

# Vivek Gopalakrishnan

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I am a combined BS/MSE student in the Department of Biomedical Engineering at Johns Hopkins University. My research focuses on developing machine learning methods to analyze multi-subject neuroimaging data (advised by [Dr. Joshua T. Vogelstein](#) and [Dr. Carey E. Priebe](#)). Currently, I am building a Random Forest (RF)-based computer vision algorithm to perform robust and interpretable brain tumor segmentation. I also lead a Design Team of undergraduate biomedical engineers (advised by [Dr. Elizabeth Logsdon](#) and [Dr. Rani Hasan](#)). We are building a dynamic fusion image guidance system for minimally invasive heart surgery.

## Education

- 08/21 **Massachusetts Institute of Technology and Harvard Medical School**, Cambridge, MA.  
(Incoming) Doctor of Philosophy (Ph.D.) in Medical Engineering and Medical Physics.  
○ **Concentration Area:** Computer Science.
- 08/20 – 05/21 **Johns Hopkins University**, Baltimore, MD.  
Master of Science and Engineering (M.S.E.) in Biomedical Engineering.  
○ **Advisors:** Professors Joshua T. Vogelstein (primary) and Carey E. Priebe (secondary).  
○ **Concentration Area:** Biomedical Data Science.  
○ **Thesis:** *Multiscale Statistical Hypothesis Testing for  $k$ -Sample Graph Inference*.
- 08/17 – 05/21 **Johns Hopkins University**, Baltimore, MD.  
Bachelor of Science (B.S.) in Biomedical Engineering.  
○ **Advisor:** Professor René Vidal.  
○ **Concentration Area:** Biomedical Data Science.

## Research and Engineering Experience

- 01/20 – now **Design Team Leader**, [Dept. of Biomedical Engineering](#), Johns Hopkins University.  
○ Team leader and project manager for a team of eight undergraduate engineers.  
○ Developing a dynamic fusion image guidance system for minimally invasive heart surgery.  
○ **Skills used:** *Computer vision, tensorflow, Python, and Git*.
- 09/18 – now **Undergraduate Research Assistant**, [Neurodata Lab](#), Johns Hopkins University.  
○ Developing Random Forest-based computer vision algorithm for brain tumor segmentation.  
○ Developed novel machine learning methods for analyzing populations of graph-valued objects [3, 1].  
○ Discovered neuro-connectively similar subtypes of autism using joint embeddings of multi-network connectomes [4, 7].  
○ **Skills used:** *Graph theory, statistical learning theory, Python, Cython, and Git*.
- Summer 2018 **Summer Student Researcher**, [Ghebremichael Lab](#), Ragon Institute of MGH, MIT and Harvard.  
○ Developed predictive models of disease progression and immune recovery in HIV-positive children with TB co-infection [2].  
○ Identified biomarkers for antiretroviral toxicity by applying machine learning methods to HIV-patient data [5].  
○ **Skills used:** *Survival analysis, ROC models, R, and Git*.
- 12/17 – 05/18 **Design Team Member**, [Dept. of Biomedical Engineering](#), Johns Hopkins University.  
○ Designed and implemented a clinical machine learning algorithm to predict the onset of lung failure in pediatric patients.  
○ **Skills used:** *Representation learning, sparse dictionary learning, Python, and Git*.

- 06/17 – 07/17 **Summer Researcher**, *Fondazione Bruno Kessler*, Trento, Italy.
- Implemented a deep learning algorithm to quantitatively assess crop damage from images taken by farmers.
  - **Skills used:** *Computer vision, Keras, Python, and Git.*
- 06/16 – 06/17 **High School Researcher**, *Tufts University BioSeq Program*, Tufts University.
- Used next-generation sequencing (NGS) to generate a novel human oral microbiome data set.
  - Analyzed sequence data using dimensionality reduction and hidden Markov models to identify microbial biomarkers of oral health.
  - Presented at the 2017 Intel International Science and Engineering Fair, Los Angeles, CA.
  - **Skills used:** *DNA library construction, next-generation sequencing, dimensionality reduction, hidden Markov models, and R.*

## Publications and Preprints

- [1] Jaewon Chung, Eric Bridgeford, Jesus Arroyo, Benjamin D. Pedigo, Ali Saad-Eldin, **Vivek Gopalakrishnan**, Liang Xiang, Carey E Priebe, and Joshua T Vogelstein. “Statistical Connectomics”. *Annual Review of Statistics and Its Application* (Mar. 2021). DOI: <https://doi.org/10.1146/annurev-statistics-042720-023234>.
- [2] **Vivek Gopalakrishnan**, Eliezer Bose, Usha Nair, Yuwei Cheng, and Musie Ghebremichael. “Pre-HAART CD4+ T-Lymphocytes as Biomarkers of Post-HAART Immune Recovery in HIV-Infected Children with or without TB Co-Infection”. *BMC Infectious Diseases* (Oct. 2020). DOI: [10.1186/s12879-020-05458-w](https://doi.org/10.1186/s12879-020-05458-w).
- [3] **Vivek Gopalakrishnan**, Jaewon Chung, Eric Bridgeford, Benjamin D. Pedigo, Jesús Arroyo, Lucy Upchurch, G. Allan Johnson, Nian Wang, Youngser Park, Carey E. Priebe, and Joshua T. Vogelstein. “Multiscale Comparative Connectomics”. *arXiv:2011.14990* (Nov. 2020). arXiv: [2011.14990](https://arxiv.org/abs/2011.14990).
- [4] Nian Wang, Robert J Anderson, David G Ashbrook, **Vivek Gopalakrishnan**, Youngser Park, Carey E Priebe, Yi Qi, Rick Laoprasert, Joshua T Vogelstein, Robert W Williams, and G Allan Johnson. “Variability and Heritability of Mouse Brain Structure: Microscopic MRI Atlases and Connectomes for Diverse Strains”. *NeuroImage* (Aug. 2020). DOI: [10.1016/j.neuroimage.2020.117274](https://doi.org/10.1016/j.neuroimage.2020.117274).
- [5] Jong Soo Lee, Elijah Paintsil, **Vivek Gopalakrishnan**, and Musie Ghebremichael. “A Comparison of Machine Learning Techniques for Classification of HIV Patients with Antiretroviral Therapy-Induced Mitochondrial Toxicity from Those Without Mitochondrial Toxicity”. *BMC Medical Research Methodology* (Nov. 2019). DOI: [10.1186/s12874-019-0848-z](https://doi.org/10.1186/s12874-019-0848-z).

## Conference Presentations

- [6] **Vivek Gopalakrishnan** and Joshua T Vogelstein. “Statistical Methods for Multiscale Comparative Connectomics”. *NeuroMatch*. Oct. 2020. URL: [https://www.neuromatch.io/abstract?submission\\_id=recARY71P6SjXY3xK](https://www.neuromatch.io/abstract?submission_id=recARY71P6SjXY3xK).
- [7] **Vivek Gopalakrishnan** and Joshua T Vogelstein. “Towards Discovering Heterogeneity in Autism via Multi-Network Connectomics”. *Biomedical Engineering Society (BMES)*. Philadelphia, PA, Oct. 2019.

## Skills

Programming	Python, R, C++, git, $\LaTeX$
DevOps	GitHub, AWS, Docker, CircleCI
APIs	NumPy, Pandas, scikit-learn, Keras, TensorFlow, PyTorch, Matplotlib, Seaborn, Plotly
Bioinformatics	Microbiome and B cell repertoire analysis

Wet Lab Microfabrication, 3-D tissue culture, NGS library construction

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## Teaching

- Fall '20 **TA – Linear Algebra**, *AS.MATH.201*, Johns Hopkins University.
- Fall '20 **TA – Computational Cardiology Lab**, *EN.BME.487*, Johns Hopkins University.
- Fall '20 **TA – NeuroData Design**, *EN.BME.437/637*, Johns Hopkins University.
- Fall '18 **Head PILOT Leader**, *Dept. of Academic Support*, Johns Hopkins University.
- to Spring '20
  - Led group tutoring sessions ( $\approx 10$  students/group), and wrote weekly problem sets and lectures.
  - Led weekly meetings to train junior PILOT leaders in mathematics and pedagogy.

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## Fellowships and Awards

- 2020 **Provost's Undergraduate Research Award**, *Office of Undergraduate Research*, Johns Hopkins University.
- 2019 **INBT Research Award**, *Institute for NanoBioTechnology*, Johns Hopkins University.
- 2019 **Joseph C. Pistritto Research Fellowship**, *Dept. of Computer Science*, Johns Hopkins University.
- 2018 **AWS Cloud Credits for Research Grant**, *Dept. of Computer Science*, Johns Hopkins University.
- 2017 **Second Place Winner**, *Intel International Science and Engineering Fair (ISEF)*, Category: Microbiology.
- 2017 **Internship Award**, *Intel ISEF Special Award*, Fondazione Bruno Kessler.
- 2017 **Semi-Finalist**, *Regeneron Science Talent Search*, Microbiology.
- 2017 **Second Place Winner**, *Massachusetts State Science & Engineering Fair*.
- 2016 **Second Place Winner**, *Massachusetts State Science & Engineering Fair*.