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Summary:

Bioinformatician and data analyst with an eye for details hidden in big data. A PhD with over 6 years of experience in structural immunology, India and certification in Data Science from Rutgers University, New Jersey. Fast learner, adept at working independently and in collaboration. Disseminates knowledge and experiential learning to peers.

Technical Skills:

1.Life Sciences Tools/ Techniques: **Dry-lab:** Data curation, structural data mining, High Performance Computing (HPC), Molecular Dynamics Simulation, Structure analysis, Molecular modeling, Docking, Energy calculations using MM(GB)SA/MM(PB)SA, Interaction profiling using CPPTRAJ, Phylogenetic analysis, Sequence analysis, Domain prediction, Epitope mapping. **Wet-lab:** DNA, RNA and plasmid extraction, Agarose gel electrophoresis, SDS-PAGE, PCR, btaining and handling microbial pure culture, biochemical test, Antimicrobial Susceptibility Test by disc-diffusion method.

2.Bioinformatics programs and databases: AMBER, Pymol, Chimera, VMD, MODELLER, CLUSTAL, IgBLAST, PIGS, Schrodinger Maestro, Discovery Studio suite, PISA, PDBsum, PDBfunc, Expasy proteomics tool, PDB, IMGT, SAbDab, NCBI, EBI etc.

3.Programming: Python (proficient), R (fundamentals), Java (fundamentals), Perl (fundamentals)

4.Data Science: MS Excel, Machine Learning (supervised and unsupervised), Jupyter notebook, Pandas, Matplotlib, SciPy, NumPy, API, MongoDB, PostgreSQL, HTML, CSS, D3.js, Leaflet, Tableau, Plotly, Dashboard building, Extract Transform Load (ETL), Apache- Spark, AWS S3, Scikit-learn, Keras, Tensorflow.

Projects:

PhD project:
New Paradigm in Antigen Recognition: Systems Approach of Antibody-Antigen Interaction Data: Conducted analysis of structural data of antibody-antigen complexes retrieved from PDB by performing predictive modeling, structural and sequence analysis, interaction profiling and molecular dynamics simulation in AMBER 14. Study showed optimization of antibody structures during maturation to deal with different types of infection eliciting immune response in individuals (https://bmcstructbiol.biomedcentral.com/articles/10.1186/s12900-018-0096-1).

Data Science projects:
1. LubDub:Machine Learning Based App For Non-Invasive Diagnosis Of Heart Disease: Built a predictive model to assess the potential risk of occurrence of heart disease based on analysis of big data on associated risk factors. Feature selection, data-preprocessing and various classification algorithms were leveraged to train the model using Scikit-learn and Tensorflow. Final predictive model was built using deep learning and tableau dashboard was deployed on heroku (https://lubdub-heartsense.herokuapp.com/).(Github: https://github.com/msfa12th/heartsense).

2. Paradise: An Interactive Dashboard for Top 10 Leading Death Causes in The United States: Led a team of four to deploy wrangled data from CDC on to cloud mongoDB. Several API routers were created using FLASK,

interactive visualizations were created using JavaScript libraries. Dashboard was deployed on heroku (http://livebetter.herokuapp.com/). (Github: https://github.com/Harmeet2504/full-stack-web-app-project).

3. What-if Analysis of Residential Real Estate: Led a team of four to examine the impact of parameters affecting valuation of residential real estate in counties of New Jersey. Statistical analysis and visualizations were performed using Python, Pandas, NumPy, SciPy, Matplotlib. The analysis was significant for decision making about the best places to rent or buy residential properties in New Jersey. (https://github.com/Harmeet2504/Project-What-if-analysis-of-residential-real-estate/).

Publications, book chapters, scientific proceedings and posters:

1. Kumar, A.*, **Kaur, H**.*, Jain, A., Nair, D., Salunke, D.M. (2018). Docking, thermodynamics and molecular dynamics (MD) studies of a non-canonical protease inhibitor, MP-4, from Mucuna pruriens. Scientific Reports 12;8(1): 689. doi: 10.1038/s41598-017-18733-9 (*equal authorship).

2. **Kaur, H.**, Saini, N., Mohanty, D. and Salunke, D.M. Deciphering evolution of Immune recognition in antibodies. BMC Structural Biology 2018); 18 (1): 19. doi:10.1186/s12900-018-0096-1).

3. **Kaur, H**., Salunke, DM (2015). Antibody promiscuity: Understanding the paradigm shift in antigen recognition. IUBMB Life 67:498.

4. Salunke, D.M., **Kaur, H**. and Gill, J (2013). New Paradigms in antibody specificity: Structural biology of antigen recognition by germline antibodies. Biomolecular forms and functions (Ed. M. Bansal and N. Srinivasan). World Scientific Publishing, pp. 173.

Experience:

1. **DBT Research Trainee**, Bioinformatics Infrastructure Facility (BIF), Gauhati University, May-Oct 2010.
Role: Sequence analysis and phylogenetic studies of GCH1 gene product.

2. **Research Intern**, Regional Medical Research Centre, Dibrugarh, Jun-Jul 2008.
Role: Standardization of DNA extraction and PCR protocols to study the endothelial nitric oxide synthase gene.

3. **Mentor**ed an Indian National Science Academy (INSA) trainee on a 3 months project at Regional Centre for Biotechnology, Delhi-NCR, Apr-Jun 2016.

4. **Coordinator**, student's affairs, Regional Centre for Biotechnology, Delhi-NCR, 2013-2016.

 Education:

1.Certification, Data Science (Rutgers University, New Jersey, USA), 2019- 2020.
2.PhD, Bioinformatics (UNESCO Regional Centre for Biotechnology, Faridabad, India), 2012- 2019.
3.Certification, Data Science: R Basics (HarvardX), May 2019.
Credential URL: https://courses.edx.org/certificates/b04d33adbac440c089aae6a742d22fd1
4.M.Sc., Biotechnology (Gauhati University, Guwahati, India), 2007- 2009.

Awards and Honors:

CSIR Senior Research Fellow, 2014-2017.
Best scientific poster award at Program Advisory Committee meet (PAC), RCB, 2015.
CSIR Junior Research Fellow, 2012-2014.
NCC 'B' and 'C' (Ministry of Defense, Govt. of India), 2006.
State Merit Scholarship, 2001, Govt. of Assam.