Kim et al. developed a method to catalog analytes in chromatograms of complex environmental data. It was demonstrated that this method can identify more individual analytes information (~1000 species) than operators' manual inspection (~100 species) and save time from human-instrument interactions. Here I have some major comments.

1. Although the method developed by the authors can identify more than 10 times of analytes than the conventional one (manual inspection), what scientific problems can this method help us to solve? It seems that we still do not know most of the identified analytes.
I think the limit of identified analytes in previous studies is primarily due to the lack of authentic standards. The other big problem in investigating organic aerosols is the lack of organic tracers specifically related to their sources and/or transformation.
If the total ion chromatographs of environmental data were inspected manually based on individual *m/z* ratios, at least several hundred of analytes will be identified, but mostly unknown.
Here, I have to admit that the method developed by the authors really simplified the time-consuming work for chromatograph inspection. But scientific problems should be solved to enlighten the significance of this work.

2. To keep column conditions, the GC column close to the inlet might need to be cut for quite a few centimeters after a batch of sample analysis, and retention times of analytes will vary differently. In this case, will the method be able to match the same analytes from different chromatograms in different batches?

3. How does the developed method deal with background peaks like pollution, column blood, etc? How does the method perform field blank correction?