

High-precision retention time prediction for next-generation proteomics

Biognosys' team enhances its pioneering iRT concept for high content protein quantification

July 14, 2016 – Zurich-Schlieren (CH) – Biognosys AG, a leader in next-generation proteomics, announced today a new revolutionary approach for high-precision prediction of peptide retention time (high-precision iRT) specifically designed for the targeted analysis of data independent acquisition (DIA or SWATH) data sets. The high-precision iRT approach is described in a study recently published in Proteomics by Bruderer et al. entitled “[High-precision iRT prediction in the targeted analysis of data-independent acquisition and its impact on identification and quantitation](#)”.

Accurate prediction of peptide retention times is an extremely important parameter in modern proteomic workflows. In targeted proteomic approaches such as multiple or parallel reaction monitoring (MRM or PRM) the number of peptides measured in one run can be significantly increased by scheduling the acquisition with the accurate retention time of each peptide. Similarly, discovery proteomic workflows such as [Hyper reaction monitoring \(HRM\)](#) that rely on spectral libraries for targeted analysis benefit substantially from accurately predicted retention times. DIA analysis using a spectral library with accurately predicted retention times uses narrower XIC windows resulting in **faster data processing and better specificity** of the analyzed data due to blinding out non-relevant signals.

However, it is challenging to compare retention times between chromatographic systems. To address this issue Biognosys initially developed an indexed retention time (iRT), a dimensionless value that defines chromatographic retention relative to a set of 11 non-naturally occurring peptides (Escher et al. 2012). This allows prediction of peptide retention times on any chromatographic system and the approach can be used in targeted and discovery proteomic workflows. However, the linear model it does not consider local fluctuations or non-linear gradients.

The newly developed high-precision iRT concept extends the set of original 11 iRT peptides to thousands of anchor points derived from the actual sample. These anchor points are stored in [Spectronaut](#), a professional software for DIA or SWATH data analysis, which automatically takes the available peptides in each specific sample to build a high quality spectral library. The high-precision iRT concept results in **15% more precursor IDs in a DIA analysis compared to the original iRT** and 25% more precursor IDs in a DIA run when retention time prediction was not used for spectral library generation (Bruderer et al. 2016).

High-precision iRT is automatically implemented in the latest release of Spectronaut and is also applied in Biognosys' proteomic facility thus benefiting all Biognosys customers. For more information on high-precision iRT or tools and services available for high-content protein quantification contact Biognosys at info@biognosys.ch.

About Biognosys

Biognosys is the leading proteomics company offering services and products for highly multiplexed protein quantification. Founded in 2008 as spin-off from the lab of proteomics pioneer Ruedi Aebersold at ETH Zurich, Biognosys is dedicated to transform life science with superior technology and software.

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