**Sambhawa Priya**
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## Education

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| Ph.D. in Bioinformatics and Computational Biology<br>University of Minnesota, Minneapolis, MN, USA<br>Adviser: Dr. Ran Blekhman | 11/2021 |
| M.S. in Computer Science<br>Lehigh University, Bethlehem, PA, USA | 05/2016 |
| B.E. in Computer Science<br>Manipal Institute of Technology, Karnataka, India | 05/2010 |

## Professional Experience

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| • Postdoctoral Fellow | Broad Institute of MIT and Harvard, Harvard Medical School, Massachusetts General Hospital, Boston, MA, USA | 12/2021 – Present |
| • Research Assistant | University of Minnesota, Minneapolis, MN, USA | 08/2016 – 11/2021 |
| • Graduate Research Intern | Mayo Clinic, Rochester, MN, USA | 06/2014 – 08/2014 |
| • Research and Teaching Assistant | Lehigh University, Bethlehem, PA, USA | 08/2011 – 05/2016 |
| • Undergraduate Research Intern | Carnegie Mellon University, Pittsburgh, PA, USA | 06/2009 – 08/2009 |
| • Undergraduate Research Intern | University of Lodz, Poland | 06/2008 – 08/ 2008 |

## Honors and Awards

- Doctoral Dissertation Fellowship, University of Minnesota (approx. $50,000), 08/2019 – 05/2020.
- Best Poster award in 10th Annual Bioinformatics Research Symposium, University of Minnesota, 2018.
- Microbial and Plant Genomics Institute Travel award ($489), 2018
- Bioinformatics and Computational Biology Graduate Fellowship, University of Minnesota (approx. $50,000), 08/2016 – 05/2017.
- First prize in the 2012 Semantic Web Challenge (Billion Triples Challenge Track), 2012.
- NSF Travel Grant, International Semantic Web Conference ($1,200), 2012.
- Award for Academic Excellence in Computer Science, Manipal Institute of Technology, 2009.

## Publications (google scholar link)

1. **Priya S**, Burns MB, Ward T, Mars RAT, Adamowicz B, Lock E, Kashyap PC, Knights D, Blekhman R. "Identification of shared and disease-specific host gene–microbiome associations across human diseases using multi-omic integration". *Nature Microbiology, 7, 780–795.* 2022. https://doi.org/10.1038/s41564-022-01121-z

2. Bramble MS, Vashist N, Ko A, **Priya S**, Musasa C, Spencer D, Lipson A, Mamona P, Karume K, Nsibu J, Manya H, Uy MNA, Colwell B, Boivin M, Mayambu B, Okitundu D, Mumba-Ngoyi D, Blekhman R, Tshala-Katumbay D, Vilain E. "The Gut Microbiome in Konzo". *Nature Communications, 12(1):5371.* 2021. https://doi.org/10.1038/s41467-021-25694-1

3. Mihindukulasuriya KA, Mars RAT, Johnson AJ, Ward T, **Priya S**, Lekatz HR, Kalari KR, Droit L, Zheng T, Blekhman R, D'Amato M, Farrugia G, Knights D, Handley SA, Kashyap PC. "Multi-Omics analyses show disease, diet, and transcriptome interactions with the virome". *Gastroenterology, 161 (4), 1194-1207. e8.* 2021. https://doi.org/10.1053/j.gastro.2021.06.077

4. Mars RAT, Yang Y, Ward T, Houtti M, **Priya S**, Lekatz HR, Tang X, Sun Z, Kalari KR, Korem T, Bhattarai Y, Zheng T, Bar N, Frost G, Johnson AJ, van Treuren W, Han S, Ordog T, Grover M, Sonnenburg J, D'Amato M, Camilleri M, Elinav E, Segal E, Blekhman R, Farrugia G, Swann J, Knights D, Kashyap PC. "Longitudinal

multi-omics reveals subset-specific mechanisms underlying irritable bowel syndrome". *Cell, 182:6, 1460–1473*. 2020**.** https://doi.org/10.1016/j.cell.2020.08.007.

5. Dayama G*, **Priya S***, Niccum DE, Khoruts A, Blekhman R. "Interactions between the gut microbiome and host gene regulation in cystic fibrosis". *Genome Medicine, 12:12.* 2020**.** https://doi.org/10.1186/s13073-020-0710-2. (*these authors contributed equally)**.**
6. **Priya S** and Blekhman R. "Population dynamics of the human gut microbiome: change is the only constant". *Genome Biology, 20:150.* 2019**.** https://doi.org/10.1186/s13059-019-1775-3.
7. Brooks AW, **Priya S**, Blekhman R, Bordenstein SR. "Gut Microbiota Diversity across Ethnicities in the United States". *PLoS Biology, 16(12): e2006842.* 2018. https://doi.org/10.1371/journal.pbio.2006842.
8. Burns MB, Montassier E, Abrahante J, **Priya S**, Niccum DE, Khoruts A, Starr TK, Knights K, Blekhman R. "Colorectal cancer mutational profiles correlate with defined microbial communities in the tumor microenvironment", *PLoS Genetics, 14(6): e1007376.* 2018**.** https://doi.org/10.1371/journal.pgen.1007376.
9. Hale VL, Jeraldo P, Chen J, Mundy M, Yao J, **Priya S**, Keeney G, Lyke K, Ridlon J, White BA, French AJ, Thibodeau S, Diener C, Resendis-Antonio O, Gransee J, Dutta T, Petterson XT, Blekhman R, Boardman L, Larson D, Nelson H, Chia N, "Distinct Microbes, Metabolites, and Ecologies Define the Microbiome in Deficient and Proficient Mismatch Repair Colorectal Cancers", *Genome Medicine, 10(1).* 2018. https://doi.org/10.1186/s13073-018-0586-6.
10. Clark CR, Maile M, Blaney P, Hellweg SR, Strauss A, Durose W, **Priya S**, Habicht J, Burns MB, Blekhman R, Abrahante JE, Starr TK, "Transposon mutagenesis screen in mice identifies TM9SF2 as a novel colorectal cancer oncogene", *Scientific Reports 8(1).* 2018. https://doi.org/10.1038/s41598-018-33527-3.
11. Lynch J, Tang K, **Priya S**, Sands J, Sands M, Tang E, Mukherjee S, Knights D, Blekhman R. "HOMINID: A framework for identifying associations between host genetic variation and microbiome composition". *GigaScience. 6:12, pp. 1–7.* 2017**.** https://doi.org/10.1093/gigascience/gix107.
12. **Priya S**, Jiang G, Dasari S, Zimmermann MT, Wang C, Heflin J, Chute CG. "A Semantic Web-based system for mining genetic mutations in cancer clinical trials". *AMIA Summits on Translational Science Proceedings. pp.142 –146 (PMID:26306257).* 2015. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4525254/.
13. Zhang X, Song D, **Priya S**, Daniels Z, Reynolds K, Heflin J. "Exploring Linked Data with Contextual Tag Clouds". *Journal of Web Semantics: Science, Services and Agents on the World Wide Web. vol. 34, pp. 33-39*. 2014**.** https://doi.org/10.1016/j.websem.2013.12.004.
14. **Priya S**, Guo Y, Spear M, Heflin J. "Partitioning OWL Knowledge Bases for Parallel Reasoning". *In: Proc. of Eighth IEEE International Conference on Semantic Computing (ICSC 2014). Newport Beach, CA, pp. 108-115*. 2014. https://doi.org/10.1109/ICSC.2014.34.
15. Zhang S, Song D, **Priya S**, Heflin J. "Infrastructure for Efficient Exploration of Large Scale Linked Data via Contextual Tag Clouds". *In: Alani H. et al. (eds) The Semantic Web – ISWC 2013. ISWC 2013. Lecture Notes in Computer Science, vol 8218. Springer, Berlin, Heidelberg*. 2013**.** https://doi.org/10.1007/978-3-642-41335-3_43.

**Research Presentations**

- **(Invited Talk)** "Multi-omics of host-microbiome interactions", Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden, 10/2021.
- **(Invited Talk)** "Machine Learning on Microbiome data", 14th Great Lakes Bioinformatics (GLBIO) conference, University of Minnesota, MN, 05/2021.
- **(Talk)** "Shared and disease-specific host gene-microbiome interactions across human diseases", Cold Spring Harbor meeting on The Biology of Genomes, Cold Spring Harbor, New York, 05/2021.
- **(Talk)** "A machine learning framework reveals patterns of host gene-microbiome interactions across human diseases", Cold Spring Harbor Laboratory meeting on Biological Data Science, CSHL, 11/2020.
- **(Poster)** "Shared and disease-specific host gene-microbiome interactions across human diseases", Cold Spring Harbor Laboratory meeting on Microbiome, Cold Spring Harbor, New York, 10/2020.
- **(Poster)** "Common host gene-microbiome interactions across human diseases", Cold Spring Harbor Laboratory Meeting on Microbiome, Cold Spring Harbor, New York, 07/2019.
- **(Talk)** "A Machine Learning Framework Reveals Common Molecular Interactions Between Gut Microbiome and Host Genes Across Human Disease States", 3rd Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis, Simons Foundation, New York, 04/2019.

- (**Invited Talk**) “Characterizing Host Gene-Microbiome Interactions in Human Diseases Using Machine Learning”, Machine Learning Applications to Phenomics and Genomics, Fall Symposium, Microbial and Plant Genomics Institute, University of Minnesota, 08/2018.
- (**Talk**) “Characterizing Host Gene-Microbiome Interactions in Human Diseases Using Machine Learning”, 5th Midwest Population Genetics Meeting, University of Minnesota, 08/2018.
- (**Poster**) “Interactions between the gut microbiome and host gene regulation shed light on the pathogenesis of colorectal cancer in cystic fibrosis patients”, 7th Conference on Beneficial Microbes, Madison, Wisconsin, 07/2018.
- (**Invited Talk**) “Interactions between the gut microbiome and host gene regulation shed light on the pathogenesis of colorectal cancer in cystic fibrosis patients”, 10th Annual Bioinformatics Research Symposium, University of Minnesota Rochester, 01/2018.
- (**Talk**) “A Semantic Web-based system for mining genetic mutations in cancer clinical trials”, AMIA Joint Summits on Translational Science, San Francisco, 03/2015.

## Teaching and Mentoring Experience

- Developed and taught a course module on “Introduction to Machine Learning using R” in BICB 8510 Computation and Biology (Spring 2020, Spring 2021, *UMN-Twin Cities* & *UMN-Rochester campuses*).
- Mentored graduate rotation students in *Blekhman Lab, UMN* (Fall 2018, Spring 2021)
- Teaching Assistant, *Lehigh University* (2013 – 2015).
    - Courses: *Design and Analysis of Algorithms*, *Introduction to Java*.
    - Managed classes with 50 – 140 undergraduate students.
    - Responsibilities: Conduct labs, grade homeworks and exams, design and deliver guest lectures, hold office hours, mentor students, maintain and write scripts for collection and processing of homeworks.

## Science Outreach and Service

Outreach:

- Organized science outreach activity on the topic of Human Microbiome at farmer’s market as part of Market Science outreach program. (06/2019 and 06/2017)
- Coordinator of monthly lab reading and discussion on diversity, equity and inclusion.

Service:

- Organized and conducted workshop on “Machine Learning on Microbiome data” at the 14th Great Lakes Bioinformatics (GLBIO) conference, 05/2021.
- Reviewer for PloS Computational Biology, Human Genetics, mSystems, Cell Host & Microbe (co-reviewer), Communications Biology – Nature, Scientific Data - Nature, PeerJ, IJCAI research track (2016), Biomedical Data Mining, Modeling, and Semantic Integration at ISWC (2015).
- Served in local organizing committee for International Semantic Web Conference (ISWC) 2015.

## Professional and Technical Skills

- *Programming*: R, Java, Scala, C, C++
- *Scientific skills*: microbiome analysis (metagenomics, 16S, metabolomics, viromics), human genomic analysis (RNA-sequencing, whole genome sequencing), multi-omic integration, machine learning, parallel and distributed computing.