

ONLINE INTERNATIONAL TRAINING WORKSHOP ON SINGLE CELL TRANSCRIPTOMICS

Organized by

Supported by

National Institute of Biomedical Genomics, India & Massachusetts Institute of Technology, USA



The purpose of this workshop is to introduce the methods of transcriptomic data generation and analysis at the level of single cells from diverse tissues. This workshop is supported by the *Human Cell Atlas*, an international project that aims to map every cell type in the human body, with the hope that this effort will transform our understanding of biology and disease and could lead to major advances in the way illnesses are diagnosed and treated. Although the methods that will be discussed in this workshop will be applicable to all organisms, the focus of this workshop will be on the human. The workshop will comprise live demonstration of experimental and data analysis methods. Members of the National Institute of Biomedical Genomics, India, and Massachusetts Institute of Technology, USA, will jointly teach in this online workshop. Members of the HCA will deliver special lectures.

Registration is mandatory



Go to the link:

https://docs.google.com/forms/d/1EZdmJCS_iRC8YeiWg4VgGHIHXlPwUoE7uIGe5LdotGM/edit?usp=share5LdotGM/edit?usp=share

OR scan the QR code

The number of participants is restricted to 50. Participants will be selected based on their experience and motivation. Selected participants will be notified by email.

Topics

Experimental methods

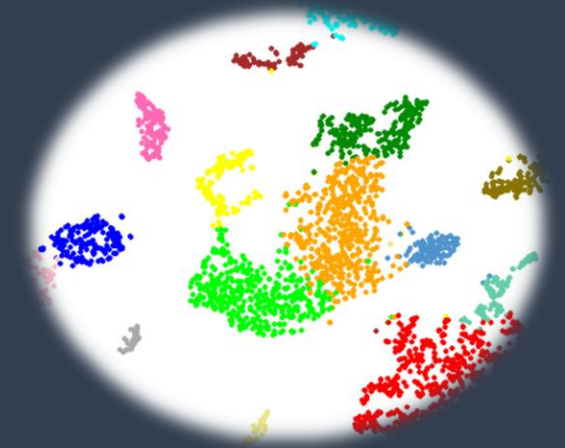
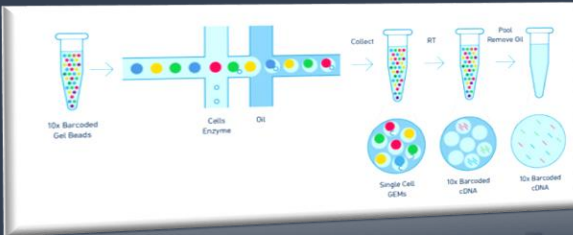
- Sample preparation for single cell sequencing;
- GEM generation and cDNA synthesis;
- cDNA amplification, clean-up and quantitation;
- Sequencing library preparation (fragmentation, size selection, adapter ligation, clean-up, index PCR, size selection, post-library cleanup and QC);
- Sequencing setup and run.

Data analysis and computational methods

- Introduction to Linux and R; Sequence data analysis: principles & approaches;
- Data download and data loading; Alignment and construction of feature-barcode counts matrix from 10x Chromium data using cellranger;
- Exploratory analysis of cellranger output using the Loupe browser;
- QA/QC, normalization and batch effect removal; Dimensionality reduction and cell type clustering; tSNE, UMAP;
- Cluster annotation; DEG identification;
- Gene expression program;
- Data integration.
- ATAC-seq, TCR-seq, BCR-seq
- Applications of single cell RNA-sequencing

Novel methodology
Seq-Well: Technology and methods.

Last date of registration: January 10, 2022.



This Workshop is open to human genomics researchers, including post-doctoral fellows.

