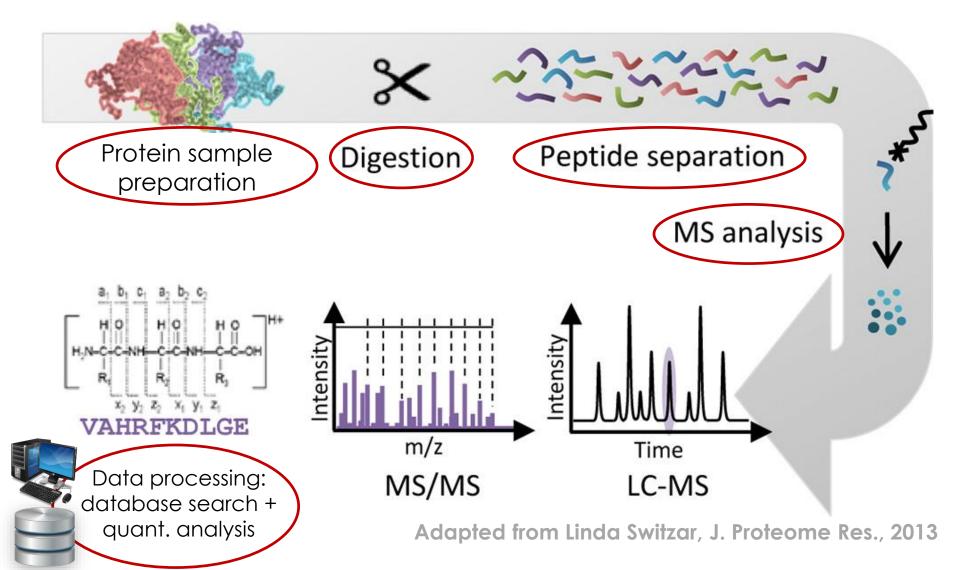




IBIP19: Integrative Biological Interpretation using Proteomics with Veit Schwämmle, Marc Vaudel and David Bouyssié









Each step of the workflow is a potential source of error

I don't find what I was expecting, what could have gone wrong?



I have very few identifications...

Can be anything from sample preparation (protein extraction for instance) to database search (wrong database used or wrong parameters

- I performed immunoprecipitation and I have identified too many proteins

 Might be improper cleaning of the sample, redo the experiment or use appopriate control
- I have a lot of missing values in my quantitative data...

If you compare very different proteomes then try a different strategy

If proteomes are supposed to be similar, you may have issues in the LC-MS setup

If you are doing label-free experiments maybe your software didn't aligned the runs correctly

- My ID/QUANT data seem to be good but I don't find any variant proteins...
 - 1. Maybe your experiment was not inducing a change in your proteome
 - 2. You may have a high biological variability => increase the number of replicates

How can I monitor/avoid problems?



USE STANDARD SAMPLES: A GOOD WAY TO MONITOR YOUR INSTRUMENT

COMPLEX MIXTURES

LC gradient optimization, test of instrument MS and MS/MS throughput performance

SINGLE PROTEIN SAMPLES (e.g. BSA, beta-gal, cytochrome C, myoglobin)

Inter-runs quality control: LC issues (RT shifts, wider peaks), m/z calibration and sensitivity

SPIKED-IN SAMPLES (e.g. UPS1/UPS2)

Benchmarking of both LC-MS instrument setup and data processing methods (requires a sufficient number of proteins)

SAMPLES OF INTEREST: TRY TO AVOID ADDITIONAL PROBLEMS

- Define appropriate experimental design (e.g. minimum number of replicates)
- Optimize sample preparation
- Tune data processing parameters





Hands-on session



https://github.com/GTPB/IBIP19/blob/master/pages/qc/