SHASHIDHAR RAVISHANKAR

Staff Scientist
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Current Role

April 2022 - Present **Staff Scientist, Warren Lab, Clinical Research Division, Fred Hutchinson Cancer Center**.

- Examining the role of T-cells within the tumor micro-environment of individuals with KS. (Manuscript in preparation)
- Identifying the diversity of Epstein Barr Virus (EBV) and its impact on the immune response. (Manuscript submitted)
- Exploring the impact of HLA Class II genotype on mNSCLC patients undergoing ICI therapy. (Published in Nature Scientific Reports)

Research Interests

- **T-Cell Specificity Prediction using Large Language Models**
- **3D Structure Prediction of T-Cell Receptor-pMHC Complexes**
- **Multi-Instance Learning for T-Cell Repertoire Level Characteristic Identification**
- **Epitope Hotspot Identification in Kaposi Sarcoma Herpesvirus (KSHV)**

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Research Experience

Oct 2019 - April 2022 **Bioinformatics Analyst, Warren Lab, Clinical Research Division, Fred Hutchinson Cancer Center**.

- Investigating the impact of extended ART on the T-cell repertoire in people living with HIV. (Frontiers in Immunology)
- Understanding the tumor micro-environment of Kaposi Sarcoma using single-cell RNA-Seq.
- Developing tools for the analysis of AIRR-Seq, scRNA-Seq analysis, and genome assembly.

Jan 2018 - Aug 2018 **SWEP Graduate Researcher, Malaria Branch, Centers for Disease Control and Prevention**.

- Developing a scalable NGS workflow for to identify variations associated with drug resistance in *P. falciparum*. (Published in Antimicrobial agents and chemotherapy and available on bioRxiv)
- Constructing the first complete genome of the simian malaria parasite *P. brasilianum*. (Nature Scientific Reports)

Jun 2015 - Aug 2015 **Bioinformatics Intern, New York Genome Center**.

- Developing a framework for Bisulfite-Seq analysis.
- Benchmarking tools for variant identification from Bisulfite-Seq data.
- Developing a tool for the detection of allele-specific methylation from Bisulfite-Seq data.

Jul 2013 - May 2014 **Junior Bioinformatics Analyst, Interpretomics India Pvt Ltd**.

- Design and implementation of a Python based pipeline for Whole Genome/Exome Sequencing, RNA-Seq, ChIP-Seq, microRNA-Seq, and HLA-Typing for NGS-based cloud platform called iOMICS.
- Developing a tool for the detection of the complete spectrum of variations in WGS/WES data. (PLOS One)

Publications

Scientific Reports, Jan 2023	**Class II HLA-DRB4 is a predictive biomarker for survival following immunotherapy in metastatic non-small cell lung cancer**. Cindy Y Jiang, Lili Zhao, Michael D Green, **Shashidhar Ravishankar**, Andrea MH Towlerton, Anthony J Scott, Malini Raghavan, Matthew F Cusick, Edus H Warren, Nithya Ramnath
Scientific Reports, Nov 2022	**The first complete genome of the simian malaria parasite *Plasmodium brasilianum***. Marko Bajic*, **Shashidhar Ravishankar***, Mili Sheth, Lori Rowe, M. Andreina Pacheco, Dhruviben S. Patel, Dhwani Batra, Vladimir Loparev, Christian Olsen, Ananias Escalante, Fredrik Vannberg, Venkatachalam Udhayakumar, John W. Barnwell, Eldin Talundzic
Front. immunol., May 2022	**Serial analysis of the T-cell receptor β-chain repertoire in people living with HIV reveals incomplete recovery after long-term antiretroviral therapy**. Andrea M. H. Towlerton*, **Shashidhar Ravishankar***, David G. Coffey, Camillie E. Puronen, Edus H. Warren
DNA repair, Jul 2021	**RNA helicase, DDX3X, is actively recruited to sites of DNA damage in live cells**. Michael J. Cargill, **Shashidhar Ravishankar**, Alicia Morales, Edus H. Warren
IJID, Jun 2021	**Targeted deep amplicon sequencing of antimalarial resistance markers in *Plasmodium falciparum* isolates from Cameroon**. Mariangela L'Episcopia, Julia Kelley, Bruna G Djeunang Dongho, Dhruviben Patel, Sarah Schmedes, **Shashidhar Ravishankar**, Edvige Perrotti, David Modiano, Naomi W Lucchi, Gianluca Russo, Eldin Talundzic, Carlo Severini
Antimicrob Agents Chemother, May 2019	**Evolution and genetic diversity of the k13 gene associated with artemisinin delayed parasite clearance in *Plasmodium falciparum***. M Andreína Pacheco, Esha R Kadakia, Zainab Chaudhary, Douglas J Perkins, Julia Kelley, **Shashidhar Ravishankar**, Michael Cranfield, Eldin Talundzic, Venkatachalam Udhayakumar, Ananias A Escalante
bioRxiv, May 2018	**Next-generation Sequence-analysis Toolkit (NeST): A standardized bioinformatics framework for analyzing Single Nucleotide Polymorphisms in next-generation sequencing data**. **Shashidhar Ravishankar**, Sarah E Schmedes, Dhruviben S Patel, Mateusz Plucinski, Venkatachalam Udhayakumar, Eldin Talundzic, Fredrik Vannberg
Antimicrob Agents Chemother , Mar 2018	**Next-Generation Sequencing and Bioinformatics Protocol for Malaria Drug Resistance Marker Surveillance**. Eldin Talundzic, **Shashidhar Ravishankar**, Julia Kelly, Dhruviben Patel, Mateusz Plucinski, Sarah Schmedes, Dragan Ljolje, Brooke Clemons, Susan Madison-Antenucci, Paul M. Arguin, Naomi W Lucchi, Fredrik Vannberg, Vekatachalam Udhayakumar
Bioinformatics, Nov 2017	**Mapping-free variant calling using haplotype reconstruction from k-mer frequencies**. Peter Audano III, **Shashidhar Ravishankar**, Fredrik Vannberg
Scientific Reports, Mar 2017	**TLR-exosomes exhibit distinct kinetics and effector function**. Swetha Srinivasan , Michelle Su , **Shashidhar Ravishankar** , James Moore , Pamela Sara Head , Brandon J Dixon, Fredrik Vannberg
Genome Announc., Feb 2017	**First full draft genome of *Plasmodium brasilianum***. Eldin Talundzic, **Shashidhar Ravishankar**, Vishal Nayak, Dhruviben S. Patel, Christian Olsen, Mili Sheth, Dhwani Batra, Vladimir Loparev, Fredrik O.Vannberg, Venkatachalam Udhayakumar,John W. Barnwell
PLOS ONE, Apr 2015	**XomAnnotate: Analysis of Heterogeneous and Complex Exome - A Step Towards Translational Medicine**. Asoke Talukder, **Shashidhar Ravishankar**, Jyothsna Prabhukumar, Francesco Blasi

Open source tools

Oct 2019 - Present **LymphoSeq2: A toolkit for exploratory data analysis of AIRR-Seq datasets**, *Dr.Edus H. Warren, Fred Hutchinson Cancer Center*.

- Calculate diversity and identify changes in the composition of immune repertoire from AIRR-Seq datasets.
- Visualize and explore immune repertoire from multiple samples.

Aug 2018 - Aug 2019 **Gentoo: Reference free clustering algorithm to identify relatedness of isolates**, *Dr.Fredrik Vannberg, Georgia Institute of Technology*.

- Reference-free algorithm to identify relatedness of isolates using k-mer frequencies.
- Weighted Jaccard distance used to estimate genomics distances from raw NGS (FASTQ) data.

May 2017 - Aug 2019 **Next-generation Sequence analysis Toolkit**, *Dr. Fredrik Vannberg, Georgia Institute of Technology, Dr. Venkatachalam Udhayakumar, Center for Disease Control*.

- Development of a toolkit for the rapid identification of mutations in the *Plasmodium falciparum* genome conferring drug resistance against standard anti-malaria drug regimes.

Aug 2016 - Jan 2018 ***Plasmodium brasilianum* genome project**, *Dr. Fredrik Vannberg, Georgia Institute of Technology, Dr. Venkatachalam Udhayakumar, Center for Disease Control*.

- Assembling the genome of the malaria-causing parasite *Plasmodium brasilianum*.
- Develop a standardized protocol for the assembly of genomic data from *Plasmodium spp*.
- Comparative analysis of the *Plasmodium malariae* and *Plasmodium brasilianum* genome.

Aug 2016 - May 2017 **Hummingbird: A K-mer based, alignment-free tool for RNA Seq analysis**, *Dr. Fredrik Vannberg, Georgia Institute of Technology*.

- k-mer based algorithm for the quantification of transcripts in RNA-Seq data.
- k-mer frequencies across indexed transcriptome used to calculate abundances at gene and isoform level.