

lamp_quick_start

October 31, 2024

1 Quick Start

In this vignette we will demonstrate how to use LAMP python package. The input data and reference files are located in <https://github.com/wanchanglin/lamp/tree/master/examples/data>.

1.1 Setup

To use LAMP, the first step is to import some python libraries including LAMP.

```
[1]: import sqlite3
import pandas as pd
from lamp import anno, stats, utils
```

1.2 Data Loading

LAMP 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. Load it into python and check its format:

```
[2]: d_data = "./data/df_pos_2.tsv"
data = pd.read_table(d_data, header=0, sep="\t")
data
```

```
[2]:
```

	name	namecustom	mz	mzmin	mzmax	rt	\
0	M151T34	M150.8867T34	150.886715	150.886592	150.886863	34.152700	
1	M151T40	M151.0402T40	151.040235	151.040092	151.040350	39.838172	
2	M152T40	M152.0436T40	152.043607	152.043451	152.043737	40.303700	
3	M153T34	M152.8838T34	152.883824	152.883678	152.883959	34.174647	
4	M153T36	M153.0195T36	153.019474	153.019331	153.019633	35.785847	
..	
395	M283T339	M283.2646T339	283.264583	283.264341	283.264809	338.763489	
396	M284T60	M284.1953T60	284.195294	284.194939	284.195536	59.593561	
397	M284T108	M284.2235T108	284.223499	284.223156	284.223692	108.406389	
398	M284T339	M284.268T339	284.267962	284.267634	284.268204	338.725056	
399	M285T34	M284.775T34	284.775031	284.774635	284.775287	34.079641	
	rtmin	rtmax	npeaks	X210	X209 \

0	33.637595	35.465548	97	97	...	4.224942e+06	3.946599e+06
1	37.556072	40.532315	95	95	...	1.419062e+06	1.251606e+06
2	38.092678	40.909428	81	81	...	1.203919e+05	9.970442e+04
3	33.637595	35.465548	98	98	...	5.592065e+06	5.761380e+06
4	34.130244	36.287354	98	98	...	7.284938e+06	1.083289e+07
..
395	338.398380	339.165948	94	94	...	3.509767e+05	4.117633e+05
396	58.844217	60.107058	59	59	...	NaN	NaN
397	107.880510	108.971046	72	72	...	7.477652e+04	7.482219e+04
398	338.268300	339.370098	84	84	...	3.697604e+04	5.398264e+04
399	33.667172	35.198181	97	97	...	3.439330e+06	3.359842e+06

	X208	X207	X206	X205	X204 \
0	3.668948e+06	3.754321e+06	3.853724e+06	3.787350e+06	3.584464e+06
1	1.214826e+06	8.143028e+05	5.331963e+05	1.930928e+06	1.479001e+06
2	9.384000e+04	4.186335e+04	NaN	2.115447e+05	1.285713e+05
3	5.845419e+06	5.576013e+06	5.552878e+06	6.132789e+06	5.891378e+06
4	1.140072e+07	8.220552e+06	9.255154e+06	7.648211e+06	7.723814e+06
..
395	3.948000e+05	4.338804e+05	5.335221e+05	6.224684e+05	7.009340e+05
396	NaN	NaN	NaN	2.558004e+04	4.020517e+04
397	3.399667e+04	7.233564e+04	1.043879e+05	2.506785e+04	2.753769e+04
398	5.340109e+04	6.557698e+04	7.656575e+04	1.040606e+05	1.063727e+05
399	3.375577e+06	3.789056e+06	3.478506e+06	3.391588e+06	5.067802e+06

	X203	X202	X201
0	3.499711e+06	3.623205e+06	4.145770e+06
1	1.076354e+06	9.293218e+05	5.298062e+05
2	9.389346e+04	7.163655e+04	4.916483e+04
3	5.418082e+06	5.036840e+06	5.733794e+06
4	5.571163e+06	5.362560e+06	9.259675e+06
..
395	3.005173e+05	3.133173e+05	8.204783e+05
396	NaN	3.162670e+04	5.446684e+04
397	NaN	NaN	NaN
398	NaN	3.059370e+04	1.358056e+05
399	3.497546e+06	3.316025e+06	3.906000e+06

[400 rows x 110 columns]

This data set includes peak list and intensity data matrix. LAMP 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, 3, 6 and 11, respectively.

Load input data with `xlsx` format for LAMP:

```
[3]: cols = [1, 3, 6, 11]
      # d_data = "./data/df_pos_2.tsv"
```

```
# df = anno.read_peak(d_data, cols, sep='\t')
d_data = "./data/df_pos_2.xlsx" # use xlsx file
df = anno.read_peak(d_data, cols, sheet_name=0)
df
```

```
[3]:
```

	name	mz	rt	QC9	QC5 \
0	M151T34	150.886715	34.152700	3.664879e+06	3.735147e+06
1	M151T40	151.040235	39.838172	7.406381e+05	7.524075e+05
2	M152T40	152.043607	40.303700	6.105241e+04	5.335546e+04
3	M153T34	152.883824	34.174647	5.141479e+06	5.496344e+06
4	M153T36	153.019474	35.785847	5.336758e+06	5.558265e+06
..
395	M283T339	283.264583	338.763489	7.330602e+05	8.243956e+05
396	M284T60	284.195294	59.593561	2.310932e+04	NaN
397	M284T108	284.223499	108.406389	3.748444e+04	2.993283e+04
398	M284T339	284.267962	338.725056	1.161886e+05	1.476514e+05
399	M285T34	284.775031	34.079641	4.063268e+06	3.807148e+06

	QC4	QC3	QC26	QC25	QC24 \
0	5.190263e+06	2.742966e+06	3.824723e+06	3.722932e+06	3.804188e+06
1	NaN	6.429245e+05	1.167016e+06	1.175981e+06	1.122533e+06
2	NaN	NaN	6.875157e+04	7.807399e+04	8.943068e+04
3	8.335846e+06	3.860588e+06	5.316874e+06	5.988232e+06	5.844917e+06
4	1.118557e+07	6.876715e+06	9.967314e+06	9.073822e+06	9.328573e+06
..
395	NaN	1.159506e+06	4.294760e+05	4.641813e+05	4.570657e+05
396	NaN	NaN	1.759336e+04	2.645392e+04	2.727266e+04
397	NaN	NaN	3.175596e+04	3.879604e+04	4.299529e+04
398	NaN	NaN	NaN	6.753490e+04	5.436219e+04
399	4.645099e+06	2.232221e+06	4.576754e+06	4.533339e+06	4.559356e+06

	...	X210	X209	X208	X207 \
0	...	4.224942e+06	3.946599e+06	3.668948e+06	3.754321e+06
1	...	1.419062e+06	1.251606e+06	1.214826e+06	8.143028e+05
2	...	1.203919e+05	9.970442e+04	9.384000e+04	4.186335e+04
3	...	5.592065e+06	5.761380e+06	5.845419e+06	5.576013e+06
4	...	7.284938e+06	1.083289e+07	1.140072e+07	8.220552e+06
..
395	...	3.509767e+05	4.117633e+05	3.948000e+05	4.338804e+05
396	...	NaN	NaN	NaN	NaN
397	...	7.477652e+04	7.482219e+04	3.399667e+04	7.233564e+04
398	...	3.697604e+04	5.398264e+04	5.340109e+04	6.557698e+04
399	...	3.439330e+06	3.359842e+06	3.375577e+06	3.789056e+06

	X206	X205	X204	X203	X202 \
0	3.853724e+06	3.787350e+06	3.584464e+06	3.499711e+06	3.623205e+06
1	5.331963e+05	1.930928e+06	1.479001e+06	1.076354e+06	9.293218e+05

2	NaN	2.115447e+05	1.285713e+05	9.389346e+04	7.163655e+04
3	5.552878e+06	6.132789e+06	5.891378e+06	5.418082e+06	5.036840e+06
4	9.255154e+06	7.648211e+06	7.723814e+06	5.571163e+06	5.362560e+06
..
395	5.335221e+05	6.224684e+05	7.009340e+05	3.005173e+05	3.133173e+05
396	NaN	2.558004e+04	4.020517e+04	NaN	3.162670e+04
397	1.043879e+05	2.506785e+04	2.753769e+04	NaN	NaN
398	7.656575e+04	1.040606e+05	1.063727e+05	NaN	3.059370e+04
399	3.478506e+06	3.391588e+06	5.067802e+06	3.497546e+06	3.316025e+06

	X201
0	4.145770e+06
1	5.298062e+05
2	4.916483e+04
3	5.733794e+06
4	9.259675e+06
..	...
395	8.204783e+05
396	5.446684e+04
397	NaN
398	1.358056e+05
399	3.906000e+06

[400 rows x 103 columns]

The argument `sep` will be ignored if the input data is an `xlsx` file. Data frame `df` now includes only `name`, `mz`, `rt` and intensity data matrix.

1.3 Metabolite Annotation

To perform metabolite annotation, users should provide their own reference file. Otherwise, LAMP will use its default reference file for annotation. Here we load the default reference file for compound annotation. Since the input data is positive mode here, we only use positive part of reference file. If `ion_mode` is empty, all reference items will be used for matching.

```
[4]: ion_mode = "pos"
ref_path = "" # if empty, use default reference file for matching
# load reference library
cal_mass = False
ref = anno.read_ref(ref_path, ion_mode=ion_mode, calc=cal_mass)
ref
```

```
[4]:
```

	compound_name	molecular_formula	monoisotopic_mass	\
34230	(-)-Salsoline	C11H15N02	193.110265	
34231	(-)-trans-carveol	C10H16O	152.120110	
34232	(-)-ureidoglycolic acid	C3H6N2O4	134.032730	
34233	(11R)-11-hydroperoxylinoleic acid	C18H32O4	312.230040	
34234	(11Z,14Z)-eicosadienoylcarnitine	C27H49NO4	451.366135	

...
83155	N(6),N(6),N(6)-trimethyl-L-lysine	C9H21N2O2+	189.160301
83156	nicotinic acid D-ribonucleotide	C11H15N09P+	336.048436
83157	phosphocholine	C5H15N04P+	184.073866
83158	S-adenosyl-L-methionine	C15H23N6O5S+	399.145060
83159	S-adenosylmethioninamine	C14H23N6O3S+	355.155232

	exact_mass	ion_type	ion_mode \
34230	232.073425	[M+39K]+	positive
34231	191.083270	[M+39K]+	positive
34232	172.995890	[M+39K]+	positive
34233	351.193200	[M+39K]+	positive
34234	490.329295	[M+39K]+	positive

...
83155	189.159751	M+	positive
83156	336.047886	M+	positive
83157	184.073316	M+	positive
83158	399.144510	M+	positive
83159	355.154682	M+	positive

	smiles \
34230	<chem>COc1cc2c(cc1O)CCN[C@H]2C</chem>
34231	<chem>C=C(C) [C@@H]1CC=C(C) [C@H](O)C1</chem>
34232	<chem>NC(=O)N[C@H](O)C(=O)O</chem>
34233	<chem>CCCCC=CC(C=CCCCCCCC(=O)O)O</chem>
34234	<chem>CCCCC/C=C\C/C=C\CCCCCCCCC(=O)OC(CC(=O)[O-])C[...]</chem>
...	...
83155	<chem>C[N+](C)(C)CCCC[C@H](N)C(=O)O</chem>
83156	<chem>O=C(O)c1ccc[n+]([C@H]2O[C@H](COP(=O)(O)O)[C@H]2O)</chem>
83157	<chem>C[N+](C)(C)CCOP(=O)(O)O</chem>
83158	<chem>C[S+](CC[C@H](N)C(=O)O)C[C@H]1O[C@H](n2cnc3c(...</chem>
83159	<chem>C[S+](CCCN)C[C@H]1O[C@H](n2cnc3c(N)ncnc32)[C@H]1O</chem>

	inchikey \
34230	YTPRLBPGGZHUPD-ZETCQYMNSA-N
34231	BAVONGHXFVOKBV-ZJUUDORDSA-N
34232	NWZYVCVIOKVTHI-SFOWXEAESA-N
34233	PLWDMWAXENHPLY-UHFFFAOYSA-N
34234	OLZWDVKTOGTVLC-UTJQPWESSA-N

...	...
83155	MXNRLFUSFKVQSK-QMMGPOBSA-O
83156	JOUIQRNQJGXQDC-ZYUZZMQFOSA-O
83157	YHHSNZFOIEMCP-UHFFFAOYSA-O
83158	MEFKEPWMEQLKI-AIRLBKTGSA-O
83159	ZUNBITIXDCPNDS-LSRJEVITSA-N

inchi	kegg_id	hmdb_id \
-------	---------	-----------

34230	InChI=1S/C11H15N02/c1-7-9-6-11(14-2)10(13)5-8(...	C09640	-X-
34231	InChI=1S/C10H16O/c1-7(2)9-5-4-8(3)10(11)6-9/h4...	C00964	-X-
34232	InChI=1S/C3H6N2O4/c4-3(9)5-1(6)2(7)8/h1,6H,(H,...	C00603	HMDB0001005
34233		-X-	-X-
34234	InChI=1S/C27H49N04/c1-5-6-7-8-9-10-11-12-13-14...	-X-	-X-
...	
83155	InChI=1S/C9H20N2O2/c1-11(2,3)7-5-4-6-8(10)9(12...	C03793	HMDB0001325
83156	InChI=1S/C11H14N09P/c13-8-7(5-20-22(17,18)19)2...	C01185	-X-
83157	InChI=1S/C5H14N04P/c1-6(2,3)4-5-10-11(7,8)9/h4...	C00588	HMDB0001565
83158	InChI=1S/C15H22N6O5S/c1-27(3-2-7(16)15(24)25)4...	C00019	HMDB0001185
83159	InChI=1S/C14H23N6O3S/c1-24(4-2-3-15)5-8-10(21)...	C01137	HMDB0000988

	chebi_id	pubchem_id	lipidmaps_id
34230	CHEBI:112	442356	-X-
34231	CHEBI:15389	-X-	-X-
34232	CHEBI:15412	439269	-X-
34233	CHEBI:134247	5230520	-X-
34234	CHEBI:73119	-X-	-X-
...
83155	CHEBI:17311	440120	-X-
83156	CHEBI:15763	53477721	-X-
83157	CHEBI:18132	1014	-X-
83158	CHEBI:15414	16757548	-X-
83159	CHEBI:15625	439415	-X-

[39150 rows x 14 columns]

The reference file must have one column: `molecular_formula` (or `formula`) if there is no column called `ion m/z` (or, `m/z`, `exact_mass`). The `exact_mass` is optional. if absent, LAMP will use `molecular_formula` to calculate 'exact_mass' based on the NIST Atomic Weights and Isotopic Compositions for All Elements. If your reference file has `exact_mass` and you still want to calculate it using NIST database, set `calc` as `True`. The `exact_mass` is used to match against a range of `mz`, controlled by `ppm`, in data frame `df`.

As the same as input data, the reference file can be `xlsx` file. Another reference file is HMDB database for urine:

```
[5]: ref_path = "./data/hmdb_urine_v4_0_20200910_v1.tsv"
ref = anno.read_ref(ref_path, calc=True)
ref
```

[5]:	id	molecular_formula	compound_name \
0	HMDB0000001	C7H11N3O2	1-Methylhistidine
1	HMDB0000002	C3H10N2	1,3-Diaminopropane
2	HMDB0000005	C4H6O3	2-Ketobutyric acid
3	HMDB0000008	C4H8O3	2-Hydroxybutyric acid
4	HMDB0000010	C19H24O3	2-Methoxyestrone
...

1606	HMDB0012308	C8H8O3	Vanillin
1607	HMDB0012322	C10H8O	2-Naphthol
1608	HMDB0012325	C5H10O5	Arabinofuranose
1609	HMDB0012451	C20H28O3	all-trans-5,6-Epoxyretinoic acid
1610	HMDB0012467	C15H13O9S	(-)-Epicatechin sulfate

```

                                inchi \
0   InChI=1S/C7H11N3O2/c1-10-3-5(9-4-10)2-6(8)7(11...
1   InChI=1S/C3H10N2/c4-2-1-3-5/h1-5H2
2   InChI=1S/C4H6O3/c1-2-3(5)4(6)7/h2H2,1H3,(H,6,7)
3   InChI=1S/C4H8O3/c1-2-3(5)4(6)7/h3,5H,2H2,1H3,(...
4   InChI=1S/C19H24O3/c1-19-8-7-12-13(15(19)5-6-18...
...
1606 InChI=1S/C8H8O3/c1-11-8-4-6(5-9)2-3-7(8)10/h2-...
1607 InChI=1S/C10H8O/c11-10-6-5-8-3-1-2-4-9(8)7-10/...
1608 InChI=1S/C5H10O5/c6-1-2-3(7)4(8)5(9)10-2/h2-9H...
1609 InChI=1S/C20H28O3/c1-15(8-6-9-16(2)14-17(21)22...
1610 InChI=1S/C15H14O9S/c16-9-3-8-5-13(24-25(20,21)...
```

	inchi_key	exact_mass
0	BRMWTNUJHUMWMS-LURJTMIESA-N	169.085127
1	XFNJVJPLKCPIBV-UHFFFAOYSA-N	74.084398
2	TYEYBOSBBBHJIV-UHFFFAOYSA-N	102.031694
3	AFENDNXGAFYKQO-VKHYHEASA-N	104.047344
4	WHEUWNKSCXYKBU-QPWUGHHJSA-N	300.172545
...
1606	MWOOGOJBHIARFG-UHFFFAOYSA-N	152.047344
1607	JWAZRIHNYRIHIV-UHFFFAOYSA-N	144.057515
1608	HMFHBZSHGGEWLO-HWQSCIPKSA-N	150.052823
1609	KEEHJLBAOLGBJZ-WEDZBJJSA-N	316.203845
1610	WTXWEAXATVSZQX-AFYWNPRSA-M	369.028028

[1611 rows x 6 columns]

Next we use HMDB reference file for compounds match. Here function argument `ppm` is used to control the m/z matching tolerance(range).

```

[6]: ppm = 5.0
      match = anno.comp_match_mass(df, ppm, ref)
      match
```

[6]:	id	mz	molecular_formula	compound_name
0	M154T37	154.062402	C8H10O3	Hydroxytyrosol
1	M164T119	164.046774	C9H8O3	Phenylpyruvic acid
2	M164T119	164.046774	C9H8O3	m-Coumaric acid
3	M164T119	164.046774	C9H8O3	4-Hydroxycinnamic acid
4	M164T119	164.046774	C9H8O3	2-Hydroxycinnamic acid
5	M164T233	164.046832	C9H8O3	Phenylpyruvic acid

6	M164T233	164.046832	C9H8O3	m-Coumaric acid
7	M164T233	164.046832	C9H8O3	4-Hydroxycinnamic acid
8	M164T233	164.046832	C9H8O3	2-Hydroxycinnamic acid
9	M164T53	164.046825	C9H8O3	Phenylpyruvic acid
10	M164T53	164.046825	C9H8O3	m-Coumaric acid
11	M164T53	164.046825	C9H8O3	4-Hydroxycinnamic acid
12	M164T53	164.046825	C9H8O3	2-Hydroxycinnamic acid
13	M167T35	167.021095	C7H5NO4	Quinolinic acid
14	M173T36_3	173.104423	C8H15NO3	Hexanoylglycine
15	M174T35	174.088395	C8H14O4	Suberic acid
16	M181T36	181.060407	C6H7N5O2	8-Hydroxy-7-methylguanine
17	M212T39	212.067866	C10H12O5	Vanillactic acid
18	M276T36	276.077397	C10H16N2O5S	Biotin sulfone

inchi \

0	InChI=1S/C8H10O3/c9-4-3-6-1-2-7(10)8(11)5-6/h1...
1	InChI=1S/C9H8O3/c10-8(9(11)12)6-7-4-2-1-3-5-7/...
2	InChI=1S/C9H8O3/c10-8-3-1-2-7(6-8)4-5-9(11)12/...
3	InChI=1S/C9H8O3/c10-8-4-1-7(2-5-8)3-6-9(11)12/...
4	InChI=1S/C9H8O3/c10-8-4-2-1-3-7(8)5-6-9(11)12/...
5	InChI=1S/C9H8O3/c10-8(9(11)12)6-7-4-2-1-3-5-7/...
6	InChI=1S/C9H8O3/c10-8-3-1-2-7(6-8)4-5-9(11)12/...
7	InChI=1S/C9H8O3/c10-8-4-1-7(2-5-8)3-6-9(11)12/...
8	InChI=1S/C9H8O3/c10-8-4-2-1-3-7(8)5-6-9(11)12/...
9	InChI=1S/C9H8O3/c10-8(9(11)12)6-7-4-2-1-3-5-7/...
10	InChI=1S/C9H8O3/c10-8-3-1-2-7(6-8)4-5-9(11)12/...
11	InChI=1S/C9H8O3/c10-8-4-1-7(2-5-8)3-6-9(11)12/...
12	InChI=1S/C9H8O3/c10-8-4-2-1-3-7(8)5-6-9(11)12/...
13	InChI=1S/C7H5NO4/c9-6(10)4-2-1-3-8-5(4)7(11)12...
14	InChI=1S/C8H15NO3/c1-2-3-4-5-7(10)9-6-8(11)12/...
15	InChI=1S/C8H14O4/c9-7(10)5-3-1-2-4-6-8(11)12/h...
16	InChI=1S/C6H7N5O2/c1-11-2-3(9-6(11)13)8-5(7)10...
17	InChI=1S/C10H12O5/c1-15-9-5-6(2-3-7(9)11)4-8(1...
18	InChI=1S/C10H16N2O5S/c13-8(14)4-2-1-3-7-9-6(5-...

	inchi_key	exact_mass	ppm_error
0	JUUBCHWRXWPFH-UHFFFAOYSA-N	154.06	-3.84
1	BTNMPGBKDVTSJY-UHFFFAOYSA-N	164.05	-3.47
2	KKSDGJDHHZEWEP-SNAWJCMRSA-N	164.05	-3.47
3	NGSWKAQJJWESNS-ZZXKVVIFSA-N	164.05	-3.47
4	PMOWTIHVNWZYFI-AATRIKPKSA-N	164.05	-3.47
5	BTNMPGBKDVTSJY-UHFFFAOYSA-N	164.05	-3.12
6	KKSDGJDHHZEWEP-SNAWJCMRSA-N	164.05	-3.12
7	NGSWKAQJJWESNS-ZZXKVVIFSA-N	164.05	-3.12
8	PMOWTIHVNWZYFI-AATRIKPKSA-N	164.05	-3.12
9	BTNMPGBKDVTSJY-UHFFFAOYSA-N	164.05	-3.16
10	KKSDGJDHHZEWEP-SNAWJCMRSA-N	164.05	-3.16

11	NGSWKAQJJWESNS-ZZXKWIFSA-N	164.05	-3.16
12	PMOWTIHVNWZYFI-AATRIKPKSA-N	164.05	-3.16
13	GJAWHXHKYYXBSV-UHFFFAOYSA-N	167.02	-4.57
14	UPCKIPHSXMXJOX-UHFFFAOYSA-N	173.11	-4.45
15	TYFQFVWCELRYAO-UHFFFAOYSA-N	174.09	-4.67
16	VHPXSVXJBWZORQ-UHFFFAOYSA-N	181.06	2.39
17	SVYIZYRTOYHQRE-UHFFFAOYSA-N	212.07	-2.86
18	QPFQYMONYBAUCY-ZKWXMUHSA-N	276.08	-2.16

match gives the compound matching results. LAMP also provides a mass adjust option by adduct library. You can provide your own adducts library otherwise LAMP uses its default adducts library.

The adducts library's format looks like:

```
[7]: add_path = './data/adducts_short.tsv'
lib_df = pd.read_csv(add_path, sep="\t")
lib_df
```

```
[7]:
```

	label	exact_mass	charge	ion_mode
0	[M+H] ⁺	1.007276	1	pos
1	[M+NH ₄] ⁺	18.033826	1	pos
2	[M+Na] ⁺	22.989221	1	pos
3	[M+Mg] ⁺	23.984493	1	pos
4	[M+K] ⁺	38.963158	1	pos
5	[M+Fe] ⁺	55.934388	1	pos
6	[M+Cu] ⁺	62.929049	1	pos
7	[M+2H] ⁺	2.015101	1	pos
8	[M+3H] ⁺	3.022926	1	pos
9	[M-H] ⁻	-1.007276	1	neg
10	[M+35Cl] ⁻	34.969401	1	neg
11	[M+Formate] ⁻	44.998203	1	neg
12	[M+Acetate] ⁻	59.013853	1	neg

The adducts library must have columns of label, exact_mass, charge and ion_mode.

We use this adducts file to adjust mass:

```
[8]: # if empty, use default adducts library
add_path = './data/adducts_short.tsv'
lib_add = anno.read_lib(add_path, ion_mode)
lib_add
```

```
[8]:
```

	label	exact_mass	charge
0	[M+H] ⁺	1.007276	1
1	[M+NH ₄] ⁺	18.033826	1
2	[M+Na] ⁺	22.989221	1
3	[M+Mg] ⁺	23.984493	1
4	[M+K] ⁺	38.963158	1
5	[M+Fe] ⁺	55.934388	1

6	[M+Cu] ⁺	62.929049	1
7	[M+2H] ⁺	2.015101	1
8	[M+3H] ⁺	3.022926	1

Now use function `comp_match_mass_add` to match compounds:

```
[9]: match_1 = anno.comp_match_mass_add(df, ppm, ref, lib_add)
      match_1
```

```
[9]:
```

	id	mz	molecular_formula	compound_name \
0	M152T40	152.043607	C5H8N2O2	Dihydrothymine
1	M154T37	154.062402	C8H8O3	p-Hydroxyphenylacetic acid
2	M154T37	154.062402	C8H8O3	3-Hydroxyphenylacetic acid
3	M154T37	154.062402	C8H8O3	ortho-Hydroxyphenylacetic acid
4	M154T37	154.062402	C8H8O3	Mandelic acid
5	M154T37	154.062402	C8H8O3	3-Cresotinic acid
6	M154T37	154.062402	C8H8O3	4-Hydroxy-3-methylbenzoic acid
7	M154T37	154.062402	C8H8O3	Vanillin
8	M157T35	157.036819	C4H10N2O2	2,4-Diaminobutyric acid
9	M157T35	157.036819	C4H10N2O2	L-2,4-diaminobutyric acid
10	M167T35	167.021095	C5H8N2O2	Dihydrothymine
11	M174T35	174.088395	C9H13NO	Phenylpropanolamine
12	M174T35	174.088395	C10H14O	Thymol
13	M174T35	174.088395	C10H14O	(S)-Carvone
14	M174T35	174.088395	C8H12O4	2-Octenedioic acid
15	M174T35	174.088395	C8H12O4	cis-4-Octenedioic acid
16	M181T36	181.060407	C8H8N2O3	Nicotinuric acid
17	M184T38	184.097942	C10H13N2	Nicotine imine
18	M185T39_2	185.082034	C5H15NO4P	Phosphorylcholine
19	M186T36	186.045606	C6H14N2O	N-Acetylputrescine
20	M187T38	187.097642	C5H15NO4P	Phosphorylcholine
21	M193T40	193.050761	C5H14N4	Agmatine
22	M200T36	200.061328	C7H16N2O	N-Acetylcadaverine
23	M201T39_1	201.051849	C10H10O3	4-Methoxycinnamic acid
24	M203T36_1	203.002108	C9H9NO	Indole-3-carbinol
25	M212T39	212.067866	C8H15NO3	Hexanoylglycine
26	M212T39	212.067866	C10H10O5	Vanilpyruvic acid
27	M217T37_1	217.018279	C10H11NO	Tryptophol
28	M221T37	221.012328	C9H11NO2	L-Phenylalanine
29	M223T38	223.008162	C4H10NO6P	O-Phosphothreonine
30	M223T40	223.096863	C12H14O4	Monoisobutyl phthalic acid
31	M226T44	226.128007	C8H18N4O2	Asymmetric dimethylarginine
32	M226T44	226.128007	C8H18N4O2	Symmetric dimethylarginine
33	M227T36	227.066175	C9H10N2O5	3-Nitrotyrosine
34	M229T38	229.069418	C4H10N3O5P	Phosphocreatine
35	M233T38	233.043479	C8H10N4O2	Caffeine
36	M245T44	245.045772	C7H15N3O3	Homocitrulline
37	M245T37_2	245.093315	C13H18O2	Ibuprofen

38	M249T38	249.038309	C8H10N4O3	1,3,7-Trimethyluric acid
39	M261T43	260.972975	C10H7NO4	Xanthurenic acid
40	M269T37_2	269.088048	C10H12N4O5	Inosine
41	M275T168	275.201932	C18H24O2	Estradiol
42	M275T168	275.201932	C18H24O2	17a-Estradiol
43	M277T181	277.217564	C18H28O2	19-Norandrosterone
44	M277T181	277.217564	C18H28O2	19-Noretiocholanolone
45	M278T71	278.148195	C11H20N2O6	Saccharopine
46	M279T233	279.233232	C18H30O2	alpha-Linolenic acid
47	M279T233	279.233232	C18H28O2	19-Norandrosterone
48	M279T233	279.233232	C18H28O2	19-Noretiocholanolone
49	M281T287	281.248903	C18H32O2	Linoleic acid
50	M281T287	281.248903	C18H30O2	alpha-Linolenic acid
51	M282T61	282.070271	C10H14N2O6	Ribothymidine
52	M282T61	282.070271	C10H14N2O6	3-Methyluridine
53	M283T37	283.103695	C11H14N4O5	1-Methylinosine

inchi \

```

0  InChI=1S/C5H8N2O2/c1-3-2-6-5(9)7-4(3)8/h3H,2H2...
1  InChI=1S/C8H8O3/c9-7-3-1-6(2-4-7)5-8(10)11/h1-...
2  InChI=1S/C8H8O3/c9-7-3-1-2-6(4-7)5-8(10)11/h1-...
3  InChI=1S/C8H8O3/c9-7-4-2-1-3-6(7)5-8(10)11/h1-...
4  InChI=1S/C8H8O3/c9-7(8(10)11)6-4-2-1-3-5-6/h1-...
5  InChI=1S/C8H8O3/c1-5-3-2-4-6(7(5)9)8(10)11/h2-...
6  InChI=1S/C8H8O3/c1-5-4-6(8(10)11)2-3-7(5)9/h2-...
7  InChI=1S/C8H8O3/c1-11-8-4-6(5-9)2-3-7(8)10/h2-...
8  InChI=1S/C4H10N2O2/c5-2-1-3(6)4(7)8/h3H,1-2,5-...
9  InChI=1S/C4H10N2O2/c5-2-1-3(6)4(7)8/h3H,1-2,5-...
10 InChI=1S/C5H8N2O2/c1-3-2-6-5(9)7-4(3)8/h3H,2H2...
11 InChI=1S/C9H13NO/c1-7(10)9(11)8-5-3-2-4-6-8/h2...
12 InChI=1S/C10H14O/c1-7(2)9-5-4-8(3)6-10(9)11/h4...
13 InChI=1S/C10H14O/c1-7(2)9-5-4-8(3)10(11)6-9/h4...
14 InChI=1S/C8H12O4/c9-7(10)5-3-1-2-4-6-8(11)12/h...
15 InChI=1S/C8H12O4/c9-7(10)5-3-1-2-4-6-8(11)12/h...
16 InChI=1S/C8H8N2O3/c11-7(12)5-10-8(13)6-2-1-3-9...
17 InChI=1S/C10H13N2/c1-12-7-3-5-10(12)9-4-2-6-11...
18 InChI=1S/C5H14NO4P/c1-6(2,3)4-5-10-11(7,8)9/h4...
19 InChI=1S/C6H14N2O/c1-6(9)8-5-3-2-4-7/h2-5,7H2,...
20 InChI=1S/C5H14NO4P/c1-6(2,3)4-5-10-11(7,8)9/h4...
21 InChI=1S/C5H14N4/c6-3-1-2-4-9-5(7)8/h1-4,6H2,(...
22 InChI=1S/C7H16N2O/c1-7(10)9-6-4-2-3-5-8/h2-6,8...
23 InChI=1S/C10H10O3/c1-13-9-5-2-8(3-6-9)4-7-10(1...
24 InChI=1S/C9H9NO/c11-6-7-5-10-9-4-2-1-3-8(7)9/h...
25 InChI=1S/C8H15NO3/c1-2-3-4-5-7(10)9-6-8(11)12/...
26 InChI=1S/C10H10O5/c1-15-9-5-6(2-3-7(9)11)4-8(1...
27 InChI=1S/C10H11NO/c12-6-5-8-7-11-10-4-2-1-3-9(...
28 InChI=1S/C9H11NO2/c10-8(9(11)12)6-7-4-2-1-3-5-...

```

29 InChI=1S/C4H10N06P/c1-2(3(5)4(6)7)11-12(8,9)10...
 30 InChI=1S/C12H14O4/c1-8(2)7-16-12(15)10-6-4-3-5...
 31 InChI=1S/C8H18N4O2/c1-12(2)8(10)11-5-3-4-6(9)7...
 32 InChI=1S/C8H18N4O2/c1-10-8(11-2)12-5-3-4-6(9)7...
 33 InChI=1S/C9H10N2O5/c10-6(9(13)14)3-5-1-2-8(12)...
 34 InChI=1S/C4H10N3O5P/c1-7(2-3(8)9)4(5)6-13(10,1...
 35 InChI=1S/C8H10N4O2/c1-10-4-9-6-5(10)7(13)12(3)...
 36 InChI=1S/C7H15N3O3/c8-5(6(11)12)3-1-2-4-10-7(9...
 37 InChI=1S/C13H18O2/c1-9(2)8-11-4-6-12(7-5-11)10...
 38 InChI=1S/C8H10N4O3/c1-10-4-5(9-7(10)14)11(2)8(...
 39 InChI=1S/C10H7N04/c12-7-3-1-2-5-8(13)4-6(10(14...
 40 InChI=1S/C10H12N4O5/c15-1-4-6(16)7(17)10(19-4)...
 41 InChI=1S/C18H24O2/c1-18-9-8-14-13-5-3-12(19)10...
 42 InChI=1S/C18H24O2/c1-18-9-8-14-13-5-3-12(19)10...
 43 InChI=1S/C18H28O2/c1-18-9-8-14-13-5-3-12(19)10...
 44 InChI=1S/C18H28O2/c1-18-9-8-14-13-5-3-12(19)10...
 45 InChI=1S/C11H20N2O6/c12-7(10(16)17)3-1-2-6-13-...
 46 InChI=1S/C18H30O2/c1-2-3-4-5-6-7-8-9-10-11-12-...
 47 InChI=1S/C18H28O2/c1-18-9-8-14-13-5-3-12(19)10...
 48 InChI=1S/C18H28O2/c1-18-9-8-14-13-5-3-12(19)10...
 49 InChI=1S/C18H32O2/c1-2-3-4-5-6-7-8-9-10-11-12-...
 50 InChI=1S/C18H30O2/c1-2-3-4-5-6-7-8-9-10-11-12-...
 51 InChI=1S/C10H14N2O6/c1-4-2-12(10(17)11-8(4)16)...
 52 InChI=1S/C10H14N2O6/c1-11-6(14)2-3-12(10(11)17...
 53 InChI=1S/C11H14N4O5/c1-14-3-13-9-6(10(14)19)12...

	inchi_key	exact_mass	adduct	ppm_error
0	NBAKTGXDIBVZOO-VKHYHEASA-N	152.04	[M+Mg] ⁺	3.52
1	XQXPVVBIMDBYFF-UHFFFAOYSA-N	154.06	[M+2H] ⁺	-0.28
2	FVMDYYGIDFPZAX-UHFFFAOYSA-N	154.06	[M+2H] ⁺	-0.28
3	CCVYRRGZDBSHFU-UHFFFAOYSA-N	154.06	[M+2H] ⁺	-0.28
4	IWYDHOAUDWTVEP-ZETCQYMHTA-N	154.06	[M+2H] ⁺	-0.28
5	WHSXTWFYRGOBGO-UHFFFAOYSA-N	154.06	[M+2H] ⁺	-0.28
6	LTFHNKUKQYVHDX-UHFFFAOYSA-N	154.06	[M+2H] ⁺	-0.28
7	MWOOGOJBHIAFG-UHFFFAOYSA-N	154.06	[M+2H] ⁺	-0.28
8	OGNSCSPNOLGXSM-UHFFFAOYSA-N	157.04	[M+K] ⁺	-3.61
9	OGNSCSPNOLGXSM-VKHYHEASA-N	157.04	[M+K] ⁺	-3.61
10	NBAKTGXDIBVZOO-VKHYHEASA-N	167.02	[M+K] ⁺	-3.83
11	DLNKOKYKWOXYQA-VXNVDRBHSA-N	174.09	[M+Na] ⁺	-3.10
12	MGSRCZKZVOBKFT-UHFFFAOYSA-N	174.09	[M+Mg] ⁺	-3.23
13	ULDHMXUKGWMISQ-VIFPVBQESA-N	174.09	[M+Mg] ⁺	-3.23
14	BNTPVRGYUHFHN-HWKANZROSA-N	174.09	[M+2H] ⁺	-1.52
15	LQVYKEXVMZXOAH-UPHRSURJSA-N	174.09	[M+2H] ⁺	-1.52
16	ZBSGKPYXQINNGF-UHFFFAOYSA-N	181.06	[M+H] ⁺	-1.99
17	GTQXYYYOJZZJHL-UHFFFAOYSA-N	184.10	[M+Na] ⁺	4.61
18	YHHSONZF0IEMCP-UHFFFAOYSA-O	185.08	[M+H] ⁺	4.80
19	KLZGKIDSEJWEDW-UHFFFAOYSA-N	186.05	[M+Fe] ⁺	3.25

20	YHHSOZFOIEMCP-UHFFFAOYSA-O	187.10	[M+3H] ⁺	4.52
21	QYPPJABKJHAVHS-UHFFFAOYSA-N	193.05	[M+Cu] ⁺	-0.69
22	RMOIHAKNOFHOF-UHFFFAOYSA-N	200.06	[M+Fe] ⁺	3.39
23	AFDXODALSZRGH-QPJXVBHSA-N	201.05	[M+Na] ⁺	-1.82
24	IVYPNXXAYMYVSP-UHFFFAOYSA-N	203.00	[M+Fe] ⁺	-3.42
25	UPCKIPHSXMXJOX-UHFFFAOYSA-N	212.07	[M+K] ⁺	-2.29
26	YGQHQTMRZPHIBB-UHFFFAOYSA-N	212.07	[M+2H] ⁺	-0.28
27	MBBOMCVGYCRMEA-UHFFFAOYSA-N	217.02	[M+Fe] ⁺	-0.79
28	COLNVLDHVKWLRT-QMMMGPBSA-N	221.01	[M+Fe] ⁺	-4.70
29	USRGIUJOYOXOQJ-GBXIJSLDSA-N	223.01	[M+Mg] ⁺	-4.06
30	RZJSUWQGFCNFS-UHFFFAOYSA-N	223.10	[M+H] ⁺	1.69
31	YDGMGEXADBMOJ-LURJTMIESA-N	226.13	[M+Mg] ⁺	2.38
32	HVPFXCBJHIIJGS-LURJTMIESA-N	226.13	[M+Mg] ⁺	2.38
33	FBTSQILOGYXGMD-LURJTMIESA-N	227.07	[M+H] ⁺	-0.32
34	DRBBFCLWYRJSJZ-UHFFFAOYSA-N	229.07	[M+NH ₄] ⁺	-0.94
35	RYYVLZVUVIJVGH-UHFFFAOYSA-N	233.04	[M+K] ⁺	-0.23
36	XIGSAGMEBXLVJJ-YFKPBYRVSA-N	245.05	[M+Fe] ⁺	0.17
37	HEFNWSXXWATRW-UHFFFAOYSA-N	245.09	[M+K] ⁺	-2.13
38	BYXCFUMGEBZDDI-UHFFFAOYSA-N	249.04	[M+K] ⁺	-0.56
39	FBZONXHGGPHHIY-UHFFFAOYSA-N	260.97	[M+Fe] ⁺	4.13
40	UGQMRVRMYASKQ-KQYNXXCUSA-N	269.09	[M+H] ⁺	0.01
41	VOXZDWNVPVJITMN-ZBRFXRBCSA-N	275.20	[M+3H] ⁺	5.00
42	VOXZDWNVPVJITMN-SFFUCWETSA-N	275.20	[M+3H] ⁺	5.00
43	UOUIARGWRPHDBX-CQZDKXCPSA-N	277.22	[M+H] ⁺	4.90
44	UOUIARGWRPHDBX-DHNVHTBWSA-N	277.22	[M+H] ⁺	4.90
45	ZDGJAHTZVHVLOT-YUMQZZPRSA-N	278.15	[M+2H] ⁺	3.44
46	DTOSIQBPBRVQHS-PDBXOOCHSA-N	279.23	[M+H] ⁺	4.93
47	UOUIARGWRPHDBX-CQZDKXCPSA-N	279.23	[M+3H] ⁺	4.93
48	UOUIARGWRPHDBX-DHNVHTBWSA-N	279.23	[M+3H] ⁺	4.93
49	OYHQOLUKZRVRQ-HZJYTRNSA-N	281.25	[M+H] ⁺	4.97
50	DTOSIQBPBRVQHS-PDBXOOCHSA-N	281.25	[M+3H] ⁺	4.97
51	DWRXFEITVBNRMK-JXOAFFINSA-N	282.07	[M+Mg] ⁺	2.10
52	UTQUILVPBZEHTK-UHFFFAOYSA-N	282.07	[M+Mg] ⁺	2.10
53	WJNGQIYEQLPJMN-IOSLPCCCSA-N	283.10	[M+H] ⁺	-0.01

1.4 Correlation Analysis

Next step is correlation analysis, based on intensity data matrix along all peaks. All results are filtered by the correlation coefficient, p-values and retention time difference. That is: keep correlation results in an retention time differences/window (such as 1 second) with correlation coefficient larger than a threshold (such as 0.5) and their correlation p-values less than a threshold (such as 0.05).

LAMP supports two correlation methods, **pearson** and **spearman**. Also parameter **positive** allows user to select only positive correlation results, otherwise positive and negative correlations will be used.

Two functions, `_tic` and `_toc`, record the correlation computation time in seconds.

```
[10]: thres_rt = 1.0
      thres_corr = 0.5
      thres_pval = 0.05
      method = "spearman" # "pearson"
      positive = True
```

```
[11]: utils._tic()
      corr = stats.comp_corr_rt(df, thres_rt, thres_corr, thres_pval, method,
                               positive)
      utils._toc()
      corr
```

Elapsed time: 1.9924170970916748 seconds.

```
[11]:
```

	name_a	name_b	r_value	p_value	rt_diff
0	M151T34	M153T34	0.80	1.267076e-23	0.02
1	M151T34	M155T34	0.71	1.752854e-16	0.20
2	M151T34	M161T34	0.78	1.869949e-21	0.14
3	M151T34	M163T34	0.69	3.239594e-15	0.20
4	M151T34	M167T35	0.51	5.776482e-08	0.73
...
1783	M283T34_1	M283T34_2	0.62	4.214876e-12	0.29
1784	M283T34_1	M285T34	0.82	5.937139e-26	0.08
1785	M283T34_2	M285T34	0.66	7.898957e-14	0.37
1786	M283T60	M284T60	0.86	1.033010e-29	0.15
1787	M283T339	M284T339	0.91	4.031333e-39	0.04

[1788 rows x 5 columns]

corr gives results of correlation coefficient(r_value), correlation p-values(p_value) and retention time difference(rt_diff).

Based on the correlation analysis, we can extract the groups and their sizes by:

```
[12]: # get correlation group and size
      corr_df = stats.corr_grp_size(corr)
      corr_df
```

```
[12]:
```

	name	cor_grp_size	cor_grp
0	M216T35	52	M217T35::M218T35::M219T34::M219T35::M221T34::M...
1	M217T35	52	M218T35::M219T34::M219T35::M221T34::M223T34::M...
2	M219T35	52	M221T34::M223T34::M225T35::M226T35::M229T34::M...
3	M215T35	52	M216T35::M217T35::M218T35::M219T34::M219T35::M...
4	M218T35	51	M219T34::M219T35::M221T34::M223T34::M225T35::M...
..
335	M245T39	1	M279T38
336	M182T42	1	M181T43
337	M265T66	1	M266T66
338	M271T197	1	M272T197

339 M171T119

1

M173T119

[340 rows x 3 columns]

1.5 Summarize Results

The final step gets the summary table in different format and save for the further analysis.

```
[13]: # get summary of metabolite annotation
sr, mr = anno.comp_summ(df, match)
```

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

```
[14]: sr
```

```
[14]:
```

	name	mz	rt	exact_mass	ppm_error	\
0	M151T34	150.886715	34.152700	NaN	NaN	
1	M151T40	151.040235	39.838172	NaN	NaN	
2	M152T40	152.043607	40.303700	NaN	NaN	
3	M153T34	152.883824	34.174647	NaN	NaN	
4	M153T36	153.019474	35.785847	NaN	NaN	
..	
395	M283T61	283.068474	60.739869	NaN	NaN	
396	M284T108	284.223499	108.406389	NaN	NaN	
397	M284T339	284.267962	338.725056	NaN	NaN	
398	M284T60	284.195294	59.593561	NaN	NaN	
399	M285T34	284.775031	34.079641	NaN	NaN	

	molecular_formula	compound_name	inchi	inchi_key
0	NaN	NaN	NaN	NaN
1	NaN	NaN	NaN	NaN
2	NaN	NaN	NaN	NaN
3	NaN	NaN	NaN	NaN
4	NaN	NaN	NaN	NaN
..
395	NaN	NaN	NaN	NaN
396	NaN	NaN	NaN	NaN
397	NaN	NaN	NaN	NaN
398	NaN	NaN	NaN	NaN
399	NaN	NaN	NaN	NaN

[400 rows x 9 columns]

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

```
[15]: mr
```

```
[15]:
```

	name	mz	rt	molecular_formula	compound_name	inchi	\
0	M151T34	150.886715	34.152700	NaN	NaN	NaN	
1	M151T40	151.040235	39.838172	NaN	NaN	NaN	
2	M152T40	152.043607	40.303700	NaN	NaN	NaN	
3	M153T34	152.883824	34.174647	NaN	NaN	NaN	
4	M153T36	153.019474	35.785847	NaN	NaN	NaN	
..	
404	M283T61	283.068474	60.739869	NaN	NaN	NaN	
405	M284T108	284.223499	108.406389	NaN	NaN	NaN	
406	M284T339	284.267962	338.725056	NaN	NaN	NaN	
407	M284T60	284.195294	59.593561	NaN	NaN	NaN	
408	M285T34	284.775031	34.079641	NaN	NaN	NaN	

	inchi_key	exact_mass	ppm_error
0	NaN	NaN	NaN
1	NaN	NaN	NaN
2	NaN	NaN	NaN
3	NaN	NaN	NaN
4	NaN	NaN	NaN
..
404	NaN	NaN	NaN
405	NaN	NaN	NaN
406	NaN	NaN	NaN
407	NaN	NaN	NaN
408	NaN	NaN	NaN

[409 rows x 9 columns]

Now we merges single format results with correlation results:

```
[16]: # merge summery table with correlation analysis
res = anno.comp_summ_corr(sr, corr_df)
res
```

```
[16]:
```

	name	mz	rt	exact_mass	ppm_error	\
0	M167T35	167.021095	34.882147	167.02	-4.57	
1	M276T36	276.077397	36.385373	276.08	-2.16	
2	M154T37	154.062402	37.183625	154.06	-3.84	
3	M181T36	181.060407	35.734801	181.06	2.39	
4	M174T35	174.088395	35.001130	174.09	-4.67	
..	
395	M279T50	279.159930	50.055451	NaN	NaN	
396	M279T79	279.163910	78.758079	NaN	NaN	
397	M282T85	282.207859	84.719202	NaN	NaN	
398	M283T47	283.110871	46.822069	NaN	NaN	
399	M284T108	284.223499	108.406389	NaN	NaN	

	molecular_formula	compound_name	\
--	-------------------	---------------	---

0	C7H5N04	Quinolinic acid
1	C10H16N2O5S	Biotin sulfone
2	C8H10O3	Hydroxytyrosol
3	C6H7N5O2	8-Hydroxy-7-methylguanine
4	C8H14O4	Suberic acid
..
395	NaN	NaN
396	NaN	NaN
397	NaN	NaN
398	NaN	NaN
399	NaN	NaN

		inchi \
0	InChI=1S/C7H5N04/c9-6(10)4-2-1-3-8-5(4)7(11)12...	
1	InChI=1S/C10H16N2O5S/c13-8(14)4-2-1-3-7-9-6(5-...	
2	InChI=1S/C8H10O3/c9-4-3-6-1-2-7(10)8(11)5-6/h1...	
3	InChI=1S/C6H7N5O2/c1-11-2-3(9-6(11)13)8-5(7)10...	
4	InChI=1S/C8H14O4/c9-7(10)5-3-1-2-4-6-8(11)12/h...	
..
395		NaN
396		NaN
397		NaN
398		NaN
399		NaN

	inchi_key	cor_grp_size \
0	GJAWHXHKYYXBSV-UHFFFAOYSA-N	25.0
1	QPFQYMONYBAUCY-ZKWXMUHSA-N	13.0
2	JUUBCHWRXWPFFH-UHFFFAOYSA-N	12.0
3	VHPXSVXJBWZORQ-UHFFFAOYSA-N	9.0
4	TYFQFVWCELRYAO-UHFFFAOYSA-N	9.0
..
395	NaN	NaN
396	NaN	NaN
397	NaN	NaN
398	NaN	NaN
399	NaN	NaN

	cor_grp
0	M171T34::M197T36::M209T34::M211T34::M213T34::M...
1	M277T36_2::M278T36::M173T36_2::M186T36::M187T3...
2	M155T38::M158T37_2::M164T36::M171T37_2::M173T3...
3	M224T36::M225T35::M226T35::M227T36::M269T37_2::...
4	M211T34::M213T34::M219T34::M221T34::M229T35::M...
..	...
395	NaN
396	NaN

397	NaN
398	NaN
399	NaN

[400 rows x 11 columns]

The result data frame **res** is re-arranged as four parts from top to bottom:

- 1st part: identified metabolites, satisfied with correlation analysis
- 2nd part: identified metabolites, not satisfied with correlation
- 3rd part: no identified metabolites, satisfied with correlation
- 4th part: no identified metabolites, not satisfied with correlation

The users should focus on the first part and perform their further analysis.

You can save all results in different forms, such as text format TSV or CSV. You can also save all results into a **sqlite3** database and use [DB Browser for SQLite](#) to view:

```
[17]: f_save = False          # here we do NOT save results
      db_out = "test.db"
      sr_out = "test_s.tsv"

[18]: 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)

      corr_df.to_sql("corr_grp", conn, if_exists="replace", index=False)
      corr.to_sql("corr_pval_rt", conn, if_exists="replace", index=False)
      match.to_sql("match", conn, if_exists="replace", index=False)
      mr.to_sql("anno_mr", conn, if_exists="replace", index=False)
      res.to_sql("anno_sr", conn, if_exists="replace", index=False)

      conn.commit()
      conn.close()

      # save final results
      res.to_csv(sr_out, sep="\t", index=False)
```

1.6 End User Usages

For end users, LAMP 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:

```
$ lamp gui
```

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

```
$ lamp cli \
--input-data "./data/df_pos_3.tsv" \
--sep "tab" \
--col-idx "1, 2, 3, 4" \
--add-path "" \
--ref-path "" \
--ion-mode "pos" \
--cal-mass \
--thres-rt "1.0" \
--thres-corr "0.5" \
--thres-pval "0.05" \
--method "pearson" \
--positive \
--ppm "5.0" \
--save-db \
--save-mr \
--db-out "./res/test.db" \
--sr-out "./res/test_s.tsv" \
--mr-out "./res/test_m.tsv"
```

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 `lamp_cli.sh` and `lamp_cli.bat` in <https://github.com/wanchanglin/lamp/tree/master/examples>. You can run them and check the results in directory `examples/res`:

- For Linux and MacOS terminal:

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

- For Windows terminal:

```
$ lamp_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 LAMP functions in your python scripts, there are no such requirements.