UE 5BM578
« Workshop in immunological data analysis »

Projects

1

Expectations/aims

- Train you in the analysis of –omics 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

2

What we have seen so far…

- Differential expression analysis – differentially expressed genes
- Volcano plot – visualize differentially expressed genes
- Heamap – visualize gene expressions in samples
- Hierarchical clustering – identify groups of genes / samples
- MDS – identify outliers / test the quality of a gene signature
- Venn – overlap between gene signatures
- EnrichR – functional enrichment analysis
- Stringdb – protein-protein interactions
- Reactome – specific pathway analysis
- Public databases / pubmed – extrapolate your interpretations

3

Think that we have not seen, but that you can explore…

- Boxplot representation – representation of gene expression values
- Kmeans – clustering at the genes or samples levels
- Correlogram – visualization of correlation between variables
- PCA – principal component analysis
- WGCNA – gene co-expression network
- MLR - multivariate analyses and machine learning methods

- Crossed analyses – direct comparisons with similar experiments

4

Groups

étudiant	Groupe1	Groupe2	Groupe3	Groupe4
Fabien_Francois	x			
Antonin_Bourdin	x			
Candice_Gautier	x			
Solal_Bellaiche	x			
Aurélie_Sémervil_	x			
Guillaume_Chyzak		x		
Alexandre_Martinez		x		
Hosnia_Shalabi		x		
Minh-Anh_Huynh		x		
Huy_Chau			x	
Marc-Antoine_Silvestrini			x	
Anays_Piotin			x	
Adrien Touzé			x	
Victor_Desplats			x	
Raphael_Becquart				x
Raphaël_Degrave				x
Lucie_Gaspard-Boulinc				x
Léa Toledano				x
Mathilde_Bied				x

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

5

Last things to keep in mind

- These projects are made to challenge you !
- I know that most you never used R before this workshop

- DO NOT panic and ASK questions when you are sucked (Google, me, other students)
- I will help you until the project deadline (December 22nd)
- Be organized !! Be perseverant !! Be pragmatic !!
- You will learn by making mistakes and by learning from them

- You can do them and you will success (but also work a lot…)

6

Project 1 – SARS Human

- Aim: to investigate the transcriptional differences between SARS-CoV, SARS-dORF6 and SARS-BatSRBD infections of human airway epithelial cultures, in comparisons to H1N1

- Experimental design:
  - 4 viruses (SARS-CoV, SARS-dORF6, SARS-BatSRBD and H1N1) + 1 control
  - 9 timepoints (0h, 12h, 24h, 36h, 48h, 60h, 72h, 84h, 94h) for SARS
  - 7 timepoints (0h, 06h, 12h, 18h, 24h, 36h, 48h) for H1N1
  - Transcriptomic profiles from human airway epithelial cultures (HAE)

- Questions:
  - Question 1: What are the transcriptomics mechanisms triggered by these viruses ?
  - Question 2: How much similar/different are these transcriptomics mechanisms ?
  - Question 3: To what biological mechanisms are linked these differences ?

7

Project 2 – SARS Mice

- Aim: to investigate the transcriptional differences between mice infected with icSARS CoV, SARS wild type or SARS BatSRBD viruses.

- Experimental design:
  - 3 viruses (SARS-BatSRBD, SARS-icSARS, SARS-WT) + 1 control
  - 4 timepoints (D1, D2, D4, D7)
  - 2 inoculations (10^4 PFU and 10^5 PFU for the SARS-WT)
  - Transcriptomic profiles from mice lung homogenates

- Questions:
  - Question 1: What are host response mechanisms triggered by these viruses ?
  - Question 2: How much are similar/different the different host response to these viruses ?
  - Question 3: What is the impact of the dose inoculations on the host response ?

8

Project 3 – H7N9 Human

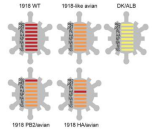
- Aim: to characterize the global transcriptomic response to H7N9 in human bronchial epithelial Calu-3 cells in comparison to Anhui01 (H7N7), NL219 (H7N7), Pan99 (H3N2), or VN1203 (H5N1) viruses

- Experimental design:
  - 4 viruses (H7N9, H7N7, H3N2, H5N1) + 1 control
  - 4 timepoints (3h, 7h, 12h, 24h)
  - Transcriptomic profiles from human bronchial epithelial Calu-3 cells

- Questions:
  - Question 1: In the H7N9 transcriptomic response similar/different to other viruses ?
  - Question 2: At which time point are transcriptome responses the most dysregulated ?
  - Question 3: What are the molecular and pathways dysregulated by H7N9, how are they different compared to other viruses ?

9

Project 4 – 1918 Mice



- Aim: to understand the response to 1918 WT and 1918-like avian viral infections in mice, and to understand the role of individual 1918 genes on the host response

- Experimental design:
  - 5 viruses (1918 WT, 1918-avian like, 1918 PB2/avian, 1918 HA /avian and DK/ALB) + 1 mock condition
  - 3 timepoints (D1,D2, and D4)
  - Transcriptomic profiles from mice lung homogenates

- Questions:
  - Question 1: What are the impact of the different viral gene insertions on the host response relative to 1918 WT and 1918-like viruses?
  - Question 2: What are the mechanisms associated to these host responses ?
  - Question 3: How are the mechanisms compared to the low-pathogenicity avian influenza virus (DK/ALB) ?

10