

		Single Cell Genomic Approaches to Study the Immune System 9 - 11 November, 2024				
Bioinformatics pre-courses online Introduction to Linux for Biologists & R Programming for Biologists	Time	Saturday 9 November	Sunday 10 November	Monday 11 November	Time	
	08:00 - 08:15	Meet at BINN Hotel lobby Walk to University	Theoretical background of the CITE-seq technology Danilo Ceschin - Felipe Gajardo	Unprecedented insights into immune system regulation with single-cell technologies Gosia Trynka	08:00 - 08:30	
	08:15 - 08:30					
	08:30 - 08:45	Wellcome slides Instructors intro Participants intro Course overview	Practical 5: The basic structure of a multimodal Seurat Object Danilo Ceschin - Felipe Gajardo	Fundamentals of single-cell ATAC-seq (scATAC-seq) analysis Evelia Coss	08:30 - 09:00	
	08:45 - 09:00					
	09:00 - 09:15		Practical 6: Background correction and normalization (DSB, CLR)	Practical 13: scATAC-seq Pre-Processing & QC Evelia Coss	09:00 - 09:30	
	09:15 - 09:30					
	09:30 - 09:45	SC basics & immune system applications (part 1) Ania Lorenc	Break	Break	09:30 - 10:00	
	09:45 - 10:00					
	10:00 - 10:15					
	10:15 - 10:30	Google collab set-up environment	Practical 6 (part 2) Danilo Ceschin - Felipe Gajardo	Practical 14: Downstream analysis for scATAC-seq Diego Ramirez	10:00 - 10:30	
	10:30 - 10:45	Break			Practical 7: Visualisation of protein levels & cell populations Danilo Ceschin - Felipe Gajardo	10:30 - 11:00
	10:45 - 11:00					
	11:00 - 11:15	SC basics & immune system applications (part 2) Ania Lorenc	Practical 8: Options for CITE-seq-based annotation Danilo Ceschin - Felipe Gajardo	Practical 15: Multiome analysis & integration Diego Ramirez	11:00 - 11:30	
	11:15 - 11:30					
	11:30 - 11:45	Practical 1: Single-cell data structure Julieth Lopez - Benilton Carvalho			11:30 - 12:00	
	11:45 - 12:00	Practical 2: Data quality control Julieth Lopez - Benilton Carvalho	Lunch	Lunch	12:00 - 12:30	
	12:00 - 12:15					
	12:15 - 12:30					
	12:30 - 12:45					
	12:45 - 13:00					
	13:00 - 13:15	Lunch	Practical 9: Normalization & integration Danilo Ceschin - Felipe Gajardo	Practical 16: Motif analysis Diego Ramirez	13:00 - 13:30	
	13:15 - 13:30		Multi-sample single-cell analysis Lucia Ramirez	Exploring results Evelia Coss	13:30 - 14:00	
	13:30 - 13:45					
	13:45 - 14:00					
	14:00 - 14:15	Practical 3: Data normalization, dimensionality reduction, clustering Julieth Lopez - Benilton Carvalho	Practical 11: Differential gene expression analysis Lucia Ramirez	Other tools used in scATAC-seq Diego Ramirez & Evelia Coss	14:00 - 14:30	
	14:15 - 14:30					
	14:30 - 14:45					
	14:45 - 15:00	Practical 4: Cell annotation: differential gene expression between clusters, automated annotation approaches	Back to the notebooks (interactive session with instructors)	Back to the notebooks (interactive session with instructors)	14:30 - 15:00	
	15:00 - 15:15					
	15:15 - 15:30		Break		Break	15:00 - 15:30
	15:30 - 15:45					
	15:45 - 16:00					
	16:00 - 16:15	Break	Immune receptor repertoires in SC technologies Anna Lorenc	Back to the notebooks (interactive session with instructors)	16:00 - 16:30	
	16:15 - 16:30					
	16:30 - 16:45	Practical 4 (part 2) Julieth Lopez - Benilton Carvalho	Practical 12: Immune receptor repertoires in single-cell technologies Anna Lorenc	Wrap-up	16:30 - 17:00	
	16:45 - 17:00					
	17:00 - 17:15		How to design a scRNaseq experiment Carla Jones			17:00 - 17:30
	17:15 - 17:30					
	17:30 - 17:45					
	17:45 - 18:00					