

## Reviewer Report

**Title: Open and re-usable annotated mass spectrometry dataset of a chemodiverse collection of 1,600 plant extracts.**

**Version: Original Submission**    **Date: 6/23/2022**

**Reviewer name: Mingxun Wang**

### Reviewer Comments to Author:

Allard et al. present a public dataset of plant extracts and their initial exploration using computational tools to mine this dataset. The authors aim to frame this as just the beginning in extracting all the discovery potential from this dataset. Main Comments Please include a citation for the MEMO tool. I would recommend a more detailed description of the usage of the TMAP visualization. For example, what exactly is the score of peaks and losses between MS/MS spectra. Was it the aligned cosine used in the molecular networking or something more akin to a shared peak count? Additionally, it seems implied that the TMAP is based upon the clustered MS/MS spectra produced by the MZMine tool, but should be made more explicit. The text for the section "Visualization of the metabolite annotations" is rather confusing and I actually cannot parse out the specific meaning here. I think the message should be related to Figure 3, where a TMAP is created utilizing the structure similarity of the putative annotations. However, the mixing of references to Figure 1 is rather confusing and I would recommend sticking with Figure 3's visualizations in carrying the story forward. Minor Comments Correction in abstract, should be: "Researchers interested in the exploitation of large and chemodiverse extracts collections should use elaborate strategies to efficiently tackle the chemical complexity and access these structures." Overall, I believe the authors limit their claims on this manuscript which is much in line with the results presented. It is not meant to be a final analysis but just the start. I do think some of the results language and presentation needs to be tightened up, as some parts as noted above are hard to comprehend and as a reader am a little confused as the message. As the authors are already limiting the scope to presenting the data, metadata (which is honestly very complete), and preliminary analysis, I think it would be good to sharpen the conclusions of the initial analysis since the merits of this paper does not rest upon an extensive results section.

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