# Molecular Matching with Ion Mobility Spectrometry using Python

## Introduction

The idea of this research is to analyze and identify how useful the Python programming language can be in comparing and identifying substances using Ion Mobility Spectrometry. Ion Mobility Spectrometry is an analytical research method that helps in separating and identifying ionized molecules.

Ion Mobility Spectrometry (IMS) is widely used in identification of molecules in fields like security, military, research etc. and is extensively used in detection of explosives, drugs and chemical weapons.

This research explores the idea of a Python-based workflow for molecular matching with IMS Data with the following steps

1. Data retrieval from an SQLite database:

The SQLite database should have two tables, *measurement* and *library* where the measurement table holds the IMS Data with which we will be working on identifying the relevant data that we need to compare and identify the substance.

1. Calculation of reduced ion mobility:

Reduced ion mobility is an important parameter with which each molecule can be differentiated.

1. Library matching:

Compare the calculated reduced ion mobility values against a reference database (which should be the library table from the SQLite database) and assign the most likely molecular identity.

## Background and Theoretical Framework

### 2.1 What is Ion Mobility Spectrometry

According to James N Dodds and Erin S Baker, Ion Mobility Spectrometry (IMS) is the study of how ions move in gases under the influence of an electric field. The idea is the setup consists of multiple chambers.[[1]](#footnote-1) When we consider a rudimentary setup of an IMS, the first chamber is where the sample gas enters. Then the sample gas is ionized using an external source by exciting the molecules. Then the ionized gas enters another chamber which has an electric field. Each molecule has a different *drift velocity* with which they travel this chamber from start to end. We should know the voltage of this electric field, the temperature, pressure and multiple factors that are required to calculate the reduced ion mobility ion mobility of each molecule in that sample.

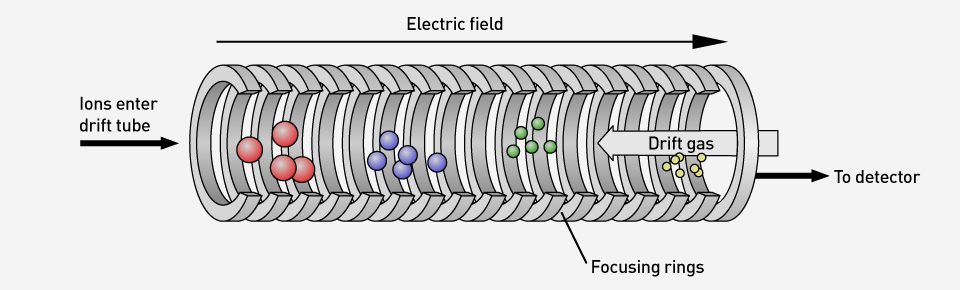


Figure 1 Ion Mobility Spectrometry cross-section [[2]](#footnote-2)

### Principles of Ion Mobility Spectrometry

In IMS, ions that are generated from a sample are introduced in the drift region. In a uniform electric field, each ion’s drift velocity is proportional to the electric field strength . is the proportionality factor between the drift velocity and the electric field strength.[[3]](#footnote-3)

The reduced ion mobility is calculated when other factors such as the temperature and pressure during drift, standard temperature *T*0 = 273 K and standard pressure *p*0 = 1013 hPa are known.

To find the value, we can use the following formula.

Where is the drift length (the length of the chamber or tube where the ionized particles move), is the drift time and is the potential difference in the chamber.

### 2.3 Molecular Matching using

Molecular matching values is straightforward. We get the value of each spectrum using the above-mentioned calculations. We match the values against a reference library. is the value calculated. For each measured value , the algorithm searches for the library entry that minimizes . Each substance in the library is represented by up to 3 positive-mode and 3 negative-mode entries, which shows slight experimental variations. A simple molecular matching absolute-deviation criterion will be used to assign the *closest* substance to each measurement.

## 3. Python for Molecular Matching

Python can be an extremely effective tool in the process of molecular matching substances in Ion Mobility Spectrometry. There are multiple reasons to use Python as the main tool for the procedure.

### 3.1 File Parsing & Data Handling

* It is possible that the values necessary for the calculation of values may not necessarily be from an SQL database. Some IMS devices have serial communication capabilities with their own APIs. Data can be stored in files which can be simple text *.txt* or *.csv* or sometimes *JSON* files. Python has a vast set of libraries for parsing different types of data and it is extremely reliable as well.
* *Pandas* *DataFrames* are very efficient in converting data into tabular form providing indexing, filtering, grouping and even being part of the I/O (CSV <-> DataFrame <-> SQL) with very few lines of code. Pandas is widely used for data handling in Python.

### 3.2 Scientific & Statistical Computation

* Mathematical calculations and operations can be done fairly easily using the Python numeric stack. Some libraries like the *math* library and *numpy* library lets us implement a lot of formulas easily and can be used to make hundreds or thousands of measurements very quickly.

### 3.3 Database Integration

* For our project, database integration helps us a lot by defining tables in the *SQLite* Database which can be easily connected to our project using very good libraries. One such library is the *SQLAlchemy* library which helps us in defining the tables that are necessary to be read and or updated in python classes.
* Portability is also a very important advantage of using Python’s database integration. Switching between SQLite to PostgreSQL or MySQL or almost any other fairly known and commonly used database frameworks can be done with minor tweaks and corrections.

### 3.4 Visualization

* Python Visualization frameworks are well-known for easy use and understanding. Plotting drift-time distributions, trends or the spectra in itself can be fairly easily done. Frameworks like *MatPlotLib, Bokeh, Seaborn* can be used to make time-series of identifications or an interactive Bokeh Plot for matching errors.

### 3.5 Reproducability & Testing

* Unit Testing is an important aspect of programming any project. *PyTest* or *unittest* frameworks are really good at writing unit tests to test the project.
  + Parsing of header sections can be tested.
  + Peak-finding logic can be tested for both the positive and the negative spectra.
  + By providing known values, accurate values can be calculated and tested.
  + Library-matching logic can be tested using edge conditions (values that are close to matching but no matches).

## 4. Computational Tools: Python Ecosystem

Since Python offers such a rich ecosystem for some instrument control and data science, we will be able to do the following methodologies in finding the values of each spectrum.

* File Parsing: Existing data if it is in *csv* format or any other format, we can parse the code using modules/libraries like *re*, *numpy* and *csv.* Retrieving data such as raw channel[[4]](#footnote-4) values, IMS parameters and arrays.
* Numerical Computation: For numerical computation, we can either write our own functions which calculate the necessary value using the formulas mentioned earlier. Or for some other operations like drift-time calculation, *numpy* is a very good tool in handling such operations. *Pandas*  can be used to provide us the tabular data management.
* Databases: *SQLAlchemy* is used along with *SQLite* which enable structured data storage of raw measurements and the reference libraries.
* Visualization: *Matplotlib* helps in visualising the spectrum, maybe after Savitzky–Golay[[5]](#footnote-5) filtration and after finding the necessary peaks for which the values are to be calculated.

## 5. Programming

Molecular matching using values is done in the following steps.

1. Raw spectrum data that is received from the sensor, meta data such as temperature, pressure, drift tube length etc. are necessary to calculate values. These values are usually sent by the IMS device used. For example, [AIRSENSE Analytics GmbH](https://airsense.com/en) from Schwerin Germany, work extensively with IMS devices and they send the data using serial communication over RS-232 connection. If the necessary API is available, the necessary data can be parsed.
2. The Raw spectrum is then parsed and saved in an SQLite database. The database has two tables, *measurements* and *library.* The measurements table holds the necessary data that is required to calculate the values and library table holds existing substances with known values for reference.
3. A module is created that will handle all SQL related functions that can be called to get the relevant data for calculation.
4. Another module called *ims.py* is created to handle all IMS calculations and algorithms.
5. *Scipy* module is used to filter noises from the raw spectrum and can be used to find peaks from the spectrum. It is not necessary to calculate value of every single point on the spectrum.

### 5.1 Raw Data Handling

Firstly the *sqlite\_helper.py* module is created which will be handling any SQLite database related functionalities. The measurements table is created using the following SQL Query.

1. CREATE TABLE measurements (

2. id INTEGER PRIMARY KEY AUTOINCREMENT,

3. measurement\_time TEXT,

4. channel\_1 REAL,

5. channel\_2 REAL,

6. channel\_3 REAL,

7. channel\_4 REAL,

8. channel\_5 REAL,

9. channel\_6 REAL,

10. channel\_7 REAL,

11. channel\_8 REAL,

12. dilution REAL,

13. temperature\_drift\_tube REAL,

14. pressure REAL,

15. pos\_voltage REAL,

16. neg\_voltage REAL,

17. tube\_length REAL,

18. pressure\_offset REAL,

19. pressure\_gradient REAL,

20. pos\_spectrum BLOB,

21. neg\_spectrum BLOB

22. );

23.

This query creates the measurement table with the important parameters like measurement time, temperature of the drift tube during measurement, pressure during measurement, potential difference during measurement (voltage), tube length and the positive and negative spectra.

Similarly, the library table is created with the following query.

CREATE TABLE library (

    id INTEGER PRIMARY KEY AUTOINCREMENT,

    substance\_name TEXT,

    k0\_pos\_1 REAL,

    k0\_pos\_2 REAL,

    k0\_pos\_3 REAL,

    k0\_neg\_1 REAL,

    k0\_neg\_2 REAL,

    k0\_neg\_3 REAL

);

A class is created in python to handle the measurement table since this table contains a bit more data compared to the library table. The class *Measurement* in the *sqlite\_helper.py* module helps us in having an idea to understand how the measurement table is structured.

### 5.2 Substance Identification

The module *substance\_identifier.py* has the methods *identify\_substances* which helps us in the comparison of the values calculated from the spectrum to the values from the library table.

The identification process is as follows:

1. Library retrieval:
   1. The function retrieves the substance library from the database using the *sqlite\_helper.get\_substance\_library()* function.
   2. The library contains the substance names and their reference values (3 positive and 3 negative).
2. Matching Algorithm:
   1. For each substance in the library the function checks if the measured positive values match the reference values within a tolerance of 0.2 (usually the tolerance is around 0.02, but for the precision, there are more compensations that must be done like temperature compensation, pressure, humidity etc. For the sake of simplicity, 0.2 as tolerance has been selected)
   2. Similarly, the negative values are matched and only non-zero reference are considered for matching.
3. Match criteria:
   1. All required positive values should match (if any specified in the library), OR
   2. All required negative values match (if any specified in the library)
4. Results collection:
   1. For each identified substance, the function collects the substance name, the positive spectrum matches, and negative spectrum matches.

### 5.3 Visualization

The *visualization.py* module helps in displaying IMS spectrum data with some interactive features.

There are two key functions in this module.

1. create\_spectrum\_plot:

Creates a static plot showing the positive and negative spectra with the peaks being annotated. The function returns a matplotlib figure object.

1. Show\_scrollable\_plots:

Creates an interactive visualization with a slider to navigate through multiple measurements.

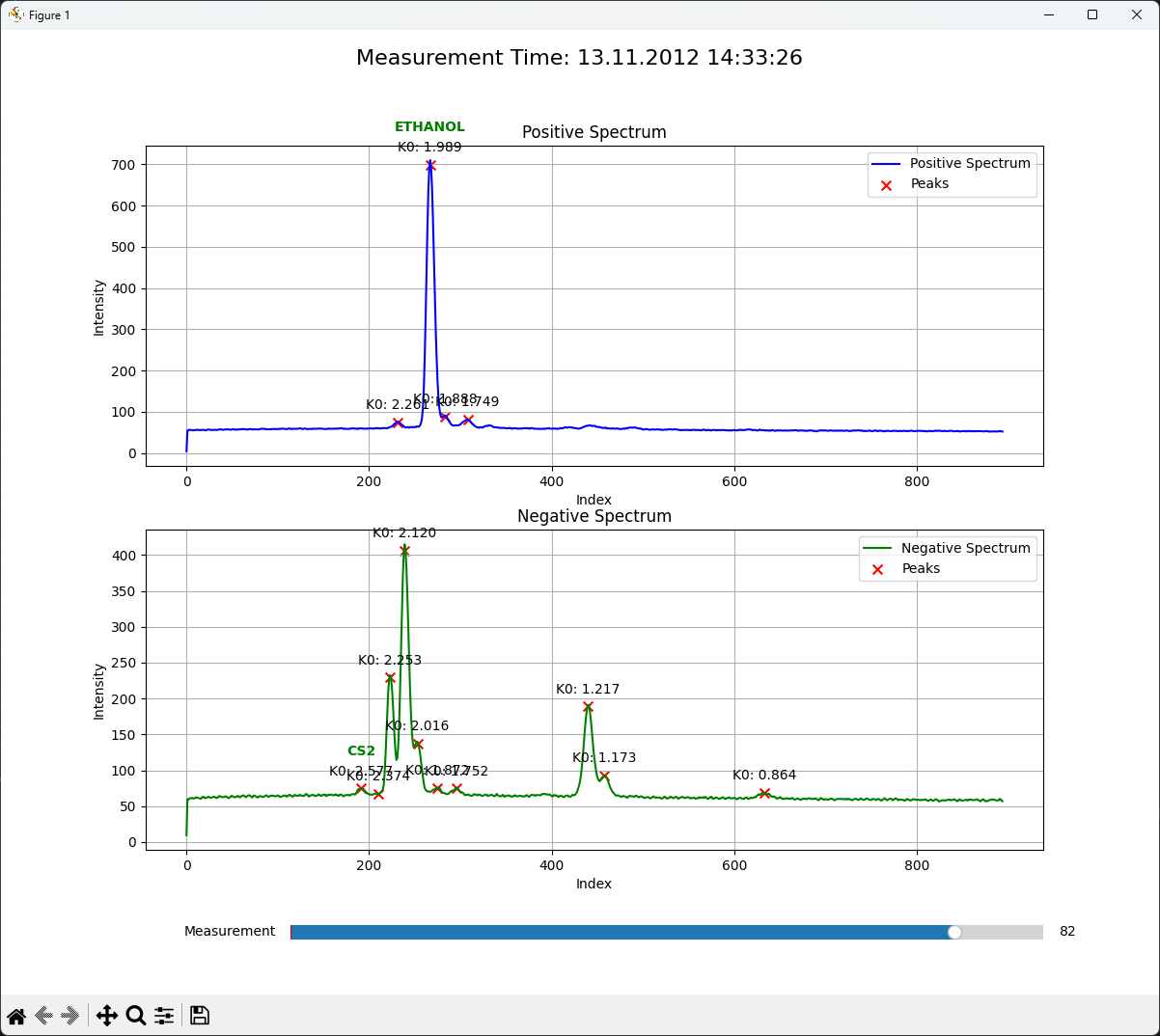


Figure 2 Visualization of the IMS spectra with Ethanol and CS2 substance matching

## 6. Conclusion

In summary, Python proved not only to fulfill all the requirements but also enable rapid, reliable development of a complete IMS data-analysis procedure with a very simple boilerplate. Libraries like *NumPy* and *Pandas* handle large spectral and channel datasets with very good efficiency. *SQLAlchemy* provides a clean, simple and maintainable SQLite interface.  
*MatPlotLib* generate high quality plots with few lines of code.   
Python’s extensive ecosystem facilitates future upgrades and maintainability of the project. Together, these strengths make Python the ideal platform for an end-to-end molecular matching procedure in IMS.

## 7. Code

The code repository for the project can be found on GitHub under this repository URL [https://github.com/kob824/IMSPeakDetector](https://github.com/kob824/IMSPeakDetector%20) for reference.

### 7.1 ims.py

1. import numpy as np

2. from scipy.signal import savgol\_filter, find\_peaks

3. import matplotlib.pyplot as plt

4.

5. def process\_spectrum(spectrum):

6.     spectrum = np.fromstring(spectrum[2:-1], sep=', ')

7.

8.     smoothed\_spectrum = savgol\_filter(spectrum, window\_length=11, polyorder=3)

9.

10.     peaks, properties = find\_peaks(smoothed\_spectrum, height=np.max(smoothed\_spectrum) \* 0.1, distance=5)

11.

12.     top\_peaks = sorted(zip(peaks, properties['peak\_heights']), key=lambda x: x[1], reverse=True)[:10]

13.

14.     return [(int(idx), float(height)) for idx, height in top\_peaks]

15.

16. def calculate\_k0\_value(peaks, temperature, pressure, voltage, drift\_tube\_length, resolution):

17.     """

18.     Calculate the k0 value based on the peaks, temperature, pressure, drift tube length, and resolution.

19.     Returns a list of K0 values for each peak.

20.

21.     The formulas needed are as follows:

22.     drift\_time = (peak\_position + position\_offset) \* (resolution / 1000000)

23.     k = length\_squared / (drift\_time \* voltage)

24.     k0 = k \* (nominal\_temperature / temperature) \* (pressure / nominal\_pressure)

25.     """

26.     nominal\_temperature = 273.15  # Kelvin

27.     nominal\_pressure = 1013.25  # kPa

28.     position\_offset = 31 + 1

29.     length\_squared = drift\_tube\_length \*\* 2

30.     temperature = temperature + 273.15  # Convert to Kelvin

31.

32.     k0\_values = []

33.     for peak in peaks:

34.         peak\_position = peak[0]  # Peak index

35.         drift\_time = (peak\_position + position\_offset) \* (resolution / 1000000)  # Drift time in seconds

36.         k = length\_squared / (drift\_time \* voltage)

37.         k0 = k \* (nominal\_temperature / temperature) \* (pressure / nominal\_pressure)

38.         k0\_values.append(k0)

39.

40.     return k0\_values

41.

### 7.2 substance\_identifier.py

1. import numpy as np

2. from modules import sqlite\_helper

3.

4. # Default tolerance for K0 value matching

5. DEFAULT\_K0\_TOLERANCE = 0.02

6.

7. def identify\_substances(pos\_k0\_values, neg\_k0\_values, tolerance=DEFAULT\_K0\_TOLERANCE):

8.     """

9.     Identify substances by comparing K0 values with the library.

10.     Returns a list of identified substances.

11.     """

12.     library = sqlite\_helper.get\_substance\_library()

13.     identified\_substances = []

14.

15.     for \_, substance in library.iterrows():

16.         substance\_name = substance['substance\_name']

17.

18.         # Check positive spectrum K0 values

19.         pos\_matches = []

20.         for i in range(1, 4):  # Check k0\_pos\_1, k0\_pos\_2, k0\_pos\_3

21.             k0\_col = f'k0\_pos\_{i}'

22.             if substance[k0\_col] > 0:  # Only check non-zero values

23.                 # Check if this K0 value matches any in our detected peaks

24.                 for k0 in pos\_k0\_values:

25.                     if abs(k0 - substance[k0\_col]) <= tolerance:

26.                         pos\_matches.append((k0\_col, k0, substance[k0\_col]))

27.                         break

28.

29.         # Check negative spectrum K0 values

30.         neg\_matches = []

31.         for i in range(1, 4):  # Check k0\_neg\_1, k0\_neg\_2, k0\_neg\_3

32.             k0\_col = f'k0\_neg\_{i}'

33.             if substance[k0\_col] > 0:  # Only check non-zero values

34.                 # Check if this K0 value matches any in our detected peaks

35.                 for k0 in neg\_k0\_values:

36.                     if abs(k0 - substance[k0\_col]) <= tolerance:

37.                         neg\_matches.append((k0\_col, k0, substance[k0\_col]))

38.                         break

39.

40.         # Count required matches (non-zero K0 values in library)

41.         required\_pos\_matches = sum(1 for i in range(1, 4) if substance[f'k0\_pos\_{i}'] > 0)

42.         required\_neg\_matches = sum(1 for i in range(1, 4) if substance[f'k0\_neg\_{i}'] > 0)

43.

44.         # Substance is identified if all required K0 values match

45.         if (len(pos\_matches) == required\_pos\_matches and required\_pos\_matches > 0) or \

46.            (len(neg\_matches) == required\_neg\_matches and required\_neg\_matches > 0):

47.             identified\_substances.append({

48.                 'name': substance\_name,

49.                 'pos\_matches': pos\_matches,

50.                 'neg\_matches': neg\_matches

51.             })

52.

53.     return identified\_substances

54.

### 7.3 sqlite\_helper.py

1. import pandas as pd

2. from sqlalchemy import create\_engine, Column, Integer, String, Float, BLOB, Table, MetaData

3. from sqlalchemy.ext.declarative import declarative\_base

4. from sqlalchemy.orm import sessionmaker

5. import os

6.

7. DB\_FILE = './db/ims.db'

8. engine = create\_engine(f'sqlite:///{DB\_FILE}')

9. Base = declarative\_base()

10.

11. class Measurement(Base):

12.     \_\_tablename\_\_ = 'measurements'

13.

14.     id = Column(Integer, primary\_key=True, autoincrement=True)

15.     measurement\_time = Column(String)

16.     channel\_1 = Column(Float)

17.     channel\_2 = Column(Float)

18.     channel\_3 = Column(Float)

19.     channel\_4 = Column(Float)

20.     channel\_5 = Column(Float)

21.     channel\_6 = Column(Float)

22.     channel\_7 = Column(Float)

23.     channel\_8 = Column(Float)

24.     dilution = Column(Float)

25.     temperature\_drift\_tube = Column(Float)

26.     pressure = Column(Float)

27.     pos\_voltage = Column(Float)

28.     neg\_voltage = Column(Float)

29.     tube\_length = Column(Float)

30.     pressure\_offset = Column(Float)

31.     pressure\_gradient = Column(Float)

32.     pos\_spectrum = Column(BLOB)

33.     neg\_spectrum = Column(BLOB)

34.

35. Base.metadata.create\_all(engine)

36.

37. Session = sessionmaker(bind=engine)

38. session = Session()

39.

40. def select\_columns\_from\_db(columns, table='measurements'):

41.     """

42.     Select columns from the specified table.

43.

44.     Parameters:

45.     - columns: List of column names

46.     - table: Table name (default: 'measurements')

47.

48.     Returns:

49.     - DataFrame with selected data

50.     """

51.     if table == 'measurements':

52.         query = session.query(\*[getattr(Measurement, col) for col in columns])

53.         results = query.all()

54.         df = pd.DataFrame(results, columns=columns)

55.     else:

56.         # For other tables, use raw SQL

57.         columns\_str = ', '.join(columns)

58.         query = f"SELECT {columns\_str} FROM {table}"

59.         df = pd.read\_sql\_query(query, engine)

60.

61.     return df

62.

63. def load\_csv\_and\_insert(csv\_file):

64.     df = pd.read\_csv(csv\_file, header=0)

65.     print("DataFrame head:")

66.     print(df.head())

67.

68.     for index, row in df.iterrows():

69.         try:

70.             measurement = Measurement(

71.                 measurement\_time = row["measurement\_time"],

72.                 channel\_1 = float(row["channel\_1"]),

73.                 channel\_2 = float(row["channel\_2"]),

74.                 channel\_3 = float(row["channel\_3"]),

75.                 channel\_4 = float(row["channel\_4"]),

76.                 channel\_5 = float(row["channel\_5"]),

77.                 channel\_6 = float(row["channel\_6"]),

78.                 channel\_7 = float(row["channel\_7"]),

79.                 channel\_8 = float(row["channel\_8"]),

80.                 dilution = float(row["dilution"]),

81.                 temperature\_drift\_tube = float(row["temperature\_drift\_tube"]),

82.                 pressure = float(row["pressure"]),

83.                 pos\_voltage = float(row["pos\_voltage"]),

84.                 neg\_voltage = float(row["neg\_voltage"]),

85.                 tube\_length = float(row["tube\_length"]),

86.                 pressure\_offset = float(row["press\_offset"]),

87.                 pressure\_gradient = float(row["press\_gradient"]),

88.                 pos\_spectrum = row["pos\_spectrum"].encode('utf-8'),

89.                 neg\_spectrum = row["neg\_spectrum"].encode('utf-8')

90.             )

91.             session.add(measurement)

92.         except ValueError as ve:

93.             print(f"Error converting row {index}: {ve}")

94.

95.     session.commit()

96.     print(f"Inserted {len(df)} records into the database.")

97.

98. def get\_substance\_library():

99.     """

100.     Retrieve the substance library with K0 values from the database.

101.     """

102.     columns = ["id", "substance\_name",

103.                "k0\_pos\_1", "k0\_pos\_2", "k0\_pos\_3",

104.                "k0\_neg\_1", "k0\_neg\_2", "k0\_neg\_3"]

105.

106.     return select\_columns\_from\_db(columns, table='library')

107.

### 7.4 visualization.py

1. import matplotlib.pyplot as plt

2. import numpy as np

3. from matplotlib.widgets import Slider

4.

5. # Constants for annotation and visualization

6. K0\_ANNOTATION\_OFFSET = (0, 10)

7. SUBSTANCE\_ANNOTATION\_OFFSET = (0, 25)

8. K0\_MATCH\_TOLERANCE = 0.02

9. PEAK\_MARKER\_SIZE = 50

10.

11. def create\_spectrum\_plot(spectrums, peaks\_data, identified\_substances=None):

12.     """

13.     Create a plot showing spectra with peaks and identified substances.

14.

15.     Parameters:

16.     - spectrums: dictionary with 'pos' and 'neg' arrays

17.     - peaks\_data: dictionary with 'pos' and 'neg' peak information (index, height)

18.     - identified\_substances: list of identified substances with their K0 matches

19.     """

20.     fig, (ax1, ax2) = plt.subplots(2, 1, figsize=(12, 10))

21.

22.     # Plot positive spectrum

23.     if 'pos' in spectrums and spectrums['pos'] is not None and len(spectrums['pos']) > 0:

24.         ax1.plot(spectrums['pos'], color='blue', label='Positive Spectrum')

25.

26.         if 'pos' in peaks\_data and peaks\_data['pos']:

27.             peak\_indices = [p[0] for p in peaks\_data['pos']]

28.             peak\_heights = [p[1] for p in peaks\_data['pos']]

29.             ax1.scatter(peak\_indices, peak\_heights, color='red', s=PEAK\_MARKER\_SIZE, marker='x', label='Peaks')

30.

31.             # Annotate peaks with K0 values

32.             for i, (idx, height) in enumerate(zip(peak\_indices, peak\_heights)):

33.                 ax1.annotate(f"K0: {peaks\_data['pos\_k0s'][i]:.3f}",

34.                             (idx, height),

35.                             textcoords="offset points",

36.                             xytext=K0\_ANNOTATION\_OFFSET,

37.                             ha='center')

38.

39.                 # Mark identified substances

40.                 if identified\_substances:

41.                     for substance in identified\_substances:

42.                         for match in substance['pos\_matches']:

43.                             if abs(peaks\_data['pos\_k0s'][i] - match[2]) <= K0\_MATCH\_TOLERANCE:

44.                                 ax1.annotate(f"{substance['name']}",

45.                                            (idx, height),

46.                                            textcoords="offset points",

47.                                            xytext=SUBSTANCE\_ANNOTATION\_OFFSET,

48.                                            ha='center',

49.                                            color='green',

50.                                            weight='bold')

51.

52.     # Plot negative spectrum

53.     if 'neg' in spectrums and spectrums['neg'] is not None and len(spectrums['neg']) > 0:

54.         ax2.plot(spectrums['neg'], color='green', label='Negative Spectrum')

55.

56.         if 'neg' in peaks\_data and peaks\_data['neg']:

57.             peak\_indices = [p[0] for p in peaks\_data['neg']]

58.             peak\_heights = [p[1] for p in peaks\_data['neg']]

59.             ax2.scatter(peak\_indices, peak\_heights, color='red', s=PEAK\_MARKER\_SIZE, marker='x', label='Peaks')

60.

61.             # Annotate peaks with K0 values

62.             for i, (idx, height) in enumerate(zip(peak\_indices, peak\_heights)):

63.                 ax2.annotate(f"K0: {peaks\_data['neg\_k0s'][i]:.3f}",

64.                             (idx, height),

65.                             textcoords="offset points",

66.                             xytext=K0\_ANNOTATION\_OFFSET,

67.                             ha='center')

68.

69.                 # Mark identified substances

70.                 if identified\_substances:

71.                     for substance in identified\_substances:

72.                         for match in substance['neg\_matches']:

73.                             if abs(peaks\_data['neg\_k0s'][i] - match[2]) <= K0\_MATCH\_TOLERANCE:

74.                                 ax2.annotate(f"{substance['name']}",

75.                                            (idx, height),

76.                                            textcoords="offset points",

77.                                            xytext=SUBSTANCE\_ANNOTATION\_OFFSET,

78.                                            ha='center',

79.                                            color='green',

80.                                            weight='bold')

81.

82.     ax1.set\_title('Positive Spectrum')

83.     ax1.set\_xlabel('Index')

84.     ax1.set\_ylabel('Intensity')

85.     ax1.legend()

86.     ax1.grid(True)

87.

88.     ax2.set\_title('Negative Spectrum')

89.     ax2.set\_xlabel('Index')

90.     ax2.set\_ylabel('Intensity')

91.     ax2.legend()

92.     ax2.grid(True)

93.

94.     plt.tight\_layout()

95.     return fig

96.

97. def show\_scrollable\_plots(data\_list):

98.     """

99.     Create a scrollable interface to navigate through multiple spectrum plots.

100.

101.     Parameters:

102.     - data\_list: List of dictionaries containing spectrum data for each measurement

103.     """

104.     if not data\_list:

105.         print("No data to display")

106.         return

107.

108.     # Create a figure that will persist

109.     fig, (ax1, ax2) = plt.subplots(2, 1, figsize=(12, 10))

110.     # Slider position adjustment

111.     SLIDER\_BOTTOM\_MARGIN = 0.15

112.     plt.subplots\_adjust(bottom=SLIDER\_BOTTOM\_MARGIN)

113.

114.     # Function to update the plot

115.     def update\_plot(idx):

116.         ax1.clear()

117.         ax2.clear()

118.

119.         current\_data = data\_list[idx]

120.

121.         # Plot positive spectrum

122.         if current\_data['spectrums']['pos'] is not None:

123.             pos\_spectrum = current\_data['spectrums']['pos']

124.             ax1.plot(pos\_spectrum, color='blue', label='Positive Spectrum')

125.

126.             if current\_data['peaks\_data']['pos']:

127.                 peak\_indices = [p[0] for p in current\_data['peaks\_data']['pos']]

128.                 peak\_heights = [p[1] for p in current\_data['peaks\_data']['pos']]

129.                 ax1.scatter(peak\_indices, peak\_heights, color='red', s=PEAK\_MARKER\_SIZE, marker='x', label='Peaks')

130.

131.                 # Annotate peaks with K0 values

132.                 for i, (idx, height) in enumerate(zip(peak\_indices, peak\_heights)):

133.                     ax1.annotate(f"K0: {current\_data['peaks\_data']['pos\_k0s'][i]:.3f}",

134.                                 (idx, height),

135.                                 textcoords="offset points",

136.                                 xytext=K0\_ANNOTATION\_OFFSET,

137.                                 ha='center')

138.

139.                     # Mark identified substances

140.                     if current\_data['identified\_substances']:

141.                         for substance in current\_data['identified\_substances']:

142.                             for match in substance['pos\_matches']:

143.                                 if abs(current\_data['peaks\_data']['pos\_k0s'][i] - match[2]) <= K0\_MATCH\_TOLERANCE:

144.                                     ax1.annotate(f"{substance['name']}",

145.                                                (idx, height),

146.                                                textcoords="offset points",

147.                                                xytext=SUBSTANCE\_ANNOTATION\_OFFSET,

148.                                                ha='center',

149.                                                color='green',

150.                                                weight='bold')

151.

152.         # Plot negative spectrum

153.         if current\_data['spectrums']['neg'] is not None:

154.             neg\_spectrum = current\_data['spectrums']['neg']

155.             ax2.plot(neg\_spectrum, color='green', label='Negative Spectrum')

156.

157.             if current\_data['peaks\_data']['neg']:

158.                 peak\_indices = [p[0] for p in current\_data['peaks\_data']['neg']]

159.                 peak\_heights = [p[1] for p in current\_data['peaks\_data']['neg']]

160.                 ax2.scatter(peak\_indices, peak\_heights, color='red', s=PEAK\_MARKER\_SIZE, marker='x', label='Peaks')

161.

162.                 # Annotate peaks with K0 values

163.                 for i, (idx, height) in enumerate(zip(peak\_indices, peak\_heights)):

164.                     ax2.annotate(f"K0: {current\_data['peaks\_data']['neg\_k0s'][i]:.3f}",

165.                                 (idx, height),

166.                                 textcoords="offset points",

167.                                 xytext=K0\_ANNOTATION\_OFFSET,

168.                                 ha='center')

169.

170.                     # Mark identified substances

171.                     if current\_data['identified\_substances']:

172.                         for substance in current\_data['identified\_substances']:

173.                             for match in substance['neg\_matches']:

174.                                 if abs(current\_data['peaks\_data']['neg\_k0s'][i] - match[2]) <= K0\_MATCH\_TOLERANCE:

175.                                     ax2.annotate(f"{substance['name']}",

176.                                                (idx, height),

177.                                                textcoords="offset points",

178.                                                xytext=SUBSTANCE\_ANNOTATION\_OFFSET,

179.                                                ha='center',

180.                                                color='green',

181.                                                weight='bold')

182.

183.         ax1.set\_title('Positive Spectrum')

184.         ax1.set\_xlabel('Index')

185.         ax1.set\_ylabel('Intensity')

186.         ax1.legend()

187.         ax1.grid(True)

188.

189.         ax2.set\_title('Negative Spectrum')

190.         ax2.set\_xlabel('Index')

191.         ax2.set\_ylabel('Intensity')

192.         ax2.legend()

193.         ax2.grid(True)

194.

195.         fig.suptitle(f"Measurement Time: {current\_data['measurement\_time']}", fontsize=16)

196.         fig.canvas.draw\_idle()

197.

198.     # Initial plot

199.     update\_plot(0)

200.

201.     # Add slider

202.     SLIDER\_X\_POSITION = 0.25

203.     SLIDER\_Y\_POSITION = 0.05

204.     SLIDER\_WIDTH = 0.65

205.     SLIDER\_HEIGHT = 0.03

206.     ax\_slider = plt.axes([SLIDER\_X\_POSITION, SLIDER\_Y\_POSITION, SLIDER\_WIDTH, SLIDER\_HEIGHT])

207.     slider = Slider(

208.         ax=ax\_slider,

209.         label='Measurement',

210.         valmin=0,

211.         valmax=len(data\_list) - 1,

212.         valinit=0,

213.         valstep=1

214.     )

215.

216.     # Connect the slider to the update function

217.     def update(val):

218.         update\_plot(int(slider.val))

219.

220.     slider.on\_changed(update)

221.     plt.show()

222.

223.

### 7.5 main.py

1. from modules import sqlite\_helper

2. from modules.ims import process\_spectrum, calculate\_k0\_value

3. from modules.substance\_identifier import identify\_substances, DEFAULT\_K0\_TOLERANCE

4. from modules.visualization import show\_scrollable\_plots

5. import numpy as np

6. import pandas as pd

7.

8. # Constants

9. K0\_TOLERANCE = 0.2  # The tolerance used specifically in this script

10.

11. def main():

12.     # csv\_file = r"./data/HCl 10ppm.csv"

13.     # sqlite\_helper.load\_csv\_and\_insert(csv\_file)

14.

15.     df = sqlite\_helper.select\_columns\_from\_db(["measurement\_time", "pos\_spectrum", "neg\_spectrum",

16.                                               "temperature\_drift\_tube", "pressure", "pos\_voltage",

17.                                               "neg\_voltage", "tube\_length"])

18.

19.     # Most of the rows in the database have either positive or negative spectrum data, not both

20.     # We need to merge them based on the presence of data in either spectrum

21.     # Process and merge the data to combine appropriate positive and negative spectra

22.     merged\_data = []

23.     i = 0

24.     while i < len(df):

25.         current\_row = df.iloc[i].copy()

26.         pos\_spectrum = current\_row["pos\_spectrum"]

27.         neg\_spectrum = current\_row["neg\_spectrum"]

28.

29.         pos\_spectrum\_array = np.fromstring(pos\_spectrum[2:-1], sep=', ')

30.         neg\_spectrum\_array = np.fromstring(neg\_spectrum[2:-1], sep=', ')

31.

32.         # Case 1: Both spectra have data - no need to merge

33.         if not np.all(pos\_spectrum\_array == 0) and not np.all(neg\_spectrum\_array == 0):

34.             merged\_data.append(current\_row)

35.             i += 1

36.             continue

37.

38.         # Case 2: Current row has positive spectrum but no negative spectrum

39.         if not np.all(pos\_spectrum\_array == 0) and np.all(neg\_spectrum\_array == 0):

40.             # Look ahead for a row with negative spectrum data

41.             next\_neg\_idx = -1

42.             for j in range(i+1, len(df)):

43.                 next\_neg\_array = np.fromstring(df.iloc[j]["neg\_spectrum"][2:-1], sep=', ')

44.                 next\_pos\_array = np.fromstring(df.iloc[j]["pos\_spectrum"][2:-1], sep=', ')

45.

46.                 # If we find a row with negative data and no positive data

47.                 if not np.all(next\_neg\_array == 0) and np.all(next\_pos\_array == 0):

48.                     next\_neg\_idx = j

49.                     break

50.

51.             if next\_neg\_idx != -1:

52.                 # Merge the data - keep metadata from current row with positive spectrum

53.                 merged\_row = current\_row.copy()

54.                 merged\_row["neg\_spectrum"] = df.iloc[next\_neg\_idx]["neg\_spectrum"]

55.                 merged\_data.append(merged\_row)

56.                 i = next\_neg\_idx + 1  # Skip to after the last used row

57.             else:

58.                 # No matching negative spectrum found

59.                 i += 1

60.             continue

61.

62.         # Case 3: Current row has negative spectrum but no positive spectrum

63.         if np.all(pos\_spectrum\_array == 0) and not np.all(neg\_spectrum\_array == 0):

64.             # Look behind for the most recent row with positive spectrum data

65.             prev\_pos\_idx = -1

66.             for j in range(i-1, -1, -1):

67.                 prev\_pos\_array = np.fromstring(df.iloc[j]["pos\_spectrum"][2:-1], sep=', ')

68.

69.                 # If we find a row with positive data

70.                 if not np.all(prev\_pos\_array == 0):

71.                     prev\_pos\_idx = j

72.                     break

73.

74.             if prev\_pos\_idx != -1:

75.                 # We've already processed this by looking ahead from the positive spectrum row

76.                 i += 1

77.             else:

78.                 # No matching positive spectrum found before this

79.                 i += 1

80.             continue

81.

82.         # Case 4: Both spectra are empty

83.         i += 1

84.

85.     visualization\_data = []

86.

87.     for i, row in enumerate(merged\_data):

88.         measurement\_time = row["measurement\_time"]

89.         pos\_spectrum = row["pos\_spectrum"]

90.         neg\_spectrum = row["neg\_spectrum"]

91.         temperature = row["temperature\_drift\_tube"]

92.         pressure = row["pressure"]

93.         pos\_voltage = row["pos\_voltage"]

94.         neg\_voltage = row["neg\_voltage"]

95.         drift\_tube\_length = row["tube\_length"]

96.         resolution = 32.392

97.

98.         pos\_spectrum\_array = np.fromstring(pos\_spectrum[2:-1], sep=', ')

99.         neg\_spectrum\_array = np.fromstring(neg\_spectrum[2:-1], sep=', ')

100.

101.         # Skip if either spectrum is empty

102.         if np.all(pos\_spectrum\_array == 0) or np.all(neg\_spectrum\_array == 0):

103.             print(f"Skipping spectrum at Measurement Time: {measurement\_time} (contains zeros in one spectrum)")

104.             continue

105.

106.         print(f"\nProcessing Measurement Time: {measurement\_time} (Entry {i+1}/{len(merged\_data)})")

107.

108.         pos\_top\_peaks = []

109.         pos\_k0\_values = []

110.         if not np.all(pos\_spectrum\_array == 0):

111.             pos\_top\_peaks = process\_spectrum(pos\_spectrum)

112.             pos\_k0\_values = calculate\_k0\_value(pos\_top\_peaks, temperature, pressure, pos\_voltage, drift\_tube\_length, resolution)

113.             print(f"Positive Spectrum:")

114.             print(f"Top 10 Peaks: {pos\_top\_peaks}")

115.             print(f"K0 Values: {pos\_k0\_values}")

116.

117.         neg\_top\_peaks = []

118.         neg\_k0\_values = []

119.         if not np.all(neg\_spectrum\_array == 0):

120.             neg\_top\_peaks = process\_spectrum(neg\_spectrum)

121.             neg\_k0\_values = calculate\_k0\_value(neg\_top\_peaks, temperature, pressure, neg\_voltage, drift\_tube\_length, resolution)

122.             print(f"Negative Spectrum:")

123.             print(f"Top 10 Peaks: {neg\_top\_peaks}")

124.             print(f"K0 Values: {neg\_k0\_values}")

125.

126.         # Identify substances based on K0 values

127.         # identified\_substances = identify\_substances(pos\_k0\_values, neg\_k0\_values, tolerance=0.02)

128.         identified\_substances = identify\_substances(pos\_k0\_values, neg\_k0\_values, tolerance=K0\_TOLERANCE)

129.

130.         if identified\_substances:

131.             print(f"\nIdentified Substances:")

132.             for substance in identified\_substances:

133.                 print(f"- {substance['name']}")

134.                 if substance['pos\_matches']:

135.                     print(f"  Positive spectrum matches:")

136.                     for match in substance['pos\_matches']:

137.                         print(f"    {match[0]} library value: {match[2]:.3f}, measured: {match[1]:.3f}")

138.                 if substance['neg\_matches']:

139.                     print(f"  Negative spectrum matches:")

140.                     for match in substance['neg\_matches']:

141.                         print(f"    {match[0]} library value: {match[2]:.3f}, measured: {match[1]:.3f}")

142.         else:

143.             print("\nNo substances identified in this spectrum.")

144.

145.         print("="\*50)

146.

147.         # data for visualization

148.         visualization\_data.append({

149.             'measurement\_time': measurement\_time,

150.             'spectrums': {

151.                 'pos': pos\_spectrum\_array,

152.                 'neg': neg\_spectrum\_array

153.             },

154.             'peaks\_data': {

155.                 'pos': pos\_top\_peaks,

156.                 'neg': neg\_top\_peaks,

157.                 'pos\_k0s': pos\_k0\_values,

158.                 'neg\_k0s': neg\_k0\_values

159.             },

160.             'identified\_substances': identified\_substances

161.         })

162.

163.     print(f"\nFound {len(visualization\_data)} complete spectra (with both positive and negative data)")

164.     print (f"\nTotal matches found: {sum(len(data['identified\_substances']) for data in visualization\_data)}")

165.

166.     show\_scrollable\_plots(visualization\_data)

167.

168. if \_\_name\_\_ == "\_\_main\_\_":

169.     main()

170.

1. Ion Mobility Spectrometry: Fundamental Concepts, Instrumentation, Applications, and the Road Ahead (<https://pmc.ncbi.nlm.nih.gov/articles/PMC6832852/>) [↑](#footnote-ref-1)
2. https://www.analyticon.eu/en/ion-mobility-spectrometry.html [↑](#footnote-ref-2)
3. https://en.wikipedia.org/wiki/Ion\_mobility\_spectrometry#Ion\_mobility [↑](#footnote-ref-3)
4. Channels are the sensor values that are measured by the multiple sensors present during IMS measurement. In this project, we will be using an 8 channel IMS measurement. [↑](#footnote-ref-4)
5. https://docs.scipy.org/doc/scipy/reference/generated/scipy.signal.savgol\_filter.html [↑](#footnote-ref-5)