

# ALACI 2024 - Pre-Congress Course 3RD FRANCO-AUSTRAL COURSE ON BIOINFORMATICS APPLIED TO IMMUNOLOGY

# COMPUTATIONAL TOOLS APPLIED TO THE ANALYSIS OF SINGLE CELL "OMICS" 10/31/2024-11/02/2024

**GOAL:** To provide graduate students and young researchers from Latin American countries with the fundamentals of single-cell transcriptomics and proteomics. During this course attendees will learn how to use available R-based computational and statistical methods to analyse immune cell datasets. The course is organised in such a manner that, during the mornings, the theoretical aspects of the different technologies will be discussed after listening to a keynote speaker work and during the afternoons, experts in computational and statistical methods will provide personalized training to analyse immune cell datasets (from the literature or the papers exposed during the morning). Although several virtual courses have been implemented in the last few years, we still believe that in-person meetings allow maximum interaction. Consequently, the afternoon session will be organised in a way that one professor/organiser will assist a group of 4-5 students. One assigned paper with an associated data set will be provided to each group to be analysed during the course and a final presentation of the result will be evaluated on the last day. The focus will be on implementing commonly used software and pipelines (eg CellRanger, Seurat, ArchR). We expect to foment productive, high-level discussions and to create a nurturing and supportive environment for early-career investigators and trainees that will consequently impact the quality of our research, teaching and health systems.

**DIRECTED TO:** The course is intended for graduate students pursuing their doctorate, as well as postdoctoral fellows and young researchers involved in research in basic, applied and clinical immunology.

# Registration open until the 30th September

https://forms.gle/MH8MDgvB8nedxnqNA

ADMISSION PROCESS Admission will be subject to selection based on merit, geographic distribution, and gender equality among applicants. Interested parties must send a CV and a summary of their work along with a motivation letter that justifies the need to implement these tools in their research work. Candidates must demonstrate knowledge and experience in using the "R" programming language and a good understanding of English MINIMUM AND MAXIMUM NUMBER OF STUDENTS:

Minimum: 20 Maximum: 40

#### COST:

Members of a national immunology society belonging to ALACI (<a href="https://www.alaci.org/en/sociedades-afiliadas/">https://www.alaci.org/en/sociedades-afiliadas/</a>), AINCA members, or participants from low or middle-income countries according to the World Bank Classification: 40 US dollars.

Non-ALAC members, non-AINCA members, or persons from high-income countries according to the World Bank Classification: 60 US dollars.

Fellowships will be available for ALACI MEMBERS considering academic and scientific training, geographical distribution, and gender balance. Candidates must demonstrate knowledge and experience in using the "R" programming language and a good understanding of English.

#### **SCIENTIFIC ORGANIZERS**

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## **Coordinators**

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#### Teaching Staff

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# **TENTATIVE PROGRAM**

Day 1	
09:00 a 9:45	General introduction and presentation of the
	course. Presentation of the participants
09:45 a 10:15	Overview of gene regulation
	overview or gene regulation
10:15 a 10:45	Aplications of scRNA/TCRseq/ATAQ seq
10:45 a 11:00	Coffee Break
11:00 a 13:00	Theoretical concepts on how to run a scRNA/ TCRseq experiment
13:00 a 14:30	Lunchtime
14:30 a 16:30	Bioinformatics analysis of single cell transcriptomics
16:30 a 18:30	"Hands on computer training"
Day 2	
09:00 a 10:30	Tools and public initiatives on single cell
	genomics
10:30 a 11:00	Coffee Break
11:00 a 12:00	General concepts of T cell biology and TCR

12:00 a 13:00	Hands on training TCR data analysis
13:00 a 14:30	Lunchtime
14:30 a 15:30	Hands on training TCR data analysis
15:30 a 16:00	Coffee Break
16:00 a 18:30	scATACseq: Introductory concepts.  Biological and technological introduction QC and filtering Dimensionality reduction and visualization Clustering and peak calling Gene score prediction and motif analysis
Day 3	
9:00 a 10:30	Spectral flow cytometry. Basic concepts of full spectrum cytometry.  Deconvolution.  Demonstration of autofluorescence extraction. Spectral data analysis applying dimensionality reduction
10:30 a 11:00	Coffee Break
11:00 a 13:00	"Hands on computer training"
13:00 a 14:30	Final Conclusions