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To the editors of

Journal of Chromatography B.

February 21, 2014

**Revised manuscript “Straightforward interpretation of metabolomics, proteomics, transcriptomics, and genomics data by comprehensive visualization and pathway enrichment using a single software tool”, submitted under manuscript number JCB-13-943**

Dear Dr. Theodoridis,

We thank you and the expert reviewers for the very helpful and knowledgeable comments and advices to improve the content and clarity of our manuscript. All suggestions have been respected and point by point answers to the comments of the reviewers have been attached.

Based on our long standing experiences in the development and application of metabolomics and lipidomics approaches one of our foci at the moment is on one of the major present bottle necks of metabolomics studies, which is a sophisticated evaluation and biochemical interpretation of the data, in particular when systems biology approaches are performed. Of course, there are also challenging analytical limitations like the comprehensive profiling of polar or low abundant metabolite pattern. However, in general it is very easy to generate a huge amount of very complex data by metabolomics approaches that need to be evaluated and interpreted using novel bioinformatics tools.

We are happy that you share our point of view, that it is quite important to illustrate in a special metabolomics issue of JCB not only chromatographic aspects, but also to shine a light on tools not directly related with improvements of chromatographic aspects, but dealing with other current limitations of metabolomics analyses.

As suggested by the referees, we revised diverse paragraphs where an inappropriate terminology was used and included a comparison of InCroMAP to existing software for the visualization of metabolomics data. Furthermore, we modified Figure 2 which now shows results from an illustrative example application. In the revised manuscript we also added more detailed descriptions of the implemented algorithms (e.g., for the integrated pathway enrichment), the required pre-processing steps and the procedures used for ID mapping.

We hope that the revised version of our manuscript is now acceptable for publication and we thank you again for your kind consideration.

Sincerely yours,

Lars Rosenbaum

(for the authors)