CONTACT INFO

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Melbourne, Australia

scholar.google.com/citations?user=z95fSCAAAAAJ

https://github.com/Susmitha-Nair?tab=repositories

RESEARCH INTERESTS

RESEARCH DESIGN AND ANALYSIS
ARTIFICIAL INTELLIGENCE
DRUG DISCOVERY
STATISTICS
DATA VISUALIZATION
NGS
MULTI-OMIC DATA ANALYSIS
BIOINFORMATICS
ANNOTATION
HEALTH RESERACH
PROTEIN-PROTEIN INTERACTION
MOLECULAR BIOLOGY

PROFESSIONAL SKILLS

R
PYTHON
JAVA
SQL
PARALLEL PROGRAMMING
HIGH PERFORMANCE COMPUTING
BIOCONDUCTOR
DAVID
ALPHAFOLD
PYMOL
dbSNP
MICROSOFT OFFICE
GSEA
PRESENTATION SKILLS
UNIX
MANUSCRIPT PREPARATION
PROJECT MANAGEMENT

SUSMITHA SHANKAR, Ph.D.

BIOINFORMATICIAN | STATISTICIAN | DATA SCIENTIST | AI EXPERT

Experienced bioinformatics researcher with a doctorate in computational molecular biology and master's in computer science and engineering, specializing in big data analysis, statistics and advanced machine learning Adept at leading interdisciplinary research teams and contributing to high-impact publications. Proven ability to communicate complex scientific concepts to diverse audiences and collaborate with global research institutions. Passionate about leveraging AI and advanced analytics to drive business transformation and innovative solutions in the biotech and other technological industries. Seeking to bring deep technical expertise, strong communication, leadership and collaborative approach to teams tackling with complex business challenges in artificial intelligence, enabling digital transformation.

POSITIONS

May 2024 - May 2020

Researcher, International PhD Programme

Institute Of Molecular Biology, Johannes Gutenberg Universität, Mainz, Germany

- Led the bioinformatics research - from designing research protocols, advising on experimental designs to analysis and interpretation, to understand protein quality control
- Developed end-to-end pipeline for annotating, preprocessing, managing and effectively multi-omics data from various sequencing techniques in yeast and human genome.
- Successfully inferred certain sequence motifs and biophysical properties that help in protein degradation, using optimized deep learning and natural language processing (NLP) model, which could further be used to design PROTAC-like drug enzymes to target carcinogenic proteins
- Deciphered the role of various biophysical properties and molecular mechanisms affecting protein localizations, using statistical analysis and effective visualization

May 2020 - May 2017

Research Fellow – Data Analyst

Amrita School Of Engineering, Bangalore, India

- Led the team of 5 research students, on the research for drug repurposing using multi-omics data such as genomic, transcriptomic and proteomics data, and clinical trial drug databases from sources such as FDA and clinicalTrials.org, using statistical approaches and machine learning
- Predicted therapeutic effects of drugs and their side effects using various machine learning and network-based models

May 2020 - May 2018

Supervisor – Data Science

CubeBioAI, Bangalore, India

- Led the data analytics team working on project "Mathematical interpretation of various molecular fingerprints in various deep neural network to predict Adverse Drug Reactions in health"
- Mentored research assistants working on project "Use of deep learning and statistical techniques for predicting functional similarity among transcriptomic profiles from LINCS L1000 data"
- Introduced analysis of RNA-seq data, drug databases as well as protein-protein interaction databases to bioinformatics Master's students in the form of a graded course

PUBLISHED WORKS

2023

Nature Communications

Orphan quality control by an SCF ubiquitin ligase directed to pervasive C-degrons

S Shankar, Ka-Yiu Edwin Kong, Frank Rühle, Anton Khmelinskii
doi.org/10.1038/s41467-023-44096-z

2020

Chemical Biology and Drug Design

Predicting Adverse Drug Reactions of Two-drug Combinations using Structural and Transcriptomic Drug Representations to Train an Artificial Neural Networks
S Shankar, I Bhandari, DT Okou, G Srinivasa, P Athri
doi.org/10.1111/cbdd.13802

2019

Biomedical and Pharmacology Journal

Integrated system for easier and effective access to drug information
S Shankar, S Thangam
dx.doi.org/10.13005/bpj/1736

EDUCATION

2024 - 2020

Doctor Of Philosophy

Computational Molecular Biology
Institute Of Molecular Biology, Johannes Gutenberg University, Germany
Grade: 1.0/1.0 (highest)
Status: Magna cum laude (very good)
Thesis: Dissecting Specificity of Short Linear Motifs in Protein Quality Control.

2019 - 2017

Master Of Technology

Computer Science And Engineering
Amrita Vishwa Vidyapeetham, India
Cumulative Grade: 9.01/10
Thesis: Development of effective data integration techniques for drug-based information management system

2017 - 2013

Bachelor Of Technology

Computer Science And Engineering
Amrita Vishwa Vidyapeetham, India
Cumulative Grade: 8.55/10
Project Report: Treatment of cancer protein by treating the first neighbor protein

PROJECTS

Apr 2024 - Apr 2021

Visual Pooled-to-arrayed Screening Reveals Compartment Specific Determinants Of Tail-anchored Proteins

Institute Of Molecular Biology, Mainz, Germany

- Initiated and collaborated with experimental biologists.
- Analyzed microscopy data for understanding the localization of mutated proteins after deep mutational scanning using statistical method such as PCA, t-SNE and machine learning models such as Random Forest. Correlating the localization with composition of amino acids, hydrophobicity, volume and other biophysical properties indicated 67% of proteins with low hydrophobicity localizes in mitochondria.

Oct 2020 - Dec 2019

Predicting Adverse Drug Reactions Of Two-drug Combinations Using Structural And Transcriptomic Drug Representations To Train An Artificial Neural Network

Amrita School of Engineering, Bangalore, India

- Predicted side effects due to combinations of drugs from PharmGKB database using their transcriptomic profile on 20k human genes. 34,549 common drug pairs between these two databases were used to train an artificial neural network (ANN), to predict 243 ADRs that were induced by at least 10% of the drug pairs. The model predicts the occurrence of these ADRs with an average accuracy of 82% across a multifold cross-validation

Jun 2019 - Apr 2018

Integrated System For Easier And Effective Access To Drug Information

Amrita School of Engineering, Bangalore, India

- Integrated drug databases from openFDA, namely adverse events, product label and enforcement, validated with ClinicalTrials.org, coupled with visualization platform using big data technologies such as Hadoop for the study of drugs and their adverse effects.
- Concatenation- based approach and the use of technologies such as SQL Server, dotnet core and creation of multiple threads running parallelly in asynchronous fashion has reduced the computational process time by 50% and ensures ACID properties.

VOLUNTEERING

Present - Jan 2023

Events Organizer and IT support

Neuroscience Graduates' Colloquium

- Organized 3 industry related talk for scientific students from Johannes Gutenberg University, Mainz, Germany

Nov 2023 - Nov 2022

IPP Representative

Institute of Molecular Biology

- Organized 2 academic talks for PhD students in Institute of Molecular Biology, Mainz, Germany
- Participated in organizing funds for international conference travels for doctoral students

CONFERENCE, WORKSHOPS AND SEMINARS

Sept 2023

Basel Computational Biology Conference

Basel, Switzerland

- Presented poster titled “Deep Learning based analysis infers degron for human protein termini” before 250+ participants

May 2023

Protein Quality Control : From molecular mechanisms to therapeutic intervention.

Dubrovnik, Croatia

- Presented poster and gave oral presentation on “Deep Learning to infer degron motif in yeast C-terminome” before 750+ researchers

May 2023

Research Slam

Mainz, Germany

- Presented Slam talk titles – “What does not kill you, makes you smarter” in IPPSlam before 150 participants

REFERENCES

Reference available upon request