

Interactive comment on “A Novel Approach for Simple Statistical Analysis of High-Resolution Mass Spectra” by Yanjun Zhang et al.

Anonymous Referee #1

Received and published: 18 May 2019

This manuscript reports a novel “binPMF” method that can be used to improve the deconvolution of organic factors using atmospheric mass spectral data that don't have adequate mass resolution for unambiguous ion speciation. The authors applied this method to both ambient and synthetic data and demonstrated that the combination of mass spectral binning with positive matrix factorization is an effective approach to better resolve chemical information and to improve the separation of different sources and processes. This is an exciting new development in data analysis for real-time mass spectrometry and this work is of very high quality. The manuscript is very well written and the topic is a good fit for AMT. I thus recommend the manuscript be accepted for publication as is.

Interactive comment on Atmos. Meas. Tech. Discuss., doi:10.5194/amt-2019-59, 2019.

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