

October 18, 2022

Dear editors, Dear Magnus, Michael, and Veit:

Enclosed you will find a manuscript entitled: “Triqler for Protein Summarization of Data from Data Independent Acquisition Mass Spectrometry”. The manuscript describes the applicability of our software, Triqler, to Data Independent Acquisition Mass Spectrometry. We think the manuscript would be suitable for your “Third Special Issue on Software Tools and Resources”.

We have previously published a methods to derive protein relative quantities using a combined model for identification and quantification errors, which we called Triqler. The method accurately models the major error sources of a quantitative proteomics experiment, and can accurately assess the overall errors made in inferences from quantitative proteomics to a level where we routinely can report FDRs of quantities. The model’s efficiency can in large part be attributed to its ability to quantify and integrate errors in the identification process with the errors of the quantification process. Triqler was designed for Data-Dependent Acquisition mass spectrometry in mind. However, here we demonstrate that the method is well suited for processing data from Data Independent Mass spectrometry as well.

The manuscript is an original contribution and none of the work it describes has been published elsewhere. The manuscript will remain with you and will not be submitted elsewhere, until you made a decision as to its suitability for publication. We suggest the following five experts in the analysis of proteomics data as potential reviewers:

- Professor Lieven Clement, Gent University,
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Sincerely,

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