Bioinformatics Training

Instructor-led course

Provided by: Bioinformatics

This course has 2 scheduled runs. To book a place, please choose your preferred date:

2025

Thu 27 Mar	**[Full]**
Thu 10 Jul	Not bookable

[Show past events]

Single-cell RNA-seq analysis (IN-PERSON)

Prerequisites

Description

Recent technological advances have made it possible to obtain genome-wide transcriptome data from single cells using high-throughput sequencing. This course offers an **introduction to single-cell RNA sequencing** (scRNA-seq) analysis. Participants will gain hands-on experience with key software packages and methodologies for processing, analyzing, and interpreting scRNA-seq data. Key topics include data preprocessing, quality control, normalization, dimensionality reduction, batch correction and data integration, cell clustering and differential expression and abundance analysis. By the end of the course, students will be equipped with the skills to independently conduct and critically analyse data from scRNA-seq experiments.

If you do not have a University of Cambridge Raven account please book or register your interest here.

If for any reason the above links do not work, please email Research Informatics Training Team with details of your course enquiry.

Additional information

- ♿ The training room is located on the first floor and there is currently **no wheelchair or level access**.
- Our courses are **only free for registered University of Cambridge students**. All other participants will be charged according to our charging policy.
- Attendance will be taken on all courses and **a charge is applied for non-attendance**. After you have booked a place, if you are unable to attend any of the live sessions, please email the Research Informatics Training Team.
- Further details regarding eligibility criteria are available here.
- Guidance on visiting Cambridge and finding accommodation is available here.

Target audience

- Everyone is welcome to attend the courses, please review the **relevant policies.**

Prerequisites

Essential

- Basic understanding of high-throughput sequencing technologies.
  - Watch this iBiology video for an excellent overview.
- A working knowledge of the **UNIX command line** (course registration page).
  - If you are not able to attend this prerequisite course, please work through our Unix command line materials ahead of the course (up to section 7).
- A working knowledge of **R** (course registration page).
  - If you are not able to attend this prerequisite course, please work through our R materials ahead of the course.

Desirable

- Experience with analysis of bulk RNA-seq data is strongly recommended (course registration page).
- A working knowledge of running analysis on High Performance Computing (HPC) clusters (course registration page).

Topics covered

Bioinformatics, *Data handling*, *Data mining*, *Data visualisation*, *Functional genomics*, *Transcriptomics*

Objectives

During this course you will learn about:

- Different scRNA-seq technologies and what kind of data you obtain from each.
- Processing raw sequencing data from the commonly-used 10x Chromium platform using *cellranger*.
- Use several R/Bioconductor packages for downstream analysis of scRNA-seq data, including: data normalization, correction for batch effects, dimensionality reduction methods (PCA, t-SNE and UMAP), cell clustering and differential expression and abundance analysis.

Aims

After this course you should be able to:

- Describe the range of single-cell sequencing technologies available, their pros and cons and which you may want to use for your experiments.
- Process raw single-cell sequencing data and assess the quality of your data.
- Normalise scRNA-seq data.
- Visualise the data and apply dimensionality reduction.
- Apply methods for batch correction and data integration.
- Identify groups of similar cells by clustering and identify marker genes to differentiate them.
- Apply differential expression and cell abundance between conditions.

Format

Presentations, demonstrations and practicals

System requirements

Participants **can make use of the computers in the training room.**

Timetable

Day 1	**Topics**
Session 1	Introduction to single-cell technologies
Session 2	Library structure and cell calling using the `cellranger` software.
Session 3	Quality control and exploratory analysis of scRNA-seq using R/Bioconductor
Day 2	**Topics**
Session 1	Data normalisation
Session 2	Feature selection and dimensionality reduction
Session 3	Batch correction and data integration
Day 3	**Topics**
Session 1	Cell clustering
Session 2	Identification of cluster marker genes
Session 3	Differential expression and abundance analysis

Registration Fees

- **Free** for registered **University of Cambridge students**
- **£ 60/day** for all **University of Cambridge staff, including postdocs**, **temporary visitors (students and researchers)** and participants from **Affiliated Institutions**. Please note that these charges are **recovered by us at the Institutional level**
- It remains the participant's responsibility to acquire prior approval from the relevant group leader, line manager or budget holder to attend the course. It is requested that people booking only do so with the agreement of the relevant party as costs will be charged back to your Lab Head or Group Supervisor.
- **£ 60/day** for all **other academic participants** from external Institutions and charitable organizations. These charges must be **paid at registration**
- **£ 120/day** for all **Industry participants**. These charges must be **paid at registration**
- Further details regarding the charging policy are available here

Duration

3

Frequency

A number of times per year

Related courses

- Introduction to the Unix command line (IN-PERSON)
- Introduction to R (ONLINE LIVE TRAINING)
- Bulk RNA-seq analysis (IN-PERSON)
- Working on HPC clusters (IN-PERSON)
- Extracting biological information from gene lists (ONLINE LIVE TRAINING)

Theme

Bioinformatics