Genomics Research & Technology Hub (GRT Hub)

Suzanne Sandmeyer, PhD
Director

Mission and Leadership

MISSION

To provide emerging and state-of-the-art genomics technologies and training to CFCCC members

To fulfill this mission, **GRT Hub**:

- Supports adoption of current and developing – omics technologies to combat cancer
- Trains and supports cancer center researchers in the strategic application of -omics technologies
- Promotes rigorous analytical approaches in –omics including: providing user training, bioinformatic and statistical analysis, and support for data interpretation and documentation, archiving, and sharing

LEADERSHIP

Suzanne Sandmeyer, PhD
Director
Genomic Technologies

Remi Buisson, PhD
Assistant Director
GRT Hub SR

Melanie Oakes, PhD
Manager
Technical Operations

Jenny Wu, PhD
Director, Bioinformatics
Transcriptomic Analysis

Ivan Chang, PhD
Bioinformatics Engineer
Data Sharing

Home Page

Instruments Page

PacBio Revio Long-Read Sequencer

10X Genomics Xenium Analyzer

10X Genomics CytAssist

Illumina NovaSeq X Plus Short-Read Sequencer

Illumina NovaSeq X Plus Short-Read Sequencer

The Illumina NovaSeq X Plus installed in the middle of June, comes with state-of-the-art short read sequencing. Two flow cells (2*8 lanes) produce up to 25 B reads each (2x150bp) in 48 hr while maintaining quality of 85% >Q30 and reducing price by 30 %. According to Illlumina specifications, technical improvements include reduced input requirements, higher density flow cells, XLAP-SBS chemistry, new optics, enzymes, and modifications in cycle blocking and unblocking. Dragen software can be used to facilitate analysis. FASTQ files will continue to be made available to users. This reduces runs for short read 30X coverage with 128 genomes per dual flow cell and deeper sequencing for single cell transcriptomics.

More Information from the Manufacturer

Related Services: Short-read Sequencing & Library Construction |

Seminars

Upcoming

Genetics, Biomedical Computing and Genomics Seminar Series – "Harnessing alternative polyadenylation and tandem repeat to understand the genetic basis of human diseases"

Friday 11/01/2024
10:00 to 11:00 a.m. (PST)
Zoom Only - This seminar will not be recorded.

Ya (Allen) Cui, PhD
Research Assistant Professor in the Wei Li lab
UCI Department of Biological Chemistry

Dr. Ya (Allen) Cui is a research assistant professor in Prof. Wei Li's lab in the Department of Biological Chemistry at the University of California Irvine. Dr. Cui will open his own lab early next year. Dr. Cui's research is focused on understanding the genetic association of tandem repeat (TR) and alternative polyadenylation (APA) association with complex traits and diseases, such as cancer, neurological, cardiovascular, and metabolic diseases. Dr. Cui will present his recently developed alternative polyadenylation transcriptome-wide association method (3'aTWAS) to identify APA-linked susceptibility risk genes (Nature Communications 2023) and an extremely exciting new research direction: TR-gnomAD, now known as TR-Atlas, a biobank-scale TR reference map for diverse ancestries (Cell 2024 and Nature Genetics accepted).

Zoom Link

Previous

Genetics, Biomedical Computing and Genomics Monthly Seminar
Tuesday 06/04/2024
10:00 to 11:00 a.m. PST

Emerging Genetic Drivers of Human Diseases: A genome-wide spectrum of tandem repeat expansions in 338,963 humans

In this talk, Dr. Li will present an extremely exciting new research direction: the Tandem Repeat Genome Aggregation Database (UCI TR-gnomAD; *Cell* 2024). This groundbreaking project has positioned UCI as a leader in human and medical genetics. TR-gnomAD provides the first genetic reference maps for approximately 0.8 million Tandem Repeat (TR) expansions, such as the CAG expansion in Huntington's disease, across 340,000 humans. It revolutionizes TR-based disease-association studies, health disparity research, and clinical diagnostics. The international research and medical communities, including scientists, physicians, and genetic counselors, will heavily rely on TR-gnomAD for interpreting TR expansions in genetic diseases,
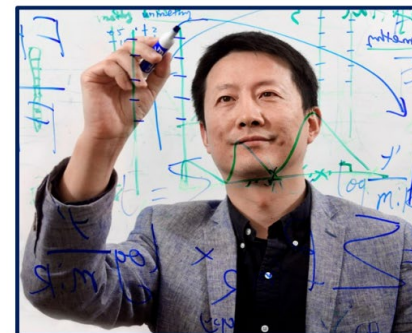
Genetics, Biomedical Computing and Genomics Monthly Meeting – "Translational Science at CFCCC-Opportunities for Collaboration and Clinical Trials", Farshid Dayyani, MD, PhD
Tuesday 05/07/2024
10:00 to 11:00 a.m. (PT)

Dr. Dayyani is a Professor of Clinical Medicine in the Division of Hematology/Oncology at University of California Irvine and board certified in Medical Oncology. He is also the Associate Director for Translational Science and the Medical Director of the Clinical Trials Unit at the Chao Family Comprehensive Cancer Center at UC Irvine.

Dr. Dayyani performs clinical and translational research in gastrointestinal and hepatobiliary carcinomas. He manages a wide portfolio of investigator initiated, NCI funded and industry sponsored clinical trials to develop novel treatment options and establish new biomarkers. He obtained his MD/PhD from LMU Munich, Germany, followed by a research fellowship and residency in internal medicine at Harvard Medical School, Boston. He then completed a combined clinical and research fellowship in medical oncology at the UT MD Anderson Cancer Center, Houston, TX. Dr. Dayyani also has industry experience as Global Clinical Lead for Oncology at Roche Diagnostics, Int. in Rotkreuz, Switzerland, prior to joining UC Irvine.

Workshops

Upcoming

Workshop on Spatial Transcriptomic Data Analysis with an Emphasis on 10x Genomics Visium

Tuesday 11/12/2024
9:00 a.m. to 1:00 p.m. (PST)
Sprague Hall, Room 105

This workshop will introduce data analysis workflow with both sequencing- and imaging-based spatial transcriptomics platforms, using 10x Genomics Visium and Xenium as examples. The topics will include an overview of preprocessing and data visualization with both 10x Genomics proprietary software and the state-of-the-art open-source software. New topics such as Visium HD and Xenium 5k data analysis will be discussed including cellular niche and spatial differential analysis methods. A guided tour will be provided on how to run the latest visualization and data exploration tools to support spatial transcriptomics via command line and Jupyter Hub on HPC3. *Attendees are encouraged to bring their own project data for analysis and discussion.*

Registration is required – $50 and limited to 20 attendees

Register Today!

Previous Workshops

Spatial Transcriptomic Data Analysis & Software

Tuesday 02/27/2024
8:00 a.m. to 12:00 p.m. - Light continental breakfast provided
Sprague Hall, Room 105

Genomics Research and Technology Hub (GRT Hub) Workshop

Required: Personal laptop (Mac or Windows) and HPC3 account

Instructors: Jenny Wu, PhD and Ivan Chang, PhD

This workshop introduces data analysis workflow with both sequencing and imaging based spatial transcriptomics platforms, using 10x Visium and Xenium as examples. The topics included an overview of data quality control, preprocessing and visualization, cellular segmentation etc. with 10x proprietary software and state of the art Open-source software. A guided tour was provided on how to run the latest visualization and data exploration tools to support spatial transcriptomics via both the command line and the Jupyterhub of HPC3.

- Computing on the HPC3 for Spatial Omics Ivan Chang, PhD 📄
- Introduction to 10x Visium and Xenium spatial platform data analysis workflow and analytical tools Jenny Wu, PHD 📄
- Interactive Computing on the HPC3 for Spatial Omics, Ivan Chang, PhD ▶
- Introduction to 10x Visium and Xenium Spatial Platform Data Analysis, Jenny Wu, PhD ▶

10x Genomics Spatial Workshop Series – Three Sessions

Thursday 01/11/2024 – Wednesday 01/24/2024
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Webinar

Because cells reside within microenvironments, their functions are influenced by the network cells surrounding them, sending and receiving messages. Spatially resolved biology, including whole transcriptomic and targeted in situ methods, allows scientists to build a more complete view of cellular function in a morphological context, representing a paradigm shift in the study of biological systems. Visium from 10x Genomics is a NGS-based spatial discovery platform that allows whole transcriptome profiling of tissues. The Xenium In Situ platform is an imaging-based solution that provides precise localization of thousands of RNA targets with subcellular resolution, offering true single cell spatial analysis. Insights from these spatial techniques can be combined with single cell data to bring greater resolution and enable a deeper understanding of gene expression patterns, helping researchers develop and refine hypotheses.

January 11, 2024 – Xenium – Accelerating the Master of Biology 📄
January 18, 2024 – Xenium 📄
January 24, 2024 – Visium Gene Expression 📄

Experimental Planning

Staff of the GRT Hub are experts excited to assist you in the overall conception and framing of the experimental workflow. If you are new to using the Hub or working with a particular instrument or technique, it is advised to meet as much in advance as possible with the Hub Manager, Melanie Oakes, PhD, in order to understand the workflow, expertise and resources that may be required as well as the time frame and cost to go from concept to product. In addition, for planning with regard to numbers of samples required for statistical robustness, meeting with the Director for Bioinformatics, Jenny Wu, PhD, is advised. For understanding your own computer resources that may be required, meeting with our expert in bioinformatic engineering, Ivan Chang, PhD, may also be helpful, particularly if your experiments are data intensive and you are new to UCI or the HPC3.

Grant Applications

Strategic planning for grants including experimental workflow, time for execution, data collection and analysis performed in the GRT Hub should be addressed as much in advance of the grant deadline as possible to ensure time to provide complete support. Direct assistance in grant writing is a recharged expense, however, grant planning, costing etc. is not.

Letters of support (LOS) The GRT Hub can provide either a standard LOS, or a customized version. In either case, when requesting such a letter, please provide the PI name(s), agency and title of the grant, and abstract or other brief description of the goal and aims of the research and nature of genomics experimental workflow. Please follow-up by letting us know if your application was successful or if we can assist with the resubmission.

Budgeting for GRT Hub genomics iLab has a complete list of the rates for work in the GRT Hub; however, these rates do not necessarily include supplies, so you are advised when starting a new series of experiments to confer with the GRT Hub staff to accurately project both the cost of reagents and the recharge rate from the Hub covering the Hub's expenses in service contracts and staff time. Also, please check with your specific center regarding any supplements related to   membership in the Cancer Center or Skin P30 and with the Manager for any volume related discounts.

Budgeting for computational staff time, computing cycles, hardware and software resources. NIH now appropriately stresses budgeting for data analysis including expert time compensation and computational resources. Staff can advise on the extent of these types of resources likely to be required and the suitability of HPC3 to support.

Publications

As the experimental workflow is reduced to and progresses into the data collection phase, it will be important to rigorously collect data and evaluate in real time to ensure that the expected data types are going to actually fulfill SOPs the needs for addressing the hypothesis or discovery mission. Upon completion of the experiment with appropriate records of the work, the staff can, on a recharge basis, assist with drafting parts of the experimental design, data collection, and analysis, and graphical displays, in which they were involved or before which they can be provided with complete documentation to facilitate the draft description. It is appropriate when there are creative contributions by the staff to include them in authorship on publications. This benefits the staff obviously, but in also your own efforts when you cite them as experts involved in your next grant application or letter of support from the GRT Hub.

Publications

When our services have provided data that will be used in a manuscript, we would appreciate acknowledgement of the shared instrumentation grants and support from the Chao Comprehensive Cancer Center at UCI, Complexity, Cooperation and Community in Cancer and the Skin Biology Resource-Based Center at UCI.

The following publications have acknowledged these services and support:

How to Acknowledge the GRT Hub in your Publications

Publication Acknowledgement

Publications
Sergei Butenko, Raji R. Nagalla, Christian F. Guerrero-Juarez, Francesco Palomba, Li-Mor David, Ronald Q. Nguyen, Denise Gay, Axel A. Almet, Michelle A. Digman, Qing Nie, Philip O. Scumpia, Maksim V. Plikus & Wendy F. Liu. Hydrogel crosslinking modulates macrophages, fibroblasts, and their communication, during wound healing. (2024) nature 2024 August 09. doi.org/10.1038.
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UCI Chao Family Comprehensive Cancer Center