Hari **Sharma**

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Summary

- Organized and detail-oriented computational scientist skilled at working on multiple projects and collaborating to drive scientific efforts to successful outcomes.
- Expertise in quantitative and statistical analysis on complex datasets.
- Excellent communication skills and proven ability to thrive in a fast-paced environment.

Technical Skills

Programming	Python | SQL | BASH | C++
DATA SCIENCE & MACHINE LEARNING	Deep Learning/Neural Networks (TensorFlow | Keras | Image Processing with CNNs) | Unsupervised Learning (K-Means | Clustering | PCA) | Linear & Logistic Regression (Scikit-Learn) | Data Processing & Visualization (Pandas | Matplotlib | Altair | Seaborn) | REST API Development | Big Data with PySpark | Cloud computing with AWS
INDUSTRY KNOWLEDGE	Computational Drug Discovery | Computational Molecular Modeling | Cheminformatics | Structural Biology

Education

The Data Incubator
Data Scientist Certification - Fellowship Program — *Apr 2023 - May 2023*

University of Connecticut — *Storrs, CT, USA*
PhD in Physics — *Jan 2015 - Aug. 2019*

University of Connecticut — *Storrs, CT, USA*
M. S in Physics — *Aug 2012 - Dec. 2014*

Experience

StemSynergy Therapeutics INC. — *Franklin, TN, USA*
Senior Scientist — *Oct. 2021 - Present*

- Lead multiple projects involving the computational aspects of drug discovery using state-of-the art technologies.
- Collaborated with experimental chemist and biologist and contributed towards the design of future experiments.
- Analyzed the data (Gigabyets) obtained from large scale molecular dynamics (MD) simulations using self written python scripts.
- Wrote BASH shell scripts for performing fully automated molecular dynamics simulation using GROMACS software suite.
- Administered linux computer cluster nodes with GPU's and CPU's (4 nodes), installaed open source molecular modeling simulation softwares relevant for drug discovery and lead computational part of the research.

Vanderbilt University — *Nashville, TN, USA*
Postdoc Scholar — *Sept. 2019 - Sept. 2021*

- Contributed towards the ligand docking algorithm in ROSETTA (C++ codebase) macromolecular modeling suite to carry out docking of ensembles of congeneric series of ligand simultaneously into protein and their mutant variants.
- Communicated results to collaborators and provided recommendations for future experiments.
- Mentored rotating graduate student.

University of Connecticut — *Storrs, CT, USA*
Graduate Research Assistant — *Aug 2012 - Aug 2019*

- Assembled and administered linux computer cluster nodes with installation of open source molecular modeling software suites.
- Wrote python scripts from scratch to analyze the gigabytes of data obtained from MD simulations.
- Implemented an algorithm using Graph theory and matrix algebra that is able to compute the end points of a cloud of data points oriented in a flexible contour where data points are dynamic.