OMB No. 0925-0001 and 0925-0002 (Rev. 10/2021 Approved Through 09/30/2024)

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Gopalakrishnan, Vanathi

eRA COMMONS USER NAME (credential, e.g., agency login): VANATHI

POSITION TITLE: Associate Professor of Biomedical Informatics (tenured), Computational & Systems Biology, Bioengineering, Clinical and Translational Science

EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| BMS College of Engineering, Bangalore, India | B.E. | 1988 | Computer Engineering |
| University of Pittsburgh, Pittsburgh, PA | M.S. | 1991 | Computer Science |
| University of Pittsburgh, Pittsburgh, PA | Ph.D. | 1999 | Computer Science |

**A. Personal Statement**

I am a tenured associate professor of Biomedical Informatics at the University of Pittsburgh, with joint appointments in Computational & Systems Biology, Bioengineering, Clinical and Translational Science. I am primarily a data scientist, with a multidisciplinary background in engineering, computer science, machine learning, and their applications to biomedical research. My primary research focus has been on the development of novel hybrid rule learning algorithms for the predictive and integrative modeling of biomedical data obtained from molecular profiling studies, radiologic imaging and clinical textual reports. I direct the **PRoBE laboratory for *Pattern Recognition from Biomedical Evidence*.** I am fundamentally interested in technologies for data mining and discovery that allow incorporation of prior knowledge. Fundamental research areas of interest involve extensions to rule learning via the incorporation of (1) Bayesian Statistics, (2) prior rule models, and (3) knowledge obtained through mining of ontologies or the literature. My research over the past two decades has focused on the development, application and evaluation of symbolic, probabilistic and hybrid machine learning methods to the modeling and analysis of high-dimensional, sparsely-populated biomedical datasets for early detection of disease and its progression.

**I recently completed a successful term as the elected Director (and Chair) of the Intelligent Systems Program (ISP), a premier multidisciplinary graduate program at the University of Pittsburgh dedicated to applied artificial intelligence (AI). I also pioneered the Bioinformatics Curriculum within the NLM-funded Biomedical Informatics Training Program (BMITP), and have successfully supervised >12 doctoral students in this area (2 minorities), with current doctoral trainees at the University of Pittsburgh also comprising minorities. I have previously contributed as a co-founder of a successful breast cancer detection company that is now part of NASDAQ:ICAD.**

**I have an extensive background in developing and testing real-world models from large datasets in collaboration with biomedical scientists.** I have been the creator and co-creator of novel hybrid classification rule learning methods such as Bayesian Rule Learning (BRL) and Transfer Rule Learner (TRL), and as the PI on NIH-funded R01’s, overseen their application to biomarker discovery and validation for the early detection of ALS, lung cancer, and esophageal adenocarcinoma. This project builds upon these strengths and my ongoing collaboration as a co-investigator on:

1U24 TR004111-01 (Reis & Visweswaran); NIH/NCATS

08/01/2022- 05/31/2027

ENACT: Translating Health Informatics Tools to Research and Clinical Decision Making

My key related publications include:

A1. Ganchev, P., Malehorn, D., Bigbee, W. L., **Gopalakrishnan, V**. Transfer Learning of Classification Rules for Biomarker Discovery and Verification from Molecular Profiling Studies. J Biomed Inform. 2011 Dec;44 Suppl 1:S17-23. Epub 2011 May 6. (*Won a Distinguished Paper Award at the AMIA TBI Summit on Translational Bioinformatics in 2011*). PMID: 21571094 PMCID: PMC3706089.

A2. Bigbee, W. L**\***., **Gopalakrishnan, V.\*,** Weissfeld J, L., Wilson, D. O., Dacic, S. Lokshin, A. E., Siegfried, J. M. A Multiplexed Serum Biomarker Immunoassay Panel Discriminates Clinical Lung Cancer Patients from High-Risk Individuals Found to be Cancer-Free by CT Screening. J Thorac Oncol. 2012 Apr;7(4):698-708. (**\*These authors contributed equally to the study**). PMID: 22425918 PMCID: PMC3308353. (Cited 84 times as per google scholar on 2/28/2021).

A3. Ogoe, H.A., Visweswaran, S., Lu, X., **Gopalakrishnan, V.** Knowledge Transfer via Classification Rules using Functional Mapping for Integrative Modeling of Gene Expression Data. BMC Bioinformatics. 16 (2015): 226. PMID: 26202217. PMCID: PMC4512094.

A4. Balasubramanian JB, **Gopalakrishnan V**. Tunable structure priors for Bayesian rule learning for knowledge integrated biomarker discovery. World J Clin Oncol. 2018 Sep 14;9(5):98-109. doi: 10.5306/wjco.v9.i5.98. PMID: 30254965; PMCID: PMC6153126.

**Positions and Employment**

2/2019 – present Associate Professor of Clinical and Translational Science, UPitt

9/2019 – 8/2022 Director of the Intelligent Systems Program, School of Computing and Information, UPitt.

2/2018 – present Associate Professor of Bioengineering, Swanson School of Engineering, UPitt.

2/2017 - present Co-Director of the Bioengineering, Biotechnology and Innovation (BBI) Area

of Concentration for Medical Curriculum within the School of Medicine, UPitt.

6/2012 - 6/2014 Director (& mentor) of the Computer Science, Biology and Biomedical Informatics (CoSBBI)

Summer Program for High School Students (rising Juniors and Seniors) for the first two years of this University of Pittsburgh Cancer Institute’s innovative program.

12/2011 – present Associate Professor (tenured) of Biomedical Informatics, Intelligent Systems and Computational & Systems Biology, University of Pittsburgh, School of Medicine.

7/2006 – 11/2011 Assistant Professor of Computational Biology, UPitt (joint appointment)

8/2002 – 11/2011 Assistant Professor of Intelligent Systems, UPitt (secondary appointment)

7/2006 – 11/2011 Assistant Professor, Department of Biomedical Informatics, UPitt (tenure-track)

8/2002 – 6/2006 Assistant Professor, Department of Medicine (SMI), UPitt (tenure-track)

7/2000 – 7/2002 Visiting Assistant Professor, Department of Medicine, Section of Medical Informatics (SMI), University of Pittsburgh, Pittsburgh, PA

7/2000 – 7/2002 Visiting Assistant Professor of Intelligent Systems, University of Pittsburgh (UPitt)

Spring 2000 Part-Time Faculty, Intelligent Systems Program, University of Pittsburgh. Introduced and taught a new Graduate level core course called Introduction to Bioinformatics.

1996 – 1998 Co-founder of Intelligent Systems, M.D., Inc., Florida, USA. (now NASDAQ:ICAD)

1989 – 1997 Research Assistant, Intelligent Systems Laboratory, University of Pittsburgh, Pittsburgh, PA.

Summer 1991 Software Engineer, Systems Modeling Corporation, Sewickley, PA.

1988 – 1989 Systems Executive, Wipro Information Technology Limited, Bangalore, India.

**Other Experience and Memberships (non-consecutive) in Professional and Scientific Societies**

2021 - Executive Committee Member, Biomedical Informatics Training Program, UPitt

2006 - Lung & Thoracic Malignancies Program, University of Pittsburgh Cancer Institute (UPCI)

2004 - Association for Computing Machinery (ACM)

2004 - American Association for Advancement of Science (AAAS)

2000 - The American Association for Artificial Intelligence (AAAI)

2000 - The American Medical Informatics Association (AMIA)

2000 - The International Society for Computational Biology (ISCB)

Peer Review Experience Overview

2023 NIH NIAID Special Emphasis Panel

2022 NIH MOSAIC K99/R00 Review Panel

2021 NSF Convergence Accelerator Review Panelist

2020 NIH Several Panels including S10 Instrumentation grant reviews and Rapid SARS-CoV-2 proposal

2019 NIH K99 Reviewing for NIGMS

2018 NIH Maximizing Investigators' Research Award for Early Stage Investigators

2018 NIH BDMA Winter study section panelist

2017 NIH Special emphasis panelist: Imaging and Biomarkers for Early Detection of Aggressive Cancer

2015 NIH Winter BDMA Study Section Review Panelist,

2015 NIH Special emphasis panelist: Imaging and Biomarkers for Early Cancer Detection

2015-16 NIH Academic Industrial Partnership (AIP) Review Meeting

2014 Expert Committee Review for the Canada Foundation for Innovation: Integrating ‘Big Data’ for Health

2013 NIH P41 Special Review Panelist and NIH P51 Review Panelist

2011 NSF Review Panelist (Informatics / BIG Data)

2009 NIH (NCRR/NCATS) SBIR Grants and Contracts Review Study Section

**Honors**

2020 Distinguished Alumni Honor, B.M. S. College of Engineering, Computer Science & Engineering Dept.

2018 Pitt Innovator Award (for Coronary Artery Disease intelligent detection via Metabolomic Expression)

2015 AMIA TBI Marco Ramoni Distinguished Paper Award: Co-author and Senior Author **(see C3d)**

2011 AMIA Translational Bioinformatics (TBI) Distinguished Paper Award: Co-and Senior Author (**see A1**)

2006 Pitt Innovator Award (for licensing RL-Wrap: Wrapper-based Rule Learning)

1994 W.M. Keck Fellowship in Computational Biology

1988 Best TraineeAward, Wipro Information Technology Limited, Bangalore, India.

**C. Contributions to Science**

* 1. Novel computational frameworks for enabling macromolecular crystallization: The art of growing a good X-ray diffractible quality crystal of a protein or other macromolecule can be infused with scientific theory to enable bench scientists to better understand how protein nucleation and growth take place. My first contribution to interdisciplinary science began with my doctoral dissertation work which produced novel insights into the process of macromolecular crystallization via the development and assessment of computational models. This pioneering research in a niche area of bioinformatics was published in important conferences and journals (see 1a – 1d), and led to new research by other groups and robotic companies to improve the science of macromolecular crystallization to provide better monitoring tools and experimental design conditions.

1. Hennessy, D., **Gopalakrishnan, V**., Buchanan, B.G., Subramanian, D., Rosenberg, J.M. Induction of Rules for Biological Macromolecule Crystallization, In: Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology (1994) 179-187.
2. **Gopalakrishnan, V.**, Buchanan, B.G., Rosenberg, J.M. Intelligent Aids for Parallel Experiment Planning and Macromolecular Crystallization. In: Proceedings of the Eight International Conference on Intelligent Systems for Molecular Biology (2000) 171-180.
3. **Gopalakrishnan, V.**, Buchanan, B.G., Rosenberg, J.M. A Simple Simulator of Protein Crystallization, Journal of Applied Crystallography 35(6) (2002) 727-733.
4. **Gopalakrishnan, V.**, Livingston, G., Hennessy, D., Buchanan, B., Rosenberg, J.M. Machine-Learning Techniques for Macromolecular Crystallization Data, Acta Crystallogr D Biol Crystallogr 60 (2004)1705-1716.
5. Development of novel rule learning methodologies for predictive modeling and classifier construction from both data and prior knowledge: Over the past two decades, I have collaborated with world-renowned faculty at the University of Pittsburgh to develop and test hybrid machine learning methods that combine the strengths of Bayesian network learning with symbolic rule-based inference to provide clinicians and bench scientists with predictive models that are parsimonious, easily interpretable, and accurately capture uncertainty. My laboratory has produced many innovative methods for modeling biomedical data that include new and efficient methods for discretizing continuous valued data (c), and transfer learning of classification rules between two related datasets (A1). Moreover, we use ontologies and literature mining methods to capture prior knowledge and use them as input to our classification algorithms (b, and A3).
   1. **Gopalakrishnan, V.**, Lustgarten, J. L., Visweswaran, S., Cooper, G.F. Bayesian Rule Learning for Biomedical Data Mining. Bioinformatics. 26(5) (2010) 668-675. PMID: 20080512; PMCID: PMC2852212.
   2. Lu, X., Zhai, C., **Gopalakrishnan, V.**, Buchanan, B.G. Automatic annotation of protein motif function with Gene Ontology terms, BMC Bioinformatics 5 (2004) 122. PMCID: PMC517493.
   3. Lustgarten, J. L., Visweswaran, S., **Gopalakrishnan, V**., Cooper, G. F. Application of an efficient Bayesian discretization method to biomedical data. BMC Bioinformatics. 2011;12:309. PubMed PMID: 21798039; PMCID: PMC3162539.
   4. Balasubramanian JB, Boes RD, **Gopalakrishnan V**. A novel approach to modeling multifactorial diseases using Ensemble Bayesian Rule Classifiers. J Biomed Inform. 2020 Jul;107:103455. doi: 10.1016/j.jbi.2020.103455. Epub 2020 Jun 1. PMID: 32497685.
6. Application of our methods to biomarker discovery and validation from omic data: I have been collaborating locally, regionally and nationally with several research groups to apply our novel predictive modeling methods to discover and validate biomarkers for early detection and monitoring of various diseases including Amyotrophic Lateral Sclerosis, Ulcerative Colitis and Cancers of the Lung, Breast and Esophagus. Four representative publications are given below:
7. Ranganathan, S., Williams, E., Ganchev, P., **Gopalakrishnan, V.,** Lacomis, D., Urbinelli, L., Newhall, K., Cudkowicz, M. E., Brown, R. H., Jr., Bowser, R. Proteomic profiling of cerebrospinal fluid identifies biomarkers for amyotrophic lateral sclerosis. J Neurochem. 2005;95(5):1461-71. PubMed PMID: 16313519; PMCID: PMC1540444.
8. Ryberg, H., An, J., Darko, S., Lustgarten, J. L., Jaffa, M., **Gopalakrishnan, V.**, Lacomis, D., Cudkowicz, M., Bowser, R. Discovery and verification of amyotrophic lateral sclerosis biomarkers by proteomics. Muscle Nerve. 2010;42(1):104-11. PubMed PMID: 20583124; PMCID: PMC2975276.
9. Zaidi, A.H, **Gopalakrishnan, V**., Kasi, P. M., Zeng, X., Malhotra, U., Balasubramanian, J., Visweswaran, S., Sun, M., Flint, M. S., Davison, J. M., Hood, B. L., Conrads, T. P., Bergman, J.J., Bigbee, W. L., Jobe, B. A. Evaluation of a 4-protein serum biomarker panel – biglycan, annexin-A6, myeloperoxidase and protein S100-A9 (B-AMP©) – for the detection of esophageal adenocarcinoma. Cancer. 2014 Aug 5. PMID: 25100294. PMCID: PMC4441619 (Impact Factor = 5.201).
10. Lopez Pineda, A., **Gopalakrishnan, V**. Novel Application of Junction Trees to the Interpretation of Epigenetic Differences among Lung Cancer Subtypes. *Winner of the 2015 Marco Ramoni Distinguished Paper Award in Translational Bioinformatics.* AMIA Jt Summits Transl Sci Proc. 2015 Mar 23;2015:31-5. eCollection 2015. San Francisco, CA, USA. PMID: 2630622 PMCID:PMC4525224.
11. Mining big imaging data sets for clinically relevant information and image-derived markers related to injuries and diseases of brain and heart. I am highly interested in research that involves combining omic-biomarkers and imaging-derived markers to increase the precision for disease detection, monitoring and treatment. Towards that end, my laboratory has been developing novel methods to extract image-derived markers from fMRI data, brain tumor diffusion MR data (4a), and cardiac imaging data (4b-d).
12. Ceschin, R. Panigraphy, A., **Gopalakrishnan, V.** sfDM: Open Source Software for Temporal Analysis and Visualization of Brain Tumor Diffusion MR using Serial Functional Diffusion Mapping. Cancer Inform. 2015 Feb 1;14(Suppl 2):1-9. doi: 10.4137/CIN.S17293. eCollection 2015. PMCID: PMC4315050.
13. Menon, P. G., Morris, L., Staines, M., Lima, J., Lee, D. C., **Gopalakrishnan, V**. Novel MRI-derived quantitative biomarker for cardiac function applied to classifying ischemic cardiomyopathy within a Bayesian rule learning framework. Proceedings of the SPIE 9034, Medical Imaging 2014: Image Processing, 90341L (21 March 2014) pp: 90341L-90341L-6. PMCID: PMC4440803.
14. **Gopalakrishnan, V**., Menon, P.G., Madan, S. cMRI-BED: A novel informatics framework for cardiac MRI biomarker extraction and discovery applied to pediatric cardiomyopathy classification. Biomed Eng Online. 2015;14 Suppl 2:S7. Epub 2015 Aug 13. PMCID: PMC4547147.
15. Liu Y, **Gopalakrishnan V**. An Overview and Evaluation of Recent Machine Learning Imputation Methods Using Cardiac Imaging Data. Data (Basel). 2017. Mar;2(1). doi: 10.3390/data2010008. Epub 2017 Jan 25. PMCID: PMC5325161.
16. Training next generation of scientists. The UPCI runs a highly selective program in the summer to train high school students in laboratory and computational work. Students whom I mentored have won best poster awards, and gone on to present in national conferences. A sample publication in the Journal of Pathology Informatics illustrates this service to science, while also bringing out novel contributions made by these students and their research mentors.
17. Dutta-Moscato, J., **Gopalakrishnan, V**., Lotze, M. T., Becich, M.J. Creating a Pipeline of Talent for Informatics: STEM Initiative for High School Students in Computer Science, Biology and Biomedical Informatics (CoSBBI). Journal of Pathology Informatics. 2014; Editorial in J Pathol Inform 2014;5:12. PMID: 24860688. PMCID: PMC4030307.
18. Firdous, A., **Gopalakrishnan, V.**, Vo, N., & Sowa, G. Challenges and opportunities for omics-based precision medicine in chronic low back pain. European Spine Journal. 2022 Dec 24:1-15. PMID: 36565345

## Complete List of Published Work in MyBibliography:

https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/41925325/