# Bioinformatics Core

Ambient RNA Contamination Correction (SoupX)

About Us

The Bioinformatics Core at UVA is headed by Dr. Pankaj Kumar, a Ph.D. in Computational Biology, with 15+ years of experience in data science (https://www.ncbi.nlm.nih.gov/myncbi/pankaj.kumar.2/bibliography/public/). It provides analysis of high-throughput sequencing, omics (proteomics, metabolomics, gene expression) and other genomics data. It provides expert advice in designing the experiments to make analysis possible and can assist with grant proposals to incorporate bioinformatics analysis in research plans. The Bioinformatics Core at UVA serves as a centralized resource for providing expert and timely bioinformatics consulting and data analysis solutions. The core offers services to investigators both within and outside UVA. The Bioinformatics Core's mission is to build and maintain an infrastructure that enables the application of strong bioinformatics analysis with a measurable impact on the ability of UVA investigators to both publish their work and obtain new funding. The core not only helps with data analysis on the data generated in PI's lab but also helps with any publicly available data on cyberspace. The bioinformatics core also helps and guides the PI to get the restricted raw sequencing data hosted by dbGaP.

The Bioinformatics Core provides expert advice in

Computational Biology
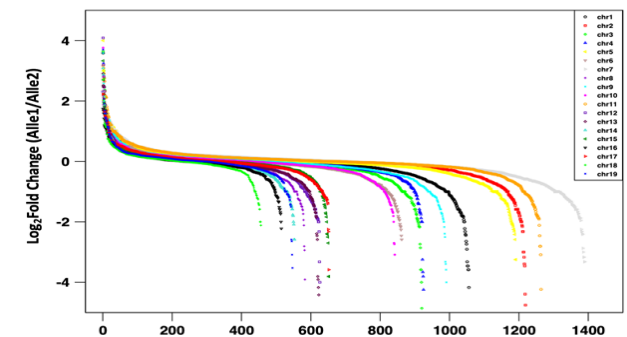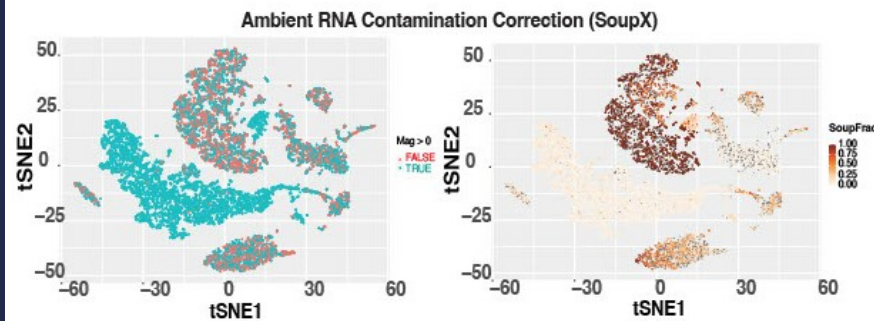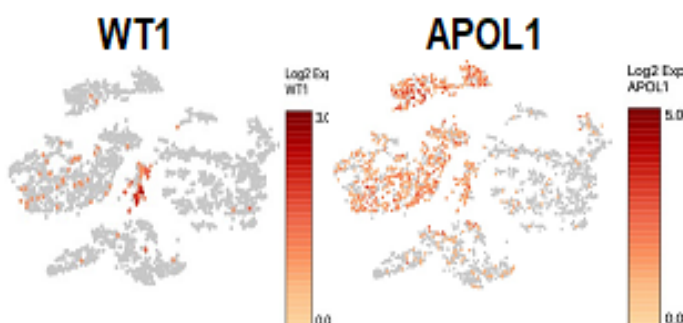
Instrumentation

- Dedicated access to three 72-core 376GB high-memory servers
- Shared access to 92 multi-core high-memory computing nodes; >5,000 cores and >50,000 GB RAM total as part of a high-performance computing cluster

Our Services

- Custom bioinformatics / biostatistical support
- Gene expression profiling: RNA-seq (bulk), microarray, Small RNA-seq and Allele-specific gene expression analysis
- Single Cell RNA-seq (scRNA-seq) (expression profiling, cluster generation, cluster annotation, Marker gene identification, trajectory analysis, pathway analysis, etc.)
- Single Cell ATAC-seq (scATAC-seq) analysis, Integrated scRNA-seq and scATAC-seq data analysis
- DNA variation (SNP and GWAS), Copy number variation (Aneuploidy, insertion/deletion etc.)
- Analyzing genomic data generated by DNA-protein binding assays (ChIP-seq, CHIRP-seq, etc.) and RNA-protein binding assays (CLIP-seq, PAR-CLIP, CLASH, etc.)
- DNA methylation: sequence-based analysis and array-based analysis
- Microbiome data analysis (16S rRNA, shotgun metagenomics, etc.)
- Pathway and functional analysis
- Proteomics and Metabolomics data analysis (Targeted & Untargeted)
- Developing data-specific predictive models, conducting survival analysis (using molecular and clinical data)
- CRISPR screening experimental design and data analysis
- Power Analysis (Estimation of sample size)
- Data Management and Sharing plan write up during grant submission and preparing, uploading and sharing the data as per NIH guidelines

Enhancing Research, Rigor and Reliability

Our Team

Pankaj Kumar, PhD - Director
Assistant Professor of Biochemistry & Molecular Genetics

Anwaruddin Mohammad, MS - Senior Bioinformatics Analyst

Guruprasad Varma Kondu, MS - Bioinformatics Analyst Intermediate

Contact

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Bioinformatics Core Website:
med.virginia.edu/bioinformatics-core/

Request services on:
uva.corefacilities.org/account/login

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