

In-Source Decay during Matrix-Assisted Laser Desorption/Ionization Combined with the Collisional Process in an FTICR Mass Spectrometer

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SUPPORTING INFORMATION

The batch processing script for exporting peak lists is found on page 2, the source code for MatrixPeaksRemover.java (to remove matrix peaks) is on pages 3-8, and the source code for MatrixSubtractImaging.java (to plot ion images) is on pages 9-12.

The batch processing script for use with DataAnalysis software (Bruker Daltonics) is a simple four line script that results in the peak lists for all of the spectra from a FTMS imaging dataset to be exported into text files. Each of the text files is labeled with the X-Y coordinates of the spectrum location on the tissue section. The number 5 in the third line of code means that the sixth portion (determined by number of back slashes) of the complete path of a spectrum folder will be used as the file name of each exported peak list.

```
Sub Form_OnLoad
```

```
    Analysis.Spectra(1).MassListFind 100, 2600
```

```
    Analysis.Spectra(1).ExportMassList "D:\users\Tyler\" + Split(Analysis.Path, "\")(5) + ".txt", daASCII
```

```
End Sub
```

The MatrixPeaksRemover code is used to remove MALDI matrix peaks from the peak lists of an MS imaging dataset, thereby allowing enhanced spectral interpretation without the interference of matrix cluster ion peaks.

```

1  /*
2  * MatrixPeaksRemover.java
3  *
4  * Created on 22-feb.-2012, 16:49:26
5  */
6
7  /**
8  *
9  * @author Tyler A. Zimmerman, Ph. D.
10 */
11
12 import java.io.*;
13 import javax.imageio.*;
14 import java.awt.image.*;
15 import java.awt.*;
16 import java.lang.*;
17 import java.lang.Math.*;
18 import java.util.*;
19 import java.util.Arrays.*;
20 import java.util.Collections;
21 import java.io.File;
22
23 public class MatrixPeaksRemover
24 {
25     public static void main(String args[ ]) throws IOException
26     {
27
28         String[] filename = new String[3];
29         filename[0]="D:\\Tyler";           //Path of the working directory (where all the files are)
30         filename[1]="Matrix peak list for 1-5 DAN.txt"; //Text file containing the peak list of the matrix alone
31         filename[2]="Processed spectra text files"; //The name of the peak list containing directory (within the working directory)
32         ReadLines(filename);
33     }
34
35     static void ReadLines(String[] filename) throws IOException
36     {
37
38         String WorkingPath = filename[0];
39
40         if (WorkingPath.endsWith("\\") == false | WorkingPath.endsWith("/") == false)
41         {
42             WorkingPath = WorkingPath + "\\";           //Ensures a slash in the path
43         }                                               //
44                                                         //
45         String userDir = WorkingPath + filename[2];     //Creates complete path
46                                                         //to the peak list directory
47         File dir = new File(userDir);                   //
48                                                         //
49         String[] childrenTemp = dir.list();              //Gathers file names
50                                                         //of text files
51         String[] children = new String[childrenTemp.length]; //
52                                                         //
53         for (int i = 0; i <= childrenTemp.length-1; i++) //Creates complete path
54         {                                                 //to peak lists

```

```

55         children[i] = WorkingPath + filename[2] + "\\\" + childrenTemp[i];    //
56     }                                                                    //
57                                                                    //
58     String[] SplitName = new String[5];                                    //This next step splits
59                                                                    //the file names so as
60     double[][] Coord = new double[children.length][2];                  //to recover the X-Y
61                                                                    //coordinates of the
62     for (int i = 0; i <= children.length-1; i++)                          //peak lists from
63     {                                                                    //their file names
64         SplitName = children[i].split("0X");                             //
65                                                                    //The structure of this whole section of code
66         if (SplitName.length > 1)                                         //will reflect the actual file structure
67         {                                                                    //
68             Coord[i][0] = Integer.valueOf(SplitName[1].substring(0, 3)).intValue(); //The X-Y positions
69             Coord[i][1] = Integer.valueOf(SplitName[1].substring(4, 7)).intValue(); //are assigned to the
70             }                                                            //variable "Coord"
71     }                                                                    //
72
73     int Rownum = 0;
74     int a = 0;
75
76     Double MassList[][] = new Double[children.length][5000];            //The variable MassList has
77     Double Intensity[][] = new Double[children.length][5000];          //dimensions of the total
78                                                                    //number of peak lists, by
79     for (int i = 0; i <= children.length-1; i++)                          //a number large enough
80     {                                                                    //to include all the
81         Rownum = 0;                                                       //individual peaks.
82                                                                    //Same dimensions for the
83         LineNumberReader InrM = new LineNumberReader(new FileReader(children[i])); //variable Intensity.
84         InrM.setLineNumber(1);                                           //All values are read
85         StreamTokenizer stokM = new StreamTokenizer(InrM);              //from the peak lists
86         stokM.parseNumbers();                                           //conatining text files.
87         stokM.eolIsSignificant(true);                                    //
88         stokM.nextToken();
89
90         StreamTokenizer stok = new StreamTokenizer(InrM);
91
92         while (stokM.ttype != StreamTokenizer.TT_EOF)
93         {
94             while (stokM.ttype != StreamTokenizer.TT_EOF)
95             {
96                 for (int colnum=1; colnum<=4; colnum++)
97                 {
98                     if (Rownum >= 1)
99                     {
100                         if (colnum==1) {MassList[i][Rownum-1]=stokM.nval;}
101                         if (colnum==2) {a = 0;}
102                         if (colnum==3) {Intensity[i][Rownum-1]=stokM.nval;}
103                     }
104
105                     if (colnum==4) {stokM.nextToken();
106                                     Rownum++;
107                                     break;}
108
109                     stokM.nextToken();
110                 }
111                 if (stokM.ttype == StreamTokenizer.TT_EOF) {break;}
112             }
113             if (stokM.ttype == StreamTokenizer.TT_EOF) {break;}
114         }

```

```

114     }
115
116     Double MassListRevSort[][] = new Double[MassList.length][5000]; //The values are sorted in descending order
117     Double IntensityRevSort[][] = new Double[MassList.length][5000]; //to allow for more accurate ISD sequencing
118                                     //from the cleaned peak lists that will
119     int LengthCount = 0; //eventually be outputted from this code.
120                                     //See Zimmerman et al., Anal. Chem. 2011, 83, 6090.
121     for (int i = 0; i <= MassList.length-1; i++) //
122     {
123         for (int j = 0; j <= 5000-1; j++)
124         {
125             if (MassList[i][j] == null)
126             {
127                 LengthCount = j-1+1;
128                 break;
129             }
130         }
131
132         if (LengthCount > 5)
133         {
134             Double MassListTemp[] = new Double[LengthCount]; //This creates temporary MassList and Intensity
135             Double IntensityTemp[] = new Double[LengthCount]; //variables that are first sorted and then
136                                     //entered into new arrays called MassListRevSort
137             for (int j = 0; j <= MassListTemp.length-1; j++) //and IntensityRevSort.
138             { //
139                 MassListTemp[j] = MassList[i][j];
140                 IntensityTemp[j] = Intensity[i][j];
141             }
142
143             for (int lastPlace = MassListTemp.length-1; lastPlace > 0; lastPlace--)
144             {
145                 int minLoc = 0; //
146                                     //The actual sorting takes place inside this for loop.
147                 for (int k = 0; k <= lastPlace; k++) //
148                 {
149                     if (MassListTemp[k] < MassListTemp[minLoc])
150                     {
151                         minLoc = k;
152                     }
153                 }
154
155                 Double Temp = MassListTemp[minLoc];
156                 MassListTemp[minLoc] = MassListTemp[lastPlace];
157                 MassListTemp[lastPlace] = Temp;
158
159                 Double Temp1 = IntensityTemp[minLoc];
160                 IntensityTemp[minLoc] = IntensityTemp[lastPlace];
161                 IntensityTemp[lastPlace] = Temp1;
162             }
163
164             for (int j = 0; j <= MassListTemp.length-1; j++)
165             {
166                 MassListRevSort[i][j] = MassListTemp[j];
167                 IntensityRevSort[i][j] = IntensityTemp[j];
168             }
169         }
170     }
171
172     BufferedReader inM = new BufferedReader(new //
                                     //The same steps to read the MS

```

```

173 FileReader(WorkingPath + filename[1])); //imaging peak lists are applied here to
174 int MlineCount = 0; //read the single text file containing
175 //the peak list of the MALDI matrix
176 do //alone.
177 { //
178 String lineM = inM.readLine(); //
179 if (lineM == null) break; //
180 MlineCount++;
181 } while (true);
182
183 Double MatrixPeaks[] = new Double[MlineCount];
184
185 int rownum = 0;
186
187 LineNumberReader lnrM = new LineNumberReader(new FileReader(WorkingPath + filename[1]));
188 lnrM.setLineNumber(1);
189 StreamTokenizer stokM = new StreamTokenizer(lnrM);
190 stokM.parseNumbers();
191 stokM.eolIsSignificant(true);
192 stokM.nextToken();
193
194 StreamTokenizer stok = new StreamTokenizer(lnrM);
195
196 while (stokM.ttype != StreamTokenizer.TT_EOF)
197 {
198 while (stokM.ttype != StreamTokenizer.TT_EOF)
199 {
200 for (int colnum=1; colnum<=2; colnum++)
201 {
202 if (colnum==1) {MatrixPeaks[rownum]=stokM.nval;}
203
204 if (colnum==2) {stokM.nextToken();
205 rownum++;
206 break;}
207 stokM.nextToken();
208 }
209
210 if (stokM.ttype == StreamTokenizer.TT_EOF) {break;}
211 }
212
213 if (stokM.ttype == StreamTokenizer.TT_EOF) {break;}
214 }
215
216 int RemovedCount = 0; //
217 //This for loop is where the actual
218 for (int i = 0; i <= MassListRevSort.length-1; i++) //matrix peak subtraction takes place
219 { //from the values in MassListRevSort,
220 for (int j = 0; j <= 5000-1; j++) //by setting the values equal to zero
221 { //if there is a peak that corresponds to
222 for (int k = 0; k <= MatrixPeaks.length-1; k++) // a matrix peak.
223 {
224 if (MassListRevSort[i][j] != null && MassListRevSort[i][j] <= MatrixPeaks[k] + 0.001 &&
225 MassListRevSort[i][j] >= MatrixPeaks[k] - 0.001)
226 {
227 MassListRevSort[i][j] = 0.0; //
228 IntensityRevSort[i][j] = 0.0; //The values above of +/-0.001 Da
229 RemovedCount++; //define the mass window around each
230 } //MALDI matrix peak that is used to
231 } //perform subtraction on all the MS

```

```

232     }                                     //imaging peak lists. This value can
233 }                                         //be edited by the user.
234                                     //
235 Double BinsIntensity[] = new Double[40000]; //Now begins the code for creating the TIC (total ion count)
236 int BinsIntensityCount[] = new int[40000]; //spectrum that is created by summing all the MS imaging peak
237                                     //list intensities into appropriate sized mass bins. If creating a TIC using
238 for (int i = 0; i <= BinsIntensity.length-1; i++) //0.01 Da bins over a 40 Da range, the number of bins needed is 40,000.
239 {                                     //
240     BinsIntensity[i] = 0.0;           //The BinsIntensity variable is initialized with zeros in place of
241 }                                     //of null values that tend to cause errors, in this for loop.
242                                     //
243 Double MassIncrement = 600.0;         //The MassIncrement variable is designed to increase in increments
244 int MassIncrementCount = 0;           //over the mass range desired, starting with this value.
245                                     //These for loops do the actual summing of peak intensities over the entire MS
246 for (int i = 0; i <= BinsIntensity.length-1; i++) // imaging dataset based on the parameters selected
247 {                                     // based on the example case of using a 0.01 Da bin size.
248     for (int j = 0; j <= MassListRevSort.length-1; j++)
249     {
250         for (int k = 0; k <= 5000-1; k++)
251         {
252             if (MassListRevSort[j][k] != null && MassListRevSort[j][k] != 0.0 && IntensityRevSort[j][k] != null
253                 && IntensityRevSort[j][k] != 0.0 && MassListRevSort[j][k] <= MassIncrement + 0.01 &&
254                 MassListRevSort[j][k] >= MassIncrement)
255             {
256                 BinsIntensity[MassIncrementCount] += IntensityRevSort[j][k];
257                 BinsIntensityCount[MassIncrementCount]++;
258             }
259         }
260     }
261
262     MassIncrement += 0.01;             //
263     MassIncrementCount++;              //This part of the code increases the MassIncrement over the entire
264                                     // mass range of 40 Da. The MassIncrementCount increases the
265                                     // array indices over successive runs of the for loop.
266     System.out.println(MassIncrementCount); //This code creates a visual printout in the MS-DOS
267     System.out.println(MassIncrement);      //command prompt of the progress estimated.
268     System.out.println("-----");         //through the for loop, so that the computational time can be
269                                     //estimated.
270
271 FileOutputStream out1;                 //
272 PrintStream p1;                       //This code creates a new text file in the working
273 out1 = new FileOutputStream(WorkingPath + "TICMassList" + ".txt"); //directory and
274 p1 = new PrintStream(out1);            //prints the TIC spectrum to this text file called
275                                     //TICMassList.txt, the value of which can be
276 for (int i = 0; i <= BinsIntensity.length-1; i++) // plotted in M/S Excel
277 {                                     //for visualization of the TIC spectrum.
278     if (BinsIntensity[i] != null)
279     {
280         p1.println(BinsIntensity[i]);
281     }
282 }
283 p1.close();
284
285 for (int i = 0; i <= MassListRevSort.length-1; i++) //
286 {                                     //This code creates a text file in the working directory for each X-Y
287     FileOutputStream out;             // position of the tissue MS imaging dataset, and prints
288     PrintStream p;                    // the corresponding "cleaned" peak lists to each text file,
289                                     //where MALDI matrix peak have been removed. Then, the code
290                                     //ends
291     out = new FileOutputStream(WorkingPath + "X" + Integer.toString((int)Coord[i][0]) + "_Y" +
292         Integer.toString((int)Coord[i][1]) + ".txt");

```

```

291         p = new PrintStream( out );
292
293         for (int j = 0; j <= 5000-1; j++)
294         {
295             if (MassListRevSort[i][j] != null)
296             {
297                 if (MassListRevSort[i][j] != 0.0)
298                 {
299                     p.println(MassListRevSort[i][j] + "\t" + IntensityRevSort[i][j]);
300                 }
301             }
302         }
303
304         p.close();
305     }
306 }

```


The MatrixSubtractImaging software is used to plot select 2D ion images from an MS imaging dataset using the peak lists, and within a user-defined mass window. Plotting of ion images with this software can be done either before or after use of the above software to remove MALDI matrix peaks.

```

1  /*
2   * MatrixSubtractImaging.java
3   *
4   * Created on 22-feb.-2012, 11:41:14
5   */
6
7  /**
8   *
9   * @author Tyler A. Zimmerman, Ph. D.
10  */
11
12  import java.io.*;
13  import javax.imageio.*;
14  import java.awt.image.*;
15  import java.awt.*;
16  import java.lang.*;
17  import java.lang.Math.*;
18  import java.util.*;
19  import java.util.Arrays.*;
20  import java.util.Collections;
21  import java.io.File;
22
23  public class MatrixSubtractImaging
24  {
25      public static void main(String args[ ]) throws IOException
26      {
27
28          String[] filename = new String[5];
29          filename[0]="D:\\Tyler";           //Path of the working directory (where all the files are)
30          filename[1]="Example.bmp";         //The user chooses an output image name for the ion images
31          filename[2]="Text files";         //The name of the peak list containing directory (within the working directory)
32          filename[3]="630.32";             //The theoretical mass of the analyte to plot an ion image of
33          filename[4]="0.2";                //The mass tolerance window for plotting ion images
34          ReadLines(filename);
35      }
36
37  static void ReadLines(String[] filename) throws IOException
38  {
39
40      if (!(filename[1].toLowerCase().endsWith(".bmp")) && !(filename[1].toLowerCase().endsWith(".png"))) //
41          && !(filename[1].toLowerCase().endsWith(".jpg")) //Tests image format
42          {System.out.println("Error: ouput image can only end in .jpg, .png, or .bmp");} //
43
44      String WorkingPath = filename[0];
45
46      if (WorkingPath.endsWith("\\") == false | WorkingPath.endsWith("/") == false)
47      {
48          WorkingPath = WorkingPath + "\\"; // Ensures a slash in the path
49      } //
50      //
51      String userDir = WorkingPath + filename[2]; //Creates complete path
52      //to the peak list directory
53      File dir = new File(userDir); //
54      //
55      String[] childrenTemp = dir.list(); //Gathers file names
56      //of text files
57      String[] children = new String[childrenTemp.length]; //

```

```

58                                     //
59 for (int i = 0; i <= childrenTemp.length-1; i++) //Creates complete path
60 { //to peak lists
61     children[i] = WorkingPath + filename[2] + "\\\" + childrenTemp[i]; //
62 } //
63 //This next step splits
64 String[] SplitNameX = new String[2]; //the file names so as
65 String[] SplitNameX1 = new String[2]; //to recover the X-Y
66 String[] SplitNameY = new String[2]; //coordiniates of the
67 String[] SplitNameY1 = new String[2]; //peak lists from
68                                     //their file names
69 double[][] Coord = new double[children.length][2]; //
70
71 for (int i = 0; i <= children.length-1; i++)
72 {
73     SplitNameX = children[i].split("X");
74     SplitNameY = children[i].split("_Y");
75
76     System.out.println(Arrays.toString(SplitNameX));
77     System.out.println(Arrays.toString(SplitNameY));
78
79     if (SplitNameX.length > 1 && SplitNameY.length > 1)
80     {
81         if (SplitNameX[1].split("_").length > 1)
82         {
83
84             SplitNameX1 = SplitNameX[1].split("_");
85             SplitNameY1 = SplitNameY[1].split("\\.");
86
87             Coord[i][0] = Integer.valueOf(SplitNameX1[0]).intValue(); //The X-Y positions
88             Coord[i][1] = Integer.valueOf(SplitNameY1[0]).intValue(); //are assigned to the
89             } //variable "Coord"
90         } //
91     }
92
93 int Rownum = 0;
94 int a = 0;
95
96 Double MassList[][] = new Double[children.length][5000]; //The variable MassList has
97 Double Intensity[][] = new Double[children.length][5000]; //dimensions of the total
98 //number of peak lists by
99 for (int i = 0; i <= children.length-1; i++) //a number large enough
100 { //to include all the
101     Rownum = 0; //individual peaks.
102     //Same dimensions for the
103     LineNumberReader InrM = new LineNumberReader(new FileReader(children[i])); //variable Intensity.
104     InrM.setLineNumber(1); //All values are read
105     StreamTokenizer stokM = new StreamTokenizer(InrM); //from the peak lists
106     stokM.parseNumbers(); //conatining text files.
107     stokM.eolIsSignificant(true); //
108     stokM.nextToken();
109
110     StreamTokenizer stok = new StreamTokenizer(InrM);
111
112     while (stokM.ttype != StreamTokenizer.TT_EOF)
113     {
114         while (stokM.ttype != StreamTokenizer.TT_EOF)
115         {
116             for (int colnum=1; colnum<=3; colnum++)
117             {
118                 if (colnum==1) {MassList[i][Rownum]=stokM.nval;}
119             }

```

```

120                                     if (colnum==2) {Intensity[i][Rownum]=stokM.nval;}
121
122                                     if (colnum==3) {stokM.nextToken();
123                                                         Rownum++;
124                                                         break;}
125
126                                     stokM.nextToken();
127                                     }
128                                     if (stokM.ttype == StreamTokenizer.TT_EOF) {break;}
129                                     }
130                                     if (stokM.ttype == StreamTokenizer.TT_EOF) {break;}
131                                     }
132     }
133
134     Double MassCenter = Double.valueOf(filename[3]);           //
135     Double MassWindow = Double.valueOf(filename[4]);           //The appropriate mass window
136     Double MassLow = MassCenter - MassWindow;                  //for ion image plotting
137     Double MassHigh = MassCenter + MassWindow;                  //is defined with these
138                                                                //variables.
139     double MaxX = 0;                                           //
140     double MaxY = 0;
141
142     for (int i = 0; i <= Coord.length-1; i++)                  //
143     {                                                            //The maximum X and Y
144         if (Coord[i][0] > MaxX)                                  //coordinates are found
145         {                                                        //in order to output an
146             MaxX = Coord[i][0];                                  //image of appropriate size.
147         }                                                        //
148
149         if (Coord[i][1] > MaxY)
150         {
151             MaxY = Coord[i][1];
152         }
153     }
154
155     int width = (int)MaxX;
156     int height = (int)MaxY;
157
158     String format = "JPG";                                       //
159                                                                //The type of image to output
160     if (filename[1].toLowerCase().endsWith(".png"))              //is taken from the user input
161         {format = "PNG";}                                        //at the very top of this code.
162                                                                //
163     if (filename[1].toLowerCase().endsWith(".bmp"))
164         {format = "BMP";}
165
166     BufferedImage image = new BufferedImage(width + 10, height + 10, BufferedImage.TYPE_INT_RGB);
167
168     Double IntensityMap[] = new Double[Coord.length];
169
170     for (int i = 0; i <= MassList.length-1; i++)                //
171     {                                                            // This tests if the mass resides within the user-
172         for (int j = 0; j <= 5000-1; j++)                        //defined region of interest.
173         {                                                        //
174             if (MassList[i][j] != null && MassList[i][j] >= MassLow && MassList[i][j] <= MassHigh)
175             {
176                 IntensityMap[i] = Intensity[i][j];
177             }
178         }
179     }
180
181     double MaxIntensity = 0;

```

```

182 double IntensitySum = 0;
183
184 double MaxInd = 0;
185
186 for (int i = 0; i <= IntensityMap.length-1; i++)
187 {
188     if (IntensityMap[i] != null && IntensityMap[i] > MaxIntensity)
189     {
190         MaxIntensity = IntensityMap[i];           //The maximum intensity value
191         MaxInd = i;                               //throughout the dataset in
192     }                                              //the user-defined mass region
193     }                                              //is found.
194     }                                              //
195     String[] SplitTemp = filename[1].split("\\."); //Important values are added to the output image name
196
197     String OutImageName = SplitTemp[0] + "_mz" + MassCenter + "+-" + MassWindow + "_lmax" + (int)MaxIntensity + "." +
198     SplitTemp[1];
199
200     double colorValue = 0;
201
202     for (int i = 0; i <= IntensityMap.length-1; i++)
203     {
204         if (IntensityMap[i] != null)
205         {
206             colorValue = IntensityMap[i] / (MaxIntensity); //The color value is scaled to the
207             //maximum intensity value found above.
208             if (colorValue > 1) //
209             { //The color values are normalized to 1.
210                 colorValue = 1; //
211             } //
212
213             Graphics graphics = image.getGraphics();
214             Color color = new Color((int)(colorValue * 255), (int)(colorValue * 255), (int)(colorValue * 255));
215             graphics.setColor(color);
216             graphics.fillRect((int)Coord[i][0] - 1, (int)Coord[i][1] - 1, 1, 1); //
217         } //A 2D ion image
218     } //is outputted
219     //and the code
220     ImageIO.write(image, format, new File(WorkingPath + OutImageName)); //ends.
221 } //

```