

SPANDANA MAKENENI

makeneni@gmail.com • (706)-206-4487 • Philadelphia, PA

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

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| • 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

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

Relevant Portfolio Projects

Survival Analysis on Lung cancer

- Employed Kaplan-Meier curves and Cox proportional hazard model to estimate 1-year and 5-year survival rates on two types of non-small cell lung cancers using clinical trial data of ~800 patients obtained from the cancer genome atlas program (TCGA)
- Explored demographic, pathological, and smoking history characteristics and identified statistically-significant covariates that influence survival rates

Injection Drug User population estimates- Code for Philly Datathon 2020

- Worked with a team of 4 participants to assist a non-profit organization, Prevention Point, which works with communities affected by drug use.
- Integrated and analyzed data from multiple public databases and employed indirect estimation methods (multiplier method and Poisson estimation) to estimate the number of intravenous drug users in the city of Philadelphia
- The calculated estimates will aid prevention point to secure funding for Naxalone kits to prevent deaths resulting from drug overdose.

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 peer-reviewed publications (3 first author), presentations at national conferences, and publication of an automated web tool

US Residency: US permanent resident, no sponsorship required.

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. Thieker, **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 *International Conference on Bioinformatics and Computational Biology (BIOCOMP 2011, Las Vegas, NV, July 18-21, 2011)*