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Atmospheric Measurement Techniques Discussions



# *Interactive comment on* "Evaluation of hierarchical agglomerative cluster analysis methods for discrimination of primary biological aerosol" *by* I. Crawford et al.

**Anonymous Referee #1**

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Review of Crawford et al. for AMTD

This manuscript presents a new method for performing cluster analysis on data taken by the Wide-band Integrated Bioaerosol Sensor (WIBS). Previous cluster analysis software for use with the WIBS has been severely limited in terms of the amount of data that could be processed (∼10ˆ4 particles). This typically requires heavy subsampling of the particles and brings into question the representativeness of the clusters. The authors test the performance of various clustering algorithms using laboratory calibration particles and then apply the best-performing algorithm to ambient data collected during the BEACHON-RoMBAS. They find that the bacterial concentrations are increased



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and the fungal concentrations decreased in the new clustering method relative to the old. In general this manuscript is well written and represents a nice advancement of the field. I do have some specific comments as outlined below:

1. Is this WIBS-4 from Droplet Measurements in Boulder? If so, that should probably be stated somewhere. If not, what does the "4" signify and how is this instrument different from other published WIBS measurements? 2. I would like to know a bit more about any calibrations that might have been done for the instrument used in BEACHON. First, was there any independent verification that the size derived from the lookup table was accurate? It is hard to see in the log-scale plots for the lab data how closely the WIBS-reported size matches with the PSL size for the different test particles. Also, I believe the users manual for the DMT WIBS states that only side-scatter is utilized for sizing rather than the forward to side ratio. Please check on this. 3. Similarly, were there any calibrations for the asymmetry factor measurement? Has the WIBS's ability to report a reasonable AF been determined for small sizes? I thought it only really worked for some of the larger particles and even then I thought it was relatively unverified. 4. It seems like there is quite a lot of detail on the instrumental side and less on the statistics. This may also be driven by my expertise (which is not computation or statistics) but I would like to know a little bit more about what a "linkage" is, what the different linkages mean and what the different normalization strategies are. I realize that these definitions are likely in the literature and textbooks but, especially given that one of the major outcomes of the paper seems to be that the Ward linkage with either z-score or range normalization is the best performer, it would be appropriate to have a brief explanation for the layperson in the paper itself. 5. It also seems really odd to me to only test the clustering using PSL spheres which are so obviously and easily differentiated by eye without any fancy analyses. Couldn't you test the clustering performance with at least lab-generated bacteria and fungal populations? That would improve confidence in the ambient clusters greatly. 6. I would love to see some size distributions for the clusters from the BEACHON data. Does the "bacterial" cluster also actually look like bacteria in addition to "behaving" like bacteria? Similarly for the fungal clusters



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which I would expect to also have well-behaved size distributions at larger sizes than you see for the bacterial populations. 7. I think you should be careful not to present the increase in bacterial concentrations and decrease in fungal concentrations with the new clustering methods as closer to “true” than the WASP parameterization. Right now these clustering methods are different statistical treatments with little “ground-truth” for either although this paper will likely convince the reader that the new methods are better. It would be best to simply describe how they differ and why you think that might be. Also, I believe the explanation for how the new clustering generates more bacteria-attributed particles is that WASP is miscategorizing some bacteria as fungi? But the fungal concentrations dropped by 10 /L while the bacterial concentrations increased by 80 or 90 per liter so reclassification of WASP fungal signals can only explain a minor fraction of the bacterial increase in the new algorithm. Are there also many many more unattributed particles in WASP?

Smaller technical comments include: 1. You could use some references for the offline techniques in your “Detection methods” section of the introduction. 2. In figures 3 and 4 it would be nice if the colors were consistent for a given calibration particle. 3. Tables 2 and 3 seem not quite harmonized. The point in table 2 was that for large data sets the z-score normalization slightly outperforms the range but then in table 3 the range normalization looks better for all sample sizes tested. 4. P 7316, line 19, I believe you mean that the range-normalized result has 4 clusters not 5. 5. I believe that on the right side of figure 7 the blue points represent Z1 vs B3? Also these labels are a little unfriendly. Perhaps also include in parenthesis the identities (bacteria and fungi) that you attribute to the sum of the clusters.

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Interactive comment on Atmos. Meas. Tech. Discuss., 8, 7303, 2015.