DIY: Using MS²PIP predicted spectral libraries for DIA data extraction

In our manuscript we only show the benefit of MS²PIP predicted libraries on a HeLa dataset published by Searle et al. Nevertheless, before putting this story on paper, we evaluated our workflow on both public and in-house datasets.

One of these datasets was a public Yeast dataset, which was published together with the HeLa dataset. As this dataset is smaller, we provide our workflow as a Do)It-Yourself tutorial on our GitHub. We would like to challenge you to try out our workflow on the Yeast dataset. That way you can go through the different steps and at the same time see the added value of this new peptide centric approach.

The Yeast dataset itself can be downloaded online from the MassIVE proteomics repository: <ftp://massive.ucsd.edu/MSV000082805>. The repository contains both raw as peak picked data, so it is up to you whether you want to skip the raw file processing with the MSConvert GUI.

For convenience, we have included all intermediate results to allow skipping the more computational steps such as e.g. MS²PIP spectral library prediction.

Please share your results and experiences as much as possible via social media (Twitter,...). We would be very grateful to you. If you encounter any problems, please contact us by e-mail: bart.vanpuyvelde@ugent.

Then the only thing left for me to do is to wish you all the best with the challenge!

With kind regards,

Bart