

# lirtmats\_quick\_start

December 4, 2025

## 1 Quick Start

This python script describes how to use LiRTMaTS python package. The input data and retention time reference files used here are in <https://github.com/wanchanglin/lirtmats/tree/master/examples/data>.

### 1.1 Setup

The users need to load python package LAMP before using LiRTMaTS. It's functions used here are for loading data set and summarising the matching results. For details, see <https://github.com/wanchanglin/lamp>.

```
[1]: import sqlite3
import pandas as pd
from lamp import anno
import lirtmats.lirtmats as rtm
```

### 1.2 Data Loading

LiRTMaTS supports text files separated by comma (,) or tab (\t). The Microsoft's XLSX is also supported, using argument `sheet_name` to indicate which sheet is used for input data. The default is 0 for the first sheet.

Here we use a small example data set with `tsv` format. This data set includes peak list and intensity data matrix. LiRTMaTS requires peak list's name, m/z value and retention time. User needs to indicate the locations of feature name, m/z value, retention time and starting points of data matrix from data. Here they are 1, 2, 3 and 4, respectively.

```
[2]: cols = [1, 2, 3, 4]
data_fn = "./data/df_pos_3.tsv" # use tsv file
df = anno.read_peak(data_fn, cols, sep='\t')
df
```

```
[2]:      name        mz         rt       D121       A122 \
0    M102T899  102.034153  898.850160  1.404584e+07  3.689953e+06
1    M102T849  102.034154  849.085350  1.473961e+07        NaN
2    M105T45   105.042677   45.353942  5.520865e+05  1.813279e+05
3    M105T54   105.054961   54.350049  6.669635e+05  4.833251e+06
4  M105T48_1   105.074216   47.538626  6.310113e+05        NaN
```

...	...	...	...	...	...	...	...
1995	M299T296	299.233645	295.569540	8.125150e+04	1.020165e+05		
1996	M300T43_1	299.919504	42.832066	5.042924e+04		NaN	
1997	M300T62	300.119720	62.428854		Nan	3.914945e+05	
1998	M300T285_2	300.124255	285.061758		Nan	4.602130e+05	
1999	M300T288	300.181271	287.944377	7.880306e+05	1.738638e+06		
							\
	A125	A126	A127	A128	B131		
0	3.598363e+06	1.138875e+07	4.887524e+06	2.104782e+06	7.288258e+06		
1	5.934387e+06		Nan	4.607624e+06	5.969186e+06	3.367949e+06	
2	2.734923e+05	2.342655e+05	6.241395e+04	1.068277e+05	1.192451e+05		
3	2.137479e+06	1.552473e+06	1.753294e+06	2.301363e+06		NaN	
4	5.199302e+05	4.302566e+05	5.650141e+05	3.635406e+05	1.096530e+06		
...	...	...	...	...	...	...	
1995	2.209362e+05	3.557402e+05	6.039153e+05		Nan	2.330915e+05	
1996		NaN	2.222376e+05	3.763288e+05	2.094474e+05	1.163715e+05	
1997	5.182468e+05	7.492101e+05	1.546338e+06	5.741346e+05	9.712791e+05		
1998	4.559729e+05	9.718658e+05	3.864969e+05	3.877729e+05	1.315307e+06		
1999	1.113482e+06	4.063701e+06	3.788191e+06	1.201084e+06	2.988076e+06		
							\
	E214	E215	E216	H234			
0	3.125203e+06	3.608369e+06		Nan	4.763811e+06		
1	1.276006e+07	1.490770e+07	2.880142e+06	4.263577e+06			
2	3.092946e+04	1.788324e+05	1.810794e+05	3.225256e+05			
3	1.186390e+06	3.001167e+06	2.558921e+06		NaN		
4	7.882748e+05		Nan	9.822090e+05	4.974403e+05		
...	...	...	...	...	...		
1995	3.872671e+05	1.632064e+05	7.224218e+04	3.678394e+04			
1996	4.035525e+05	2.032260e+05	2.700920e+05		NaN		
1997	8.554399e+05	7.431820e+05	8.878200e+05		NaN		
1998	2.418197e+06	2.917536e+06	9.108396e+05	4.583314e+05			
1999	2.907005e+06	3.365814e+06	2.761628e+06	1.865813e+06			
							\
	H235	H236	H237	H238	H239		
0	2.281365e+06		Nan	3.404450e+06	3.720441e+06	4.539032e+05	
1		NaN		Nan	4.437697e+06	6.777076e+06	
2		NaN	3.734778e+05	1.935349e+05		NaN	1.094705e+05
3		NaN	1.695460e+06		Nan	1.834140e+06	1.029692e+06
4	3.604541e+05	1.340656e+06		Nan		NaN	6.020203e+05
...	...	...	...	...	...	...	
1995	9.526812e+04	5.785549e+04	6.183749e+05		Nan	2.915690e+04	
1996	2.675647e+05	2.695188e+05	2.750383e+05	2.882957e+05	6.720465e+04		
1997	3.625514e+05	4.987110e+05	1.393237e+06	5.217566e+05		NaN	
1998	4.022556e+05	2.673259e+05		Nan		NaN	8.926295e+04
1999	1.956308e+06		Nan	2.918514e+06		NaN	

```

0          NaN
1  6.341930e+06
2  1.946732e+05
3  4.382618e+05
4  3.597655e+05
...
1995        ...
1996  3.352428e+05
1997  1.257126e+05
1998  2.126753e+04
1999        NaN

```

[2000 rows x 40 columns]

Data frame df now includes only name, mz, rt and intensity data matrix.

### 1.3 Retention Time Matching

To perform retention time matching, users use either default retention time library or their own reference file. The reference file must have one column: `rt_lib` which is used for retention time matching with a range or torrance in seconds. Also the column `ion_mode` should be required for indication of positive or negative mode matching. If `ion_mode` is not included in the reference file, all rows will be used for matching.

```
[3]: ion_mode = "pos"
# ref_path = "" # if empty, use default reference file for matching
ref_path = "./data/rt_lib_202509.tsv"
ref = rtm.read_rt(ref_path, ion_mode=ion_mode)
ref
```

	identifier	metabolite_name	rt_lib	\
0	ACMG_aqC18_POS_0001	MS5029_Isovaleraldehyde	24.6	
1	ACMG_aqC18_POS_0002	L057_Dihydroxyfumaric acid hydrate	27.0	
2	ACMG_aqC18_POS_0003	L061_Benzoic acid	27.0	
3	ACMG_aqC18_POS_0004	L052_Spermine	28.2	
4	ACMG_aqC18_POS_0005	L021_Spermidine	30.0	
...	...	...	...	...
2827	ACMG_aqC18_POS_1412	LIM3312_Cholesterol	659.4	
2828	ACMG_aqC18_POS_1413	L013_5alpha-Cholestan-3-one	672.6	
2829	ACMG_aqC18_POS_1414	LIM3310_5alpha-Cholest-7-en-3beta-ol	675.0	
2830	ACMG_aqC18_POS_1415	L0302_5alpha-Cholestanol	681.6	
2831	ACMG_aqC18_POS_1416	L045_10Z-Nonadecenoic acid	723.6	
		inchikey	ion_mod	
0	QPUYECUOLPXSFR-UHFFFAOYSA-N	positive		
1	SEKGMJVHSBBHRD-WZHZAFAFSA-M	positive		
2	DMBUODUULYCPAK-UHFFFAOYSA-N	positive		
3	XDSPGKDYYRNYJI-IUPFWZBJS-A	positive		

```

4      HELXLJCILKEWJH-NCGAPWICSA-N  positive
...
2827   ASOSVCXGWPDUGN-UHFFFAOYSA-N  negative
2828   XQCZBXHVTFVIFE-UHFFFAOYSA-N  negative
2829   WLFXSECCHULRRO-UHFFFAOYSA-N  negative
2830   YCIMNLLNPGFGHC-UHFFFAOYSA-N  negative
2831   QIGBRXMKCJKVMJ-UHFFFAOYSA-N  negative

```

[2832 rows x 5 columns]

`rt_tol` is a threshold for the retention time matching window. The unit is seconds and the default value is 5.

```
[4]: rt_tol = 5
res = rtm.comp_match_rt(df, ref, rt_tol)
res
```

```
[4]:          id        rt      identifier \
0      M105T45  45.353942  ACMG_aqC18_POS_0280
1      M105T45  45.353942  ACMG_aqC18_POS_0281
2      M105T45  45.353942  ACMG_aqC18_POS_0282
3      M105T45  45.353942  ACMG_aqC18_POS_0283
4      M105T45  45.353942  ACMG_aqC18_POS_0284
...
150065  ...      ...
150065  M300T288  287.944377  ACMG_aqC18_POS_0942
150066  M300T288  287.944377  ACMG_aqC18_POS_0943
150067  M300T288  287.944377  ACMG_aqC18_POS_0944
150068  M300T288  287.944377  ACMG_aqC18_POS_0945
150069  M300T288  287.944377  ACMG_aqC18_POS_0945

          metabolite_name  rt_lib      inchikey \
0  L0309_Asymmetric dimethylarginine  40.5  ZDLNXNCMJBOYJV-YFKPBRYVSA-N
1  MS5037_Ribonic acid gamma-lactone  40.5  DAUAQNGYDSHRET-UHFFFAOYSA-N
2  L018_L-Dihydroorotic acid       40.5  KCDXJAYRVLXPFO-UHFFFAOYSA-N
3  L030_Stachydrine             40.5  ITECRQ00EQWFPE-UHFFFAOYSA-N
4  L072_Amino adipic acid        40.5  JYPHNHPXFNEZBR-UHFFFAOYSA-N
...
150065  ...
150066  ...
150067  ...
150068  ...
150069  ...

          ion_mod  rt_range
0  positive      5
1  positive      5
2  positive      5
3  positive      5
```

4	positive	5
...	...	...
150065	negative	5
150066	negative	5
150067	negative	5
150068	positive	5
150069	negative	5

[150070 rows x 8 columns]

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## 1.1 Summarize Results

The function `comp_summ` in package LAMP summarises the retention time matching.

```
[5]: sr, mr = anno.comp.summ(df, res)
```

This function combines peak table with retention time matching results and returns two results in different formats. `sr` is single row results for each peak id in peak table `df`:

[6]: sr

0 L0488\_Maleic acid::L0488\_Maleic acid::L0321\_L...  
1 L0481\_3-Hydroxydecanedioic acid::LIM3308\_Suber...  
2 MS5018\_Dimethyl maleate::MS5018\_Dimethyl malea...  
3 NaN  
4 NaN  
...  
1995 ... NaN  
1996 L005\_Vitamin K1::L005\_Vitamin K1::LIM3314\_Phyl...  
1997 L0306\_Syringic acid::L0315\_ortho-Hydroxyphenyl...  
1998 MS5012\_Diethyl malonate::MS5019\_Trimethylacet...  
1999 LIM3312\_Aspartame::MS5023\_Ethyl levulinate::MS...

rt\_lib \  
0 48.9::48.9::49.2::49.2::50.4::50.4::50.4::50.4...  
1 249.00000000000003::249.00000000000003::249.00...  
2 223.2::223.2::223.8::223.8::223.8::223.8::223...  
3 NaN  
4 NaN  
...  
1995 ... NaN  
1996 642.6::642.6::643.2::643.2::647.1::647.1  
1997 232.2::232.2::232.2::232.2::232.2::232.2::232...  
1998 262.2::262.2::262.2::262.2::262.2::262.2::262...  
1999 237.6::237.6::237.6::237.6::237.6::237.6::237...

inchikey \  
0 JJVNINGBGBWJH-UHFFFAOYSA-N::JJVNINGBGBWJH-UH...  
1 FVWJYYTZTCVBKE-ROUWMTJPSA-N::TVZGACDUOSZQKY-UH...  
2 KIWFQJKWBHZMDT-UHFFFAOYSA-N::KIWFQJKWBHZMDT-UH...  
3 NaN  
4 NaN  
...  
1995 ... NaN  
1996 ZFDIRQKJPRINOQ-HYXAFXHYSA-N::ZFDIRQKJPRINOQ-HY...  
1997 AFBPFSWMIHJQDM-UHFFFAOYSA-N::OISVCGZHKNMSJ-UH...  
1998 KEVYVLWNCKMXJX-UHFFFAOYSA-N::WTJVINHCBCLGX-ZD...  
1999 MBDOYVRWFFCFHM-SNAWJCMRSA-N::XPFVYQJUAUNWIW-UH...

ion\_mod  
0 positive::negative::positive::negative::positi...  
1 positive::positive::negative::negative::positi...  
2 positive::negative::positive::positive::positi...  
3 NaN  
4 NaN  
...  
1995 ... NaN  
1996 positive::negative::positive::negative::positi...

```

1997 positive::positive::positive::positive::positi...
1998 positive::positive::positive::negative::negati...
1999 positive::positive::positive::positive::negati...

```

[2000 rows x 9 columns]

mr is multiple rows format if the match more than once from the reference file:

[7]: mr

```

[7]:
      name          mz        rt      identifier \
0     M100T54  100.075925  53.810924  ACMG_aqC18_POS_0389
1     M100T54  100.075925  53.810924  ACMG_aqC18_POS_0389
2     M100T54  100.075925  53.810924  ACMG_aqC18_POS_0390
3     M100T54  100.075925  53.810924  ACMG_aqC18_POS_0390
4     M100T54  100.075925  53.810924  ACMG_aqC18_POS_0391
...
...   ...
...   ...
150218  M934T242  933.932365  242.395371  ACMG_aqC18_POS_0775
150219  M934T242  933.932365  242.395371  ACMG_aqC18_POS_0772
150220  M934T242  933.932365  242.395371  ACMG_aqC18_POS_0773
150221  M934T242  933.932365  242.395371  ACMG_aqC18_POS_0774
150222  M934T242  933.932365  242.395371  ACMG_aqC18_POS_0775

                           metabolite_name rt_lib \
0                      L0488_Maleic acid    48.9
1                      L0488_Maleic acid    48.9
2                     L0321_L-Theanine    49.2
3                     L0321_L-Theanine    49.2
4                    L0310_Dihydrothymine    50.4
...
...   ...
...   ...
150218            L035_2-Methoxybenzoic acid  247.2
150219            MS5015_Phenylglyoxal  247.2
150220  MS5021_Ethyl 2-methylacetate  247.2
150221            L012_Homoveratrumic acid  247.2
150222            L035_2-Methoxybenzoic acid  247.2

           inchikey ion_mod rt_range
0  JJVNINGBHGBWJH-UHFFFAOYSA-N  positive    5.0
1  JJVNINGBHGBWJH-UHFFFAOYSA-N negative    5.0
2  SULYEHHGGXARJS-UHFFFAOYSA-N  positive    5.0
3  SULYEHHGGXARJS-UHFFFAOYSA-N negative    5.0
4  YPTJKHVBDCKNF-UHFFFAOYSA-N  positive    5.0
...
...   ...
...   ...
150218  RFKITWRHKUYMRJ-UHFFFAOYSA-N  positive    5.0
150219  QWIZNVHXZRPDR-WSCXOGSTSA-N negative    5.0
150220  BHTRKEVKTKCXOH-LBSADWJPSA-N negative    5.0
150221  SEBFKMXJBCUCAI-UHFFFAOYSA-N negative    5.0
150222  RFKITWRHKUYMRJ-UHFFFAOYSA-N negative    5.0

```

```
[150223 rows x 9 columns]
```

All of results can be saved into a `sqlite3` database and use [DB Browser for SQLite](#) to view. Or save these results in other formats, such as TSV, CSV or XLSX, separately.

```
[8]: f_save = False          # here we do NOT save results
db_out = "test.db"
sr_out = "test_s.tsv"
mr_out = "test_m.tsv"
xlsx_out = "test.xlsx"
```

```
[9]: if f_save:
    # save all results into a sqlite3 database
    conn = sqlite3.connect(db_out)
    df[["name", "mz", "rt"]].to_sql("peaklist",
                                    conn,
                                    if_exists="replace",
                                    index=False)
    mr.to_sql("anno_mr", conn, if_exists="replace", index=False)
    sr.to_sql("anno_sr", conn, if_exists="replace", index=False)

    conn.commit()
    conn.close()

    # save results into text files
    sr.to_csv(sr_out, sep="\t", index=False)
    mr.to_csv(mr_out, sep="\t", index=False)

    # save results into Excel format
    with pd.ExcelWriter(xlsx_out, mode="w", engine="openpyxl") as writer:
        sr.to_excel(writer, sheet_name="single-row", index=False)
        mr.to_excel(writer, sheet_name="multiple-row", index=False)
```

It should be noted that saving of Excel file takes much longer time than text files.

## 1.5 End User Usages

LiRTMaTS provides two computation options: command line interface(CLI) and graphical user interface (GUI).

To use GUI, you need to open a terminal and type in:

```
$ lirtmats gui
```

To use CLI, open a terminal and type in command with required arguments, something like:

```
lirtmats cli \
--input-data "./data/df_pos_3.tsv" \
--input-sep "tab" \
--col-idx "1, 2, 3, 4" \
```

```
--rt-path "" \
--rt-sep "tab" \
--rt-tol "5.0" \
--ion-mode "pos" \
--save-db \
--summ-type "xlsx" \
```

Execution of this command line will produce `df_pos_3_rtm.db` and `df_pos_3_rtm.xlsx` in the directory `./data/`. If the `summ-type` is `tsv` or `csv`, files `df_pos_3_rtm_s.tsv` or `df_pos_3_rtm_s.csv` and `df_pos_3_rtm_m.tsv` or `df_pos_3_rtm_m.csv` will be saved into `./data`.

For the best practice, you can create a bash script `.sh` (Linux and MacOS) or Windows script `.bat` to contain these CLI arguments. Change parameters in these files each time when processing new data set.

For example, there are `lirtmats_cli.sh` and `lirtmats_cli.bat` in <https://github.com/wanchanglin/lirtmats/tree/master/examples>.

- For Linux and MacOS terminal:

```
$ chmod +x lirtmats_cli.sh
$ ./lirtmats_cli.sh
```

- For Windows terminal:

```
$ lirtmats_cli.bat
```

Note that if users use `xlsx` files for input data and reference file when using GUI or CLI, all data must be in the first sheet. If you use LiRTMaTS functions in your python scripts, there are no such requirements.