

Kasthuri Kannan, PhD

Associate Professor, UT MD Anderson Cancer Center

✉ kskannan@mdanderson.org ☎ (551) 284 9106 📍 2130 W Holcombe Blvd. Houston. TX 77494
🔗 <https://kannan-kasthuri.github.io/> 🇺🇸 US Citizen 🔗 [linkedin.com/in/kasthuri-kannan-0a05b43](https://www.linkedin.com/in/kasthuri-kannan-0a05b43)

PROFILE

Data scientist with 15 years experience primarily working in cancer research. Recognized for managing and hands-on approach with large-scale data, statistical modeling, and image processing. A team player.

Actively seeking an opportunity to excel in an industrial setting.

EDUCATION

Doctor of Philosophy (Computer Science)

Texas A&M University

2002 – 2008
College Station, Texas

Master of Science (Mathematics)

Texas A&M University

2000 – 2002
College Station, Texas

Master of Science (Mathematics)

Indian Institute of Technology, Madras

1998 – 2000
Chennai, India

Bachelor of Science (Mathematics)

University of Madras

1995 – 1998
Chennai, India

SKILLS

Leadership

● ● ● ● ●

Managing data science and bioinformatics projects

Data Science/Machine Learning/AI

● ● ● ● ●

Math, CS, Statistics and Programming
Ethical hacking, Domain knowledge, LLMs

Software (Representative)

● ● ● ● ●

Python, R, Java, Cypher, SQL, Bioinformatics tools,
Unix/HPC/Bash, Neo4j, MySQL, PostgreSQL, HTML,
Javascript, Spatstat, Pytorch, Tensorflow

Bioinformatics & Image Processing

● ● ● ● ●

Pipeline development and data engineering
Geospatial analysis

PROFESSIONAL EXPERIENCE

UT MD Anderson Cancer Center

Associate Professor

02/2020 – present
Houston, TX

- Leading graph database development for multi-omics data integration
- Establishing spatial modeling of pathology images using R spatstat
- Supervising post-doctoral fellows and students

New York University

Assistant Professor

11/2013 – 08/2019
New York, NY

- Established bioinformatics pipelines and investigated cancer datasets
- Directed and taught data science and machine learning courses

Memorial Sloan-Kettering Cancer Center

Research Fellow/Associate

04/2011 – 10/2013

New York, NY

- Established mutation pipeline for Brain/Head & Neck cancers
- Discovered ATRX mutations in lower grade gliomas
- Provided directed insights in various cancer studies through data analysis

Pennsylvania State University

Research Associate

10/2010 – 03/2011

State College, PA

- Organized data analysis pipelines
- Offered bioinformatics consultation to researchers
- Managed sequencing tasks

Stowers Institute for Medical Research

Research Specialist II

01/2008 – 09/2010

Kansas City, MO

- Developed image processing methods for worm and fly tracking
- Implemented an automated data workflow to process yeast cell images
- Responsible for high quality image acquisition and microscope maintenance

Knowledge Based Systems, Inc

Internship

01/2007 – 12/2008

College Station, TX

- Delivered data driven directed insights for aircraft movement operations
- Proposed cost and time saving measures for managing air force logistics

ACTIVE DATA SCIENCE PROJECTS

Geospatial modeling of tissues — Spatial point processes are powerful statistical frameworks for studying point patterns. By representing cells as points and annotating the measurements taken on those cells, such as gene expression at single cell level, it is appropriate to study their interactions using point processes. We extensively use spatstat, an R package, to model interactions and derive directed insights in cancers.

Biomarker discovery using graph database — Graph databases can help identify biomarkers by efficiently representing complex biological networks. By enabling powerful queries and community detection algorithms, graph databases make exploring the relationships between multiple genes easier, thus facilitating the discovery of potential biomarkers critical for diagnostics or therapeutic targets. We use Neo4j, a property graph database, and algorithms from the Graph Data Science Library (GDS) to derive insights and propose actionable biological targets.

Biomarker validation using Graph Convolution Networks (GCNs) — Insilico validation of biomarkers is critical for providing actionable biological targets for experiments and prognosis. We apply graph convolutional networks to validate critical biomarkers discovered through the graph database. GCNs enhance biomarker discovery by leveraging the structure of biological networks, such as gene-gene interactions, and learning meaningful node/edge representations. By aggregating information from a node's neighbors, GCNs capture local and global patterns, allowing the model to predict relationships between genes and diseases more effectively.

INVITED TALKS (REPRESENTATIVE)

Mayo Clinic (2023), National University of Singapore (2022), Texas A&M University (2021), Courant Institute of Mathematical Sciences (2019), Institute of Mathematical Sciences, w/ honorarium (2018)

PUBLICATIONS

Authored/co-authored 32 peer reviewed articles, that includes very high-impact journals.

Please refer https://pubmed.ncbi.nlm.nih.gov/?term=kasthuri+kannan&sort=date&sort_order=desc 