1 – Write a definition of epigenetics.

Epigenetics is the study of the epigenetic variations in the genome of any organism. This genetic variations in DNA or in Histones can affect the expression of certain genes without infering in the DNA sequence.

2 – How would you expect to find a region of constitutive heterochromatin in terms of nucleosome positioning, DNA methylation and histone modifications?

3 – Which is/are the chromatin state/s most highly associated with the following histone modifications:

- H3K27ac : active promoter and enhancer
- H3K9me3 : heterochromatin
- H3K36me3 : Tx elongation
- H3K27me3 : repressed state
- H3K4me3 : active promoter

4 – What kind of information is provided by ATAC-seq?

5 – Rewrite the following terms in hierarchical order:

Nucleosomes, A/B compartments, FIREs, TADs, chromosome territories.

(From bigger to small:)

- Chromosome territories
- Nucleosomes
- A/B compartments
- TADs
- FIREs

6- Explain all you know about the specific omics technique you presented.

The technique I presented was Methyl-Seq.

This technique is based on bisulfite sequencing, a sequencing technique where we can know where are methylations located in any given genome.

This bisulfite technique is based on a discovery from the 70s. It was discovered that the addition of Sodium Bisulfide to Cytosines made them turn into Uracil. Later in the 90s it was discovered that this conversion wasn't produced if the cytosine was methylated.

So basically, in this method we want to add Sodium bisulfite to every Cytosine and see if they turn into Uracil or not. Later, we would have to compare our reads from NGS with normal reads of that specie and compare which Guanines are real and which are from methylated Cytosines that did not turned into Uracil.

This technique is quite reliable because 70-80% of CpG sites are methylated, so Cytosines are a good target if we are looking for methylations in the genome.

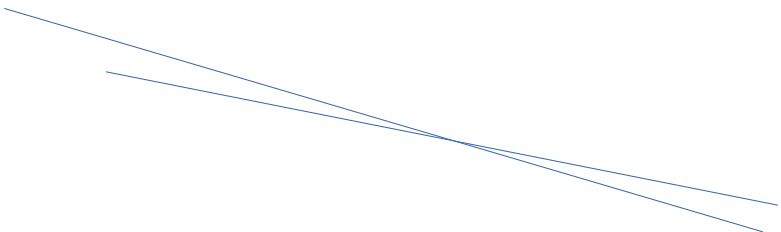
This technique is harder and more slow than others because here we have to work with a whole genome, while other techniques are specific for a certain region.

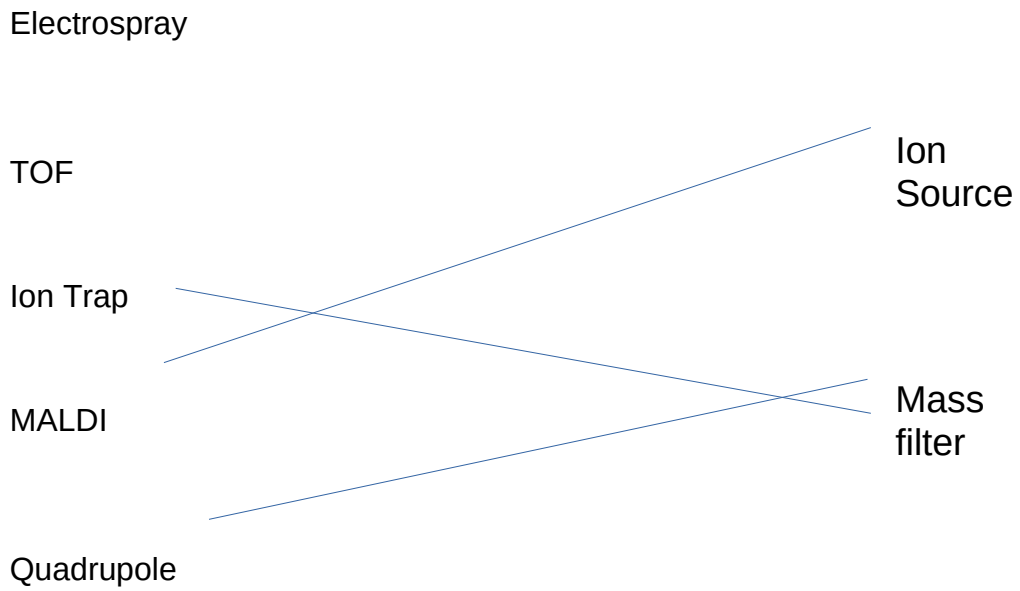
7 – What are UMIs, and what purpose do they serve?

8 – What are the advantages of using nuclei instead of cells in single-nuclei RNA-seq?

9 – What is the Louvain algorithm designed for in the context of single-cell?

10 – Pair with arrows:





11 – Describe the purpose of the second MS step in an MS/MS applied to protein identification.