Sagar Utturkar, Ph.D.

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Introduction:

Skilled bioinformatics scientist with 10+ years of experience in analyses of large-scale NGS data. I work in close collaboration with bench scientists for effective data interpretation, experimental design, hypothesis generation and grant applications.

Skills:

- Proficient in data processing, analyses, and interpretation of NGS workflows for RNAseq (Bulk, single-cell RNAseq and Spatial transcriptomics, TTseq), DNAseq (WGS/WES variant discovery), functional genomics (CRISPR, miRNA), epigenomics (ATAC-Seq, ChIP-Seq), Databases (TCGA, KidsFirst, GEO, NCBI, cBioPortal).
- Highly skilled in R, R-markdown, Python, Bash, and power-user of HPC Linux environment.
- Expert in generating custom data visualization (tidyverse, ggplot) with scientific data.
- Excellent communication skills to convey results to both computational and noncomputational collaborators.
- Co-manage the bioinformatics core facility, lead junior bioinformaticians for successful and timely completion of high-impact projects.

Research and Professional Experience:

Staff Scientist - Purdue University, USA **2022 -Present**

- Lead the bioinformatics core facility to support oncology group (20+ faculty) and high-impact projects.
- Utilizing emerging technologies single-cell RNAseq (10X Chromium), spatial transcriptomics (10X Visium) and perform integrated analysis to support drug discovery.
- Actively involved in scientific premise seeking to develop dogs as a model system to study human cancers. I am Co-PI on multiple grants that support immunotherapy research and Phase I/II clinical trials in dogs.

Senior Bioinformatics Scientist - Purdue University, USA **2019 -Present**

- Lead the bioinformatics component (bulk and single-cell RNA-seq, ChIP-seq, Variant calling (WGS/WES), miRNA and methylation analysis) for interdisciplinary cancer genomics projects.
- Developed custom bioinformatics pipelines to automate bioinformatic workflows with integrated visualizations using R-programming, Python and HPC Clusters
- Leveraged single-cell RNA-seq data from chemotherapy administered pet dogs to study the changes in the immune cell populations and subsequent comparisons with TCGA (human) data.
- Customized analysis of TCGA/GTEX and public cancer genomics data (KidsFirst, St. Jude’s, ICDC) to determine correlation with experimental results and generated preliminary data for grant applications.
- Developed R-shiny App for customized exploration of single-cell RNA-seq data.
- Contributed towards conceptualizing research ideas in grant applications that lead in 5 funded research grants and 10+ publications in cancer genomics.
- Support bioinformatics education by providing training and guidance to graduate students and post-doc.

Bioinformatics Scientist - Purdue University, USA **2017 - 2019**

- Independently managed end-to-end workflows for various Cancer bioinformatics projects.
- Implemented R-markdown for generating beautiful HTML reports in semi-automated fashion.
- Correlated scientific data with published literature and public databases.
- Designed and automated bioinformatics pipelines using Python, R, Bash and HPC clusters.
- Maintained GitHub Repository for C^3B Bioinformatics Core to support reproducible research.

Bioinformatics Analyst - Purdue University, USA **2016 - 2017**

- Provided bioinformatics analysis and consultation services for bioinformatics applications of RNA-Seq, Metagenomics, Meta-transcriptomics, genome assembly, miRNA analysis and annotation.
- Analyzed sequencing data from bacterial, mammalian and various non-model organisms, developed customized workflows, assisted in manuscript preparations and data deposition.
- Designed custom pipelines and maintained GitHub repositories to support high throughput data analytics.
- Conducted hands-on bioinformatics workshops to train the research staff in bioinformatics applications.
- Actively participated in writing research grants to enhance funding opportunities.

Graduate Research Assistant - Oak Ridge National Laboratory, USA **2010 - 2016**

- Evaluated *de novo* and hybrid assembly methods using PacBio, Illumina, 454, and Ion Torrent NGS platforms and designed microbial genome finishing strategies.
- Single-cell genomics analysis of uncultured bacteria from *Populus deltoides* root microbiome.
- Linux Shell, and Perl scripting for pipeline development, data retrieval/conversion.
- Graduate teaching assistant at the University of Tennessee, Knoxville.

Bioinformatics Software Engineer **Persistent Systems Ltd., India** **2008 – 2010**

- Algorithm testing for instrument control and analysis software from Life Technologies.
- Developed automated test suite using Perl for algorithm consistency check.
- Developed and executed test cases, identified software defects, and reported in bug tracking system.
- Provided bioinformatics domain support for internal developers and customers.

Education:

University of Tennessee, USA	**Ph.D.**	**Bioinformatics**	2015
Nottingham Trent University, UK	**M.S.**	**Bioinformatics**	2007
University of Mumbai, India	**B.S.**	**Biotechnology**	2006

Selected Publications: Google Scholar

- Dhawan D, Ramos-Vara JA, **Utturkar SM**, Ruple A, Tersey SA, Nelson JB, Cooper BR, Heng HG, Ostrander EA, Parker HG, Hahn NM, Adams LG, Fulkerson CM, Childress MO, Bonney PL, Royce C, Fourez LM, Enstrom AW, Ambrosius LA, Knapp DW. Identification of a naturally-occurring canine model for early detection and intervention research in high grade urothelial carcinoma. Front Oncol. 2022 Nov 11;12:1011969. doi: 10.3389/fonc.2022.1011969. PMID: 36439482; PMCID: PMC9692095.
- Hegazy YA, Cloutier SC, **Utturkar SM**, Das S, Tran EJ. The genomic region of the 3' untranslated region (3'UTR) of PHO84, rather than the antisense RNA, promotes gene repression. Nucleic Acids Res. 2023 Aug 25;51(15):7900-7913. doi: 10.1093/nar/gkad579. PMID: 37462073; PMCID: PMC10450162.
- Wang J, Toregrosa-Allen S, Elzey BD, **Utturkar SM**, Lanman NA, Bernal-Crespo V, Behymer MM, Knipp GT, Yun Y, Veronesi MC, Sinn AL, Pollok KE, Brutkiewicz RR, Nevel KS, Matosevic S. Multispecific targeting of glioblastoma with tumor microenvironment-responsive multifunctional engineered NK cells. Proc Natl Acad Sci U S A. 2021 Nov 9;118(45):e2107507118. doi: 10.1073/pnas.2107507118. PMID: 34740973; PMCID: PMC8609337.
- Alpsoy A, **Utturkar SM**, Carter BC, Dhiman A, Torregrosa-Allen SE, Currie MP, Elzey BD, Dykhuizen EC. BRD9 Is a Critical Regulator of Androgen Receptor Signaling and Prostate Cancer Progression. Cancer Res. 2021 Feb 15;81(4):820-833. doi: 10.1158/0008-5472.CAN-20-1417. Epub 2020 Dec 21. PMID: 33355184; PMCID: PMC8026650.
- Venis SM, Moon HR, Yang Y, **Utturkar SM**, Konieczny SF, Han B. Engineering of a functional pancreatic acinus with reprogrammed cancer cells by induced PTF1a expression. Lab Chip. 2021 Sep 28;21(19):3675-3685. doi: 10.1039/d1lc00350j. PMID: 34581719; PMCID: PMC9175079.
- Knapp DW, Dhawan D, Ramos-Vara JA, Ratliff TL, Cresswell GM, **Utturkar SM**, Sommer BC, Fulkerson CM, Hahn NM. Naturally-Occurring Invasive Urothelial Carcinoma in Dogs, a Unique Model to Drive Advances in Managing Muscle Invasive Bladder Cancer in Humans. Front Oncol. 2020 Jan 21;9:1493. doi: 10.3389/fonc.2019.01493. PMID: 32039002; PMCID: PMC6985458.
- Xing Z, Russon MP, **Utturkar SM**, Tran EJ. The RNA helicase DDX5 supports mitochondrial function in small cell lung cancer. J Biol Chem. 2020 Jul 3;295(27):8988-8998. doi: 10.1074/jbc.RA120.012600. Epub 2020 May 6. PMID: 32376686; PMCID: PMC7335798.
- AlAbdi L, Saha D, He M, Dar MS, **Utturkar SM**, Sudyanti PA, McCune S, Spears BH, Breedlove JA, Lanman NA, Gowher H. Oct4-Mediated Inhibition of Lsd1 Activity Promotes the Active and Primed State of Pluripotency Enhancers. Cell Rep. 2020 Feb 4;30(5):1478-1490.e6. doi: 10.1016/j.celrep.2019.11.040. PMID: 32023463; PMCID: PMC7316367.
- Wurch L, Giannone RJ, Belisle BS, Swift C, **Utturkar SM**, Hettich RL, Reysenbach AL, Podar M. Genomics-informed isolation and characterization of a symbiotic Nanoarchaeota system from a terrestrial geothermal environment. Nat Commun. 2016 Jul 5;7:12115. doi: 10.1038/ncomms12115. PMID: 27378076; PMCID: PMC4935971.