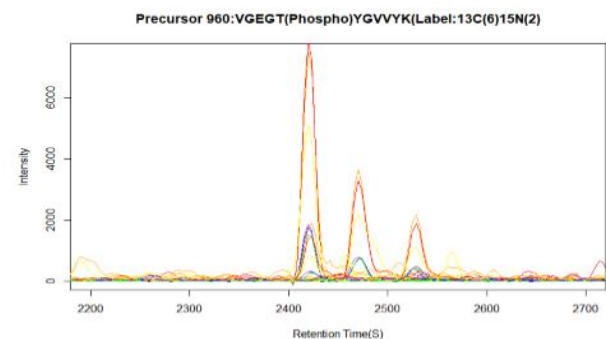
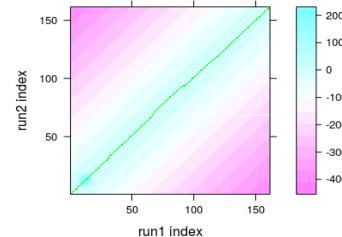


Cartoon example of **retention time alignment** to Sample A, Using GCalinR and gas-chromatography data. (1)



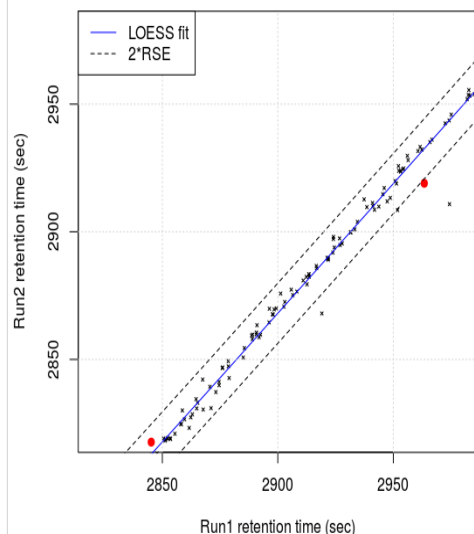
Manually plotted single peptide across 3 runs  
Demonstrating **retention time drift**.

Hybrid alignment through the similarity matrix  
for 15605\_YFMPVHGEYR/3



DIAInR **Hybrid alignment** for a single peptide (2)

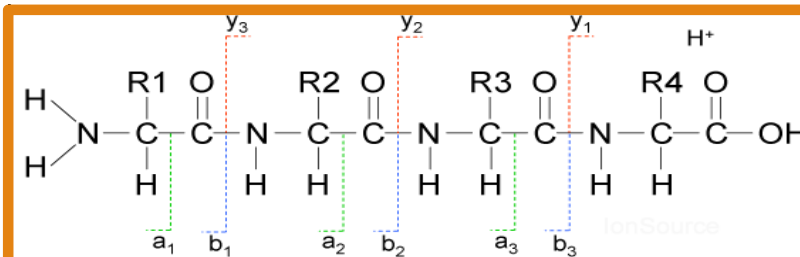
Non-linear global alignment



DIAInR **global alignment** using all detected-peaks between two samples. (2)

# LC-DrawAlignR -

An R Package for Visualizing Chromatogram Alignment in Liquid Chromatography for Targeted Proteomics with a Focus on PTM's



Using unique **Identification Transitions** (Y & B ions) to separate isomers (3)

## Unmet needs:

- ❖ Support Plotting Aligned Ms2 Chromatograms in targeted proteomics (DIA, SWATH-MS, etc.)
- ❖ Post-Translational Modifications (Phosphoproteomic)/Unique Transitions