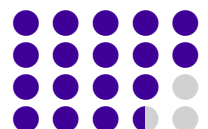
PROGRAMMING

Python

Perl

R

C++



COMPLETED PROJECTS

PACKMAN API

github.com/Pranavkhade/PACKMAN

📦 20000+ Downloads

📍 Featured on PDB website.

GOFindBias

github.com/Pranavkhade/GOFindBias

📦 Information Theory

clinical_SVs

github.com/collaborativebioinformatics/clinical_SVs

📦 Structural Variants

📍 Hackathon

PUBLICATIONS

📖 Book Chapters

- Jernigan, R. L., Khade, P. M., Kumar, A., & Kloczkowski, A. (2021). *Using surface hydrophobicity together with empirical potentials to identify protein-protein binding sites. application to the interactions of e-cadherins*. Computer Simulations of Aggregation of Proteins and Peptides, Springer US.

📄 Journal Articles

- Many others in the review process. (0).
- Khade, P. M. [Pranav M.], Scaramozzino, D., Kumar, A., Lacidogna, G., Carpinteri, A., & Jernigan, R. L. (2021). Hdanm: A new comprehensive dynamics model for protein hinges. *Biophysical Journal*. doi:<https://doi.org/10.1016/j.bpj.2021.10.017>
- Scaramozzino, D., Khade, P. M., Jernigan, R. L., Lacidogna, G., & Carpinteri, A. (2020). Structural Compliance - A New Metric for Protein Flexibility. *Proteins*. doi:10.1002/prot.25968
- Khade, P. M. [Pranav M], Kumar, A., & Jernigan, R. L. (2019). Characterizing and Predicting Protein Hinges for Mechanistic Insight. *Journal of molecular biology*. doi:10.1016/j.jmb.2019.11.018

👥 Conference Proceedings

- Khade, P. M. [Pranav M.], Scaramozzino, D., Kumar, A., & Jernigan, R. L. (2021). Hd-anm a computationally efficient, highly customizable and comprehensive elastic network model. (Vol. 120, 115a). doi:<https://doi.org/10.1016/j.bpj.2020.11.912>
- Kumar, A., Khade, P. M., Scaramozzino, D., Dorman, K., & Jernigan, R. L. (2021). Generating protein ensembles by applying forces to an improved elastic network model. (Vol. 120, 115a). doi:<https://doi.org/10.1016/j.bpj.2020.11.915>
- Khade, P. M. [Pranav M.], Kumar, A., & Jernigan, R. L. (2020). Using alpha shapes to characterize protein packing and capture the multiscale aspects of allostery. (Vol. 118, 40a). doi:<https://doi.org/10.1016/j.bpj.2019.11.401>

CONFERENCES

- Conference on Modeling of Protein Interactions 2018, KS
- 102nd Indian Science Congress, Mumbai
- International Conference on Mathematical Multiscale Modeling in Biology 2019, Guanacaste, Costa Rica
- Biophysical Society Annual Meeting (2020), San Diego, California
- The Society of Mathematical Biology (eSMB) 2020 (<https://smb2020.org/Pranav-Khade/>)
- Intelligent Systems for Molecular Biology (2020)
- Biophysical Society Annual Meeting (2021), Online

REFEREES

Dr. Robert L. Jernigan

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Dr. Karin Dorman

@ Iowa State University

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