SPANDANA MAKENENI

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Data Science Portfolio: https://smakeneni.github.io

Summary

- Core expertise in bioinformatics, programming, and derivation of insights from large complex scientific datasets
- Excellent communicator experienced at integrating computational and experimental results through multidisciplinary collaborations
- Demonstrated understanding and practical experience with data visualization tools, advanced statistical modeling, and machine learning algorithms as evidenced by data science portfolio
- Motivated to drive successful outcomes in health sciences via synergistic passion for data analysis, a strong scientific background, and an eagerness to maintain cutting edge knowledge of the rapidly evolving data science tools

Skills

- Programming: R (tidyverse, dplyr, ggplot2, plotly, bioconductor, flexdashboard, shiny, markdown), Shell scripting, C++, HTML/CSS, familiar with Python, MATLAB, and AWS
- Tools: Git, Jupyter, familiar with D3.js and SQL
- Techniques: Advanced statistical modeling and regression, survival analysis, machine learning (regression, classification, and clustering algorithms)

Relevant coursework

- Data Science Specialization from Johns Hopkins (Coursera)   **Completed 2019**
- Data Scientist with R (Datacamp)   **Completed 2019**
- Statistical Analysis in R for Public Health (Coursera)   **Completed 2020**

Education

- **Ph.D.,** Bioinformatics, University of Georgia   **May 2015**
- **B.Tech**, Industrial Biotechnology, Bharath University (India)   **May 2007**

Work Experience

Postdoctoral research associate, University of Sciences   **May 2016 – October 2019**

- Achieved a 5-fold improvement in the accuracy of 3D-structure prediction of arylamide foldamer/carbohydrate complexes by employing a density-based clustering algorithm and optimizing molecular dynamics and carbohydrate simulation workflows
- Collaborated on multiple projects with researchers at Ludwig-Maximilians University in Munich and delivered computational structure predictions that guided chemical synthesis and experimental testing of foldamer molecules
- Conceived, designed, and supervised completion of research projects for 7 undergraduate and summer intern students
- Built interdepartmental connectivity and stimulated scientific exchange and collaboration by initiating and organizing a bi-weekly department seminar series that included 3 departments and 5 labs across all computational disciplines at USciences

Postdoctoral research associate, University of Georgia   **May 2015 - May 2016**

- Implemented a user friendly web-based tool that vastly expanded access to expert computational modeling tools used to predict antibody-carbohydrate complexes
- Managed the computational aspects of a collaborative research project with a lab in Israel aimed at optimizing antibodies that bind glycan epitopes on cancer cells resulting in a publication

Graduate Researcher, University of Georgia   **2008-2015**

- Enabled more accurate quantitation and communication of carbohydrate conformation throughout the glycobiology scientific community by developing, implementing, and publishing an algorithm that characterizes pyranose conformations more accurately than existing methods
- Improved the accuracy and standardization of antibody carbohydrate complex structure prediction by designing, developing, and validating a protocol that successfully predicts the structure of the complex
- Accelerated multiple structural glycobiology projects within the Woods lab by developing automated pipelines for routine data analysis and data preparation procedures
- Validated computational methods through comparison to experimental data via local and long-distance collaborations
- Impacted the structural glycobiology field by communicating results broadly via 7 pier-reviewed publications (3 first author), presentations at national conferences, and publication of an automated web tool

Publications

- **Spandana Makeneni**, Zhiwei Liu, Ivan Huc, Vojislava Pophristic, "Unsupervised learning to filter false positive foldamer-carbohydrate complex predictions" *Manuscript in preparation*
- Ron Amon, Oliver C Grant, Shani Leviatan Ben-Arye, **Spandana Makeneni**, Robert J Woods, Vered Padler-Karavani, "A combined computational-experimental approach to define the structural origin of antibody recognition of sialyl-Tn, a tumor-associated carbohydrate antigen", *Nature SciRep* 8*,* 10786 (2018).
- **Spandana Makeneni**, David F. Thieker, Robert J. Woods, "Enriching the pose prediction accuracy in molecular docking via pose-clustering and MD simulations", *Journal of Chemical Information and Modeling* 2018 58 (3), 605-614
- Anita K. Nivedha, David F. Theiker, **Spandana Makeneni**, Huimin Hu, Robert J. Woods, "Vina-Carb: Improving Glycosidic Angles During Carbohydrate Docking", *Journal of Chemical Theory and Computation* 2016, 12(2), 892-901.
- Parnian Lak, **Spandana Makeneni,** Robert J. Woods, and Todd L. Lowary "Specificity of Furanoside–Protein Recognition through Antibody Engineering and Molecular Modeling", *Chemistry: A European Journal 2015*, 21(3), 1138-48
- **Spandana Makeneni**, Ye Ji, David C. Watson, N.Martin Young, Robert J. Woods, "Predicting the origins of anti-blood group antibody specificity: A case study of the ABO A- and B- antigens", *Frontiers in Immunology* 2014, 5, 397.
- **Spandana Makeneni**, Lachele B. Foley, Robert J. Woods, "BFMP: A method for discretizing and visualizing pyranose conformations", *Journal of Chemical Information and Modeling* 2014, 54(10), 2744-2750.
- Anita K. Nivedha, **Spandana Makeneni**, Lachele B. Foley, Matthew B. Tessier, Robert J. Woods, "The importance of ligand conformational energies in carbohydrate docking: Sorting the wheat from the Chaff", *Journal of Computational Chemistry* 2014, 35(7), 526-39.
- David Luper, **Spandana Makeneni**, "Telomerase Gene Prediction Using Support Vector Machines", 2011 I*nternational Conference on Bioinformatics and Computational Biology* (BIOCOMP 2011,Las Vegas, NV, July 18-21, 2011)