

A searchable database and mass spectral comparison tool for aerosol mass spectrometry (AMS) and aerosol chemical speciation monitor (ACSM)

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Abstract. The Aerodyne Aerosol Mass Spectrometer (AMS) and Aerosol Chemical Speciation Monitor (ACSM) are the most widely applied tools for in-situ chemical analysis of the non-refractory bulk composition of fine atmospheric particles. The mass spectra (MS) of many AMS and ACSM observations from field and laboratory studies have been reported in peer-reviewed literature and many of these MS have been submitted to an open-access website. With the increased reporting of such data sets, the database interface requires revisions to meet new demands and applications. One major limitation of the web-based database is the inability to automatically search the database and compare previous MS with the researcher's own data. In this study, a searchable database tool for the AMS and ACSM mass spectral dataset was built to improve the efficiency of data analysis using Igor Pro, consistent with existing AMS and ACSM software. The database tool incorporates the published MS and sample information uploaded on the website. This tool allows the comparison of a target mass spectrum with the reference MS in the database, calculating cosine similarity, and provides a range of MS comparison plots, reweighting, and mass spectrum filtering options. The aim of this work is to help AMS users efficiently analyze their own data for possible source or atmospheric processing features by comparison to previous studies, enhancing information gained from past and current global research on atmospheric aerosol.

1. Introduction

Atmospheric aerosol particles have adverse effects on human health and impact visibility, the hydrological cycle, and climate changes through direct and indirect radiative properties (Ramanathan et al., 2001; Bäumer et al., 2008; Kampa and Castanas, 2008; IPCC, 2021). Globally, the dominant constituent of dry fine-mode respirable aerosol particles is organic matter (OM), commonly referred to as organic aerosol (OA). Understanding the characteristics, sources, and processes of OA is key in developing aerosol-related control policies and air quality and climate models. However, OA is chemically complex, with thousands of different compounds detected in single samples (Goldstein and Galbally, 2007). The compositional complexity of OA arises from diverse primary sources and reactions of organic species in the atmosphere that produce secondary OA (SOA) material from gas-to-particle conversion or chemically aged OA (De Gouw and Jimenez, 2009).

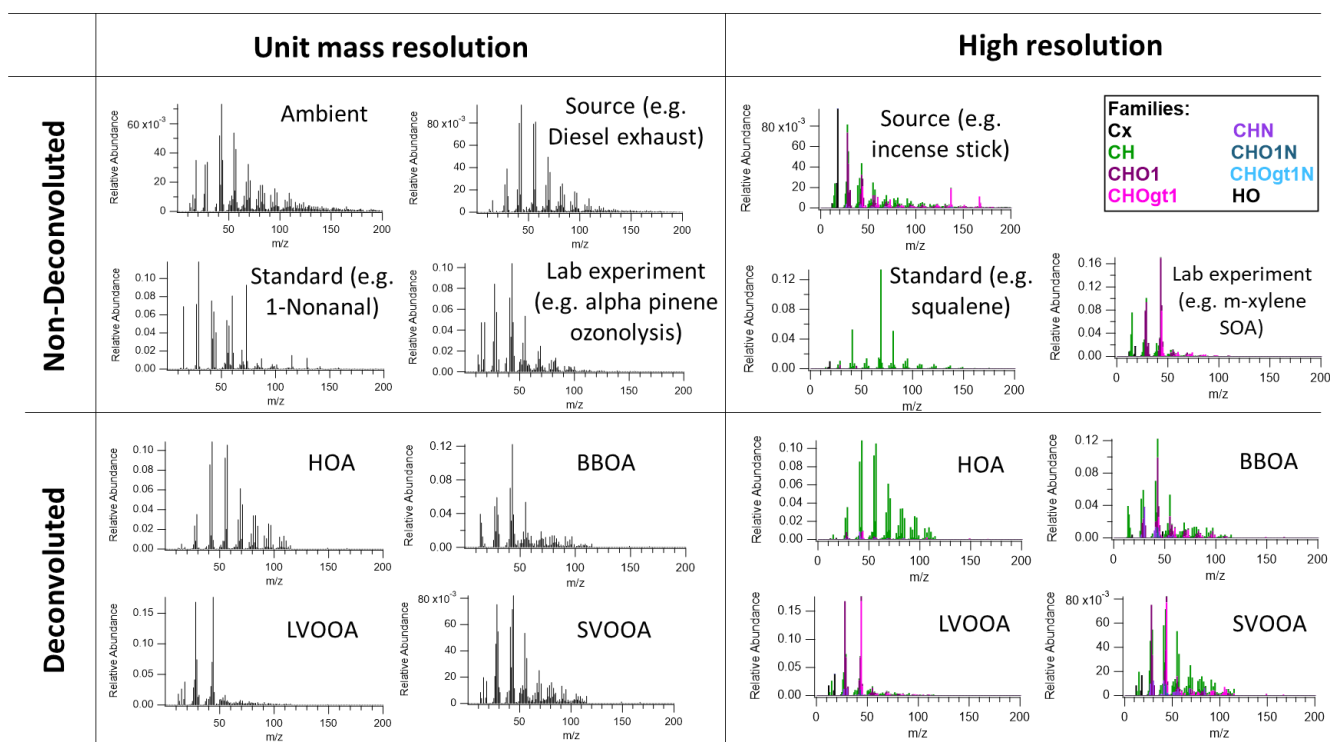
Aerosol Mass Spectrometry (AMS) has widely been applied to atmospheric science research for analysis of the bulk chemical composition of fine particles. It allows one to measure the non-refractory components of the particles with high time resolution, most typically reporting mass concentrations of total fine OA, sulfate, nitrate, ammonium, and chloride (e.g. Jayne et al., 2000; Jimenez et al., 2003; Allan et al., 2004; DeCarlo et al., 2006; Canagaratna et al., 2007; Baltensperger et al., 2010). The AMS has frequently been used in both field and laboratory studies. In field studies, the AMS has characterized atmospheric particles in environments such as urban, rural, remote, forested, ocean, and agricultural regions (e.g. Allan et al., 2004, 2006; Phinney et al., 2006; Aiken et al., 2009; He et al., 2011; Bates et al., 2012; Cleveland et al., 2012; Dall'Osto et al., 2013; Hao et al., 2014; Xu et al., 2014; Lee et al., 2015; Modini et al., 2015; Xu et al., 2015; Young et al., 2016; Kim et al., 2017). In addition, AMS has been used on many platforms such as mobile labs, aircraft, and ships as well as stationary sites (e.g. Bahreini

45 et al., 2003; Zorn et al., 2008; Mohr et al., 2011; Coggon et al., 2012; Drewnick et al., 2012; Claeys et al., 2017; Pirjola et al.,
46 2017; Robinson et al., 2018; Shilling et al., 2018). For laboratory studies, particles generated from a variety of sources,
47 including wood burning, cooking, trash burning, coal and fuel combustion, etc., have been characterized using AMS (e.g.
48 Canagaratna et al., 2004; Schneider et al., 2006; Aiken et al., 2008; Weimer et al., 2008; Mohr et al., 2009; Chirico et al., 2010;
49 He et al., 2010; Adam et al., 2011; Heringa et al., 2011; Wang et al., 2013; Collier et al., 2015; Fortenberry et al., 2018).
50 Furthermore, AMS has been employed to analyze SOA formed from different oxidation experiments using environmental
51 chambers or flow tube reactors with varying oxidants, aging processes, concentrations, humidity levels, temperatures,
52 precursors, etc. (e.g. Bahreini et al., 2005; Kroll et al., 2005, 2006; Murphy et al., 2007; Ng et al., 2007, 2008; Chhabra et al.,
53 2010; Lambe et al., 2011, 2012; Loza et al., 2014; Riva et al., 2016; Boyd et al., 2017; Lim et al., 2019).

54 The Aerosol chemical speciation monitor (ACSM) also has been used to analyze the bulk chemical composition of
55 non-refractory components with a very similar sampling and detection technology as the AMS. The key difference is that the
56 ACSM was developed with reduced complexity (e.g. no particle size measurement) and performance (Ng et al., 2011). A major
57 advantage of ACSM over AMS is that it provides a smaller size, lower cost, simpler operation, and less attention from site
58 managers than AMS. In addition, ACSM data are analyzed with the same techniques that are used for the AMS. Therefore, the
59 ACSM has been deployed for long-term monitoring at locations including urban (e.g. Ng et al., 2011; Sun et al., 2011;
60 Budisulistiorini et al., 2013; Carbone et al., 2013; Budisulistiorini et al., 2014; Aurela et al., 2015; Petit et al., 2015;
61 Budisulistiorini et al., 2016; Reyes-Villegas et al., 2016; Rattanavaraha et al., 2017; Sun et al., 2018; Kommula et al., 2021),
62 suburban (Zhang et al., 2018), rural (e.g. Tiitta et al., 2014; Canonaco et al., 2015; Fröhlich et al., 2015a; Parworth et al., 2015;
63 Bressi et al., 2016; Budisulistiorini et al., 2016; Schlag et al., 2016; Zhao et al., 2020), remote (e.g. Budisulistiorini et al., 2015;
64 Fröhlich et al., 2015b; Ripoll et al., 2015; Michoud et al., 2017), and forested areas (e.g. Fröhlich et al., 2013; Minguillón et
65 al., 2015; Heikkinen et al., 2020).

66 According to the broad and diverse application of the AMS and ACSM, data analysis procedures have also been
67 advanced to improve efficiency and accuracy to interpret the data. These advances have made it possible to divide the quantified
68 OA mass concentrations obtained from AMS and ACSM into hydrocarbon-like OA (HOA, a surrogate for primary OA (POA)
69 directly emitted from fossil fuel combustion) and oxygenated OA (OOA, a surrogate for SOA generated from a chemical
70 reaction or phase partitioning). Furthermore, OOA can be subdivided into low-volatility OOA (LV-OOA or more-oxidized
71 OOA, MO-OOA) and semi-volatile OOA (SV-OOA or less-oxidized OOA, LO-OOA) when combined with methods such as
72 thermal-denuding inlets and positive matrix factorization (PMF) analysis (Paatero and Tapper, 1994; Zhang et al., 2005; Lanz
73 et al., 2007; Ulbrich et al., 2009; Zhang et al., 2011). In addition, these deconvolved OA have been specifically characterized
74 depending on source types such as biomass burning (BBOA) and cooking (COA), increasing the utility of source apportionment
75 of atmospheric aerosols (Paatero and Tapper, 1994; Ulbrich et al., 2009; Mohr et al., 2009). This improvement in data analysis,
76 in addition to the higher performance and mass spectral resolution of modern time-of-flight (ToF) MS detectors often deployed
77 with the AMS and ACSM, has led to a growing number of reported measurements under various sample configurations and
78 conditions.

79 Mass spectra (MS) from the AMS and ACSM provide powerful information to interpret the OA data. A mass spectrum
80 with specific marker ions, or specific ratios of ions, can often be related to a source or chemical process. Here we broadly
81 classify MS types by mass resolution (unit mass resolution or UMR vs. high mass resolution or HR) and extent of MS separation
82 through data processing (non-deconvoluted/deconvoluted). UMR indicates that the signal at each mass is separated from the
83 next 'integer' m/z . In contrast, HR is able to quantify multiple HR ion fragments at a nominal m/z , which enables more detailed
84 characterization than UMR. DeCarlo et al., (2006) has demonstrated the ability to characterize HR ion fragments below a
85 nominal mass, typically m/z 120. These HR ion fragment signals can be grouped into different ion classes such as C_x , C_xH_y ,
86 $C_xH_yO_z$, etc., which are called 'HR families'. A HR mass spectrum is often plotted in a color-coded stacked bar chart of these
87 HR families. Deconvolution indicates whether or not the MS are generated from an additional analysis step like PMF. If the
88 mass spectrum is obtained from PMF, it is called a 'Deconvoluted' mass spectrum and is identified as HOA, SV-OOA, LV-
89 OOA, etc. If not separated, the mass spectrum is referred to as 'Non-deconvoluted'. A non-deconvoluted MS may be
90 representative of multiple contributing sources or aging processes if an ambient sample or can be a single source or standard
91 observed in a lab study. Figure 1 presents various examples of AMS OA MS classified by resolution and extent of MS
92 processing.



93

94 *Figure 1. Various examples of AMS OA mass spectral data divided by resolution and deconvolution. Each mass spectrum was*
 95 *plotted via the developed AMS MS comparison panel here and original data were from Alfara et al., (2004); Canagaratna et*
 96 *al., (2004); Katrib et al., (2004); Bahreini et al., (2005); Li et al., (2012); Loza et al., (2012) for non-deconvoluted MS and*
 97 *Mohr et al., (2012) for deconvoluted MS.*

98 With existing datasets growing in complexity and number according to the advancement and accessibility of
 99 technology in the aerosol science field, it is increasingly important to develop customizable databases that store previous
 100 observations and act as a reference for future studies. Previous AMS and ACSM data have often been provided in text and
 101 graphical form, such as peer-reviewed journal publications. However, as the amount of data grows, finding the appropriate data
 102 in a usable format is increasingly challenging. Previous efforts to build a database for AMS and ACSM have been made by
 103 Ulbrich et al., (2009). They collected published AMS and ACSM spectral data and metadata (e.g., instrument operating
 104 conditions, sample, and experiment details), and posted it on an open-access website (<https://cires1.colorado.edu/jimenez-group/AMSsd/>). The digital data was uploaded as an Igor Pro software (Wavemetrics, Portland, OR) text file format, with
 105 an .itx file name extension. This allows users to load or export the data in the Igor Pro software commonly used for AMS and
 106 ACSM data analysis. This is a useful repository to advertise and distribute AMS and ACSM data. However, this repository is
 107 not programmed or formatted to systematically search for appropriate results and compare them with the researcher's own data.
 108 Beyond the need to program a search method, formatting needs to be standardized compared to the current method where each
 109 spectral data is individually uploaded on the webpage with some variability in format (e.g., variable mass-to-charge (m/z)
 110 ranges).
 111

112 In this study, we introduce a searchable database tool for the AMS and ACSM mass spectral dataset. Our aim is to
 113 improve the efficiency and utility of the AMS and ACSM data analysis process, building on the existing database from Ulbrich
 114 et al., (2009). We converted the web-based database to a software-based database format using Igor-pro and developed the Igor
 115 Pro visualization interface. The interface is called 'AMS MS comparison panel' or simply 'panel' in the following sections. To
 116 demonstrate the practical application of this tool, we compared our AMS MS with reference MS in the database. This
 117 comparison demonstrates how our tool can be useful in practical applications. We believe that incorporating this comparison
 118 tool will enhance the ability of AMS and ACSM users to conveniently compare their data with previously reported studies.

119

120 2. Methods

121 The developed database is based on the existing open-access website by Ulbrich et al., (2009), providing published
 122 AMS and ACSM mass spectral datasets. The website mainly consists of 3 separate web pages such as unit mass resolution

123 (UMR, standard vaporizer), high resolution (HR, standard vaporizer), and capture vaporizer (CV, both UMR, and HR). Capture
124 vaporizer indicates that a more recently developed particle vaporizer was installed, which can lead to different spectra primarily
125 from increased thermal decomposition (Hu et al., 2018a). For each sample, the website provides metadata in a table format
126 including spectra identification, sources, research groups, AMS instruments used, electron ionization (EI) energy, and vaporizer
127 temperature. It also provides citation information and the original figure number in the publication, sometimes with additional
128 comments. The mass spectrum is uploaded in a digital form for analysis as an .itx file, a plain text file that can be directly
129 loaded into the data analysis software Igor-Pro (Wavemetrics, Portland, OR).

130 Here, to convert this web-based information and individual mass spectrum files to the software-based database in Igor-
131 Pro, the given information was fetched from HTML using the ‘fetchURL’ function in Igor-Pro to convert the contents of the
132 HTML to strings. Metadata was extracted from these HTML strings and saved in Igor Pro. Each mass spectrum was
133 automatically downloaded to the computer first and then saved in the Igor-Pro database. When saving the mass spectrum, it
134 was aligned and normalized in a uniform format with a consistent m/z range from 1 to 600 and a sum of the spectrum summing
135 to a value of 1. In the case of high resolution MS, they were converted to a UMR mass spectrum to make the HR mass spectrum
136 directly comparable to the UMR mass spectrum, and then also saved into the Igor-Pro database. HR ion family data was also
137 converted to UMR form and saved using the same method. For example, if the HR mass spectrum has three ions as CO_2^+ (m/z
138 43.9898), $\text{C}_2\text{H}_4\text{O}^+$ (m/z 44.0262), and C_3H_8^+ (m/z 44.0626), all these three ions are considered as m/z 44 on the database panel
139 in both UMR and HR. However, for HR ion families, these ions are respectively saved to corresponding HR ion families such
140 as CHOgt1 , CHO1 , and CH (a detailed description of HR families is presented in Table S1). After creating the software-based
141 database, the visualization interface (i.e., AMS MS comparison panel) was constructed in Igor Pro to analyze the correlation
142 between MS.

143

144 2.1 Mass spectrum correlation calculation

145 The main goal of this comparison panel is to provide a convenient function to analyze similarities between the mass
146 spectrum of interest and the reference MS in the database. In this comparison tool, we chose cosine similarity to estimate mass
147 spectrum similarity. Cosine similarity has been proved to show better performance in calculating correlations between MS
148 compared to other methods (Stein and Scott, 1994; Ulbrich et al., 2009). Therefore, it is commonly used to analyze the similarity
149 between MS in analyses of AMS spectra, referring to it as the dot product with normalized spectra input or uncentered
150 correlation coefficient (e.g. Marcolli et al., 2006; Lambe et al., 2015; Day et al., 2022). On the panel here, cosine similarity is
151 referred to as the ‘Cosine score’. It measures the cosine of the angle between two vectors and is calculated by using the equation
152 below.

$$153 \text{Cosine score} = \cos(\theta) = \frac{A \cdot B}{\|A\| \|B\|} \text{ (Eqn. 1)}$$

154 where each vector A and B are corresponding to the mass spectrum of interest and each reference mass spectrum in the database,
155 respectively. $\|A\|$ and $\|B\|$ denote the magnitudes of vectors A and B, and $A \cdot B$ indicates the dot product of A and B. The possible
156 range of cosine similarity (score) is from 0 to 1, and the higher the score value, the higher the similarity between the MS.

157 In addition, the panel supplies the option to reweight the mass spectrum using Equation 2 below. Regarding the
158 comparison of MS, instrument operation parameters can cause m/z -dependent differences in the amount or detection of ions,
159 and preprocessing spectral intensities by reweighting can have a beneficial effect on improving correlations between acquisition
160 methods (Stein and Scott, 1994). The score can be adjusted by varying their mass weighting and intensity scaling factors.
161 Increasing the relative significance of the lower-abundance high m/z values can enhance the match-weighting of these more
162 distinctive ions (i.e., molecular fragments). This is achieved by increasing the mass exponent (mass weighting) or decreasing
163 the peak intensity exponent (intensity scaling factors) that corresponds to the m and n in Equation 2, respectively.

$$164 \text{Weighted intensity} = [m/z]^m [\text{Peak intensity}]^n \text{ (Eqn. 2)}$$

165 The weighted exponents default to $m=0$ and $n=1$ on the panel. After reweighting, the mass spectrum is normalized by dividing
166 each value by the sum of the reweighted mass spectrum (thus summing to unity again). Finally, the panel calculates the score
167 using the scaled mass spectrum.

168 For HR mass spectral data, the score can be calculated with only the selected HR families on the panel. For example,
169 if one selects three HR families out of 17, then it combines these three HR family MS of interest into one mass spectrum and
170 sums to unity for normalization. It then calculates the score with a normalized mass spectrum utilizing the same method
171 described above. Detailed HR family information will be described in the next section. This score is referred to as ‘Score with
172 HR family’ on the HR data comparison tab of the panel.

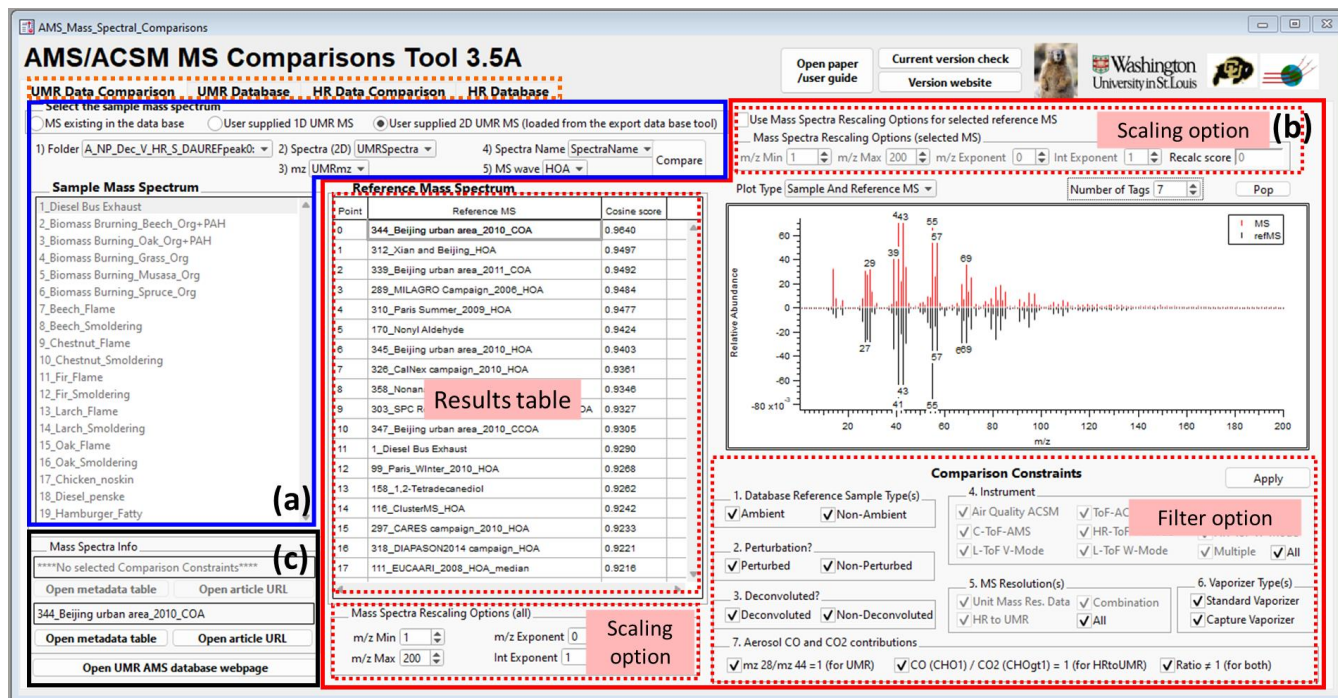
173

174 **2.2 Igor AMS mass spectral comparison panel**

175 2.2.1 Data Comparison tab

176 Figure 2 shows a screenshot of the AMS MS comparison panel. The panel is divided into four tabs (dashed line in
 177 orange of Figure 2): i) UMR Data comparison, ii) UMR Database, iii) HR Data comparison, and iv) HR Database. Both data
 178 comparison tabs for UMR and HR data consist of three regions. Figure panel section 2a (highlighted in blue) is where a new
 179 or existing mass spectrum is selected for comparison against database MS. Section 2b (highlighted in red) is where the user
 180 will set search parameters and view results, and section 2c (highlighted in black) is where metadata of selected database
 181 components can be viewed. Screenshots of other tabs are shown in the supplementary material (Figs. S1-3).

182



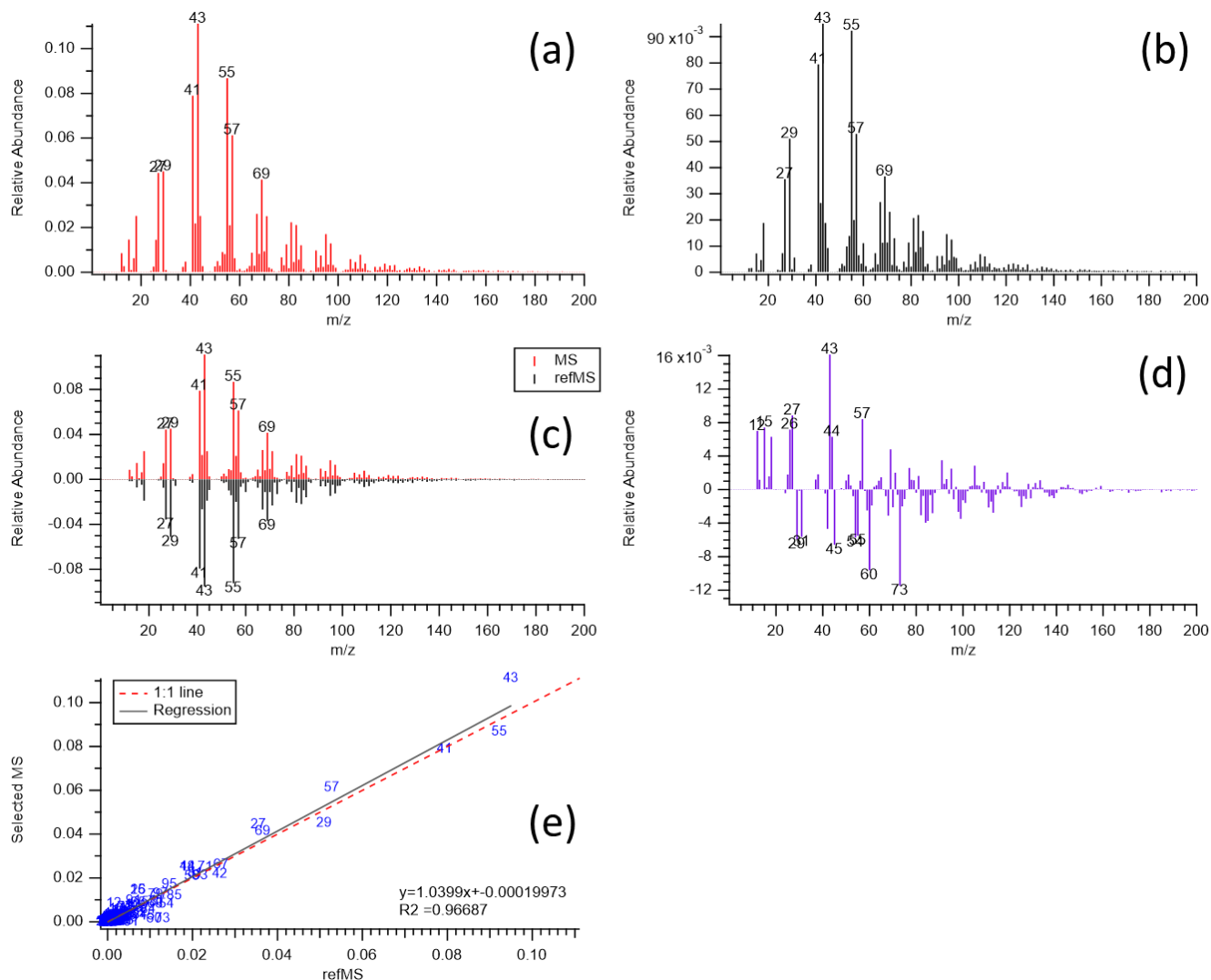
183

184 Figure 2. A screenshot of the UMR Data comparison tab in the ‘AMS MS Comparison Panel’. In box (a), the user selects their
 185 sample mass spectrum of interest, in box (b) the user views a comparison result of the sample with the database reference mass
 186 spectrum and sets the scaling option and filter option, and the box (c) provides the citation information.

187 In panel section 2a, users are able to select MS to be compared. There are two options for users to choose a mass
 188 spectrum of interest. One is to choose their own mass spectrum (‘User supplied 1D/2D UMR MS’), and the other is to select
 189 an existing mass spectrum in the database (‘MS existing in the data base’). In the case of selecting their own mass spectrum,
 190 the mass spectrum has to be in UMR with a standard m/z range. The current panel and database use a mass range of m/z 1-600.
 191 Detailed information on how to upload the user’s own data to the database panel is described in the user guide section (Chapter
 192 2 for UMR and Chapter 3 for HR) of the supplementary information.

193 Panel section 2b contains the results table, mass spectrum plots window, scaling mass spectrum options, and
 194 comparison filter options. The results table shows the list of reference spectra sorted by the calculated score (cosine similarity)
 195 in descending order. Users are able to see the reference spectrum of interest on the mass spectrum plots window by clicking on
 196 the results table. For the UMR data comparison tab, the mass spectrum plot window provides five types of mass spectrum plots
 197 (selectable with the ‘Plot Type’ drop-down above the plot shown in Fig. 2: sample mass spectrum of interest, reference mass
 198 spectrum selected, mirror-image sample and reference MS, subtraction of sample and reference MS, and the scatter plot
 199 between the sample and reference with the markers corresponding to the specific m/z value with regression information (Fig.
 200 3). For the HR data comparison tab, the panel plots a stacked mass spectrum with HR ion families such as Cx, CH, CHO1,
 201 CHOgt1, etc (Fig. S2b). These HR ion families are the same names generated by PIKA v1.23B which is an AMS data analysis
 202 tool for HR (DeCarlo et al., 2006; Sueper, 2021, <https://cires1.colorado.edu/jimenez-group/ToFAMSResources/ToFSoftware/>).
 203 The chemical formula for each HR ion family is described in Table S1. Users can select the HR ion family to be viewed on the

204 window and can calculate a ‘score with HR family’ with these selected HR families to compare the mass spectrum specifically.
 205 These various types of plots will help users visually observe the similarities and differences between the MS. The scaling mass
 206 spectrum option can reset the mass range and reweight the mass spectrum. Users are able to choose whether to apply the scaling
 207 options to all reference MS in the database (below the results table in panel section 2b) or to only one selected reference mass
 208 spectrum on the list (top right of the panel in panel section 2b) in UMR data comparison tab. For HR data, it only provides the
 209 scaling option for all reference MS. Furthermore, the panel supplies comparison constraints to filter the reference MS in the
 210 database depending on the metadata. Comparison constraint categories include sample type, perturbation, deconvolution,
 211 instrument, MS resolution, and CO and CO₂ contribution sections. Detailed descriptions of these constraints are provided in
 212 the supplementary material (Section S1).



213
 214 *Figure 3. Five types of plots provided by the panel to inform mass spectral comparisons: (a) sample mass spectrum of interest,*
 215 *(b) reference mass spectrum selected, (c) mirrored-image sample and reference MS, (d) subtraction (difference) of sample and*
 216 *reference MS, and (e) scatter plot between the sample and reference mass spectrum with the markers corresponding to the*
 217 *specific m/z values with regression information. Original data were from Ulbrich et al., (2009) and Mohr et al., (2009). In this*
 218 *example (as observed in panel d) the sample MS (HOA) contains additional m/z 43 and 57 (both of which have primary or*
 219 *secondary contributions and would need to further explore the HR results to distinguish), and the reference MS (laboratory,*
 220 *chicken cooking without skin) contains additional m/z 60 and 73 (common biomass markers or carboxylic acids).*

221
 222 Finally, in panel section 2c, users can find detailed information on the sample mass spectrum of interest and selected
 223 reference MS in the results table. The “Open metadata table” button in panel section 2c enables a new window to pop up for
 224 users to obtain information. The new window shows sample type, perturbed type, analysis, instrument type, resolution,
 225 vaporizer type, EI energy value, vaporizer temperature, experimenter’s name, group, citations, citation URLs, figure numbers

226 in the citation, and related comments (Fig. S4). In addition, users can directly open the relevant published paper in a web
227 browser via the panel (“Open article URL” button in panel section 2c) if the URL address of the paper is saved in the database.

228

229 2.2.2 Database tab

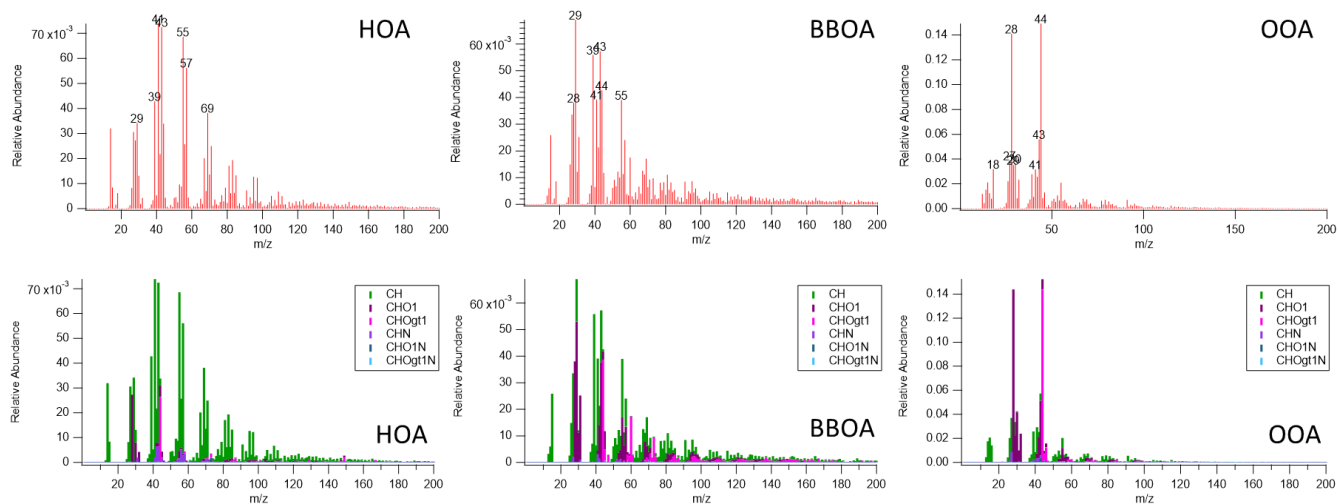
230 Both database tabs of UMR and HR (Figs. S1, S3) display reference MS in the database. Users can simply observe
231 the reference mass spectrum in the database with metadata without correlation calculation. Users can scan the MS stored in the
232 database through this tab and easily obtain the corresponding reference metadata.

233

234 3. Application of the AMS MS database and comparison panel

235 Here, we used PMF factor mass spectral data from the DAURE campaign (Determination of the sources of
236 atmospheric Aerosols in Urban and Rural Environments) to display the utility of the developed database and comparison panel.
237 Data for this study were acquired in high resolution during the intensive DAURE field campaign in Montseny, Spain, during
238 February-March 2009. An 8-factor solution (FPEAK=0) was chosen since this was the lowest number of factors at which the
239 HOA and BBOA factors showed a clear separation from each other and OOA. Six factors were recombined to make up the
240 OOA factor. The BBOA and HOA factors used here are those from the 8-factor solution. More details about an overview of
241 the DAURE campaign and a summary of the results can be found in Minguillón et al., (2011), Pandolfi et al., (2014), and
242 Zhang et al., (2022). For comparison, the acquired PMF factor mass spectral data in HR was converted to a UMR mass
243 spectrum. Figure 4 shows the converted PMF factor MS of HOA, BBOA, and combined OOA in UMR and stacked HR ion
244 families, respectively. In this section, we will introduce examples of ways to utilize the new comparison panel by applying
245 functions via the UMR data comparison tab and present a potential for the HR data comparison tab based on HR families and
246 ‘score with HR family’ to obtain more information to interpret the data depending on our factor MS.

247



248

249 *Figure 4. PMF factor MS from Montseny, Spain during the DAURE campaign (Minguillón et al., 2011) in UMR and stacked*
250 *HR ion families. The acquired PMF factor MS in high resolution were converted to a UMR mass spectrum and plotted by the*
251 *AMS MS comparison panel here.*

252

253 As introduced above, the developed database panel provides different ways to compare the MS with filtering or scaling
254 options. Among these options, the ‘sample type’ category in the filtering option (Fig. 2. section b) enables researchers to select
255 ‘ambient’ or ‘non-ambient’ samples in the database. The ‘Ambient’ option indicates direct measurement of ambient air and the
256 ‘non-ambient’ option includes analysis of chamber studies, source emission studies, standards, etc. The scaling option is used
257 to scale the mass spectrum using the mass range, mass exponent, and intensity exponent based on Eqn. 2. The default setting
258 of the scaling option on the panel is $m=0$ and $n=1$ on Eqn. 2. The comparison process and results for each method will be
259 described in this section with the DAURE campaign PMF factor MS as an example.

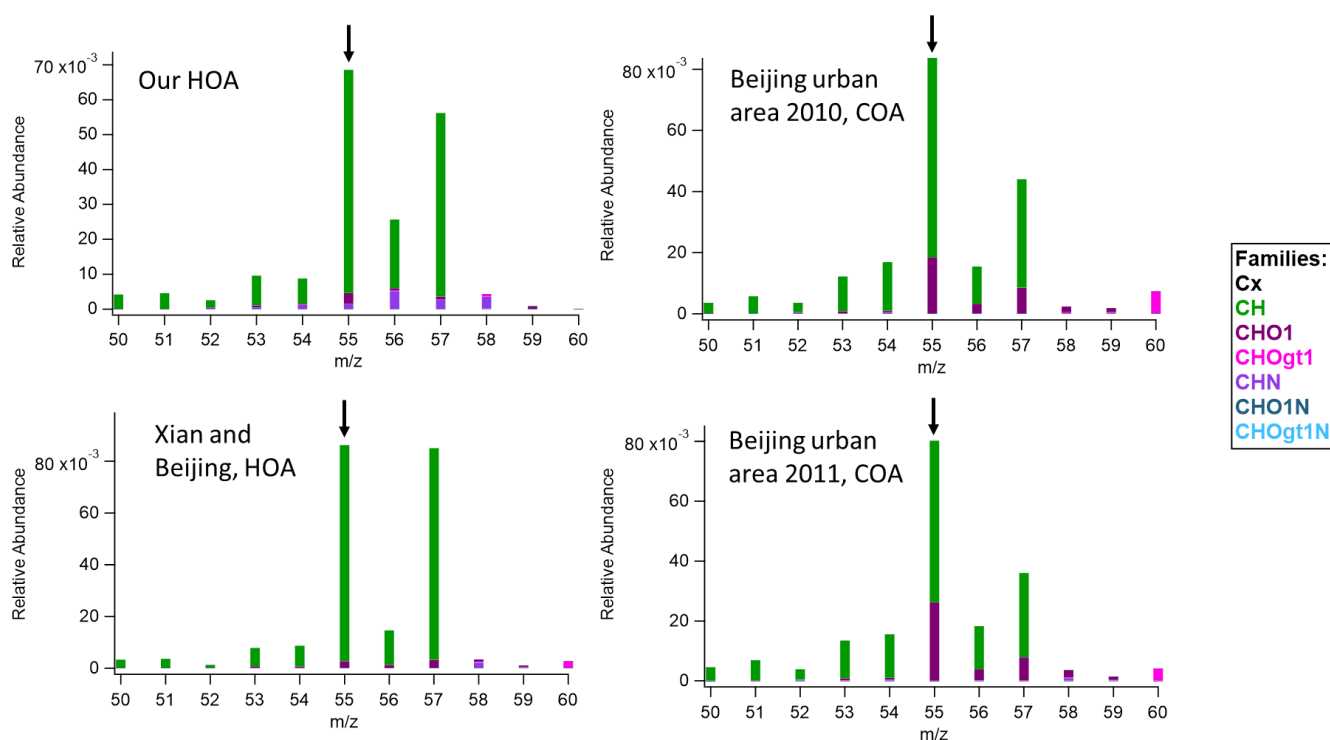
260 Selecting the ‘ambient’ option is useful when the user wants to compare their mass spectrum only with previous
 261 ambient measurements. For example, after the final PMF factors are identified, we may want to confirm if the identified PMF
 262 factors have a similar MS compared with previous studies. In this case, users can apply the ‘ambient’ sample filter to compare.
 263 Table 1 shows the comparison results with the cosine similarity when we executed a UMR comparison of the HOA factor
 264 identified from the DAURE campaign (Montseny, Spain) with the database as an example. In the results table, most of the
 265 samples in the database with a score greater than 0.9 were shown as ‘HOA’. An interesting observation that appears is that
 266 some cooking organic aerosol (COA) factors also showed a high correlation with our HOA factor. The COA factor is often
 267 identified by its characteristic mass fragment of m/z 55, and it also has the same hydrocarbon ion series (m/z 29, 43, 57, 71, for
 268 $C_nH_{2n+1}^+$ and m/z 41, 55, 69, for $C_nH_{2n-1}^+$) as the HOA (Mohr et al., 2009). The HOA factor we compared has a large m/z 55
 269 in the spectrum and that may be the main cause for some COA factors to score a high match. Therefore, we would conclude
 270 that our HOA factor might be mixed with cooking sources. However, in this case, if the user has HR family information of the
 271 mass spectrum, as we do here, one could have more information to interpret the result.

272 COA factor MS usually have a relatively high portion of CHO1 family in m/z 55 compared to HOA, which would be
 273 from the $C_3H_3O^+$ ion (Mohr et al., 2009, 2012). Figure 5 shows the comparisons of m/z 55 in stacked HR families with the top
 274 3 reference samples in Table 1. The m/z 55 in our HOA and Xian and Beijing HOA factor MS mainly consists of CH family,
 275 specifically $C_4H_7^+$, and this contribution is clearly distinguished from the COA reference MS such as Beijing urban area 2010
 276 and 2011 having larger m/z 55 contributions from CHO1 family, specifically $C_3H_3O^+$. These trends are also shown in Mohr et
 277 al., (2012) where AMS data acquired during the field campaign DAURE in Barcelona, Spain were analyzed and HOA and
 278 COA were both separated as a result. The HOA factor mass spectrum in Mohr et al., (2012) also had the m/z 55 only slightly
 279 smaller than m/z 57. However, the m/z 55 in their HOA factor mass spectrum is also predominantly contributed from the CH
 280 family as we observed here. Likewise, in their COA factor mass spectrum, m/z 55 is much larger than m/z 57 and nearly half
 281 of m/z 55 was from the CHO1 family. Therefore, we may conclude that our HOA factor is most similar to previous ‘HOA’ MS
 282 even if it has a high abundance of m/z 55. However, it also suggested that additional PMF analysis with more factors could find
 283 some contribution of COA mixed in our HOA that could perhaps be separated. This comparison shows the strength of
 284 incorporating the HR families available from HR-AMS datasets as well as simple UMR ambient comparison via the panel.

285 *Table 1. Top matches from “Ambient” sample UMR comparison results with HOA factor from the DAURE campaign (m/z 1-*
 286 *200)*

# in DB	Sample	Score	Reference
311	Beijing urban area_2010_COA	0.9640	(Hu et al., 2016)
279	Xian and Beijing_HOA	0.9497	(Elser et al., 2016)
306	Beijing urban area_2011_COA	0.9492	(Hu et al., 2016)
253	MILAGRO Campaign_2006_HOA	0.9483	(Alfarra et al., 2004)
277	Paris Summer_2009_HOA	0.9477	(Crippa et al., 2013)
312	Beijing urban area_2010_HOA	0.9403	(Hu et al., 2016)
293	CalNex campaign_2010_HOA	0.9361	(Hayes et al., 2013)
270	SPC Research Station Po Valley_2008_HOA	0.9327	(Saarikoski et al., 2012)
314	Beijing urban area_2010_CCOA	0.9305	(Hu et al., 2016)
101	Paris_Winter_2010_HOA	0.9269	(Crippa et al., 2013)

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289 *Figure 5. Segments of the MS (m/z 50-60) for our HOA and top 3 reference samples that correlated highly with our HOA in*
 290 *the “Ambient” comparison for m/z 55 HR ion families*

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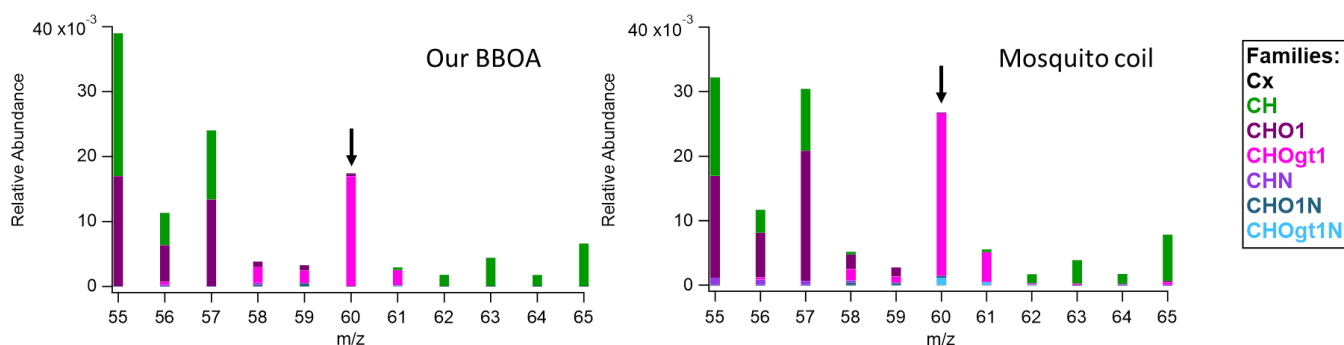
292 ‘Non-ambient’ option is convenient to compare the mass spectrum of interest with laboratory samples in the database.
 293 For example, this option is helpful when comparing a mass spectrum derived from a specific source such as BBOA. When
 294 applying the non-ambient filtering option, several non-ambient reference MS were highly correlated with our BBOA MS (Table
 295 2). The characteristic mass fragment of BBOA is m/z 60 attributed to $C_2H_4O_2^+$ (from anhydrous sugars such as levoglucosan)
 296 and this specific ion was observed in most of the MS in the list of high score matches. On the HR data comparison tab, we are
 297 able to confirm if the m/z 60 is from the oxygenated HR family (CHOgt1). In Table 2, only the mosquito coil sample included
 298 HR ion family data and we confirmed the m/z 60 was mostly from CHOgt1 ion family which is pink (Fig. 6). Since the main
 299 component of mosquito coil is biomass such as sawdust, coconut shell flour, pyrethrum, potato starch, etc, it seems to show a
 300 high correlation with our BBOA and similar HR ion family contribution in m/z 60.

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302 *Table 2. Top matches from “Non-ambient” sample UMR comparison results with the BBOA factor from the DAURE*
 303 *campaign (m/z 1-200)*

# in DB	Sample	Score	Reference
30	Ponderosa Pine Duff	0.9404	(FLAME, 2007)
41	Puerto Rican Mixed Wood	0.9337	
40	Southern Pine Needles	0.9335	
325	Mosquito Coil	0.9303	(Li et al., 2012)
38	Puerto Rican Fern	0.9296	(FLAME, 2007)
31	Alaska Core Tundra Duff	0.9275	
36	Ceanothus Leaves and Berries	0.9193	
27	Ponderosa Pine Needles and Sticks	0.9184	
39	Wax Myrtle	0.9038	
35	Lignin Powder	0.8951	

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306 *Figure 6. Enlarged MS of our BBOA and mosquito coil sample for m/z 60 HR ion family*

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308 An interesting observation from BBOA example is that when carrying out the ambient sample comparison with the
309 BBOA factor, other identifications such as HOA, SVOOA, LOOOA, COA, etc were observed as well as BBOA (Table 3) even
310 though our BBOA mass spectrum was highly correlated with biomass burning laboratory references. Since ion separation of
311 AMS mass spectrum via PMF is largely impacted by the mix of sources present at a given time, users don't always obtain a
312 'perfectly separated' mass spectrum identifying the mass spectrum as HOA, BBOA, COA, etc, but a possibly mixed mass
313 spectrum. It indicates that even if the UMR score on the panel is lower, it could be possible that there is a good match with a
314 single HR family or some families, and vice versa. For this case, 'Score with HR family' can be a useful function to gain more
315 information on similarities. When users select the HR families of interest next to the HR plot window and click the calculate
316 button below HR family selection, it combines only the selected HR families into one MS, calculates a cosine similarity in the
317 same way, and displays the results named 'score with HR family' on the results table. Table 3 shows top 10 matches from
318 ambient sample comparison results sorted by the UMR score and top 10 matches from 'score with HR family'. For BBOA, the
319 separation of the oxygenated ions provides a lot of information and is a key signature of BBOA spectra. On Table 3, we were
320 able to observe more BBOA factor mass spectrum on the list when sorting the results by the score with CHOgt1 family
321 including m/z 60. Most of the new matches showed BBOA, CCOA (coal combustion OA), HOA, and COA, not OOA like
322 when sorting the list by UMR score. UMR match scores for these reference MS are included alongside the HR Family match
323 score for comparison. We also carried out a score comparison utilizing additional HR families and family combinations (CH,
324 CHO1, and combined), but it did not provide additional insight beyond what was observed with CHOgt1 alone (Table S2).

325
326 *Table 3. Top matches from HR "Ambient" sample comparison results with the BBOA factor from the DAURE campaign (m/z*
327 *1-200) depending on UMR score and score with HR family (CHOgt1)*

Top 10 matches sorted by UMR score				
# in DB	Sample	UMR score	Reference	
293	Changdao island_2011_biomass burning	0.9632	(Hu et al., 2013)	
310	SOAS campaign_2013_SOA	0.9445	(Hu et al., 2015)	
300	Beijing urban area_2011_HOA	0.9367	(Hu et al., 2016)	
245	SOAR-1_Campaign_2005_SVOOA	0.9346	(Docherty et al., 2011)	
313	SOAS campaign_2013_LOOOA_II	0.9287	(Hu et al., 2015)	
296	Changdao island_2011_CCOA	0.9239	(Hu et al., 2013)	
315	KORUS-AQ study_2016_LOOOA	0.9164	(Hu et al., 2018b)	
269	Paris Summer_2009_SVOOA	0.9149	(Crippa et al., 2013)	
301	Beijing urban area_2011_COA	0.9097	(Hu et al., 2016)	
265	SPC Research Station Po Valley_2008_HOA	0.9050	(Saarikoski et al., 2012)	
Top 10 matches sorted by the score with HR family (CHOgt1)				
# in DB	Sample	UMR score	Score with CHOgt1	Reference
254	DAURE campaign_2009_BBOA	0.8348	0.9527	(Mohr et al., 2012)

296	Changdao island_2011_CCOA	0.9239	0.9265	(Hu et al., 2013)
259	CARES campaign_2010_HOA	0.8384	0.9216	(Setyan et al., 2012)
268	Paris Summer_2009_COA	0.8231	0.9208	(Crippa et al., 2013)
275	Xian and Beijing_COA	0.8311	0.9195	(Elser et al., 2016)
283	POPE2014 campaign_COA	0.7947	0.9079	(Struckmeier et al., 2016)
266	SPC Research Station Po Valley_2008_BBOA	0.8913	0.9061	(Saarikoski et al., 2012)
304	Beijing urban area_2010_LVVOA	0.8474	0.9052	(Hu et al., 2016)
293	Changdao island_2011_biomass burning	0.9632	0.9045	(Hu et al., 2013)
307	Beijing urban area_2010_HOA	0.8496	0.8995	(Hu et al., 2016)

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Lastly, users can use the “scaling mass spectrum” feature, which is especially helpful for up-weighting signal intensity of larger and more unique ions by increasing the mass exponent value or decreasing the intensity exponent value. When we compared the OOA factor MS with ambient samples, we observed that our OOA factor MS was highly correlated with LVVOA (or MOOOA) MS from previous studies (Table S3) showing a score of more than 0.97. We also explored cosine scores of the OOA factor with non-ambient spectra within the database. However, when we compared the OOA factor MS with non-ambient samples, top scores in the list were shown as less than 0.9 (Table 4). For OOA, the abundances of fragment ions m/z 28 (CO^+) and 44 (CO_2^+) are extremely dominant compared to other ions in the mass spectrum (typically, the m/z 28 signal is constrained to be equal to the m/z 44 signal). These prominent abundances of a few spectral peaks may affect score calculation. In the case of ‘ambient’ comparison with deconvoluted MS dominated by m/z 28 and 44, signals from other ions may not highly influence the results as shown in Table S3. On the other hand, in the case of ‘non-ambient’ comparison with non-deconvoluted MS dominated by m/z 28 and m/z 44 signals of laboratory samples, signals from other ions are more unique to the specific laboratory conditions and may reflect the lower scores as shown in Table 4. In this case, we have two options to reduce these impacts on score results: i) increase the m/z exponent value, ii) decrease the intensity exponent value, or iii) both i and ii in Eqn 2.

Table 4. Top matches from UMR “Non-ambient” sample comparison results with the OOA factor from the DAURE campaign (default setting, m/z 1-200)

# in DB	Sample	Score	Reference
141	Oxalic acid	0.8493	(Takegawa et al., 2007)
334	Chamber m-Xylene aged SOA	0.8458	(Loza et al., 2012)
321	Incense Coil	0.8385	(Li et al., 2012)
145	Adipic acid	0.8196	(Takegawa et al., 2007)
149	Glyoxylic acid	0.8132	(Takegawa et al., 2007)
331	Citric Acid (C ₆ H ₈ O ₇)	0.7661	(Hu et al., 2018b)
143	Succinic acid	0.7649	(Takegawa et al., 2007)
234	Diesel_Exhaust_2	0.7629	(Sage et al., 2008)
322	Mosquito Coil	0.7580	(Li et al., 2012)
333	Chamber m-Xylene peak growth SOA	0.7529	(Loza et al., 2012)

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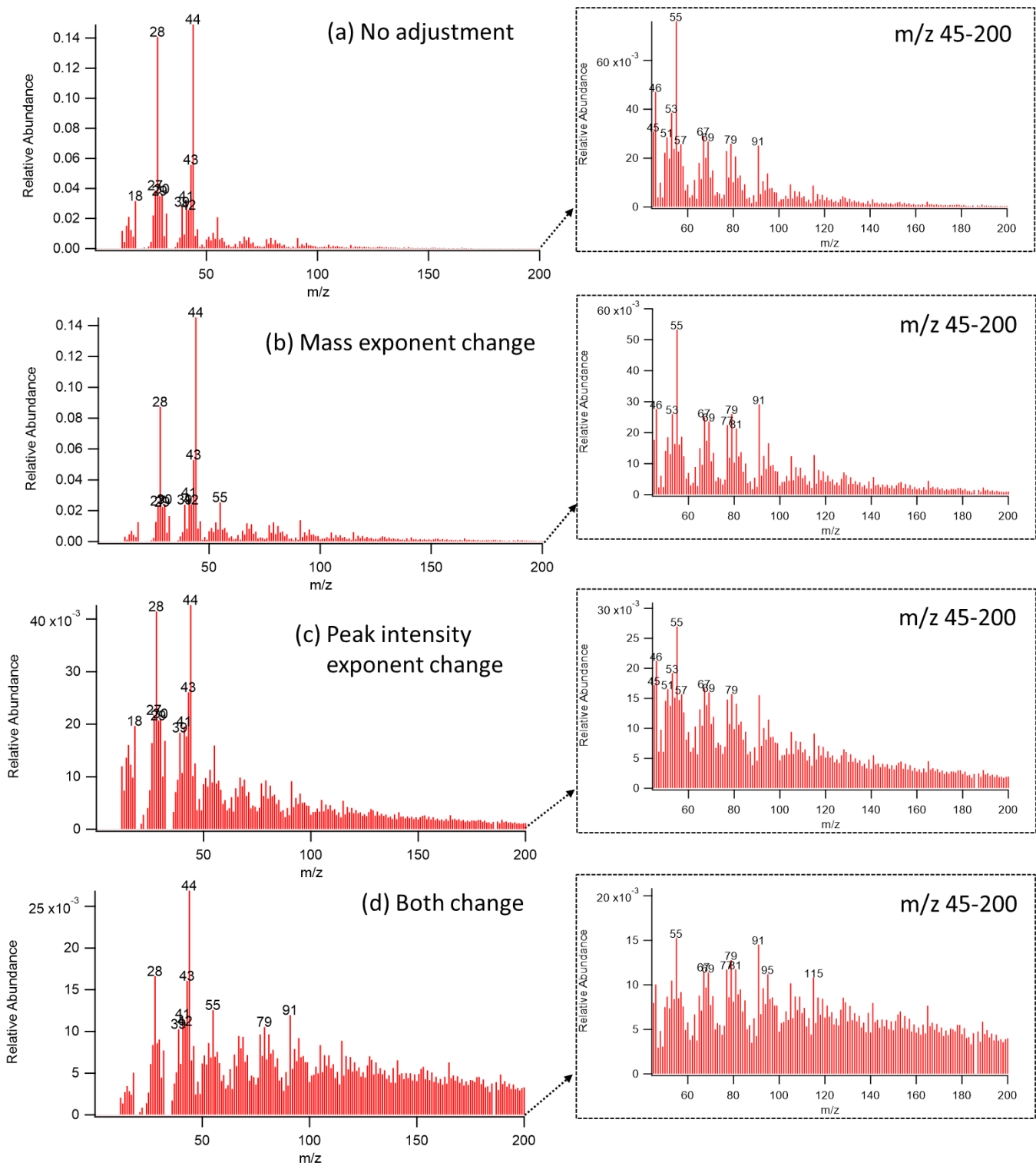
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Figure 7 shows the reweighted OOA mass spectrum generated by two exponent options. When we increased the m/z exponent from 0 to 1 (Figure 7b), we observed that the relative abundance of lower mass fragments decreased and that of larger mass fragments increased in a similar scale of relative abundance as the original MS (Figure 7a). When we decreased the peak intensity exponent from 1 to 0.5 (Figure 7c), the maximum value of relative abundance was decreased. Signal intensities other than the dominant fragments (m/z 28 and 44) were more balanced than in Figure 7a. Figure 7d is the case where we applied both mass and peak intensity exponent options. It shows the reweighted spectra with relatively smaller contributions from lower masses and higher contributions from larger masses. Table 5 shows the list of reference MS with a high correlation with our reweighted OOA factor MS with various pairs of m/z and peak intensity exponent. The scores less than 0.9 were not shown in the table and the reference samples were sorted by the maximum score among the values from each scenario. It shows that for our OOA factor MS, decreasing the intensity exponent option resulted in more scores greater than 0.9 compared to increasing the m/z exponent. Also, we observed that the reweighted OOA factor mass spectrum is mostly correlated with coils, terpene ozonolysis, aged SOA, etc. Correlations to the coils may be because both incense coil and mosquito coil have fragrances that contain aromatic compounds that can produce oxygenated aromatics during combustion.



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360 *Figure 7. The reweighted mass spectrum of DAURE OOA factor ((a): No adjustment, (b): increase m/z exponent from 0 to 1,*
 361 *(c): decrease intensity exponent from 1 to 0.5, and (d): apply (b) and (c) simultaneously). Enlarged mass spectrum with a*
 362 *restricted mass range (m/z 45-200) shown in the dashed line box.*

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365 *Table 5. Top matches from “Non-ambient” UMR sample comparison results with the OOA factor from the DAURE campaign*
 366 *depending on decreasing peak intensity exponent and increasing mass exponent. The maximum score is shown in bold.*

		m/z exponent	0	1	1	
		Peak intensity exponent	0.5	1	0.5	
# in DB	Sample		Score		Reference	
321	Incense Coil		0.9413	-	0.9316	(Li et al., 2012)
334	Chamber m-Xylene aged SOA		0.9306	-		(Loza et al., 2012)
212	Myrcene_O3		-	-	0.9252	(Bahreini et al., 2005)
322	Mosquito Coil		0.9149	-	0.9199	(Li et al., 2012)
222	Myrcene_O3		-	-	0.9176	(Bahreini et al., 2005)
32	Utah Sage, Rabbitbrush		-	-	0.9174	(FLAME, 2007)
213	Terpinolene_O3		-	-	0.9157	(Bahreini et al., 2005)
31	Utah Juniper Foliage and Sticks		-	-	0.9151	(FLAME, 2007)
205	beta-caryophyllene_O3		-	-	0.9151	(Bahreini et al., 2005)
130	Fulvic Acid		-	-	0.9142	(Alfarra, 2004)

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Setting a restricted mass range is another way to modify the score. Table 6 shows the scores of our reweighted OOA MS when setting a new mass range from m/z 45 to 200 and changing the mass and the peak intensity exponent, respectively. Increasing the mass range parameter was generally helpful to explore comparisons beyond the dominant m/z 28 and m/z 44 signals. Decreasing the peak intensity exponent showed higher scores in the list compared to the case of increasing the mass exponent. However, for our OOA, the mass exponent change was more useful to emphasize specific larger ions such as m/z 55, 91, and 115 shown in the enlarged mass spectrum in a dashed box of Figure 7b. We observed that the higher m/z range in the reweighted OOA mass spectrum is highly correlated with terpene ozonolysis and biomass burning (Table 6).

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Table 6. Top matches from “Non-ambient” sample UMR comparison results with the reweighted OOA factor from the DAURE campaign depending on the pairs of mass and intensity exponent value with restricted mass range (m/z 45-200)

		m/z exponent	0	0	1	1	
		Peak intensity exponent	1	0.5	1	0.5	
# in DB	Sample		Score		Reference		
217	Bcaryophyllene_O3		0.9097	0.9587	0.9292	0.9723	(Bahreini et al., 2005)
32	Utah Sage, Rabbitbrush		0.9052	0.9563	0.9277	0.9696	(FLAME, 2007)
205	beta-caryophyllene_O3			0.9586	0.9264	0.9693	(Bahreini et al., 2005)
212	Myrcene_O3			0.9596	0.9185	0.9693	(Bahreini et al., 2005)
31	Utah Juniper Foliage and Sticks				0.9218	0.9668	(FLAME, 2007)
222	Myrcene_O3			0.9568		0.9667	(Bahreini et al., 2005)
218	a-Humulene_O3		0.9165	0.9578	0.9285	0.9651	(Bahreini et al., 2005)
26	Southern CA Chamise					0.9579	(FLAME, 2007)
203	a-humulene_O3			0.9513	0.9156	0.9538	(Bahreini et al., 2005)
206	beta-pinene_O3		0.9139	0.9538	0.9258		(Bahreini et al., 2005)

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In addition to the comparison of the combined OOA mass spectrum, we used these scaling options to check if each of the original 6 OOA-related factors had potential characteristics to be identified before they were combined. As a result of the application of a variety of paired scalings of mass range, mass exponent value, and intensity exponent value, we observed potential characteristics between factors when using the mass range is m/z 45-200 and default exponent value ($m=0, n=1$) (Table S4). In this case, factor 1 and factor 4 were highly correlated with the oxidation of m-xylene (an anthropogenic VOC common in fossil fuels) and other potential ozonolysis products, and factor 5 and factor 6 were mostly correlated with terpene ozonolysis. Factor 2 and factor 3 showed relatively lower scores but nitrogen-related MS was shown in the results table in both factors. These results suggest that we could combine factors 1 and 4, factors 2 and 3, and factors 5 and 6 as potential OOA subcategories. When we calculated cosine similarities between these pairs of factors, it showed a high correlation with the score of 0.9576, 0.9469, and 0.9838, respectively, which supports their similarities in composition. Factors 5 and 6, in particular, had characteristic fragment ion m/z 91 which can be indicative of monoterpene oxidation matching the results we obtained. Therefore, based on a new combination of factors, we may conclude that our OOA may be mainly derived from m-xylene (anthropogenic VOC) oxidation, terpene ozonolysis, and nitrogen-related reactions. For HR data comparison, unfortunately, all non-ambient samples in this match list were originally submitted only in UMR, so HR family comparison was not available in this case. Importantly, future MS submissions from the user community should include HR MS when available.

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395 **4. Discussions**

396 The existing AMS and ACSM mass spectral database in web-based form has been converted into a searchable,
397 filterable software library coupled with a comparison panel in Igor Pro, the main analysis program currently used for AMS and
398 ACSM data. The comparison panel provides the functionality to compare the mass spectrum of interest with MS in the database
399 statistically and visually by cosine similarity and several types of mass spectral plots as UMR or stacked HR ion families.
400 Furthermore, the option to exponentially reweight the mass spectrum and filter the samples depending on their measurement
401 information (e.g. lab vs field data) can help users understand and analyze their data relative to a growing list of past
402 observations. We believe this new database can be used to improve the efficiency of data interpretation and provide new insights
403 for AMS and ACSM studies. However, we highlight considerations that users should keep in mind when using this tool for
404 more accurate AMS and ACSM data interpretation. Initially, when users set a new mass range, users should take into account
405 the maximum m/z value of their target mass spectrum for comparison. As the maximum m/z values (having none-zero value)
406 of reference mass spectra in the database may vary, adjusting the mass range can impact the cosine score. In cases where there
407 are significant signals and distinctive peaks at the higher m/z range for the target spectrum, including the higher range may
408 help identify spectra in the database that may be similar if they also contain the higher m/z range. In addition, while MS are
409 one of the AMS and ACSM data to be used for data interpretation, users should continue to consider all supporting chemical
410 and meteorological measurements together with the AMS and ACSM MS in determining factor identities. For especially AMS
411 users, it's important to consider the instrumental conditions of reference mass spectra in the database, such as the instrument
412 analysis mode (e.g. W or V mode) and particle size range, as these factors can impact the mass spectrum during AMS data
413 processing. For instrument analysis mode, in this paper, we had a limited number of V-mode spectra which was the mode of
414 our target spectra, so we conducted comparisons using the entire database to demonstrate the tool's functionality. However,
415 since W-mode analysis may result in being able to more confidently fit ions due to its higher resolution than V-mode, the
416 correlation may be different when comparing to W-mode vs V-mode. To address this, our tool offers an instrument filtering
417 option, which we recommend to use for more precise AMS data interpretation. Particle size range (due to different aerodynamic
418 lens use), although not provided by this tool, can also influence the mass spectrum. To access this information, users can utilize
419 the metadata and reference paper available online via the panel. We encourage users to carefully review the reference paper for
420 particle size details and, if needed, additional information such as a fragmentation table for their data interpretation.

421 Lastly, the AMS and ACSM users' network should further populate this digital mass spectral database in order to fully
422 realize the potential strength of such a tool. Users can download the latest version of the database as a .h5 file and the procedure
423 file for this tool through the GitHub link on the existing AMS database webpage ([https://cires1.colorado.edu/jimenez-
424 group/AMSsd/](https://cires1.colorado.edu/jimenez-group/AMSsd/)). Users can confirm the version of the database and procedure file they are using on the panel and update them
425 by downloading files at the link. Users can also follow the listed procedures for submitting new MS to the database and refer
426 to the user manual (see user guide section in supplementary material) to use this tool. As a variety of databases and tools (e.g.,
427 SoFi, SPECIEUROPE, and ICARUS) have been developed to enhance data analysis efficiency in the atmospheric field
428 (Canonaco et al., 2013; Pernigotti et al., 2016; Nguyen et al., 2023), we anticipate providing a valuable database and tool for
429 users as well. Our intention is that this database continues to grow and develop with the various types of AMS and ACSM
430 systems in operation and can serve as a useful tool to help AMS users frame their observations against a wealth of previous
431 observations obtained globally.

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433 **Code availability**

434 The code of AMS mass spectral database in this study was developed in the Igor Pro environment. The codes are available at
435 https://github.com/ActlabW/AMS_MS_DB.

436

437 **Data availability**

438 AMS mass spectra data used in this study is available at <https://cires1.colorado.edu/jimenez-group/AMSsd/>.

439

440 **Author contribution**

441 SJ developed the software code and prepared the manuscript with constructive feedback from DTS and DAD. MJW
442 conceptualized the project and framed the initial code. DTS and DAD contributed to inspecting the tool and the database. DTS,
443 DAD, AVH, and JLJ supplied AMS mass spectral data. BJW supervised the project. All authors participated in reviewing and
444 editing the manuscript.

445

446 **Competing interests**

447 The contact author has declared that none of the authors has any competing interests.

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