Saurabh Belsare, PhD

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Current Position

Mar 2020-Current	Postdoctoral Scholar, Institute for Ecology and Evolution, University of Oregon Advisor: Prof. Andrew Kern

Work Experience

July 2017-Jan 2020	Postdoctoral Scholar, Institute for Human Genetics, University of California, San Francisco Advisor: Prof. Jeff Wall

Education

Aug 2011-May 2017	PhD. in Bioengineering | GPA: 3.7/4.0 The UCB-UCSF Graduate Program in Bioengineering, University of California, Berkeley Advisor: Prof. Teresa Head-Gordon
Aug 2007-May 2011	Bachelor of Technology (Hons.) in Chemical Engineering | Minor in Biosciences | GPA: 8.67/10.0 Indian Institute of Technology, Bombay, Mumbai, India Bachelor Thesis:Computational Prediction of Loop Structures in GPCR Proteins | Advisor: Prof. Santosh Noronha

Publications & Presentations

Journal Publications

- South Asian Patient Population Genetics Reveal Strong Founder Effects and High Rates of Homozygosity – New Resources for Precision Medicine (2021) Jeffrey D. Wall, ... , **Saurabh Belsare**, ..., Andrew S. Peterson [In Review]
- Genetic profiles of 103,106 individuals in the Taiwan Biobank provide insights into the health and history of Han Chinese (2021) Chun-Yu Wei, ... , **Saurabh Belsare**, ..., Pui-Yan Kwok *npj Genomic Medicine 6, 1* DOI: 10.1038/s41525-021-00178-9
- Evaluating the quality of the 1000 Genomes Project data. (2018) **Saurabh Belsare**, Michal Sakin-Levy, Yulia Mostovoy, Steffen Durinck, Subhra Chaudhry, Ming Xiao, Andrew S. Peterson, Pui-Yan Kwok, Somasekar Seshagiri and Jeffrey D. Wall (2019) *BMC Genomics 20, 1* DOI: 10.1186/s12864-019-5957-x
- Analysis of 100 high-coverage genomes from a pedigreed captive baboon colony. (2019) Jacqueline A. Robinson, **Saurabh Belsare**, Shifra Birnbaum, Deborah E. Newman, Jeannie Chan, Jeremy P. Glenn, Betsy Ferguson, Laura A. Cox and Jeffrey D. Wall *Genome Res. 29: 848-856* DOI:10.1101/gr.247122.118
- Solvent Entropy Contributions to Catalytic Activity in Designed and Optimized Kemp Eliminases. (2017) **Saurabh Belsare**[1], Viren Pattni[1], Matthias Heyden, Teresa Head-Gordon, *J. Phys. Chem. B 122, 21, 5300-5307* DOI: 10.1021/acs.jpcb.7b07526
- Mode Specific THz Spectra of Solvated Amino Acids using the AMOEBA Polarizable Force Field. (2017) Alexander Esser[1], **Saurabh Belsare**[1], Dominik Marx, and Teresa Head-Gordon, *Phys. Chem. Chem. Phys. 19, 5579-5590* DOI: 10.1039/C6CP07388C

Invited Talks

- Studying the dynamics and solvent interactions of amino acids and proteins through biomolecular simulations (12th January 2018) Department Seminar, Department of Biosciences and Bioengineering, Indian Institute of Technology, Bombay

Conference Presentations

- Imputation in South Asian individuals using a high-coverage South Asian reference panel. (October 2019) **Saurabh Belsare** et al (American Society of Human Genetics Meeting 2019)
- Evaluating the phasing accuracy of the 1000 Genomes Project. (November 2017) **Saurabh Belsare** and Jeff Wall (Bay Area Population Genomics Meeting 2017) [Poster]
- Studying Solvation of Small Biomolecules via Molecular Dynamics using a Polarizable Force Field. (Feb 2017) **Saurabh Belsare**[1], Alexander Esser[1], Dominik Marx, and Teresa Head-Gordon (Proceedings of the Biophysical Society Meeting 2017) [Poster]
- Studying Solvation of Small Biomolecules via Molecular Dynamics using a Polarizable Force Field. (January 2017) Alexander Esser[1], **Saurabh Belsare**[1], Dominik Marx, and Teresa Head-Gordon. (Berkeley Statistical Mechanics Meeting) [Poster]
- Dynamic metrics for rationalizing directed evolution of enzymes. (August 2014) **Saurabh Belsare**, Teresa Head-Gordon (Proceedings of the American Chemical Society Meeting 2014) [Poster]
- Rationalizing Directed Evolution through Protein Dynamics. (Jan 2014)
- Homology Modeling of Protein Structure using Fragment/Profile based search method in CASP9. M. Parthiban, S. Susdalzew, **S. Belsare**, et. al. 2010 Critical assessment of methods for protein structure prediction (CASP9) - Abstract Book

[1]Equal Contribution

Research

Mar 2020-Current

Postdoctoral Research
Developing deep learning methods for genomic analysis
Advisor: Prof. Andrew Kern, Prof. Peter Ralph, Institute for Ecology and Evolution, University of Oregon

- Developing a deep learning based method for genomic analysis
- Performing imputation via deep learning
- Developing a method for ancestral haplotype reconstruction

July 2017-Jan 2020

Postdoctoral Research
Analysis of haplotype phasing and genotype imputation methods applied to human genomic data
Advisor: Prof. Jeff Wall, Institute for Human Genetics, University of California, San Francisco

- Assessing the accuracy of public databases for phasing and imputation
- Estimating recombination rates in humans and primates
- Evaluating the accuracy of a population specific reference panel for imputation
- Design of a SNP array for generating an optimal imputation study panel

July 2012-June 2017

Graduate Research
Studying dynamics of small biomolecules and enzymes, and their interactions with solvent
Advisor: Prof. Teresa Head-Gordon, Department of Bioengineering, University of California, Berkeley

- Developing computational methods to analyze dynamics of biomolecules
- Implemented codes in Fortran within existing simulation packages to enable calculations of dynamic observables
- Developing an understanding of the influence of specific residue modification on protein function
- Understanding the influence of solvent on biomolecule behavior via solvent VDOS and THz observables
- Developed scripts in python and matlab for determining observables from simulation data

May 2016-June 2017

Research Collaboration
Studying entropic contributions to enzyme solvation using a polarizable force field
Co-Advisor: Prof. Matthias Heyden, Max Planck Institut für Kohlenforschung, Mülheim

- Performed molecular dynamics simulations of Kemp Eliminase artificial enzymes and MMP enzyme using the AMOEBA polarizable force field
- Analyzed the solvation entropy trends over evolved variants in Kemp Eliminase to explain solvent contribution to improved catalytic activity
- Analyzed solvation around MMP active site with zinc cofactor, to understand influence of polarization and solvation in entropic contribution to MMP activity

May 2015-June 2017

Research Collaboration
Studying small molecule modes via classical simulations
Co-Advisor: Prof. Dominik Marx, Lehrstuhl für Theoretische Chemie, Ruhr Universität, Bochum

- Modified existing classical simulation approaches to compare with *ab-initio* simulation approaches
- Developed a formulation for localizing charges to allow mode decomposition
- Obtained significant agreement of dynamic modes predicted from classical simulations to *ab-initio* simulations

May-July 2010

Research Internship
Protein structure prediction using a homology based approach
Advisor: Dr. Michael Lappe, Structural Proteomics Group, Max Planck Institute for Molecular Genetics, Berlin

- Explored tools available for protein structure prediction and developed an efficient prediction pipeline
- Part of team participating in CASP 9 (Critical Assessment of tertiary Structure Prediction) competition
- Predicted structures for 18 out of 60 target proteins released for structure prediction
- Developed scoring function in Java assessing quality of predicted structures based on favorability of spatial location of a residue with respect to its neighbors

Aug 2010-May 2011

Undergraduate Thesis
Computational Prediction of Loop Structures in GPCR Proteins
Advisor: Prof. Santosh Noronha, Department of Chemical Engineering, Indian Institute of Technology, Bombay

- Reviewed existing ab-initio transmembrane protein folding and packing methods in in literature and identified the most suitable method for loop structure prediction
- Implemented a kinematic loop closure algorithm method to predict loop structure for proteins.
- Good loop closure was observed for test system beta adrenoceptor

Peer Reviewing

Peer reviewer for journals: Genetics, G3: Genes | Genomes | Genetics, Nucleic Acids Research, Molecular Ecology Resources, Integrative and Comparative Biology

Teaching Assistantship

BioE 131/231: Introduction to Computational Molecular Biology [Aug-Dec 2013]
Course Instructor: Prof. Ian Holmes, Department of Bioengineering, University of California, Berkeley

- Graduate student instructor (GSI) for a joint undergraduate-graduate course
- Conducted introductory programming classes, lab sessions, and office hours
- Graded homeworks and projects

Relevant Coursework

UC Berkeley: Computational Methods in Biology, Statistical Phylogenetics, Probabilistic Modeling in Computational Biology, Introduction to Protein Informatics, Thermodynamics and Statistical Mechanics, Software Engineering for Scientific Computing, Applications of Parallel Computers, Introduction to Statistical Computing
Indian Institute of Technology, Bombay: Introduction to Computational Biology, Chemistry of Biomolecules, Molecular Biology, Molecular Immunology, Genetic Engineering, Optimization, Applied Multivariate Statistics in Chemical Engineering

Computer Skills

C/C++, Python, fortran, MATLAB, R, MATHEMATICA, LaTeX, gnuplot, OpenMP