

# Metabolomic Data Analysis with MetaboAnalyst 5.0

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## 1 Background

MSEA or Metabolite Set Enrichment Analysis is a way to identify biologically meaningful patterns that are significantly enriched in quantitative metabolomic data. In conventional approaches, metabolites are evaluated individually for their significance under conditions of study. Those compounds that have passed certain significance level are then combined to see if any meaningful patterns can be discerned. In contrast, MSEA directly investigates if a set of functionally related metabolites without the need to preselect compounds based on some arbitrary cut-off threshold. It has the potential to identify subtle but consistent changes among a group of related compounds, which may go undetected with the conventional approaches.

Essentially, MSEA is a metabolomic version of the popular GSEA (Gene Set Enrichment Analysis) software with its own collection of metabolite set libraries as well as an implementation of user-friendly web-interfaces. GSEA is widely used in genomics data analysis and has proven to be a powerful alternative to conventional approaches. For more information, please refer to the original paper by Subramanian A, and a nice review paper by Nam D, Kim SY.<sup>1, 2</sup>

## 2 MSEA Overview

Metabolite set enrichment analysis consists of four steps - data input, data processing, data analysis, and results download. Different analysis procedures are performed based on different input types. In addition, users can also browse and search the metabolite set libraries as well as upload their self-defined metabolite sets for enrichment analysis. Users can also perform metabolite name mapping between a variety of compound names, synonyms, and major database identifiers.

## 3 Data Input

There are three enrichment analysis algorithms offered by MSEA. Accordingly, three different types of data inputs are required by these three approaches:

- A list of important compound names - entered as a one column data (*Over Representation Analysis (ORA)*);
- A single measured biofluid (urine, blood, CSF) sample- entered as tab separated two-column data with the first column for compound name, and the second for concentration values (*Single Sample Profiling (SSP)*);

<sup>1</sup>Subramanian *Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles.*, Proc Natl Acad Sci USA. 2005 102(43): 15545-50

<sup>2</sup>Nam D, Kim SY. *Gene-set approach for expression pattern analysis*, Briefings in Bioinformatics. 2008 9(3): 189-197.

- A compound concentration table - entered as a comma separated (.csv) file with the each sample per row and each metabolite concentration per column. The first column is sample names and the second column for sample phenotype labels (*Quantitative Enrichment Analysis (QEA)*)

You selected Over Representation Analysis (ORA) which requires a list of compound names as input.

## 4 Data Process

The first step is to standardize the compound labels. It is an essential step since the compound labels will be subsequently compared with compounds contained in the metabolite set library. MSEA has a built-in tool to convert between compound common names, synonyms, identifiers used in HMDB ID, PubChem, ChEBI, BiGG, METLIN, KEGG, or Reactome. **Table 1** shows the conversion results. Note: 1 indicates exact match, 2 indicates approximate match, and 0 indicates no match. A text file contain the result can be found the downloaded file *name\_map.csv*

Query	Match	HMDB	PubChem	KEGG	SMILES
1	HMDB0000169	HMDB0000169	18950	C00936	C([C@@H]1[C@H]([C@@H](C=C1)O)O
2	HMDB0000190	HMDB0000190	61503	C00186	C([C@@H](C(=O)O)O
3	HMDB0000122	HMDB0000122	5793	C00221	C([C@@H]1[C@H]([C@@H](C=C1)O)OC(=O)C1(C(C(C(O1)CO)O)O
4	HMDB0029965	HMDB0029965	94214		
5	HMDB0000125	NA	NA	NA	NA
6	HMDB0000078	HMDB0000078	439498	C01419	C([C@@H](C(=O)NCC(=O)C)O
7	HMDB0240253	NA	NA	NA	NA
8	HMDB0038670	NA	NA	NA	NA
9	HMDB0061717	NA	NA	NA	NA
10	HMDB0000725	HMDB0000725	5810	C01157	C1[C@H](CN[C@@H]1C=CC=C1)O
11	HMDB0002712	HMDB0002712	64960	C07326	C1[C@@H]([C@H]([C@@H](C=C1)O)O
12	HMDB0000247	HMDB0000247	5780	C00794	C([C@H]([C@H]([C@H]([C@@H](C=C1)O)O)O
13	HMDB0000660	HMDB0000660	439709	C02336	C([C@@H]1[C@H]([C@@H]([C@@H](C=C1)O)O)O
14	HMDB0000532	HMDB0000532	10972		
15	HMDB0003219	HMDB0003219	439645	C08355	C(C(C(C(C(C(=O)CO)O)O)O)O
16	HMDB0000211	HMDB0000211		C00137	O[C@H]1[C@H](O)[C@C](O)O
17	HMDB000161	HMDB000161	5950	C00041	C([C@@H](C(=O)O)N
18	HMDB0001264	HMDB0001264	7786	C05422	C([C@H]([C@H]1C=CC=C1)O)O
19	HMDB61711	HMDB0061711	13130		
20	HMDB0001401	HMDB0001401	5958	C00092	C([C@@H]1[C@H]([C@@H]([C@@H](C=C1)O)O)O
21	HMDB0000645	HMDB0000645	123912	C00446	C([C@@H]1[C@H]([C@@H]([C@@H](C=C1)O)O)O
22	HMDB0002108	HMDB0002108	384585100	C22040	CSC([C@H]([C@H]([C@H]([C@@H](C=C1)O)O)O)O
23	HMDB0001078	HMDB0001078	439198	C00275	C([C@@H]1[C@H]([C@@H]([C@@H](C=C1)O)O)O
24	HMDB0001373	HMDB0001373	439335	C00882	CC(C)(COP(=O)(O)OP(=O)(O)O
25	HMDB0000210	HMDB0000210	6613	C00864	CC(C)(C)C(C(=O)NC(=O)O)O
26	HMDB0011732	HMDB0011732	50	C03342	C(C(C(C(C(=O)C(=O)O)C(=O)O)O)O
27	HMDB0000875	HMDB0000875	5570	C01004	C[N+]=CC=CC=C(C(=O)O)O
28	HMDB0001262	HMDB0001262	439586	C01835	C([C@@H]1[C@H]([C@@H]([C@@H](C=C1)O)O)O
29	HMDB0001423	HMDB0001423	87642	C00010	CC(C)(COP(=O)(O)OP(=O)(O)O
30	HMDB0002092	HMDB0002092	811	C00490	=C(CC(=O)O)C(=O)O
31	HMDB0007112	HMDB0007112	9543736	C00165	CCCCCCCCCCCCCCCCCCCC
32	HMDB0004827	HMDB0004827	7016563	C10172	C[N+]=CC[C@H]1C(=O)O
33	HMDB0002329	HMDB0002329	971	C00209	C(=O)(C(=O)O)O
34	HMDB0001254	HMDB0001254	439217	C00352	C([C@@H]1[C@H]([C@H]([C@@H](C=C1)O)O)O
35	HMDB0000177	HMDB0000177	6274	C00135	C1=CN=C(N1)C([C@H]([C@@H](C=C1)O)O)O
36	HMDB0012141	HMDB0012141	440279	C04272	CC(C)([C@H](C(=O)O)O)O
37	HMDB0001049	HMDB0001049	123938	C00669	C(CC(=O)N[C@@H](CS(=O)(=O)C)O)O
38	HMDB0000011	HMDB0000011	92135	C01089	C[C@H](CC(=O)O)O
39	HMDB0240578	NA	NA		NA
40	HMDB0000001	HMDB0000001	92105	C01152	CN1C=C(N=C1)C([C@@H](C=C1)O)O
41	HMDB0000355	HMDB0000355	1662	C03761	CC(CC(=O)O)(CC(=O)O)O
42	HMDB0000259	HMDB0000259	5202	C00780	C1=CC2=C(C=C1O)C=C2
43	HMDB0010395	HMDB0010395	24779476	C04230	CCCC/C=C\CC/C=C/C\
44	HMDB0000560	HMDB0000560	5312409		CCCC/C=C\CC/C=C/C\
45	HMDB0002000	HMDB0002000	5281119	C08322	CCC/C=C\CCCCCCC
46	HMDB0013133	HMDB0013133	53481628		CC(C(=O)O)C(=O)O)O
47	HMDB0028844	HMDB0028844	88079		CCC(C)C(NC(=O)CN)O
48	HMDB0240506	NA	NA		NA
49	HMDB001348	HMDB001348	5283588	C00550	CCCCCCCCCCCCCCCC
50	HMDB0009003	HMDB0009003	5289133	C00350	CCCCCCCCCCCCCCCC
51	HMDB0013127	HMDB0013127	53481617		CC(CC(=O)O)C([C@H](C=C1)O)O
52	HMDB0000126	HMDB0000126	439162	C00093	C([C@H](COP(=O)(O)O)O)O
53	HMDB0240316	NA	NA		NA
54	HMDB0003426	HMDB0003426	479	C00831	CC(C)(CO)C(C(=O)O)O
55	HMDB0000855	HMDB0000855	439924	C03150	C1=CC(=C[N+](=C1)O)O
56	HMDB0000917	HMDB0000917	122340	C17644	C([C@H](CCC(=O)O)O)C(=O)O
57	HMDB0003331	HMDB0003331	27476	C02494	CN1C=NC2=C(C1=N)C=C2
58	HMDB0000023	HMDB0000023	87	C06001	C([C@H](CO)C(=O)O)O
59	HMDB0004645	HMDB0004645	104858		C(CC(=O)O)N[C@@H](C=C1)O





234	HMDB0000929	L-Tryptophan	HMDB0000929	6305	C00078	C1=CC=C2C(=C1)C(=O)NCC(C)CC(N)C(=O)NCC
235	HMDB0028929	Leucyl-Glycine	HMDB0028929	97364	C00500	CC\1=C/C(=C=C2C=CC
236	HMDB0001008	Biliverdin	HMDB0001008	5353439	C00500	CC\1=C/C(=C=C2C=CC
237	HMDB0061684	N-Acetylsoleucine	HMDB0061684	7036275	C02067	C1=C(C(=O)NC(=O)N
238	HMDB0000767	Pseudouridine	HMDB0000767	15047	C02067	C1=C(C(=O)NC(=O)N
239	HMDB0012458	7alpha-Hydroxy-3-oxo-4-cholestenoate	HMDB0012458	3081085	C17337	C1=C(C(=O)OC(CC(=O)[O-]
240	HMDB0000201	L-Acetyl carnitine	HMDB0000201	7045767	C02571	CCCCCCCCCCCC(=O)NCC
241	HMDB0000832	Capryloylglycine	HMDB0000832	84290	C00165	CCCCCCC/C=C\CCCCC
242	HMDB0007132	DG(16:1(9Z)/18:2(9Z,12Z)/0:0)	HMDB0007132	9543699	C02918	C[N+]=1=CC=CC(=C1)C
243	HMDB0000699	1-Methylnicotinamide	HMDB0000699	457	C14536	COCl1=C(C=C2C(=C1)C
244	HMDB0005781	Glycitein	HMDB0005781	5317750	NA	CCCCCCCCCCCCCCC/
245	HMDB0011352	PE(P-16:0/20:4(5Z,8Z,11Z,14Z))	HMDB0011352	52925126	NA	NA
246	HMDB000506	NA	NA	NA	NA	CCCC(=O)NCC(=O)O
247	HMDB0000927	Valerylglycine	HMDB0000927	4737557	C02477	CC1=C(C(=C2CC[C@H](C
248	HMDB0001893	Alpha-Tocopherol	HMDB0001893	14985	C05283	C(=C(=O)N[C@H](C)C
249	HMDB0011738	N2-gamma-Glutamylglutamine	HMDB0011738	150914	C02057	CCCCCCCCCCCCCCC/
250	HMDB0011152	PE(P-16:0e:0:0)	HMDB0011152	42607469	C02057	CCCCC/C=C\C/C=C\
251	HMDB0011538	MG(0:0/18:2(9Z,12Z)/0:0)	HMDB0011538	5365676	C00157	C/C=C(\C)(C(=O)NCC
252	HMDB0000959	Tiglylglycine	HMDB0000959	6441567	C00376	C1=NC2=C(C(=N1)N[
253	HMDB0000912	Succinyladenosine	HMDB0000912	20849086	C00121	C([C@H]1[C@H](C)C
254	HMDB0000283	D-Ribose	HMDB0000283	5779	C00300	CN(CC(=O)O)C(=N)N
255	HMDB000064	Creatine	HMDB000064	586	C00791	CN1C(=O)=N=C1N
256	HMDB0000562	Creatinine	HMDB0000562	588	C00157	CCCCCCCCCCCCCCC(=O)
257	HMDB0007883	PC(14:0/20:4(5Z,8Z,11Z,14Z))	HMDB0007883	24778634	C00086	CC1=C(C(=C1)C(=C
258	HMDB0001358	Retinal	HMDB0001358	6436079	C02989	C(=O)(N)N
259	HMDB0013130	Glutaryl carnitine	HMDB0013130	71317118	C03410	CS(=O)CCC(C(=O)O)N
260	HMDB0000833	N-Glycolylneuraminic acid	HMDB0000833	16738688	C00082	CC/C=C\C/C=C\C/C
261	HMDB0002095	Malonylcarnitine	HMDB0002095	22833583	C00082	C(=O)O)N=C(N)N
262	HMDB0000158	L-Tyrosine	HMDB0000158	6057	C01762	C1=NC2=C(N1[C@H]3[
263	HMDB0000294	Urea	HMDB0000294	2447	NA	NA
264	HMDB0002005	Methionine sulfoxide	HMDB0002005	847	NA	CCCCCCCC(=O)OCC
265	HMDB11580	MG(20:5(5Z,8Z,11Z,14Z,17Z)/0:0/0:0)	HMDB0011580	53480988	C02140	CC(=O)N[C@H]1[C@H](C
266	HMDB0000128	Guanidoacetic acid	HMDB0000128	763	C01103	C1=C(N(=C(O)N1C=O)N
267	HMDB0000299	Xanthosine	HMDB0000299	64959	C01551	C1(=C(=O)NC(=O)N1)N
268	HMDB0041724	NA	NA	NA	C07588	C1=CC=C(C(=C1)C(=
269	HMDB0000651	Decanoylcarnitine	HMDB0000651	10245190	C00318	C[N+](C)(C)C[C@H](C)
270	HMDB0001176	Cytidine monophosphate N-acetylneuraminic acid	HMDB0001176	448209	C00128	CC(=O)N[C@H]1[C@H](C
271	HMDB0010325	Ethyl glucuronide	HMDB0010325	18392195	C02140	CCO[C@H]1[C@H](C)C
272	HMDB0001547	Corticosterone	HMDB0001547	5753	C01103	C1=C(N(=C(O)N1C=O)N
273	HMDB0000788	Orotidine	HMDB0000788	92751	C01551	C1(=C(=O)NC(=O)N1)N
274	HMDB0000462	Allantoin	HMDB0000462	204	C07588	C1=CC=C(C(=C1)C(=
275	HMDB0000840	Salicyluric acid	HMDB0000840	10253	C00318	C[N+](C)(C)C[C@H](C)
276	HMDB0000062	L-Carnitine	HMDB0000062	2724480	C01657	CC(=O)N[C@H](C)C
277	HMDB0000866	N-Acetyl-L-tyrosine	HMDB0000866	68310	C07921	C1[C@H](CC1=CC=C(C(=
278	HMDB0014903	Metyrosine	HMDB0014903	441350	C13861	CCCCCCCCCCCCCCCC
279	HMDB0007102	DG(16:0/18:1(9Z)/0:0)	HMDB0007102	5282283	C00134	C(CC)CN
280	HMDB0001414	Putrescine	HMDB0001414	1045	C00144	CC(C)CC(=O)NCC(=O)
281	HMDB00678	Isovalerylglycine	HMDB0000678	546304	C02427	(C(CCNC(=O)N)C[C@@H](C
282	HMDB0000679	Homocitrulline	HMDB0000679	65072	NA	NA
283	HMDB0061677	NA	NA	NA	NA	NA
284	HMDB0001397	Guanosine monophosphate	HMDB0001397	6804	C00144	C1=NC2=C(N1[C@H]3[
285	HMDB11760	Cer(d18:0/16:0)	HMDB0011760	5283572	C00157	CCCCCCCCCCCCCCCC
286	HMDB0007969	PC(16:0/16:1(9Z))	HMDB0007969	6443788	C01620	C([C@H]1[C@H](C)C(=C
287	HMDB0006469	Linoleyl carnitine	HMDB0006469	6450015	C00647	C[C@H](C)C(=O)NCC
288	HMDB0000943	Threonic acid	HMDB0000943	151152	C00805	CC1=NC=C(C(=C1)C(=
289	HMDB0029159	gamma-Glutamylthreonine	HMDB0029159	53861142	C00165	CCCCCCCCCCCCCCCC
290	HMDB0001555	Pyridoxamine 5'-phosphate	HMDB0001555	1053	C00165	CCCCCCCCCCCCCCCC
291	HMDB0001895	Salicylic acid	HMDB0001895	338	C00024	CC(=O)SCCN(=O)CC
292	HMDB0007103	DG(16:0/18:2(9Z,12Z)/0:0)	HMDB0007103	9543695	C00024	[C@H]1[C@H](C)C
293	HMDB0007249	DG(18:2(9Z,12Z)/18:3(6Z,9Z,12Z)/0:0)	HMDB0007249	14275409	C00191	CC(=O)N[C@H](C)C
294	HMDB0000479	3-Methylhistidine	HMDB0000479	64969	C01152	CN1C=NC=C1C[CA@H](C
295	HMDB13326	trans-2-Dodecenoylcarnitine	HMDB0013326	53481671	C02043	CCCCCCCC/C=C/C=C/C
296	HMDB0000696	L-Methionine	HMDB0000696	6137	C00073	CSCC[C@H](C)C(=O)O
297	HMDB0001206	Acetyl-CoA	HMDB0001206	444493	C00024	CC(=O)SCCN(=O)CC
298	HMDB0000127	D-Glucuronic acid	HMDB0000127	94715	C00191	[C@H]1[C@H](C)C
299	HMDB0011756	N-Acetylleucine	HMDB0011756	70912	C02727	CC(C)C[C@H](C)C(=O)
300	HMDB0000671	Indolelactic acid	HMDB0000671	92904	C02043	C1=CC=C2C(=C1)C(=
301	HMDB0094710	3-[3-(Sulfoxy)phenyl]propanoic acid	HMDB0094710	187488	C00165	OC(=O)CCC1=CC(OS(=O)O)C
302	HMDB0004194	N1-Methyl-4-pyridone-3-carboxamide	HMDB0004194	440810	C05843	CN1C=CC(=O)C(=C1)C(=
303	HMDB001874	D-threo-Isocitric acid	HMDB001874	5318532	C00451	C([C@H]1[C@H](C)C(=C
304	HMDB0000206	N6-Acetyl-L-lysine	HMDB0000206	92832	C02727	CC(=O)NCCCC[C@H](C)C
305	HMDB0000014	Deoxycytidine	HMDB0000014	13711	C00881	C1[C@H](C)C(=O)OCC
306	HMDB0003464	4-Guanidinobutananoic acid	HMDB0003464	500	C01035	C(CC(=O)O)CN=C(N)N
307	HMDB0240592	NA	NA	NA	NA	NA
308	HMDB0059586	NA	NA	NA	NA	NA
309	HMDB0013205	9-Decenoylcarnitine	HMDB0013205	53481651	C00599	C[N+](C)(C)CC(CC(=O)C
310	HMDB0000921	Cholestenone	HMDB0000921	91477	C01697	C([C@H]1[C@H](C)C(=C
311	HMDB0000107	Galactitol	HMDB0000107	11850	C00157	CCCCCCCCCCCCCCCC
312	HMDB0007982	PC(16:0/20:4(5Z,8Z,11Z,14Z))	HMDB0007982	10747814	C00157	CC(=O)N[C@H]1[C@H](C)C
313	HMDB0002817	N-Acetylglucosamine 6-phosphate	HMDB0002817	439219	C00612	CCCCCCCCCCCCCCCC
314	HMDB0001276	N1-Acetylpermidine	HMDB0001276	496	C05598	CCCC/C=C\C/C=C\
315	HMDB0000821	Phenylacetylglucine	HMDB0000821	68144	C00157	CCCC/C=C\C/C=C\
316	HMDB0008138	PC(18:2(9Z,12Z)/18:2(9Z,12Z))	HMDB0008138	5288075	C00157	CN1CCC[C@H]1C(=O)O
317	HMDB0094696	N-Methyl-proline	HMDB0094696	643474	C16512	CCCCCCCCCCCCCCCC
318	HMDB0002100	Palmitoylthanolamide	HMDB0002100	4671	C16512	CCCCCCCCCCCCCCCC
319	HMDB11578	MG(20:4(5Z,8Z,11Z,14Z)/0:0/0:0)	HMDB0011578	16019980	C00165	CCCCCCCC/C=C\CCCC
320	HMDB0007218	DG(18:1(9Z)/18:1(9Z)/0:0)	HMDB0007218	9543716	C00165	CCCCCCCC/C=C\CCCC

321	HMDB0012097	SM(d18:1/14:0)	HMDB0012097	11433862	C00127	CCCCCCCCCCCC/C=CN(C(=O)N=C1N)
322	HMDB0011691	Cytidine 2',3'-cyclic phosphate	HMDB0011691	53481030	NA	NA
323	HMDB0005320	NA	NA	NA	NA	NA
324	HMDB000162	L-Proline	HMDB000162	145742	C00148	C1C[C@H](NC1)C(=O)O
325	HMDB0001070	Octanoyl-CoA	HMDB0001070	380	C01944	CCCCCC(=O)SCCN
326	HMDB0013128	Valerylcarnitine	HMDB0013128	53481619	CC5852	CCCC(-=O)O[C@H]([C@H](C)C)C
327	HMDB0000669	Ortho-Hydroxyphenylacetic acid	HMDB0000669	11970	C05852	C1=CC=C(C(=C1)OC(=O)C
328	HMDB0011686	p-Cresol glucuronide	HMDB0011686	154035	CC1=CC=C(C=C1)O[CH]	
329	HMDB0028995	Phenylalanyl-Glycine	HMDB0028995	98207	NC(CC1=CC=CC=C1)[C@H](C)C	
330	HMDB0009784	PI(16:0/18:2(9Z,12Z))	HMDB0009784	92918	C00626	[H][C@@](COC(=O)CC)C
331	HMDB0000982	5-Methylcytidine	HMDB0000982	6642	C03912	CC1=CN(C(=O)N=C1N)C
332	HMDB0001301	1-Pyrroline-5-carboxylic acid	HMDB0001301	6451814	CN1C=NC=C1CC(=O)O	
333	HMDB04988	Pi-Methylimidazoleacetic acid	HMDB0004988	9546749	C00350	CCCCCCCCCCCCCCCC
334	HMDB0008994	PE(18:0/18:2(9Z,12Z))	HMDB0008994	6083	C00020	C1=NC2=C(C(=N1)N)C
335	HMDB0000045	Adenosine monophosphate	HMDB0000045	439371	C15980	CCC(C)C(=O)SCCN(C(=O)O
336	HMDB0001041	2-Methylbutyryl-CoA	HMDB0001041	5283591	C00550	CCCCCCCCCCCCCCCC
337	HMDB0010168	SM(d18:0/16:0)	HMDB0010168	67427	CC(=O)N[C@@H](CC)C	
338	HMDB0004620	N-a-Acetyl-L-arginine	HMDB0004620	5283565	C00195	CCCCCCCCCCCCCCCC
339	HMDB0004950	Ceramide (d18:1/18:0)	HMDB0004950	58	C00109	CCC(=O)C(=O)O
340	HMDB0000005	2-Ketobutyric acid	HMDB0000005	22885096	CC[C@H](C)[C@@H](C)C	
341	HMDB0011170	gamma-Glutamylisoleucine	HMDB0011170	4433	C16741	C(C[C@H](C)(C(=O)O)N
342	HMDB0000450	5-Hydroxylysine	HMDB0000450	NA	NA	NA
343	HMDB0061636	NA	NA	NA	NA	NA
344	HMDB0000133	Guanosine	HMDB0000133	6802	C00387	C1=NC2=C(N1[C@H]3[C
345	HMDB0003518	Homocitric acid	HMDB0003518	439459	C01251	C(C[C@H](C)C(=O)O)(C
346	HMDB0002024	Imidazoleacetic acid	HMDB0002024	96215	C02835	C1=C(NC=N1)CC(=O)O
347	HMDB0032055	N-Acetylhistidine	HMDB0032055	273260	C02997	CC(=O)NC(CC1=CN=C
348	HMDB0005779	PE(O-18:1(1Z)/20:4(5Z,8Z,11Z,14Z))	HMDB0005779	9547058	C00350	CCCCCCCCCCCCCCCC
349	HMDB002331	Imidazoleacetic acid riboside	HMDB002331	440569	C05131	C1=C(N=CN1[C@H]2[C
350	HMDB0029151	gamma-Glutamylhistidine	HMDB0029151	7017195	C1=C(NC=N1)C[C@H](C	
351	HMDB0001257	Spermidine	HMDB0001257	1102	C00315	C(CCNCCCN)CN

The second step is to check concentration values. For SSP analysis, the concentration must be measured in *umol* for blood and CSF samples. The urinary concentrations must be first converted to *umol/mmol\_creatinine* in order to compare with reported concentrations in literature. No missing or negative values are allowed in SSP analysis. The concentration data for QEA analysis is more flexible. Users can upload either the original concentration data or normalized data. Missing or negative values are allowed (coded as *NA*) for QEA.

## 5 Selection of Metabolite Set Library

Before proceeding to enrichment analysis, a metabolite set library has to be chosen. There are seven built-in libraries offered by MSEA:

- Metabolic pathway associated metabolite sets (*currently contains 99 entries*);
- Disease associated metabolite sets (reported in blood) (*currently contains 344 entries*);
- Disease associated metabolite sets (reported in urine) (*currently contains 384 entries*)
- Disease associated metabolite sets (reported in CSF) (*currently contains 166 entries*)
- Metabolite sets associated with SNPs (*currently contains 4598 entries*)
- Predicted metabolite sets based on computational enzyme knockout model (*currently contains 912 entries*)
- Metabolite sets based on locations (*currently contains 73 entries*)
- Drug pathway associated metabolite sets (*currently contains 461 entries*)

In addition, MSEA also allows user-defined metabolite sets to be uploaded to perform enrichment analysis on arbitrary groups of compounds which researchers want to test. The metabolite set library is simply a two-column comma separated text file with the first column for metabolite set names and the second column for its compound names (**must use HMDB compound name**) separated by "; ". Please note, the built-in libraries are mainly from human studies. The functional grouping of metabolites may not be valid. Therefore, for data from subjects other than human being, users are suggested to upload their self-defined metabolite set libraries for enrichment analysis.

## 6 Enrichment Analysis

Over Representation Analysis (ORA) is performed when a list of compound names is provided. The list of compound list can be obtained through conventional feature selection methods, or from a clustering algorithm, or from the compounds with abnormal concentrations detected in SSP, to investigate if some biologically meaningful patterns can be identified.

ORA was implemented using the *hypergeometric test* to evaluate whether a particular metabolite set is represented more than expected by chance within the given compound list. One-tailed p values are provided after adjusting for multiple testing. **Figure 2** below summarizes the result.

## Enrichment Overview (top 25)

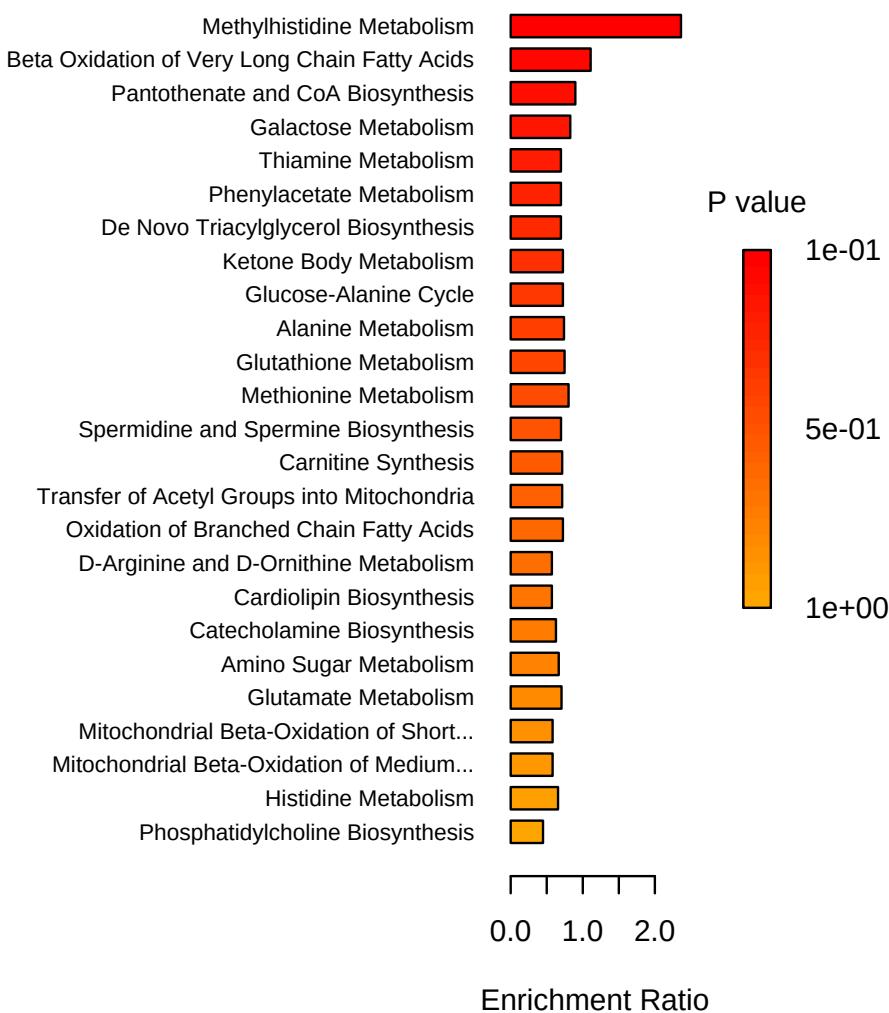


Figure 1: Summary Plot for Over Representation Analysis (ORA)

Table 2: Result from Over Representation Analysis

	total	expected	hits	Raw p	Holm p	FDR
Methylhistidine Metabolism	4	1.27	3	9.78E-02	1.00E+00	1.00E+00
Beta Oxidation of Very Long Chain Fatty Acids	17	5.41	6	4.69E-01	1.00E+00	1.00E+00
Pantothenate and CoA Biosynthesis	21	6.69	6	7.05E-01	1.00E+00	1.00E+00
Galactose Metabolism	38	12.10	10	8.21E-01	1.00E+00	1.00E+00
Thiamine Metabolism	9	2.87	2	8.36E-01	1.00E+00	1.00E+00
Phenylacetate Metabolism	9	2.87	2	8.36E-01	1.00E+00	1.00E+00
De Novo Triacylglycerol Biosynthesis	9	2.87	2	8.36E-01	1.00E+00	1.00E+00
Ketone Body Metabolism	13	4.14	3	8.36E-01	1.00E+00	1.00E+00
Glucose-Alanine Cycle	13	4.14	3	8.36E-01	1.00E+00	1.00E+00
Alanine Metabolism	17	5.41	4	8.42E-01	1.00E+00	1.00E+00
Glutathione Metabolism	21	6.69	5	8.50E-01	1.00E+00	1.00E+00
Methionine Metabolism	43	13.70	11	8.58E-01	1.00E+00	1.00E+00
Spermidine and Spermine Biosynthesis	18	5.73	4	8.75E-01	1.00E+00	1.00E+00
Carnitine Synthesis	22	7.00	5	8.79E-01	1.00E+00	1.00E+00
Transfer of Acetyl Groups into Mitochondria	22	7.00	5	8.79E-01	1.00E+00	1.00E+00
Oxidation of Branched Chain Fatty Acids	26	8.28	6	8.84E-01	1.00E+00	1.00E+00
D-Arginine and D-Ornithine Metabolism	11	3.50	2	9.11E-01	1.00E+00	1.00E+00
Cardiolipin Biosynthesis	11	3.50	2	9.11E-01	1.00E+00	1.00E+00
Catecholamine Biosynthesis	20	6.37	4	9.23E-01	1.00E+00	1.00E+00
Amino Sugar Metabolism	33	10.50	7	9.41E-01	1.00E+00	1.00E+00
Glutamate Metabolism	49	15.60	11	9.49E-01	1.00E+00	1.00E+00
Mitochondrial Beta-Oxidation of Short Chain Saturated Fatty Acids	27	8.60	5	9.63E-01	1.00E+00	1.00E+00
Mitochondrial Beta-Oxidation of Medium Chain Saturated Fatty Acids	27	8.60	5	9.63E-01	1.00E+00	1.00E+00
Histidine Metabolism	43	13.70	9	9.63E-01	1.00E+00	1.00E+00
Phosphatidylcholine Biosynthesis	14	4.46	2	9.66E-01	1.00E+00	1.00E+00
Butyrate Metabolism	19	6.05	3	9.69E-01	1.00E+00	1.00E+00
Ethanol Degradation	19	6.05	3	9.69E-01	1.00E+00	1.00E+00
Homocysteine Degradation	9	2.87	1	9.69E-01	1.00E+00	1.00E+00
Lactose Degradation	9	2.87	1	9.69E-01	1.00E+00	1.00E+00
Sphingolipid Metabolism	40	12.70	8	9.69E-01	1.00E+00	1.00E+00
Mitochondrial Beta-Oxidation of Long Chain Saturated Fatty Acids	28	8.91	5	9.71E-01	1.00E+00	1.00E+00
Lactose Synthesis	20	6.37	3	9.77E-01	1.00E+00	1.00E+00
Threonine and 2-Oxobutanoate Degradation	20	6.37	3	9.77E-01	1.00E+00	1.00E+00
Pentose Phosphate Pathway	29	9.23	5	9.78E-01	1.00E+00	1.00E+00
Pyruvaldehyde Degradation	10	3.18	1	9.79E-01	1.00E+00	1.00E+00
Glycolysis	25	7.96	4	9.80E-01	1.00E+00	1.00E+00
Propanoate Metabolism	42	13.40	8	9.80E-01	1.00E+00	1.00E+00
Beta-Alanine Metabolism	34	10.80	6	9.81E-01	1.00E+00	1.00E+00
Betaine Metabolism	21	6.69	3	9.83E-01	1.00E+00	1.00E+00
Phytanic Acid Peroxisomal Oxidation	26	8.28	4	9.85E-01	1.00E+00	1.00E+00
Glycine and Serine Metabolism	59	18.80	12	9.85E-01	1.00E+00	1.00E+00
Glycerol Phosphate Shuttle	11	3.50	1	9.86E-01	1.00E+00	1.00E+00
Phosphatidylinositol Phosphate Metabolism	17	5.41	2	9.87E-01	1.00E+00	1.00E+00
Phosphatidylethanolamine Biosynthesis	12	3.82	1	9.90E-01	1.00E+00	1.00E+00
Nicotinate and Nicotinamide Metabolism	37	11.80	6	9.91E-01	1.00E+00	1.00E+00
Thyroid hormone synthesis	13	4.14	1	9.93E-01	1.00E+00	1.00E+00
Urea Cycle	29	9.23	4	9.94E-01	1.00E+00	1.00E+00
Glycerolipid Metabolism	25	7.96	3	9.95E-01	1.00E+00	1.00E+00
Nucleotide Sugars Metabolism	20	6.37	2	9.95E-01	1.00E+00	1.00E+00
Gluconeogenesis	35	11.10	5	9.96E-01	1.00E+00	1.00E+00
Fatty Acid Biosynthesis	35	11.10	5	9.96E-01	1.00E+00	1.00E+00
Cysteine Metabolism	26	8.28	3	9.96E-01	1.00E+00	1.00E+00
Starch and Sucrose Metabolism	31	9.87	4	9.96E-01	1.00E+00	1.00E+00
Warburg Effect	58	18.50	10	9.97E-01	1.00E+00	1.00E+00
Ammonia Recycling	32	10.20	4	9.97E-01	1.00E+00	1.00E+00
Citric Acid Cycle	32	10.20	4	9.97E-01	1.00E+00	1.00E+00
Fructose and Mannose Degradation	32	10.20	4	9.97E-01	1.00E+00	1.00E+00
Retinol Metabolism	37	11.80	5	9.98E-01	1.00E+00	1.00E+00
Sulfate/Sulfite Metabolism	22	7.00	2	9.98E-01	1.00E+00	1.00E+00
Selenoamino Acid Metabolism	28	8.91	3	9.98E-01	1.00E+00	1.00E+00
Fatty acid Metabolism	43	13.70	6	9.98E-01	1.00E+00	1.00E+00
Pyruvate Metabolism	48	15.30	7	9.99E-01	1.00E+00	1.00E+00
Arginine and Proline Metabolism	53	16.90	8	9.99E-01	1.00E+00	1.00E+00
Caffeine Metabolism	24	7.64	2	9.99E-01	1.00E+00	1.00E+00
Estrone Metabolism	24	7.64	2	9.99E-01	1.00E+00	1.00E+00
Mitochondrial Electron Transport Chain	19	6.05	1	9.99E-01	1.00E+00	1.00E+00
Inositol Phosphate Metabolism	26	8.28	2	9.99E-01	1.00E+00	1.00E+00
Bile Acid Biosynthesis	65	20.70	10	9.99E-01	1.00E+00	1.00E+00
Vitamin B6 Metabolism	20	6.37	1	1.00E+00	1.00E+00	1.00E+00
Ubiquinone Biosynthesis	20	6.37	1	1.00E+00	1.00E+00	1.00E+00
Riboflavin Metabolism	20	6.37	1	1.00E+00	1.00E+00	1.00E+00
Inositol Metabolism	33	10.50	3	1.00E+00	1.00E+00	1.00E+00
Phenylalanine and Tyrosine Metabolism	28	8.91	2	1.00E+00	1.00E+00	1.00E+00
Phospholipid Biosynthesis	29	9.23	2	1.00E+00	1.00E+00	1.00E+00
Folate Metabolism	29	9.23	2	1.00E+00	1.00E+00	1.00E+00
Valine, Leucine and Isoleucine Degradation	60	19.10	8	1.00E+00	1.00E+00	1.00E+00

Fatty Acid Elongation In Mitochondria	35	11.10	3	1.00E+00	1.00E+00	1.00E+00
Aspartate Metabolism	35	11.10	3	1.00E+00	1.00E+00	1.00E+00
Lysine Degradation	30	9.55	2	1.00E+00	1.00E+00	1.00E+00
Tryptophan Metabolism	60	19.10	7	1.00E+00	1.00E+00	1.00E+00
Androgen and Estrogen Metabolism	33	10.50	2	1.00E+00	1.00E+00	1.00E+00
Plasmalogen Synthesis	26	8.28	1	1.00E+00	1.00E+00	1.00E+00
Pterine Biosynthesis	29	9.23	1	1.00E+00	1.00E+00	1.00E+00
Porphyrin Metabolism	40	12.70	2	1.00E+00	1.00E+00	1.00E+00
Purine Metabolism	74	23.60	8	1.00E+00	1.00E+00	1.00E+00
Pyrimidine Metabolism	59	18.80	5	1.00E+00	1.00E+00	1.00E+00
Steroid Biosynthesis	48	15.30	2	1.00E+00	1.00E+00	1.00E+00
Steroidogenesis	43	13.70	1	1.00E+00	1.00E+00	1.00E+00
Tyrosine Metabolism	72	22.90	4	1.00E+00	1.00E+00	1.00E+00
Arachidonic Acid Metabolism	69	22.00	1	1.00E+00	1.00E+00	1.00E+00

## 7 Appendix: R Command History

```
[1] "mSet<-InitDataObjects(\"conc\", \"msetora\", FALSE)"
[2] "cmpd.vec<-c(\"HMDB0000169\", \"HMDB0000190\", \"HMDB0000122\", \"HMDB0029965\", \"HMDB0000125\", \"")
[3] "mSet<-Setup.MapData(mSet, cmpd.vec);"
[4] "mSet<-CrossReferencing(mSet, \"hmdb\");"
[5] "mSet<-CreateMappingResultTable(mSet)"
[6] "mSet<-SetMetabolomeFilter(mSet, F);"
[7] "mSet<-SetCurrentMsetLib(mSet, \"smpdb_pathway\", 2);"
[8] "mSet<-CalculateHyperScore(mSet)"
[9] "mSet<-PlotORA(mSet, \"ora_0\", \"net\", \"png\", 72, width=NA)"
[10] "mSet<-PlotEnrichDotPlot(mSet, \"ora\", \"ora_dot_0\", \"png\", 72, width=NA)"
[11] "mSet<-CalculateHyperScore(mSet)"
[12] "mSet<-PlotORA(mSet, \"ora_1\", \"net\", \"png\", 72, width=NA)"
[13] "mSet<-PlotEnrichDotPlot(mSet, \"ora\", \"ora_dot_1\", \"png\", 72, width=NA)"
[14] "mSet<-SaveTransformedData(mSet)"
[15] "mSet<-PreparePDFReport(mSet, \"guest16292574549826598929\")\n"
```

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The report was generated on Sat Mar 20 21:24:04 2021 with R version 4.0.2 (2020-06-22).