

# Workshop « Statistical challenges in scRNA-seq data analysis »

Institut de Mathématiques de Toulouse, 11-12/10/22  
Salle Katherine Johnson (1R3 1<sup>er</sup> étage)

Tuesday Oct 11, 2022

13:30-13:45	Welcome (café, thé)	
13:45-14:00	Introduction	
14:00-14:45	Laura Cantini	Single-cell multi-omics integration
14:45-15:15	Geert-Jan Huizing	Optimal transport for cell-cell similarity inference and its implications in multi-omics integration of paired data
15:15-15:30	Jules Samaran	Unpaired single-cell data integration
15:30-16:00	Coffe break	
16:00-16:30	Boris Hejblum	Testing conditional cumulative distribution functions for differential expression analysis of scRNA-seq data
16:30-17:00	Kalidou Ba	Cell population abundance prediction from bulk RNA-seq data using scRNA-seq references
17:00- 17:30	Benjamin Hivert	Post-clustering inference in low and high-dimension

Wednesday Oct 12, 2022

08:30-09:00	Welcome (café, thé)	
09:00-09:30	Anthony Ozier-Lafontainre	Kernel-Based differential expression analysis
09:30-10:00	Hugues van Assel	Generative Probabilistic model underlying UMAP, tSNE, et al.
10:00-10:30	Bastien Batardière	Improved finite-sum optimization: AdaGrad with SAGA-type gradient estimator
10:30-11:00	Coffe break	
11:00-11:30	Nicolas Enjalbert Courrech	Convex clustering for scRNA-seq data
11:30-12:00	François Bachoc	Inference after convex clustering
12:00-12:15	Closing remarks	