Questions	Answers (Time location in video)
Can Skyline also work with sample specific internal endogenous peptides as iRTs instead of relying on spike-in peptides?	live answered (1:07:56)
Does the RT binding of 5 min really gives a final window of 10 min. I rather see this to give a window of 5 minutes.	live answered (1:09:28)
how to evaluate mPrompt scoring model in skyline batch?	live answered (1:10:57)
Can Skyline work with FAIMS multi-CV raw files from Thermo?	live answered
The username and password are the credentials for Private panorama folders? Do we have to write them in every section or is it possible to configure the server as in Skyline?	The username and password fields are only required for a private Panorama file. Since we're using public files in this webinar, no username and password are necassary today. Currently, you do need to enter them for every private file, but we are working on making this more convenient and trying to emulate Skyline more closely.
Is the new version of R (4.1.0) compatible with the recent batch set-up, if MSstats is also updated	I have not tried running the R script with R-4.1.0, but it will likely work. Since Bruderer.bcfg uses R-4.0.3, however, you will have to change the R version to be able to run the configuration.
Can we import raw files that has certain keywords? That seems to be doable when importing from remote server but not from a local folder?	The Skyline command we use in Skyline Batch requires that the data files to be imported are in their own folder (with nothing else in it). This is the case whether or not the data is downloaded from a remote source. The keywords you are referencing only impacts which files are DOWNLOADED into the data folder. However, Skyline Batch will still import everything from within that data folder. When you run with local files, you will have to copy the data you wish to import into it's own data folder to avoid importing undesired files.
Hi Brendan, Whatif the assay library doesnot contain iRT spiked in?	live answered (answered before at 1:09:28)
So how do I make my own transition library.. that's probably in an earlier tutorial on DIA.. which one?	live answered (1:18:45)
Is it necessary to include iRT peptides?	live answered (answered before at 1:09:28)
How can I adapt the Skyline batch workflow for targeted quantification from a PRM data? My workflow involves an external calibration curve and I will be reporting the concentration from the interpolated data? Thanks	live answered (1:27:25)
can skyline DIA works in quantitative analysis of MS data better than other methods?	live answered (1:25:48)
Is it ideal to keep the ppm 15 or is it less accurate ? I kept 10ppm for my data, but very less peptides showed curves within +- 10 .	live answered (1:23:44)
How do you generate library from dda raw files. Pointers to prior seminars..	live answered (1:20:29)
could we use download spectralibrary to search DIA without IRT information?	live answered (1:22:42)
In the transition setting filter tab, what is the difference between using ions from filter ion charge and type vs from product ion? when do you use the two settings?	live answered (1:28:45)
How does it select product ions for quantification?	live answered (1:31:03)