Complete Hands-on Single-Cell RNA-sequencing (scRNA-seq) Analysis Training Using Command-Line & R (Seurat)

BioCode's training offers an extensive opportunity to gain practical experience in the analysis of scRNA-seq data for detection of cellular and tumor heterogeneity between a tissue (tumor, normal, control) in different organisms and diseases. However, BioCode's training will primarily concentrate on humans . The primary focus of BioCode's training is on cancer. However, you can implement the teachings on any organism, disease and condition.

BioCode's training covers the basics of scRNA-seq and sequencing platforms used in NGS experiments, followed by a detailed step-by-step guide on how to obtain raw transcriptomics (scRNA-seq) datasets and perform mapping & demultiplexing and quantification (generation of count matrix) on them, all of which will be done on Linux (Ubuntu/macOS).

BioCode's training then moves on to teach the student how to preprocess the data, including quality control (removal of dead cells, mitochondrial reads-leaked cells), and how to dimension reduction, clustering and cell annotation to obtain the cell types present inside the tissue(s) under study.

The main focus of BioCode's training is on identification of different cell types present in a tissue and differential expression analysis between those cells, where the student will learn how to identify genes that are expressed differently through the scRNA sequencing pipeline. This process involves differentially expressed genes, and annotating them to determine their functional significance through functional enrichment (Gene Ontologies) and pathways (KEGG) analysis.

The student will also learn how to identify and shortlist diagnostic and prognostic biomarkers for the disease or cancer under study, the resulting biological pathways that are dysregulated files to obtain meaningful insights into the underlying dysregulation of the molecular biology with respect to the disease.

BioCode's training provides a comprehensive in-depth hands-on experience into scRNA-seq data analysis, including the process of obtaining, processing, and analyzing

transcriptomics data to identify biomarkers that are dysregulated and reasons for cellular and tumor heterogeneity.

Target Audience

Thi is a complete hands-on training on single-cell RNA-seq datasets aimed towards researchers and students at any stages of their career ladder looking to learn the hottest bioinformatics analysis pipeline that is pretty much a requirement of any lab around the world. By the end of this training, you will have a complete understanding of how to execute scRNA-seq projects by yourself for any number of samples, datasets and conditions. No prior experience is required, however basics of molecular biology is required

Training Features

- **Pipeline**: Single-Cell RNA-sequencing (NGS)
- **Packages**: Seurat & scType
- **Mode**: Step-by-step hands-on training (onsite or online)
- **Dataset**: raw obtained from cancer tissue
- **For**: beginners & advanced features
- **Coding experience required**: None (R & Linux will be taught in this course)
- **Operating system**: Linux (no experience required, will be taught in this course)
- **Prerequisite knowledge**: basics of molecular biology

Note: Linux can be installed on your Windows computer easily, no need to install it separately.

Training Delivery

Online through Google Meet (twice a week, 2 hours/class)

- Scheduled in agreement with the student.

Student will be added on BioCode's company Slack channel

Duration: 8 classes in total (16 hours), 4 weeks

Modules

- Introduction to Single-Cell RNA-seq, Its Pipeline and Analysis
- Gene Expression and Its Significance
- Cellular and Tumor Heterogeneity

- Bulk RNA-sequencing vs. Single-Cell RNA-sequencing
- Single-Cell RNA-seq Technologies (10x Genomics, Smart-Seq, Drop-seq and more)
- Cell Isolation and Cell Lysis Protocols for Single-Cell Genomics
- Droplet Technologies: 10x Genomics
- Hands-on: Obtaining Raw Datasets for scRNA-seq Analysis
- Hands-on: Installation of Software and R Packages
- Technical Issues With Single-Cell RNA-seq Data
- UMIs, Cell Barcodes, Read Alignment and Quantification
- Hands-on: Read Alignment, Deduplication and Quantification (Count Matrix)
- Quality Control of Single-Cell Data: Filtering Dead Cells and Unwanted Data
- Batch Effect Correction
- Hands-on: Filtering Dead Cell and Low Quality Data
- Hands-on: Normalization, Identification of Highly Variable Features and Scaling
- Hands-on: Dimension Reduction and Visualization (PCA, Heatmap, JackStraw, Elbow Plot)
- Hands-on: Clustering of Cell Subpopulations
- Hands-on: Cell Annotation of Subpopulations
- Hands-on: Differential Gene Expression Analysis Between Cell Subpopulation
- Hands-on: Gene Ontology Analysis Using GeneCodis
- Hands-on: Pathways Analysis Using KEGG, PANTHER, Reactome

By the end of BioCode's training, the student will be able to take any raw scRNA-sequencing data and analyze it to obtain diagnostic or prognostic biomarkers that are dysregulated in certain types of cells that are leading to cellular heterogeneity..

Trainer

BioCode's training will be delivered and supervised by Mr. Waqar Hanif, the Founder and CEO of BioCode. Mr. Hanif is an accomplished Cancer Bioinformatician and Genomics Researcher, with a background as a Bioinformatics Scientist and Data Scientist. He possesses a wealth of experience in the field of cancer research, molecular oncology, bioinformatics pipeline development, and drug discovery and delivery. His expertise extends to addressing challenges related to multiple drug resistant cancer types, bacteria and other diseases. Participants can benefit from Mr. Hanif's extensive knowledge and practical insights gained through his notable contributions to the field. He has developed

multiple genomics pipelines that are used for industrial and academic large scale genomics data analysis.

LinkedIn: Waqar Hanif | LinkedIn

Outcomes

- **Understanding NGS Technologies**: Gain knowledge about the basics of NGS technologies and sequencing platforms used in scRNA-sequencing experiments. Understand the principles and applications of RNA sequencing in genomics research.
- **Data Acquisition and Quality Control**: Learn how to obtain raw transcriptomics (scRNA-seq) data and perform mapping, removal of barcodes, generation of count matrix, quality control to ensure the data's reliability and accuracy. Explore techniques for assessing the quality of cells.
- **Cell Clustering and Annotation**: Acquire skills in cell-cell clustering based on expression profiles and annotating those clusters with cell types to identify which cells are present inside the tissue that you are working on.
- **Differential Gene Expression Analysis**: Learn how to identify differentially expressed genes in the identified cell types, such as cancer cells, normal cells, B-cells, T-cells, epithelial cells etc. Gain hands-on experience in performing differential expression analysis Seurat.
- **Functional Enrichment Analysis**: Explore the functional significance of differentially expressed genes by performing functional enrichment analysis. Learn how to annotate genes using Gene Ontology (GO) terms and analyze dysregulated pathways using KEGG (Kyoto Encyclopedia of Genes and Genomes) analysis.
- **Biomarker Identification**: Acquire skills in identifying and shortlisting diagnostic and prognostic biomarkers specific to the disease or cancer under study. Understand the process of selecting relevant biomarkers based on their dysregulation patterns.
- **Comprehensive scRNA-seq Analysis**: Gain a comprehensive understanding of the entire scRNA-seq data analysis pipeline, including data acquisition, preprocessing, differential expression analysis, cell clustering, functional enrichment analysis, and biomarker identification. Develop the ability to analyze and interpret scRNA-seq data to gain insights into molecular dysregulation associated with diseases.

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Account Number: 3024355000009611
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