

UE 5BM572

« Workshop in advanced cytometry analyses »

Projects

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Expectations/aims

- ▶ Train you in the analysis of complex cytometry data through practice
- ▶ Teach you good practices for such complex analyses
- ▶ Challenge you on your ability to understand the aims and limits of the different methods that you used
- ▶ Test you on your ability to interpret and summarize your findings and research
- ▶ Make you work collectively as in real life

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What we have seen so far...

- ▶ How to run a SPADE analysis using R (and CytoBank)
- ▶ How to run a tSNE/viSNE analysis using R
- ▶ Generate a QC report for SPADE analyses
- ▶ Visualize cell clusters abundances
- ▶ Generate marker expression heatmaps
- ▶ Generate parallel coordinates for a given cluster
- ▶ Represent the SPADE trees (sample, selected sample, whole dataset)
- ▶ Identify Differently Abundant Clusters (volcano plots, list of DAC)
- ▶ Boxplot representation
- ▶ Generate MDS representation (all clusters/ selected clusters)
- ▶ Public databases / pubmed - extrapolate your interpretations

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What we have not seen so far...

- ▶ How to run an UMAP analysis using R
- ▶ Kmeans clustering over viSNE/tSNE analyses
- ▶ How to use other algorithms to analysis cytometry data (such as FlowSOM, Citrus, ...)

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Last things to keep in mind

- ▶ These projects are made to challenge you !
- ▶ I know that most of you never used R before this workshop
- ▶ DO NOT panic and ASK questions when you are stuck (Google, me, Romain, Gwendolyn, other students, whoever...)
- ▶ I will help you until the project deadline (January 9th)
- ▶ Be organized !! Be perseverant !! Be pragmatic !!
- ▶ You will learn by making mistakes and by learning from them
- ▶ You can do them and you will succeed (but also work a lot...)

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Project deadlines

- ▶ Report: 9/01/2022
 - ▶ Team part (15 pages: context, methods, and results)
 - ▶ Individual part (3 pages: discussion, limits,...)
- ▶ Project defense: 14/01/2022
 - ▶ (10 minutes per group + 30 minutes of questions)

Please see the MU5BM572_Content.pdf file

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Project deadlines

- ▶ Report: 9/01/2022 + **Scripts !!!**
 - ▶ Team part (15 pages: context, methods, and results)
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Project analysis aims

- ▶ One cell population per group
 - ▶ Characterize the phenotypes of cell clusters identified by different algorithms in your dataset
 - ▶ Characterize the changes in cell cluster abundances in the different conditions of your dataset
- ▶ Of course, you will have to benchmark the impact of the different algorithm parameters on your interpretations

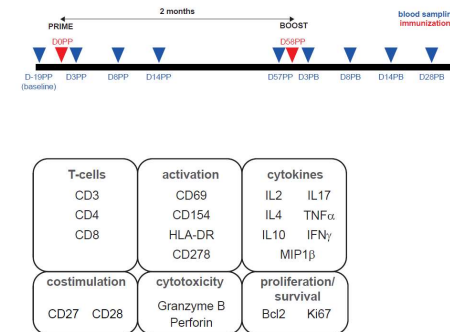
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Project topics

- Common experimental design
 - 5 macaques vaccinated with an MVA vaccine model (HIV) at two-months apart
 - Blood sample collected at different timepoints post-vaccination (post-prime and post-boost)
 - Different mass cytometry panels to characterize different innate or adaptive cell populations
- Same questions
 - What is the phenotypical diversity of the cell populations?
 - How the cell population abundances are impacted by the prime and boost?
 - Populations differentially/similarly impacted by the prime and the boost?

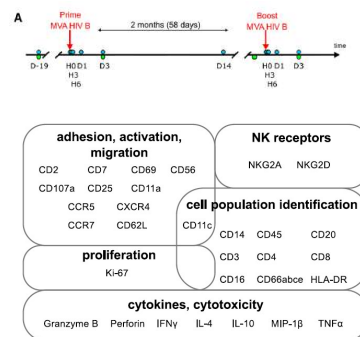
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Project 1 - Helper T cells (CD3+CD4+)



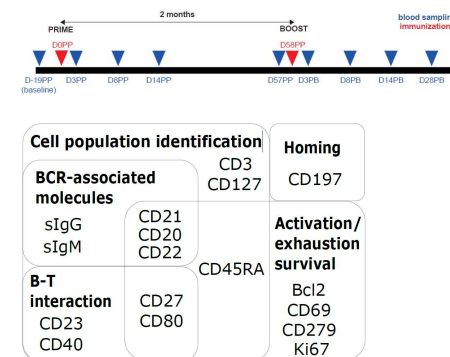
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Project 2 - NK cells (CD3-CD8+)



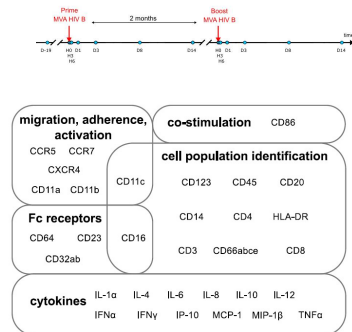
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Project 3 - B cells (CD20+)



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Project 4 - Neutrophils cells (CD66+)



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Groups

		groupe 1	groupe 2	groupe 3	groupe 4
FRANCOIS	Fabien	x			
CHYZAK	Guillaume	x			
TOLEDANO	Léa	x			
BECQUART	Raphael		x		
HUYNH	Minh-Anh		x		
BELLAICHE	Solal		x		
MARTINEZ	Alexandre			x	
SHALABI	Hosnia			x	
MARSANDE	Julie			x	
GAUTIER	Candice			x	
TOUZÉ	Adrien				x
PASCAULT	Alice				x
PIOTIN	Anays				x
DEGRAVE	Raphaël				x

These projects are equally difficult and normalized by the number of students in the different groups

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