Metabolomic Data Analysis with MetaboAnalyst 6.0

Name: guest7106216319241885243

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1 Background

The Pathway Analysis module combines results from powerful pathway enrichment analysis with pathway topology analysis to help researchers identify the most relevant pathways involved in the conditions under study.

There are many commercial pathway analysis software tools such as Pathway Studio, MetaCore, or Ingenuity Pathway Analysis (IPA), etc. Compared to these commercial tools, the pathway analysis module was specifically developed for metabolomics studies. It uses high-quality KEGG metabolic pathways as the backend knowledgebase. This module integrates many well-established (i.e. univariate analysis, over-representation analysis) methods, as well as novel algorithms and concepts (i.e. Global Test, GlobalAncova, network topology analysis) into pathway analysis. Another feature is a Google-Map style interactive visualization system to deliver the analysis results in an intuitive manner.

2 Data Input

The Pathway Analysis module accepts either a list of compound labels (common names, HMDB IDs or KEGG IDs) with one compound per row, or a compound concentration table with samples in rows and compounds in columns. The second column must be phenotype labels (binary, multi-group, or continuous). The table is uploaded as comma separated values (.csv).

3 Compound Name Matching

The first step is to standardize the compound labels used in user uploaded data. This is a necessary step since these compounds will be subsequently compared with compounds contained in the pathway library. There are three outcomes from the step - exact match, approximate match (for common names only), and no match. Users should click the textbfView button from the approximate matched results to manually select the correct one. Compounds without match will be excluded from the subsequently pathway analysis.

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
1	dimethylphenol sulfate	NA	NA	NA	NA
2	N8-acetylspermidine	N8-Acetylspermidine	HMDB0002189	123689	C01029
3	(S)-a-amino-omega-caprolactam	NA	NA	NA	NA
4	1-carboxyethylisoleucine	NA	NA	NA	NA
5	1-carboxyethylleucine	NA	NA	NA	NA
6	1-carboxyethylvaline	NA	NA	NA	NA
7	1-methyl-4-imidazoleacetate	Methylimidazoleacetic acid	HMDB0002820	75810	C05828
8	1-methylhistamine	1-Methylhistamine	HMDB0000898	3614	C05127
9	1-methylhistidine	1-Methylhistidine	HMDB0000001	92105	C01152

10	1-ribosyl-imidazoleacetate	Imidazoleacetic acid riboside	HMDB0002331	440569	C05131
11	11-beta-hydroxyandrosterone-3-glucuronide	11-beta-Hydroxyandrosterone-3-glucuronide	HMDB0010351	1864	C05643
12	7a-Hydroxypregnenolone	7alpha-Hydroxypregnenolone	HMDB0060424	9967418	C18038
13	2-aminooctanoate	DL-2-Aminooctanoic acid	HMDB0000991	69522	
14	2-dimethylaminoethanol	Dimethylethanolamine	HMDB0032231	7902	C04308
15	2-ethylphenylsulfate	NA	NA	NA	NA
16	2-hydroxy-3-methylvalerate	2-Hydroxy-3-methylpentanoic acid	HMDB0000317	10796774	
17	2-hydroxysebacate	2-Hydroxydecanedioic acid	HMDB0000424	128458	
18	2-methylbutyrylcarnitine	NA	NA	NA	NA
19	2-methylbutyrylglycine	2-Methylbutyrylglycine	HMDB0000339	193872	
20	2-methylmalonylcarnitine	NA	NA	NA	NA
21	2-methylserine	NA	NA	NA	NA
22	2,3-dimethylsuccinate	NA	NA	NA	NA
23	3-(3-amino-3-carboxypropyl)uridine	NA	NA	NA	NA
24	3-acetylphenol sulfate	NA	NA	NA	NA
25	3-amino-2-piperidone	3-Amino-2-piperidone	HMDB0000323	5200225	
26	3-ethylcatechol sulfate	O-methoxycatechol-O-sulphate	HMDB0060013	22473	
27	3-hydroxy-4-methylpyridine sulfate	NA	NA	NA	NA
28	3-hydroxybenzoate	3-Hydroxybenzoic acid	HMDB0002466	7420	C00587
29	3-methoxytyramine sulfate	NA	NA	NA	NA
30	3-methyl catechol sulfate	NA	NA	NA	NA
31	3,4-dihydroxyphenylacetate sulfate	NA	NA	NA	NA
32	3'-sialyllactose	3'-Sialyllactose	HMDB0000825	123914	
33	3alpha,21-Dihydroxy-5beta-pregnane-11,20-dione	3a,21-Dihydroxy-5b-pregnane-11,20-dione	HMDB0006755	44263347	C05478
34	4-acetylphenyl sulfate	NA	NA	NA	NA
35	4-ethyl-2-methoxyphenol sulfate	NA	NA	NA	NA
36	4-hydroxyhippurate	p-Hydroxyhippuric acid	HMDB0013678	151012	
37	4-hydroxymandelate	p-Hydroxymandelic acid	HMDB0000822	328	C03198
38	4-hydroxyphenylacetylglycine	Hydroxyphenylacetylglycine	HMDB0000735	440732	C05596
39	O-methoxycatechol-O-sulphate	O-methoxycatechol-O-sulphate	HMDB0060013	22473	
40	4-vinylcatechol sulfate	NA	NA	NA	NA
41	4-vinylguaiacol sulfate	NA	NA	NA	NA
42	4-vinylphenol sulfate	4-Vinylphenol sulfate	HMDB0062775	6426766	
43	4'-hydroxypropiophenone sulfate	NA	NA	NA	NA
44	5-hydroxy-2-methylpyridine sulfate	NA	NA	NA	NA
45	5-hydroxylysine	5-Hydroxylysine	HMDB0000450	3032849	C16741
46	5,6-dihydrothymine	Dihydrothymine	HMDB0000079	676414	C00906
47	6-Bromo-L-tryptophan	NA	NA	NA	NA
48	6-sialyl-N-acetyllactosamine	6-Sialyl-N-acetyllactosamine	HMDB0006584	16212424	
49	6'-sialyllactose	6'-Sialyllactose	HMDB0006569	643987	
50	8-methoxykynurenate	8-Methoxykynurenate	HMDB0060426	76230	C05830
51	adenosine	Adenosine	HMDB0000050	60961	C00212
52	adenosine 3',5'-cyclic monophosphate	Cyclic AMP	HMDB0000058	6076	C00575
53	O-Adipoylcarnitine	O-Adipoylcarnitine	HMDB0061677	91826562	
54	allantoic acid	Allantoic acid	HMDB0001209	203	C00499
55	alpha-CEHC	alpha-CEHC	HMDB0001518	9943542	
56	alpha-CMBHC glucuronide	NA	NA	NA	NA
57	arabitol/xylitol	NA	NA	NA	NA
58	arabonate/xylonate	NA	NA	NA	NA
59	3-Hydroxyisovalerylcarnitine	3-Hydroxyisovalerylcarnitine	HMDB0061189	53915061	
60	biopterin	Biopterin	HMDB0000468	445040	C06313
61	butyrylputrescine/isobutyrylputrescine	NA	NA	NA	NA
62	carboxy-methyl-arginine	NA	NA	NA	NA
63	cis-3,4-methylene-heptanoylcarnitine	NA	NA	NA	NA
64	Cortolone-3-glucuronide	Cortolone-3-glucuronide	HMDB0010320	53480447	
65	cyclo(gly-pro)	NA	NA	NA	NA
66	cyclo(pro-sulfo-tyr)	NA	NA	NA	NA
67	cystathionine	L-Cystathionine	HMDB0000099	439258	C02291
68	cytosine	Cytosine	HMDB0000630	597	C00380
69	delta-CEHC	NA	NA	NA	NA
70	dimethylarginine	Dimethylarginine	HMDB0251395	17801140	
71	dimethylglycine	Dimethylglycine	HMDB0000092	673	C01026
72	dopamine 4-sulfate	Dopamine 4-sulfate	HMDB0004148	123932	C13691
73	ethylmalonate	Ethylmalonic acid	HMDB0000622	11756	
74	formiminoglutamate	Formiminoglutamic acid	HMDB0000854	439233	C00439
75	gamma-CEHC glucuronide	NA	NA	NA	NA
76	gamma-CEHC sulfate	NA	NA	NA	NA
77	gamma-glutamylhistidine	gamma-Glutamylhistidine	HMDB0029151	7017195	
78	glucuronide of C12H20O3	NA	NA	NA	NA
79	glutamine conjugate of C8H12O2	NA	NA	NA	NA
80	glycine conjugate of C10H14O2	NA	NA	NA	NA
81	glycochenodeoxycholate	Chenodeoxycholic acid glycine conjugate	HMDB0000637	12544	C05466
82	Glycochenodeoxycholate-3-sulfate	Glycochenodeoxycholate-3-sulfate	HMDB0002497	21125002	
83	glycocholenate sulfate	NA	NA	NA	NA
84	glycoursodeoxycholic acid sulfate	NA	NA	NA	NA
85	guanosine-3',5'-cyclic monophosphate	NA	NA	NA	NA
86	homoarginine	Homo-L-arginine	HMDB0000670	9085	C01924
87	hydantoin-5-propionate	Hydantoin-5-propionic acid	HMDB0001212	782	C05565
88	hydroquinone sulfate	NA	NA	NA	NA
89	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine	3-Hydroxy-N6,N6,N6-trimethyl-L-lysine	HMDB0001422	439460	C01259
90	(2S,3S)-3-Hydroxyasparagine	NA	NA	NA	NA
91	isobutyrylcarnitine	Isobutyryl-L-carnitine	HMDB0000736	168379	
92	isoeugenol sulfate	NA	NA	NA	NA
93	lanthionine	Lanthionine	HMDB0240656	98504	
94	levulinate	Levulinic acid	HMDB0000720	11579	
95	methyl-4-hydroxybenzoate sulfate	Methyl-4-hydroxybenzoate sulfate	HMDB0168668	122164837	
96	N-acetyl-1-methylhistidine	NA	NA	NA	NA

97	N-Acetylcadaverine	N-Acetylcadaverine	HMDB0002284	189087	
98	N-acetylglutamate	N-Acetyl-L-glutamic acid	HMDB0001138	70914	C00624
99	N-acetylhistamine	N-Acetylhistamine	HMDB0013253	69602	C05135
100	N-acetylisoleucine	N-Acetylisoleucine	HMDB0061684	7036275	
101	N-acetylproline	N-Acetylproline	HMDB0094701	66141	
102	N-acetylputrescine	N-Acetylputrescine	HMDB0002064	122356	C02714
103	N-acetylvaline	N-Acetylvaline	HMDB0011757	66789	
104	2-(Carbamoylamino)propanoic acid	NA	NA	NA	NA
105	N-carbamoyl-L-valine	NA	NA	NA	NA
106	N-succinyl-isoleucine	NA	NA	NA	NA
107	N-succinyl-phenylalanine	NA	NA	NA	NA
108	N,N-dimethyl-pro-pro	NA	NA	NA	NA
109	N,N-Dimethylaniline	N,N-Dimethylaniline	HMDB0001020	949	C02846
110	N6-acetyllysine	Indoleacetic acid	HMDB0000197	802	C00954
111	neopterin	Neopterin	HMDB0000845	135408877	C05926
112	nicotinamide riboside	Nicotinamide riboside	HMDB0000855	439924	C03150
113	norvaline	Norvaline	HMDB0013716	439575	C01799
114	o-Tyrosine	o-Tyrosine	HMDB0006050	91482	
115	orotidine	Orotidine	HMDB0000788	92751	C01103
116	phenethylamine	Phenylethylamine	HMDB0012275	1001	C05332
117	N-Phenylacetyl-L-leucine	NA	NA	NA	NA
118	phosphate	Phosphate	HMDB0001429	1004	C00009
119	picolinoylglycine	Picolinoylglycine	HMDB0059766	11788622	
120	5alpha-Pregnan-3beta,20alpha-diol disulfate	5alpha-Pregnan-3beta,20alpha-diol disulfate	HMDB0094650	5748360	
121	Pregnenetriol sulfate	NA	NA	NA	NA
122	prolylglycine	Prolylglycine	HMDB0011178	6426709	
123	pterin	Pterin	HMDB0000802	73000	C00715
124	pyridoxal	Pyridoxal	HMDB0001545	1050	C00250
125	quinolinate	Quinolinic acid	HMDB0000232	1066	C03722
126	S-adenosylmethionine	S-Adenosylmethionine	HMDB0001185	34756	C00019
127	S-carboxymethyl-L-cysteine	S-Carboxymethyl-L-cysteine	HMDB0029415	1080	
128	sarcosine	Sarcosine	HMDB0000271	1088	C00213
129	suberate	Suberic acid	HMDB0000893	10457	C08278
130	succinimide	NA	NA	NA	NA
131	succinoyltaurine	NA	NA	NA	NA
132	succinylcarnitine	Succinylcarnitine	HMDB0061717	131802075	
133	syringol sulfate	NA	NA	NA	NA
134	tetrahydrocortisol glucuronide	NA	NA	NA	NA
135	tetrahydrocortisone	Tetrahydrocortisone	HMDB0000903	12444617	C05470
136	tetrahydrocortisone glucuronide	NA	NA	NA	NA
137	thymol sulfate	Thymol Sulfate	HMDB0062720	12456386	
138	tiglyl carnitine	Tiglylcarnitine	HMDB0002366	91825636	
139	triethanolamine	Triethanolamine	HMDB0032538	7618	C06771
140	tyramine	Tyramine	HMDB0000306	5610	C00483
141	umbelliferone sulfate	4-Methylumbelliferone sulfate	HMDB0240465		C11585
142	urea	Urea	HMDB0000294	1176	C00086

4 Pathway Analysis

In this step, users are asked to select a pathway library, as well as specify the algorithms for pathway enrichment analysis and pathway topology analysis.

4.1 Pathway Library

There are 15 pathway libraries currently supported, with a total of 1173 pathways :

- Homo sapiens (human) [80]
- Mus musculus (mouse) [82]
- Rattus norvegicus (rat) [81]
- Bos taurus (cow) [81]
- Danio rerio (zebrafish) [81]
- Drosophila melanogaster (fruit fly) [79]
- Caenorhabditis elegans (nematode) [78]
- Saccharomyces cerevisiae (yeast) [65]
- Oryza sativa japonica (Japanese rice) [83]
- Arabidopsis thaliana (thale cress) [87]
- Escherichia coli K-12 MG1655 [87]
- Bacillus subtilis [80]
- Pseudomonas putida KT2440 [89]
- Staphylococcus aureus N315 (MRSA/VSSA)[73]
- Thermotoga maritima [57]

Your selected pathway library code is **hsa** (KEGG organisms abbreviation).

4.2 Over Representation Analysis

Over-representation analysis tests if a particular group of compounds is represented more than expected by chance within the user uploaded compound list. In the context of pathway analysis, we are testing if compounds involved in a particular pathway are enriched compared to random hits. MetPA offers two of the most commonly used methods for over-representation analysis:

- Fishers'Exact test
- Hypergeometric Test

Please note, MetPA uses one-tailed Fisher's exact test which will give essentially the same result as the result calculated by the hypergeometric test.

The selected over-representation analysis method is 'Hypergeometric test'.

4.3 Pathway Topology Analysis

The structure of biological pathways represent our knowledge about the complex relationships among molecules within a cell or a living organism. However, most pathway analysis algorithms fail to take structural information into consideration when estimating which pathways are significantly changed under conditions of study. It is well-known that changes in more important positions of a network will trigger a more severe impact on the pathway than changes occurred in marginal or relatively isolated positions.

The pathway topology analysis uses two well-established node centrality measures to estimate node importance - **degree centrality** and **betweenness centrality**. Degree centrality is defined as the number of links occurred upon a node. For a directed graph there are two types of degree: in-degree for links come from other nodes, and out-degree for links initiated from the current node. Metabolic networks are directed graph. Here we only consider the out-degree for node importance measure. It is assumed that nodes upstream will have regulatory roles for the downstream nodes, not vice versa. The betweenness centrality measures the number of shortest paths going through the node. Since the metabolic network is directed, we use the relative betweenness centrality for a metabolite as the importance measure. The degree centrality measure focuses more on local connectivities, while the betweenness centrality measure focuses more on global network topology. For more detailed discussions on various graph-based methods for analyzing biological networks, please refer to the article by Tero Aittokallio, T. et al. [1]

Please note, for comparison among different pathways, the node importance values calculated from centrality measures are further normalized by the sum of the importance of the pathway. Therefore, the total/maximum importance of each pathway is 1; the importance measure of each metabolite node is actually the percentage w.r.t the total pathway importance, and the pathway impact value is the cumulative percentage from the matched metabolite nodes.

Your selected node importance measure for topological analysis is 'relative betweenness centrality'.

5 Pathway Analysis Result

The results from pathway analysis are presented graphically as well as in a detailed table.

A Google-map style interactive visualization system was implemented to facilitate data exploration. The graphical output contains three levels of view: **metabolome view**, **pathway view**, and **compound view**. Only the metabolome view is shown below. Pathway views and compound views are generated dynamically based on your interactions with the visualization system. They are available in your downloaded files.

[1] Tero Aittokallio and Benno Schwikowski. *Graph-based methods for analyzing networks in cell biology*, Briefings in Bioinformatics 2006 7(3):243-255

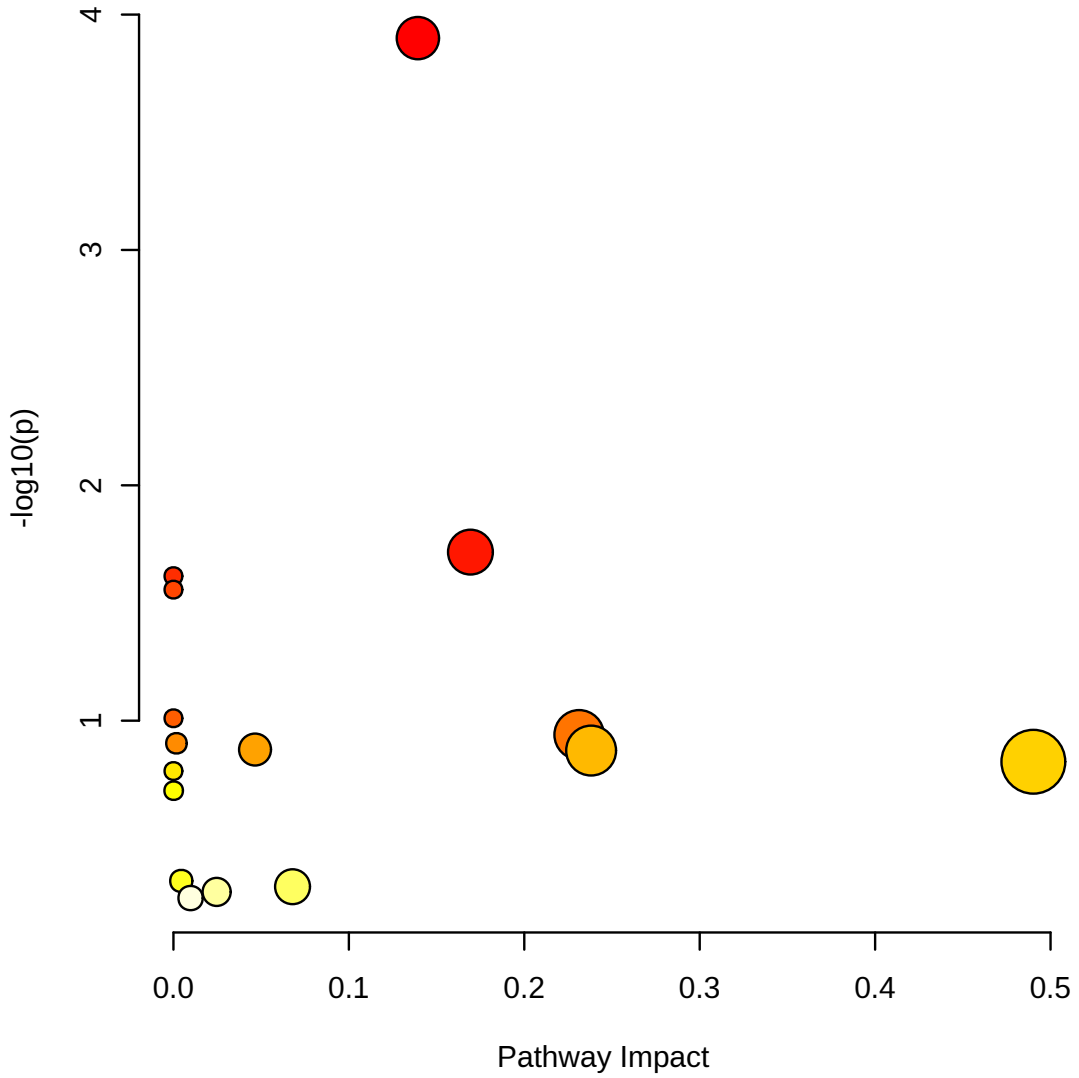

Figure 1: Summary of Pathway Analysis

The table below shows the detailed results from the pathway analysis. Since we are testing many pathways at the same time, the statistical p values from enrichment analysis are further adjusted for multiple testings. In particular, the **Total** is the total number of compounds in the pathway; the **Hits** is the actually matched number from the user uploaded data; the **Raw p** is the original p value calculated from the enrichment analysis; the **Holm p** is the p value adjusted by Holm-Bonferroni method; the **FDR p** is the p value adjusted using False Discovery Rate; the **Impact** is the pathway impact value calculated from pathway topology analysis.

Table 2: Result from Pathway Analysis

	Total	Expected	Hits	Raw p	-log10(p)	Holm adjust	FDR	Impact
Histidine metabolism	16	0.28	4	1.26E-04	3.90E+00	1.01E-02	1.01E-02	0.14
Glycine, serine and threonine metabolism	33	0.59	3	1.92E-02	1.72E+00	1.00E+00	5.55E-01	0.17
Arginine biosynthesis	14	0.25	2	2.43E-02	1.61E+00	1.00E+00	5.55E-01	0.00
Nicotinate and nicotinamide metabolism	15	0.27	2	2.77E-02	1.56E+00	1.00E+00	5.55E-01	0.00
Lysine degradation	30	0.53	2	9.77E-02	1.01E+00	1.00E+00	1.00E+00	0.00
Cysteine and methionine metabolism	33	0.59	2	1.15E-01	9.40E-01	1.00E+00	1.00E+00	0.23
Purine metabolism	70	1.24	3	1.25E-01	9.04E-01	1.00E+00	1.00E+00	0.00
Arginine and proline metabolism	36	0.64	2	1.33E-01	8.77E-01	1.00E+00	1.00E+00	0.05
Phenylalanine metabolism	8	0.14	1	1.34E-01	8.73E-01	1.00E+00	1.00E+00	0.24
Vitamin B6 metabolism	9	0.16	1	1.49E-01	8.26E-01	1.00E+00	1.00E+00	0.49
Tryptophan metabolism	41	0.73	2	1.64E-01	7.86E-01	1.00E+00	1.00E+00	0.00
Steroid hormone biosynthesis	87	1.55	3	1.98E-01	7.03E-01	1.00E+00	1.00E+00	0.00
Glycerophospholipid metabolism	36	0.64	1	4.80E-01	3.19E-01	1.00E+00	1.00E+00	0.00
Pyrimidine metabolism	39	0.69	1	5.07E-01	2.95E-01	1.00E+00	1.00E+00	0.07
Tyrosine metabolism	42	0.75	1	5.34E-01	2.73E-01	1.00E+00	1.00E+00	0.02
Primary bile acid biosynthesis	46	0.82	1	5.67E-01	2.46E-01	1.00E+00	1.00E+00	0.01

6 Appendix: R Command History

```
 [1] "mSet<-InitDataObjects(\"conc\", \"pathora\", FALSE)"
 [2] "cmpd.vec<-c(\"dimethylphenol sulfate\",\"N8-acetylspermidine\",\"(S)-a-amino-omega-caprolactam
 [3] "mSet<-Setup.MapData(mSet, cmpd.vec);"
 [4] "mSet<-CrossReferencing(mSet, \"name\");"
 [5] "mSet<-CreateMappingResultTable(mSet)"
 [6] "mSet<-PerformDetailMatch(mSet, \"dimethylphenol sulfate\");"
 [7] "mSet<-GetCandidateList(mSet);"
 [8] "mSet<-PerformDetailMatch(mSet, \"1-ribosyl-imidazoleacetate\");"
 [9] "mSet<-GetCandidateList(mSet);"
[10] "mSet<-SetCandidate(mSet, \"1-ribosyl-imidazoleacetate\", \"Imidazoleacetic acid riboside\");"
[11] "mSet<-PerformDetailMatch(mSet, \"2-ethylphenylsulfate\");"
[12] "mSet<-GetCandidateList(mSet);"
[13] "mSet<-PerformDetailMatch(mSet, \"3-(3-amino-3-carboxypropyl)uridine\");"
[14] "mSet<-GetCandidateList(mSet);"
[15] "mSet<-PerformDetailMatch(mSet, \"3-acetylphenol sulfate\");"
[16] "mSet<-GetCandidateList(mSet);"
[17] "mSet<-PerformDetailMatch(mSet, \"3-ethylcatechol sulfate\");"
[18] "mSet<-GetCandidateList(mSet);"
[19] "mSet<-SetCandidate(mSet, \"3-ethylcatechol sulfate\", \"O-methoxycatechol-O-sulphate\");"
[20] "mSet<-PerformDetailMatch(mSet, \"3-hydroxy-4-methylpyridine sulfate\");"
[21] "mSet<-GetCandidateList(mSet);"
[22] "mSet<-PerformDetailMatch(mSet, \"4-acetylphenyl sulfate\");"
[23] "mSet<-GetCandidateList(mSet);"
[24] "mSet<-PerformDetailMatch(mSet, \"6-Bromo-L-tryptophan\");"
[25] "mSet<-GetCandidateList(mSet);"
[26] "mSet<-PerformDetailMatch(mSet, \"butyrylputrescine/isobutyrylputrescine\");"
[27] "mSet<-GetCandidateList(mSet);"
[28] "mSet<-PerformDetailMatch(mSet, \"cis-3,4-methylene-heptanoylcarnitine\");"
[29] "mSet<-GetCandidateList(mSet);"
[30] "mSet<-PerformDetailMatch(mSet, \"glycocholenate sulfate\");"
[31] "mSet<-GetCandidateList(mSet);"
[32] "mSet<-PerformDetailMatch(mSet, \"(2S,3S)-3-Hydroxyasparagine\");"
[33] "mSet<-GetCandidateList(mSet);"
[34] "mSet<-PerformDetailMatch(mSet, \"N-acetyl-1-methylhistidine\");"
[35] "mSet<-GetCandidateList(mSet);"
[36] "mSet<-PerformDetailMatch(mSet, \"N-carbamoyl-L-valine\");"
[37] "mSet<-GetCandidateList(mSet);"
[38] "mSet<-PerformDetailMatch(mSet, \"N-Phenylacetyl-L-leucine\");"
[39] "mSet<-GetCandidateList(mSet);"
[40] "mSet<-PerformDetailMatch(mSet, \"Pregnenetriol sulfate\");"
[41] "mSet<-GetCandidateList(mSet);"
[42] "mSet<-PerformDetailMatch(mSet, \"tetrahydrocortisone glucuronide\");"
[43] "mSet<-GetCandidateList(mSet);"
[44] "mSet<-PerformDetailMatch(mSet, \"umbelliferone sulfate\");"
[45] "mSet<-GetCandidateList(mSet);"
[46] "mSet<-SetCandidate(mSet, \"umbelliferone sulfate\", \"4-Methylumbelliferone sulfate\");"
[47] "mSet<-SetKEGG.PathLib(mSet, \"hsa\", \"current\")"
[48] "mSet<-SetMetabolomeFilter(mSet, F);"
[49] "mSet<-CalculateOraScore(mSet, \"rbc\", \"hyperg\")"
[50] "mSet<-PlotPathSummary(mSet, F, \"path_view_0_\", \"png\", 72, width=NA, NA, NA )"
[51] "mSet<-SaveTransformedData(mSet)"
[52] "mSet<-PreparePDFReport(mSet, \"guest7106216319241885243\")\n"
```

The report was generated on Mon Oct 7 16:14:02 2024 with R version 4.2.2 (2022-10-31), OS system: Linux.