

Kasthuri Kannan
Associate Professor and Director
<https://kannan-kasthuri.github.io/>

Departments of Translational Molecular Pathology & Neurosurgery UT MD Anderson Cancer Center
Visiting Associate Professor (honorary appointment) National University of Singapore, Singapore

Professional Interests

Data Science, Systems Biology, Computational Pathology, Bioinformatics

Collaborations (representative)

1. Anand Jeyasekharan, Assistant Professor, Cancer Science Institute, National University of Singapore.
Patterns of oncogene co-expression at single cell resolution in cancer influence survival. *Cancer Discovery*. Feb. 2023.
 2. Dean Felsher, Professor, Stanford University.
MYC and Twist1 cooperate to drive metastasis by eliciting crosstalk between cancer and innate immunity. *eLife*. Jan. 2020.
 3. Jason Huse, MD, PhD, Associate Professor & Director, MD Anderson Cancer Center.
Atrx inactivation drives disease-defining phenotypes in glioma cells of origin through global epigenomic remodeling. *Nature Communications*. Mar. 2018.
 4. Matthias Karajannis, MD, MS, Chief, Pediatric Neuro-Oncology, MSKCC.
Recurrent homozygous deletion of DROSHA and microduplication of PDE4DIP containing the ancestral DUF1220 domain in pineoblastoma. *Nature Communications*. July 2018.
 5. Matija Snuderl, MD, Director, Molecular Pathology, NYU.
DNA methylation-based classification of human central nervous system tumors. *Nature*. Mar. 2018.
 6. Orrin Devinsky, MD, Director, Comprehensive Epilepsy Center, NYU.
Cardiac Arrhythmia and Neuroexcitability Gene Mutations in resected brain tissue from patients with Sudden Unexpected Death in Epilepsy. *Nature Genomic Medicine*. Mar. 2018.
 7. Adriana Heguy, PhD, Assistant Dean, Division of Advanced Research Technologies, NYU.
Why do mutant allele frequencies in oncogenes peak around .40 and rapidly decrease? *Letters in Biomathematics*. Sept. 2016.
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Skills

Proficiency	Software
Data science, Machine learning	Python, R, Scripts(Perl/Bash), C++, spatstat
Bioinformatics, Image processing	Matlab, Samtools, GATK, Bioinformatics Tools
Mathematical modeling, Statistics	MySQL, Neo4j, MS Access
Algorithms, Programming	Unix, Linux variants, Windows (all versions)

Education

Timeline	Degree	Institution
Aug. 2008	PhD Computer Science	Texas A&M University, College Station
Apr. 2002	MS Mathematics	Texas A&M University, College Station
Apr. 2000	MSc Mathematics	Indian Institute of Technology, Madras
Jun. 1998	BSc Mathematics	University of Madras, Chennai

Manuscripts submitted (blue - equal contribution/senior/last/first author)

[31] Edwin Parra, Jiexin Jiang et al. {with Cara Haymaker} Multi-omics profiling of lung squamous cell carcinoma reveals immune signatures associated with checkpoint blockade response and resistance. *Clinical Cancer Research*.

[30] Prahlad Bhat, Michael Hwang, Afroz Jahedi, Kanishka Sircar, and **Kasthuri Kannan**. Spatial Point Process Model Predicts Survival in Clear Cell Renal Cell Carcinoma. *medRxiv* (doi: <https://doi.org/10.1101/2022.02.16.22271019>).

Publications/Preprints (blue - equal contribution/senior/last/first author)

[29] Michal Marek Hoppe; Patrick Jaynes et al. {with Anand Jeyasekharan, National University of Singapore} Patterns of oncogene co-expression at single cell resolution in cancer influence survival. *Cancer Discovery (accepted)*.

[28] Afroz Jahedi, Gayatri Kumar, Lavanya Kannan, Tarjani Agrawal, Jason Huse, Krishna Bhat, and **Kasthuri Kannan**. Gibbs Process Distinguishes Survival and Reveals Contact-Inhibition Genes in Glioblastoma Multiforme. *PLoS One*. Feb. 2023. [PMID: 36795646]

[27] Varn FS, Johnson KC, Martinek J, Huse JT, Nasrallah MP, Wesseling P, Cooper LAD, Malta TM, Wade TE, Sabedot TS, Brat D, Gould PV, Wöhrer A, Aldape K, Ismail A, Sivajothi SK, Barthel FP, Kim H, Kocakavuk E, Ahmed N, White K, Datta I, Moon HE, Pollock S, Goldfarb C, Lee GH, Garofano L, Anderson KJ, Nehar-Belaid D, Barnholtz-Sloan JS, Bakas S, Byrne AT, D'Angelo F, Gan HK, Khasraw M, Migliozi S, Ormond DR, Paek SH, Van Meir EG, Walenkamp AME, Watts C, Weiss T, Weller M, Palucka K, Stead LF, Poisson LM, Noushmehr H, Iavarone A, Verhaak RGW; **GLASS Consortium**. Glioma progression is shaped by genetic evolution and microenvironment interactions. *Cell*. Jun. 2022. [PMID: 35649412]

[26] Xiangjie Sun, Jie Zhai, Baohua Sun, Edwin Roger Parra, Mei Jiang, Wencai Ma, Jing Wang, Anthony Kang, **Kasthuri Kannan**, Renganayaki Pandurengan, Shanyu Zhang, Luisa Maren Solis Soto, Cara Haymaker, Maria Gabriela Raso, Julia Mendoza Perez, Aysegul Sahin, Ignacio Wistuba, Clinton Yam, Jennifer Litton, and Fei Yang. Effector memory cytotoxic CD3+/CD8+/CD45RO+ T cell predicts good survival with less risk to recurrence in triple-negative breast cancer. *Modern Pathology*. May. 2022. [PMID: 34839351]

[25] Yam C, Yen EY, Chang JT, Bassett RL Jr, Alatrash G, Garber H, Huo L, Yang F, Philips AV, Ding QQ, Lim B, Ueno NT, **Kannan K**, Sun X, Sun B, Parra Cuentas ER, Symmans WF, White JB, Ravenberg E, Seth S, Guerriero JL, Rauch GM, Damodaran S, Litton JK, Wargo JA, Hortobagyi GN, Futreal A, Wistuba II, Sun R, Moulder SL, Mittendorf EA. Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. *Clin Cancer Research*. Jul. 2021. [PMID: 34253579]

[24] Iris Scherwitzl, Silvana Opp, Alicia M. Hurtado, Christine Pampero, Cynthia Loomis, **Kasthuri Kannan**, Minjun Yu, and Daniel Meruelo. Sindbis Virus with Anti-OX40 Overcomes the Immunosuppressive Tumor Microenvironment of Low-Immunogenic Tumors. *Molecular Therapy - Oncolytics*. Jun. 2020. [PMID: 32478167]

[23] Dhanasekaran R, Baylot V, Kim M, Kuruvilla S, Bellovin D, Adeniji N, Rajan K A, Lai I, Gabay M, Tong L, Krishnan M, Park J, Hu T, Barbhuiya M A, Gentles A J, **Kannan, K**, Tran P T and Felsher D W. MYC and Twist1 cooperate to drive metastasis by eliciting crosstalk between cancer and innate immunity. *eLife*. Jan. 2020. [PMID: 31933479]

[22] Hao Y, Ruiz R, Yang L, Neto AG, Amin MR, Kelly D, Achlatis S, Roof S, Bing R, **Kasthuri Kannan**, Brown SM, Pei Z, & Branski RC. Mitochondrial somatic mutations and lack of viral genomic variation in recurrent respiratory papillomatosis. *Scientific Reports*. Oct. 2019. [PMID: 31719597]

[21] Martin Vaeth, Yin-Hu Wang, Miriam Eckstein, Jun Yang, Gregg Silverman, Rodrigo Lacruz, **Kasthuri Kannan**, and Stefan Feske. Tissue resident and follicular Treg cell differentiation is regulated by CRAC channels. *Nature Communications*. Mar. 2019. [PMID: 30862784]

[20] Yuxiang Wang, Jie Yang, Aaron Wild, Wei Wu, Rachna Shah, Carla Danussi, Gregory Riggins, **Kasthuri Kannan**, Erik Sulman, Timothy Chan, and Jason Huse. G-quadruplex DNA drives genomic instability and

represents a targetable molecular abnormality in ATRX-deficient malignant glioma. *Nature Communications*. Feb. 2019. [PMID: 30808951]

[19] **Matija Snuderl, Kasthuri Kannan** et al. (corresponding author: Matthias A. Karajannis). Recurrent homozygous deletion of DROSHA and microduplication of PDE4DIP containing the ancestral DUF1220 domain in pineoblastoma. *Nature Communications*. July 2018. [PMID: 30030436]

[18] **Daniel Friedman, Kasthuri Kannan**, Arline Faustin, Seema Shroff, Cheddhi Thomas, Adriana Heguy, Jonathan Serrano, Matija Snuderl, Orrin Devinsky. Cardiac Arrhythmia and Neuroexcitability Gene Mutations in resected brain tissue from patients with Sudden Unexpected Death in Epilepsy. *Nature Genomic Medicine*. Mar. 2018. [PMID: 29619247]

[17] Carla Danussi, Promita Bose, Prasanna Parthasarathy, Pedro Silberman, John Van Arnem, Mark Vitucci, Oliver Tang, Adriana Heguy, Yuxiang Wang, Timothy Chan, Gregory Riggins, Erik Sulman, Frederick Lang, Chad Creighton, Benjamin Deneen, C Miller, David Picketts, **Kasthuri Kannan**, and Jason Huse. Atrx inactivation drives disease-defining phenotypes in glioma cells of origin through global epigenomic remodeling. *Nature Communications*. Mar. 2018. [PMID: 29535300]

[16] David Capper et al. *somewhere in the middle* **Kasthuri Kannan**, (corresponding author: Stefan M. Pfister). DNA methylation-based classification of human central nervous system tumors. *Nature*. Mar. 2018. [PMID: 29539639]

[15] Fanok, Melania H; Sun, Amy; Fogli, Laura K; Narendran, Vijay; Eckstein, Miriam; **Kannan, Kasthuri**; Dolgalev, Igor; Lazaris, Charalampos; Heguy, Adriana; Laird, Mary E; Sundrud, Mark S; Liu, Cynthia; Kutok, Jeff; Lacruz, Rodrigo S; Latkowski, Jo-Ann; Aifantis, Iannis; Odum, Niels; Hymes, Kenneth B; Goel, Swati; Koralov, Sergei B. Role of dysregulated cytokine signaling and bacterial triggers in the pathogenesis of Cutaneous T Cell Lymphoma. *Journal of Investigative Dermatology*. Nov. 2017. [PMID: 29128259]

[14] **Kasthuri Kannan** and Adriana Heguy. Why do mutant allele frequencies in oncogenes peak around .40 and rapidly decrease? *Letters In Biomathematics*. Sept. 2016.

[13] Snyder A, Makarov V, Merghoub T, Yuan J, Zaretsky JM, Desrichard A, Walsh LA, Postow MA, Wong P, Ho TS, Hollmann TJ, Bruggeman C, **Kasthuri Kannan**, Li Y, Elipenahli C, Liu C, Harbison CT, Wang L, Ribas A, Wolchok JD, Chan TA. Genetic basis for clinical response to CTLA-4 blockade in melanoma. *N Engl. J Med*. Dec. 2014. [PMID: 25409260]

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[11] Gerber NK, Goenka A, Turcan S, Reyngold M, Makarov V, **Kasthuri Kannan**, Beal K, Omuro A, Yamada Y, Gutin P, Brennan CW, Huse JT, Chan TA. Transcriptional diversity of long-term glioblastoma survivors. *Neuro Oncol*. Sept. 2014. [PMID: 24662514]

[10] **Allen S. Ho, Kasthuri Kannan**, David Roy, Luc G.T. Morris, Nora Katabi, Stephanie Eng, et al. The Mutational Landscape of Adenoid Cystic Carcinoma. *Nature Genetics*. July 2013. [PMID: 23685749]

[09] Ian Ganly, Julio Ricarte Filho, Stephanie Eng, Ronald Ghossein, Luc G. T. Morris, Yupu Liang, Nicholas Succi, **Kasthuri Kannan**, Qianxing Mo, James A. Fagin, and Timothy A. Chan, Genomic Dissection of Hurthle Cell Carcinoma Reveals a Unique Class of Thyroid Malignancy. *The Journal of Clinical Endocrinology & Metabolism*. May 2013. [PMID: 23543667]

[08] Luc G.T. Morris, Andrew M. Kaufman, Yongxing Gong, Deepa Ramaswami, Logan A. Walsh, Sevin Turcan, Stephanie Eng, **Kasthuri Kannan**, Yilong Zou, et al., Frequent mutation of the Drosophila tumor suppressor-related gene FAT1 in multiple human cancers leads to aberrant Wnt activation. *Nature Genetics*. Mar. 2013. [PMID: 23354438]

[07] **Kasthuri Kannan**, Akiko Inagaki, Joachim Silber, Daniel Gorovets, Jianan Zhang, et al. Whole exome sequencing identifies ATRX mutation as a key molecular determinant in lower-grade glioma. *Oncotarget*. Oct. 2012. [PMID: 23104868]

- [06] **Daniel Gorovets, Kasthuri Kannan**, Edward R Kastenhuber, Nasrin Islam-doust, Carl Campos, et al. IDH Mutation and Neuroglial Developmental Features Define Clinically Distinct Subclasses of Lower-Grade Diffuse Astrocytic Glioma. *Clinical Cancer Research*. May 2012. [PMID: 22415316]
- [05] Amitabha Majumdar, Wanda Colón Cesario, Erica White-Grindley, Huoqing Jiang, Fengzhen Ren, Mohammed “Repon” Khan, Liying Li, Edward Man-Lik Choi, **Kasthuri Kannan**, Fengli Guo, Jay Unruh, Brian Slaughter, Kausik Si. Critical Role of Amyloid-like Oligomers of Drosophila Orb2 in the Persistence of Memory. *Cell*. Feb. 2012. [PMID: 22284910]
- [04] Yan Hao, Ningyi Xu, Andrew Box, Laura Schaefer, **Kasthuri Kannan**, et al. Nuclear cGMP-Dependent Kinase Regulates Gene Expression via Activity-Dependent Recruitment of a Conserved Histone Deacetylase Complex. *PLoS Genetics*. May 2011. [PMID: 21573134]
- [03] **Kasthuri Kannan** and Vivek Sarin, A Treecode for Potentials of the Form $r^{-\lambda}$, *International Journal of Computer Mathematics*. 84, 1249-1260, Jan. 2007.
- [02] **Kasthuri Kannan** and Vivek Sarin, A Treecode for Accurate Force Calculations. *Lecture Notes in Computer Science*. 3991, pp. 92-99, May 2006.
- [01] **Kasthuri Kannan**, Hemant Mahawar and Vivek Sarin, A Multipole Based Treecode using Spherical Harmonics for the Potentials of the Form $r^{-\lambda}$. *Lecture Notes in Computer Science*. 3514, pp. 107-114, May 2005.

Invited Talks/Workshops/Interviews

CancerCon 2018. Chennai, India. Feb. 01-03, 2018

Manipal Academy of Higher Education, Manipal, India. Feb. 06, 2018

Institute of Mathematical Sciences, Chennai. India. Feb. 8, 2018, with honorarium

MedGenome symposium. Foster City, CA. Mar. 20, 2018

Beer with a Scientist Sundays, New York, NY. Apr. 01, 2018

Distinguished Lecture Series, MD Anderson Cancer Center, Houston, TX. Apr. 19, 2018

Sanford Burnham Prebys Medical Discovery Institute, San Diego, CA. May 29, 2018

Credit Suisse, Raleigh, NC. Jul. 16-19, 2019 (corporate training for employees)

Egenesis, Boston, MA. Jul. 29, 2019

GeneWiz, Short Hills, NJ. Aug. 7, 2019

University of Texas Health Science Center, San Antonio. Aug. 30, 2019

Courant Institute of Mathematical Sciences, Manhattan, NY. Sept. 24, 2019

Texas A&M University, Department of Mathematics, Oct. 25, 2021

Joint Immuno-Oncology (IO) Session, NCI. Nov. 05. 2021

Cancer Science Institute, National University of Singapore, Dec. 15, 2021

GraphConnect Conference (Neo4j), Jun. 7, 2022

Translational Molecular Pathology 2022 Retreat, Jun. 17, 2022

National University of Singapore, Cancer Science Institute (In-person visit and talk), Jul. 19, 2022

Omics Research Symposium, Pine Biotech, Aug. 30, 2022

Mayo Clinic, Science of Medicine Grand Rounds, Mar. 02, 2023, with honorarium

Employment History

Associate Professor (Translational Molecular Pathology, Neurosurgery) **Feb 2020 - present**
University of Texas MD Anderson Cancer Center, Houston, TX

- a) Systems biology architecture for glioma using GLioma AnalySiS (GLASS) consortium data. Building an integrative platform using graph database framework for hypothesis generation using Neo4j.
- b) Directing the computational pathology program. We perform spatial point process modeling of cancer tissue images obtained using multiplex immunofluorescence and CODEX technologies.
- c) NGS data analysis and spatial transcriptomics, especially GeoMx Digital Spatial Profiler data analysis
- d) Mentoring post-docs and graduate students

Assistant Professor (Pathology) **Dec 2013 - Aug 2019**
New York University Langone Health, New York, NY

- a) Directed insights through data science applied to Next Generation Sequencing data (see publications).
- b) Software and pipeline development.
- c) Statistical and mathematical modeling.
- d) Directed and taught data science and machine learning courses.

Research Associate/Fellow **Apr 2011 – Nov 2013**
Memorial Sloan-Kettering Cancer Center, New York, NY

- a) Comprehensive genomic and epigenomic analysis of the impact of first-line therapy in the molecular evolution of malignant glioma. DNA and RNA extraction from tumor specimens.
- b) Examination and discovery of genetic diversity in low grade glioma such as astrocytoma and oligodendroglioma.
- c) Analysis of genomic sequencing data (mutation discovery, copy number alterations) in glioma, head and neck and thyroid neoplasms.
- d) Development of next generation sequencing pipelines and integrated study of array (gene expression, methylation, copy number) and genetic alterations (mutations and translocations) in cancers.

Research Associate **Oct 2010 – Apr 2011**
Pennsylvania State University, State College, PA

- a) Responsible for the development of computational infrastructure for high throughput sequencing data from next-generation platforms [SOLiD and Illumina].
- b) Organized the existing data analysis pipeline (genome alignment, motif discovery to biological interpretation) and provided consultation to the researchers on core computational issues.
- c) Managed sequencing tasks at the Bioinformatics Consulting Center, Institute for Genomics, Proteomics and Bioinformatics.

Research Specialist **Jan 2008 – Sep 2010**
Stowers Institute for Medical Research, Kansas City, MO

- a) Team leader for ChIP-seq data analysis project in the Stowers Microscopy Center.
 - Developed and implemented an analytical strategy (in particular, a deconvolution model) to predict protein-binding sites in ChIP-seq data.
- b) Implemented an automated data workflow to study the growth phases of budding *S. Cerevisiae* cells.
- c) Designed image processing algorithms and software's for tracking *C. Elegans* and *Drosophila* to:

- study the foraging behavior of *C. Elegans* [please refer to *PLoS Genet.* publication].
 - analyze the mating behavior of *Drosophila* [please refer to *Cell* publication].
- d) Statistical analysis of Fluorescence Correlation Spectroscopy data, a method that characterizes proteins.
 - e) Data analysis of point spread functions in widefield and confocal microscopes using R.
 - f) Developed a dynamic web-site (PHP + MySQL) that would query and process yeast cell images.
 - g) Responsible for high quality image acquisition and microscope maintenance in the institute.

Research Intern

Jan 2007 – Dec 2007

Knowledge Based Systems, Inc., College Station, TX

- a) Offered significant ideas for logistics management in Oklahoma Air Logistics Center through data mining.
- b) Proposed several cost and time saving measures from directed insights obtained via predictive modeling.
- c) Initiated business intelligence for aircraft movement operations at the Tinker Air Force Base.

Teaching (Course Director)

- a) Programming for Data Analysis: <https://kannan-kasthuri.github.io/pda.html>
- b) Methods in Quantitative Biology: <https://kannan-kasthuri.github.io/qmb.html>
- c) Machine Learning: https://kannan-kasthuri.github.io/machine_learning.html

Last Updated: March 05, 2022