

Stealing ideas

from metabolomics data exchange repositories



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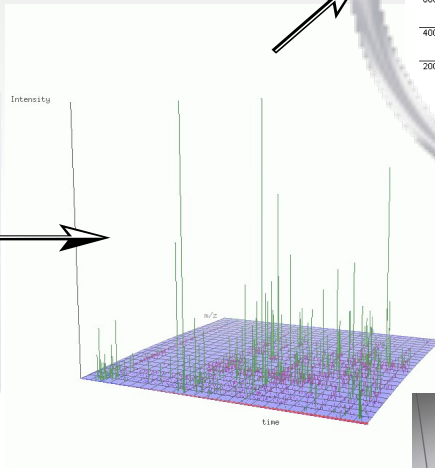
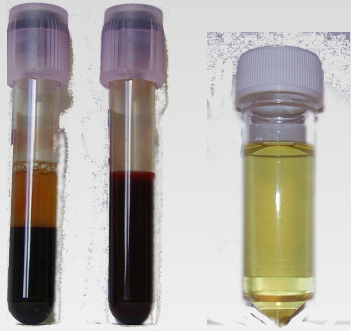


Outline

- Why would you want to care about metabolomics?
- Sharing metabolite profiling data
- Data standards in metabolomics
- Sharing reference spectra



Metabolomics @ IPB







Publications: Good Practice

- Provide Information in Supplemental Material
 - But: good looking colourful Excel doesn't help Bioinformaticians
 - Data in complex tables in PDF is even worse
- Better: submit data upstream, any data repository and provide accession numbers!

Not quite there yet:

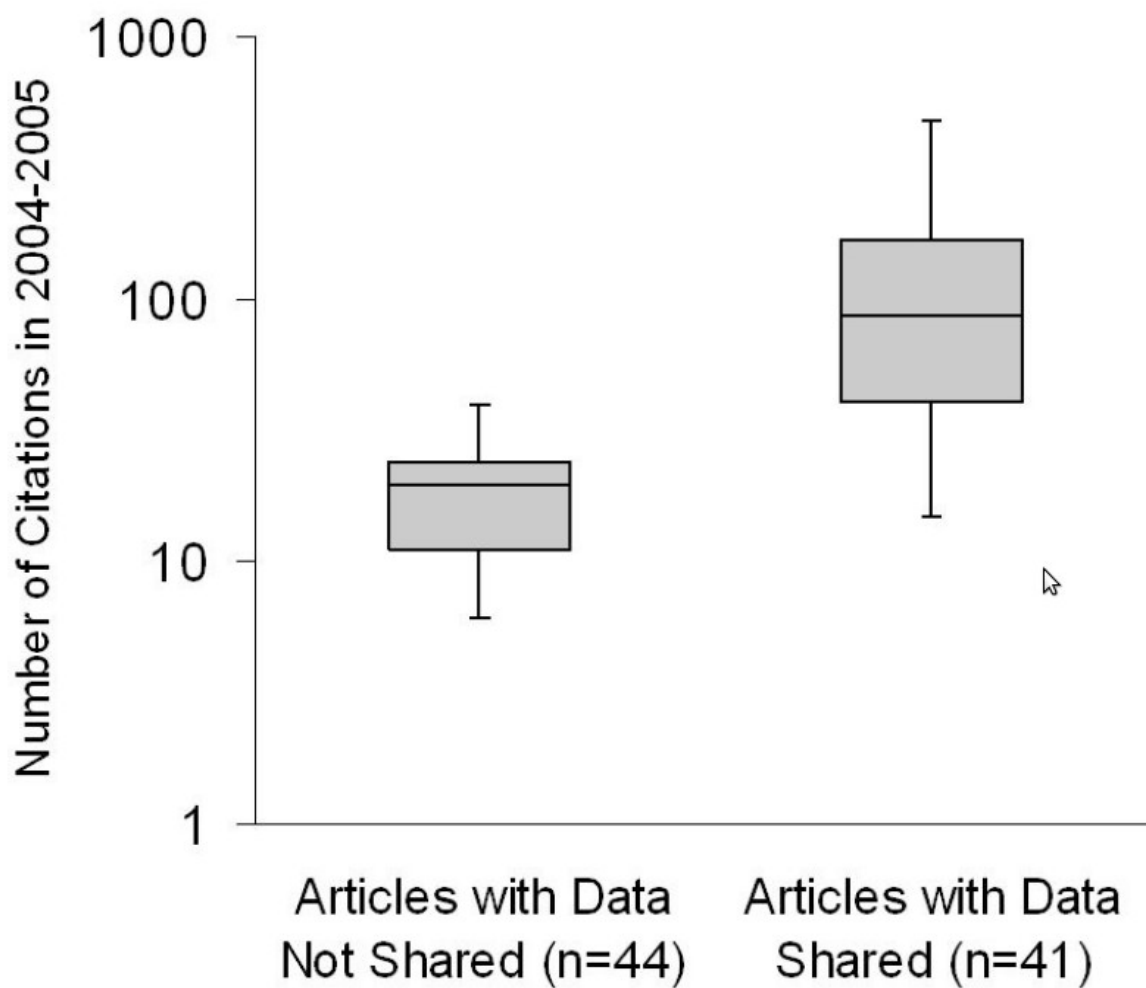
- DOI's for Data Sets
- DataCite: publication of Data Sets



Sharing Detailed Research Data Is Associated with Increased Citation Rate

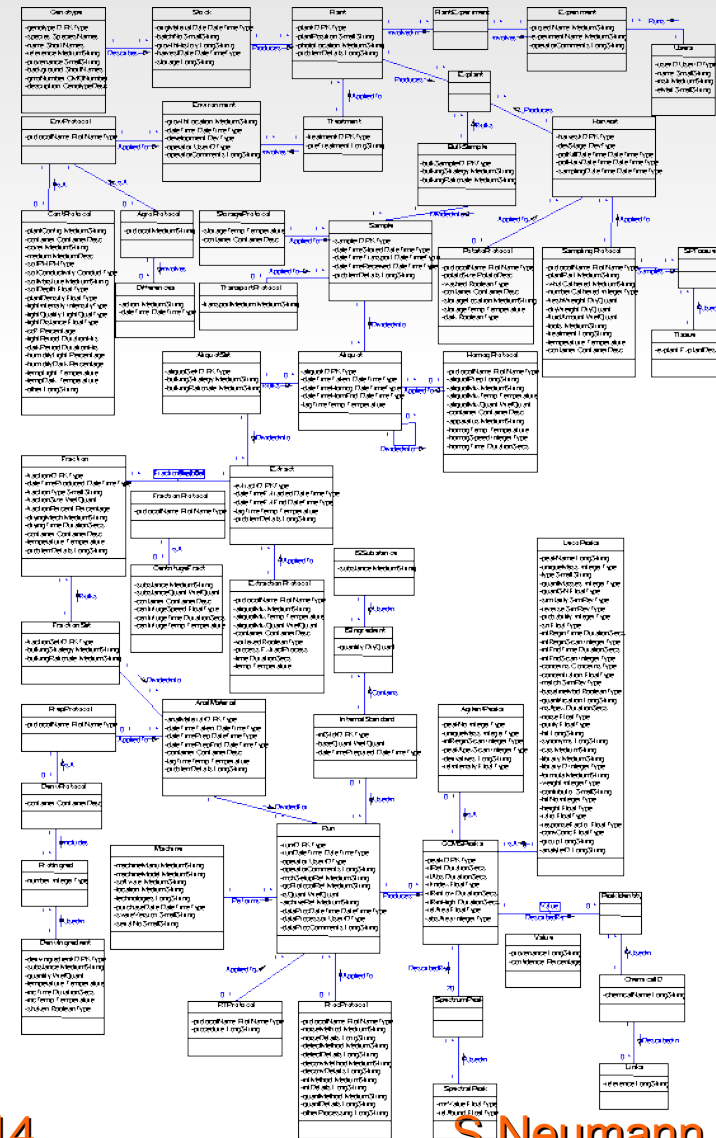
Heather A. Piwowar*, Roger S. Day, Douglas B. Fridsma

Note:
log
scale



ArMET (2004)

- One of several attempts designing biology/metabolomics databases
- Architecture for METabolomics
Nigel Hardy, Helen Jenkins
- Very detailed, not so user friendly,
→ didn't take over the world
- Other examples exist ...



MetaboLights@EBI

- EBI is a major European life-science resource
- Repository of MS/NMR Metabolomics Data
- Think: Supplemental Experimental Data
- Public data is frozen

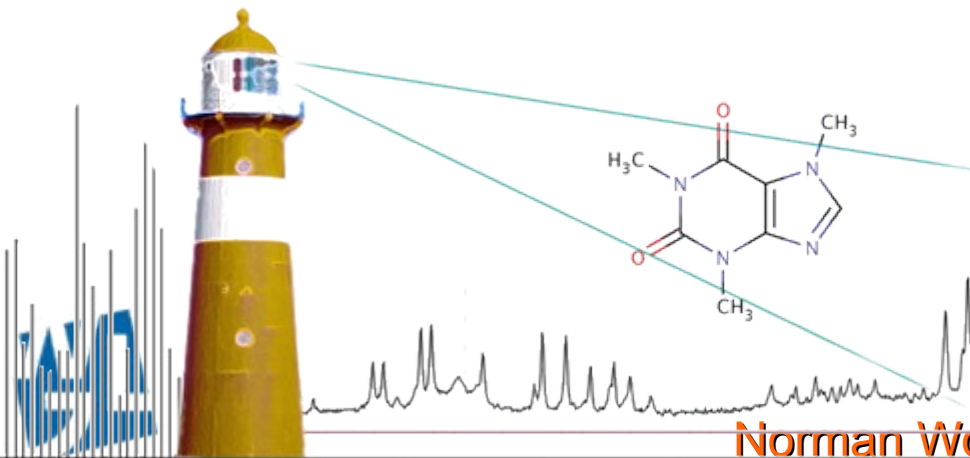
Steffen Neumann, Emmanuel Gaquerel,

Study Submission Date: 01-Feb-2012 Study Public Release Date: 02-Feb-2012

characterize changes induced in *Nicotiana attenuata* leaves 1 h and 5 days after wounding and application of Manduca sexta feeding. Using the MetaboAnalyst software, we extracted 367 buckets, which were analyzed by principal component analysis and two-factorial ANOVA. We found 128 buckets to be statistically regulated, 128 due to time effects, and 85 due to treatment effects.

Study Design Description Protocols Data Metabolite Identification

Protocol	Description
Sample collection	We used an isogenic line, obtained after 30 generations of inbreeding, of <i>Nicotiana attenuata</i> germinated as described in Krügel et al. (15). All plants were grown in the glasshouse in 1 L light supplied by Philips Sun-T Agro 400- or 600-W sodium lights (Philips, Turnhout, Belgium). <i>Manduca sexta</i> feeding were reproduced by producing with a fabric pattern wheel three rows of midvein of five fully expanded leaves per plant (5 biological replicates) and directly applying Manduca sexta feeding (OS). Treated leaves from the same plant were harvested, pooled, and flash frozen 1 h and 5 days after wounding and harvested from other plants at the same time points.
Extraction	One hundred milligrams of ground leaf tissue was weighted and transferred to a Fast Prep tube (BIO 101, Vista, USA). One milliliter of extraction buffer per 100 mg of tissue [50 mM acetate, 100 mM acetonitrile, 100 mM formic acid, 100 mM sodium acetate, 100 mM sodium formate, 100 mM sodium nitrate, 100 mM sodium phosphate, 100 mM sodium sulfate, 100 mM sodium chloride, 100 mM sodium bromide, 100 mM sodium iodide, 100 mM sodium fluoride, 100 mM sodium acetate, 100 mM sodium formate, 100 mM sodium nitrate, 100 mM sodium phosphate, 100 mM sodium sulfate, 100 mM sodium chloride, 100 mM sodium bromide, 100 mM sodium iodide, 100 mM sodium fluoride] was added, and the samples were shaken (1000 rpm, 20 min, 4 °C), the supernatant was collected in a fresh 1.5 mL Eppendorf tube and centrifuged (10000 rpm, 5 min, 4 °C). The supernatant was transferred to a HPLC vial.
Chromatography	Two microliters of the leaf extract were separated using a HPLC 1100 Series system (Agilent, 150 mm Å 2 mm i.d., 3 µm, Phenomenex Gemini NX RP-18 column with a 2 mm Å 4 mm i.d. guard column (Phenomenex, Germany). The following binary gradient was applied: 0 to 2 min isocratic 95% acetonitrile [Baker, HPLC grade], and 0.05% formic acid, 5% B (acetonitrile and 0.05% formic acid) for 5 min. The flow rate was 200 µL/min.
Mass spectrometry	Eluted compounds were detected by a MicroToF mass spectrometer (Bruker Daltonik, Bremen, Germany) with electrospray ionization source in positive and negative ion modes. Typical instrument settings: capillary voltage, 3 kV; capillary exit, 130 V; dry gas temperature, 200 °C; dry gas flow, 8 L/min. Ions were detected at a scan rate of 1 Hz. Mass calibration was performed using sodium formate clusters (10 mM solution in water containing 0.2% formic acid).



What is EMBL-EBI?

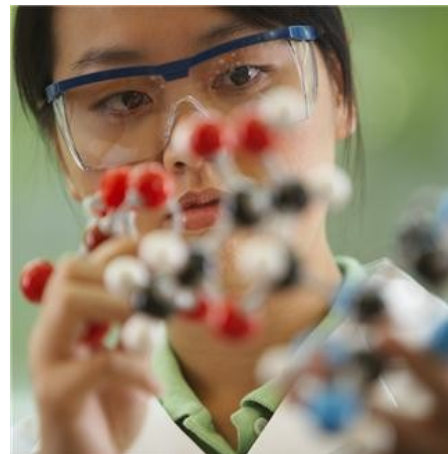
European Bioinformatics Institute

- Part of the European Molecular Biology Laboratory (Happy Birthday!)
- “Genome Campus” near Cambridge
- EU funded non-profit research institute, Europe’s hub for biological data services
570 staff from 53 nations.
- Capacity $\sim 40\text{PB}_{(08/2014)}$, mirrored data centers
- “Hardware capacity doubles every 18 months, but biological data doubles every 9 months.”



MetaboLights – Logical components

- Data Submission
 - ISAcreator (curation)
 - Online data deposition
- Repository
 - Complete metabolomics experiments/studies
 - Sharing Experiments
- Metabolite Reference Data
 - Metabolite identification
 - Curated





Data Capture Template

	A	B	C	D	E	F	G	H	I	J	K
1	Retention time [min]	Mass of ion [m/z] (peak or component)	Intensity of the ion	Intensity of the ion in the blank	Ion type		MS/MS available	Category	Proposed identification (name of the substance or n.i. for not identified)	Molecular formula	Identifier: SMILE
2					Other						
3											
7	YOUR DATA		YOUR DATA					YOUR DATA			
8	5.97	134.0711981661	1.81E+09	2.37E+07	M+H	positive	Yes	target	4&5-Methyl-Benzotriazole_167_p	C7H7N3	c12c(cc(C)cc2)nn[nH]1
9	4.69	120.0556107233	1.15E+09	1.39E+06	M+H	positive	Yes	target	Benzotriazole_166_p	C6H5N3	c12c(nn[nH]1)cccc2
10	3.93	246.1237932546	9.35E+08	0.00E+00	M+H	positive	Yes	target	4-Acetamidoantipyrine (N-Acetyl-4-Am	C13H15N3O2	CC(=O)NC=2C(=O)N(c1ccc
11	3.87	232.1081207512	5.82E+08	0.00E+00	M+H	positive	Yes	target	4-Formylaminoantipyrine (4-FAA)_1038	C12H13N3O2	O=C2C(\NC=O)=C(\C)N(C)
12	7.93	237.1022905227	3.74E+08	2.38E+06	M+H	positive	Yes	target	Carbamazepine_194_p	C15H12N2O1	N1(c2c(cccc2)C=Cc2c1ccc
13	4.09	195.0876061974	3.46E+08	6.01E+06	M+H	positive	Yes	target	Caffeine_303_p	C8H10N4O2	c12c(n(c(=O)n(c1=O)C)C)r
14	8.80	192.1382565761	2.50E+08	4.80E+06	M+H	positive	Yes	target	N-N-diethyl-3-methylbenzamide (DEET)	C12H17N1O1	c1(C(N(CC)CC)=O)cc(C)ccc
15	5.10	264.1958593355	1.69E+08	0.00E+00	M+H	positive	Yes	target	Tramadol_2567_p	C16H25N1O2	COC1=CC=CC(=C1)[C@@
16	10.40	230.1167174068	1.53E+08	0.00E+00	M+H	positive	Yes	target	Terbutylazine_284_p	C9H16Cl1N5	c1(nc(nc(n1)Cl)NCC)NC(C)(
17	4.55	198.1348923768	1.38E+08	0.00E+00	M+H	positive	Yes	target	Atrazin-2-Hydroxy_279_p	C8H15N5O1	c1(nc(nc(n1)O)NCC)NC(C)C
18	11.26	436.2341888099	1.25E+08	0.00E+00	M+H	positive	Yes	target	Valsartan_2583_p	C24H29N5O3	CCCCC(=O)N(CC1=CC=C(C
19	4.79	189.1022584029	1.20E+08	0.00E+00	M+H	positive	Yes	target	Phenazon (Antipyrin- ID 2519)_338_p	C11H12N2O1	CN1N(C(=O)C=C1C)C2=CC
20	5.49	256.0151400017	1.10E+08	0.00E+00	M+H	positive	Yes	target	Lamotrigin_2676_p	C9H7Cl2N5	Cl-c(ccc1)c(Cl)c1-c(nnc2N)
21	3.96	268.1543604517	1.09E+08	0.00E+00	M+H	positive	Yes	target	Atenololsaeure (Metoprololsaeure) 69	C14H21N1O4	CC(C)NCC(O)COc1cccc(cc1)
22	6.09	253.0972162649	8.72E+07	0.00E+00	M+H	positive	Yes	target	Carbamazepine-10-11-epoxide_916_p	C15H12N2O2	NC(=O)N2c1cccc1C4OC4
23	6.94	267.0876513875	8.28E+07	0.00E+00	M+H	positive	No	target	Valsartansaeure_2795_p	C14H10N4O2	C1=CC=C(C(=C1)C2=CC=C
24	8.55	216.1012139414	7.70E+07	0.00E+00	M+H	positive	Yes	target	Atrazin_288_p	C8H14Cl1N5	c1(nc(nc(n1)Cl)NCC)NC(C)C
25	9.57	441.1670258168	7.13E+07	0.00E+00	M+H	positive	Yes	target	Candesartan_2804_p	C24H20N6O3	c1(ccccc1c1ccc(Cn2c(nc3c
26	6.10	271.10775803	6.78E+07	0.00E+00	M+H	positive	Yes	target	Carbamazepin-10-11-dihydro-10-11-di	C15H14N2O3	c12[C@@H]([C@@H](O)c3
27	3.63	178.054250279	6.06E+07	0.00E+00	M-H	negative	Yes	target	Cyclamat_2813_n	C6H13N1O3S1	C1(CCCCC1)NS(O)(=O)=O
28	1.07	123.0916004272	5.91E+07	2.59E+06	M+H	positive	No	target	4-Dimethylaminopyridine_2833_p	C7H10N2	CN(C)C1=CC=NC=C1
29	5.74	188.0698990433	5.71E+07	6.07E+05	M+H	positive	Yes	target	Atrazine-Desethyl_309_p	C6H10Cl1N5	c1(nc(nc(n1)Cl)N)NC(C)C
30	3.56	192.0767182847	4.81E+07	0.00E+00	M+H	positive	Yes	target	Carbendazim_278_p	C9H9N3O2	c12c(cccc1)N=C(C(NC)OC)=
31	6.38	278.2114644132	4.70E+07	0.00E+00	M+H	positive	Yes	target	Venlafaxin_645_p	C17H27N1O2	CN(C)CC(C1=CC=C(C=C1)
32	7.73	202.0854156733	4.70E+07	0.00E+00	M+H	positive	Yes	target	Terbutylazin-desethyl_671_p	C7H12Cl1N5	Nc1nc(NC(C)(C)C)nc(Cl)n1
33	4.38	235.1805227377	4.51E+07	0.00E+00	M+H	positive	Yes	target	Lidocain_2572_p	C14H22N2O1	CCN(CC)CC(=O)NC1=C(C)C
34	13.21	412.9664972599	4.31E+07	8.25E+05	M-H	negative	Yes	target	Perfluoroctansaeure (PFOA)_2717_n	C8H1F15O2	O=C(O)C(F)(F)C(F)(F)C(F)(F
35	4.89	152.1434026509	3.67E+07	0.00E+00	M+H	positive	Yes	target	Amantadine_3124_p	C10H17N1	C1C2CC3CC1CC(C2)(C3)N
36	4.70	254.0594440809	3.34E+07	0.00E+00	M+H	positive	Yes	target	Sulfamethoxazol_298_p	C10H11N3O3S	c1(S(Nc2cc(C)on2)(=O)=O
37	12.04	284.1411922178	3.22E+07	0.00E+00	M+H	positive	Yes	target	Metolachlor_268_p	C15H22Cl1N1O	CCCC1=CC=CC(=C1N(C)C)C
38	2.94	184.1192596921	2.60E+07	0.00E+00	M+H	positive	Yes	target	Simazin-2-hydroxy_668_p	C7H13N5O1	c1(nc(nc(n1)Cl)NCC)NCC
39	2.94	184.1192596921	2.60E+07	0.00E+00	M+H	positive	Yes	target	Terbutylazin-desethyl-2-hydroxy_672_p	C7H13N5O1	Nc1nc(NC(C)(C)C)nc(O)n1
40	13.22	308.1525173486	2.56E+07	0.00E+00	M+H	positive	Yes	target	Tebuconazol_327_p	C16H22Cl1N3O	CC(C)(C)C(CCC1=CC=C(C=C
41	5.45	307.1113757675	2.00E+07	0.00E+00	M+H	positive	Yes	target	Fluconazol_328_p	C13H12F2N6O	OC(CN1C=NC=N1)(CN2C=



EnviLights@EBI ?

- Example: Eawag nontarget screening trial
- Same information as in DCT
- Material & Methods from Paper
- Raw data deposited as mzML files

MTBLS_DEV154: Norman Nontarget screening trial Eawag

[Share Study](#) | [View all files](#)

[Private study](#) [Make it public](#)

Submitted: **19-Jun-2014**, Release date: **17-Jun-2015**

Other identifiers: NormanNontargetTrialEawag

This Collaborative Trial is organised by the NORMAN Association (www.normannetwork.net) as part of its Joint Programme of Activities for the year 2013. The activity is a follow-up action to the NORMAN-JRC workshop in Stresa (2010), where one of the main conclusions was that comparison and harmonisation of non-target screening methods in Europe are needed. The Collaborative Trial should provide in-depth information on the methodologies used by participating laboratories. It will be carried out for the first time in the area of environmental analysis worldwide and therefore aims to result in a common publication in a prestigious refereed journal. The Collaborative Trial will be carried out with a sample from the Danube river using the liquid chromatography-high resolution-mass spectrometry (LC-HR-MS) and gas chromatography-mass spectrometry (GC-MS) methodologies available in participating laboratories. These are the results of the Eawag participation using LC-MS/MS methods.

[Study Design Description](#)

[Protocols](#)

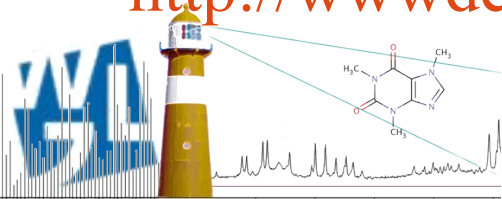
[Assay](#)

[Metabolites Identified](#)

[Study Files](#)

Description	Formula	m/z	Retention time
C8-SPC (-)	C14H20O5S	299.0958219827	8.14
C9-DATS (-)	C15H22O3S	281.121647622	13.16
C9-SPC (-)	C15H22O5S	313.1115	9.3
NP-1EC (-)	C17H26O3	277.1807672249	16.9
STA-1C (-)	C12H14O5S	269.0490519962	5.89
STA-1C (-)	C12H14O5S	269.0490611073	5.24
STA-2C (-)	C13H16O5S	283.0645284915	6.44
STA-2C (-)	C13H16O5S	283.0645314144	5.5
STA-3C (-)	C14H18O5S	297.080153284	7.51
STA-4C (-)	C15H20O5S	311.0959576936	9.02

- <http://wwwdev.ebi.ac.uk/metabolights/reviewerahRw3k0a5j>



MetaboLights – Private Data

MTBLS_DEV154: Norman Nontarget screening trial Eawag

[Share Study](#) | [View all files](#)

Private study [Make it public](#)

Submitted: **19-Jun-2014** , Release date: **17-Jun-2015**

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Study Design Description

Description

C8-SPC (-)

C9-DATS (-)

C9-SPC (-)

NP-1EC (-)

STA-1C (-)

STA-1C (-)

STA-2C (-)

STA-2C (-)

STA-3C (-)

STA-4C (-)

Public Link

This is the official link for referencing your MetaboLights study in any paper, website or other communication.

http://wwwdev.ebi.ac.uk/metabolights/MTBLS_DEV154

Private Pre-Publication Link

Share this link with reviewers and other trusted parties. Anyone with this link can access your PRIVATE study.

<http://wwwdev.ebi.ac.uk/metabolights/reviewerahRw3k0a5j>

C12H14O5S

209.0490611075

3.24

C13H16O5S

283.0645284915

6.44

C13H16O5S

283.0645314144

5.5

C14H18O5S

297.080153284

7.51

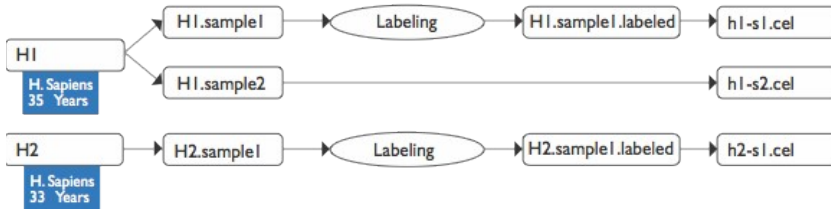
C15H20O5S

311.0959576936

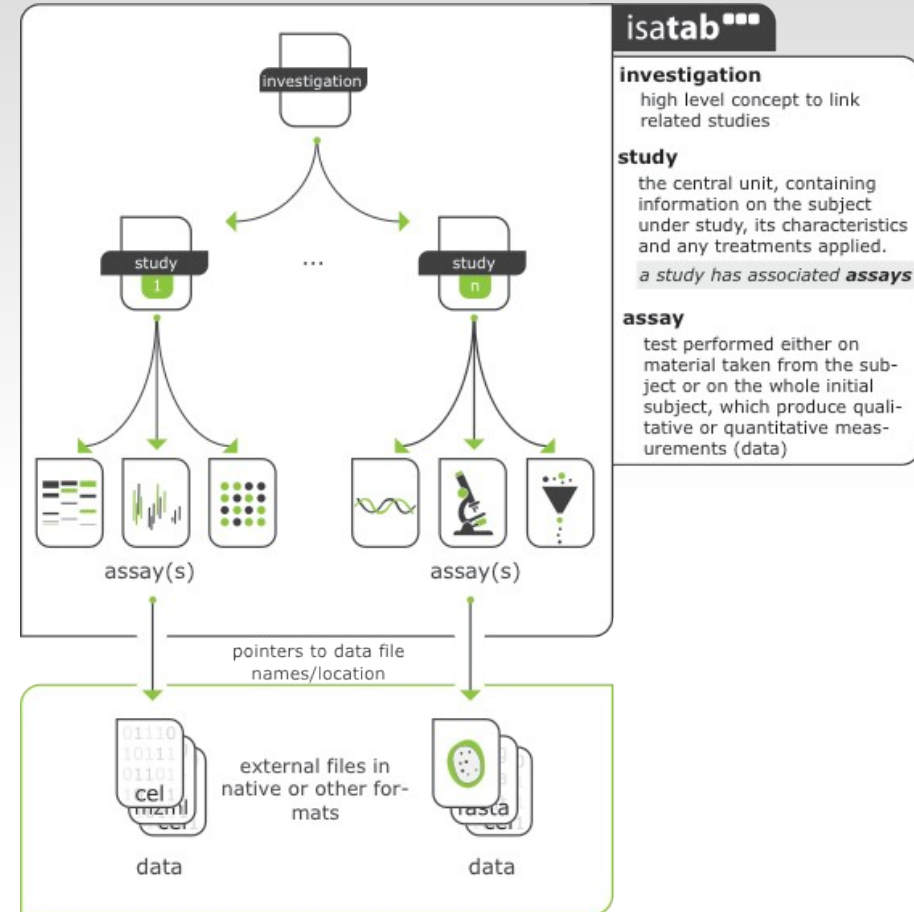
9.02

ISAtab in a nutshell

- Tab separated format
- Investigation, Study, Assay
- Checklist enforcement
- Ontology support
- Validation



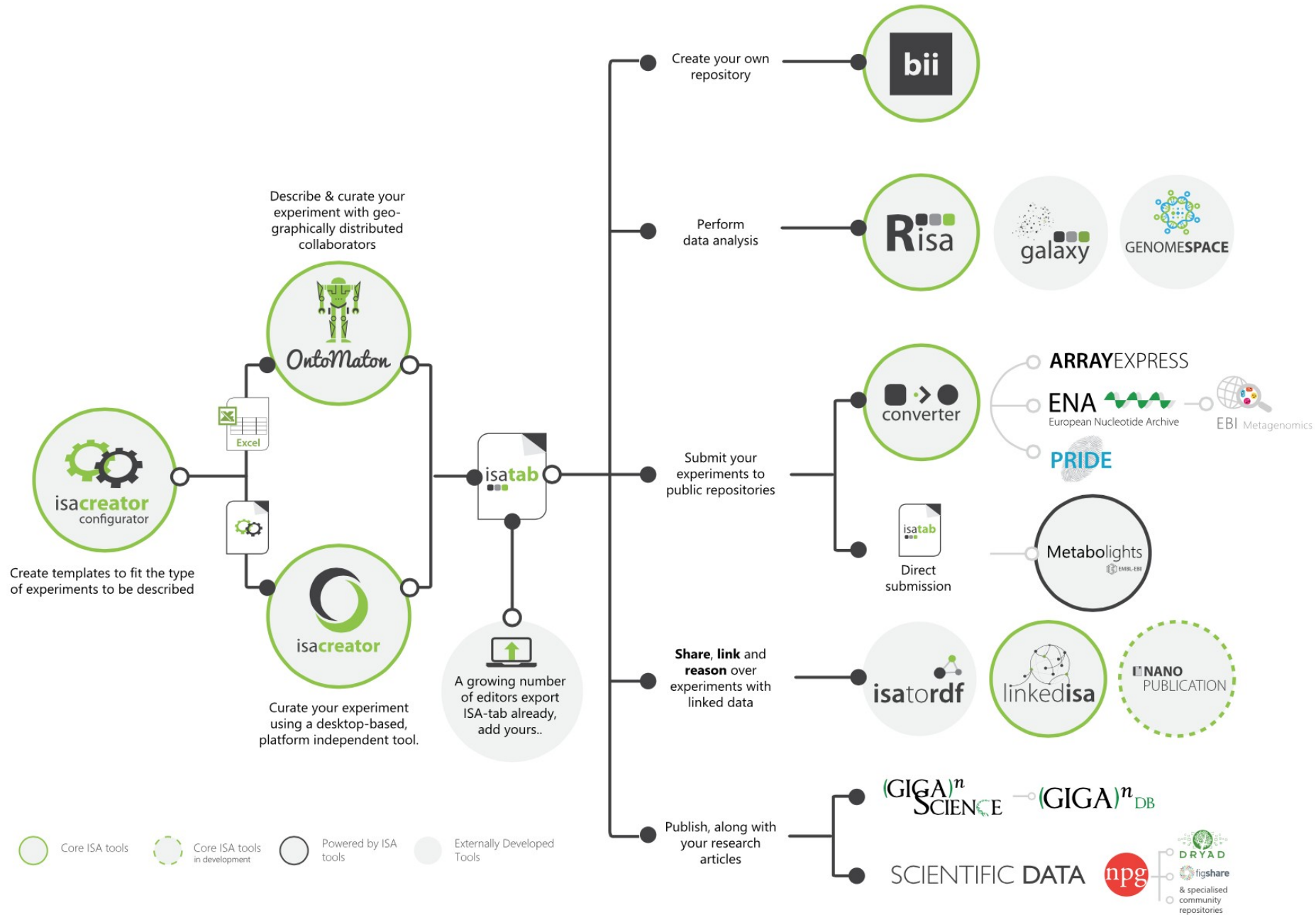
Source Name	Organism	Age	Unit	Sample Name	Protocol REF	Labeled Extract Name	Data File
H1	H. Sapiens	35	Years	H1.sample1	Labeling	H1.sample1.labeled	h1-s1.cel
H1	H. Sapiens	35	Years	H1.sample2			h1-s2.cel
H2	H. Sapiens	33	Years	H2.sample1	Labeling	H2.sample1.labeled	h2-s1.cel



ISAcreator - Metabolite Annotation plugin

● database_identifier	● chemical_formula	● smiles	● inchi	● metabolite_identification	● chemical_shift	● multiplicity
CHEBI:1148	C4H8O3	CCC(C(=O)O)O	InChI=1S/C4H8O3/c...	a-Hydroxy-n-butyrate	[0.85 .. 0.90]	t 0.90
CHEBI:60630	C5H9O3	CCCC(C(=O)[O-])O	InChI=1S/C5H10O3/...	a-Hydroxy-n-valerate	[0.90 .. 0.96]	t 0.92
CHEBI:24898	C6H13NO2	C(CCC(=O)O)CCN	InChI=1S/C6H13NO2...	isoleucine	[0.90 .. 0.96]	t 0.94
CHEBI:25017	C6H13NO2	CC(C)CC(C(=O)O)N	InChI=1S/C6H13NO2...	leucine	[0.96 .. 1.01]	t 0.96
CHEBI:57762	C5H11NO2	CC(C)C(C(=O)O)N	InChI=1S/C5H11NO2...	valine	[0.96 .. 1.01]	t 0.97
CHEBI:64669	C5H10O3	CC(C)(C(=O)OC)O	InChI=1S/C5H10O3/...	a-Hydroxyisovalerate	[0.96 .. 1.01]	
CHEBI:24898	C6H13NO2	C(CCC(=O)O)CCN	InChI=1S/C6H13NO2...	isoleucine	[1.01 .. 1.03]	d 1.01
CHEBI:35932	C6H10O3	CCCC(=O)C(=O)OC	InChI=1S/C6H10O3/...	a-keto-b-methyl-N valerate	[1.03 .. 1.09]	d 1.075
CHEBI:16530	C5H8O3	C1CC(=O)OC1CO	InChI=1S/C5H8O3/c...	2-oxoisovalerate	[1.09 .. 1.13]	d 1.11
CHEBI:16236	C2H6O	CCO	InChI=1S/C2H6O/c1...	ethanol	[1.09 .. 1.13]	t 1.11
					[1.13 .. 1.16]	
					[1.16 .. 1.18]	
CHEBI:20067	C4H8O3	CC(CC(=O)O)O	InChI=1S/C4H8O3/c...	b-hydroxy-n-butyrate	[1.18 .. 1.22]	d 1.20
				unknown_t_1.205	[1.18 .. 1.22]	t 1.205
				unknown_d_1.235	[1.22 .. 1.26]	d 1.235
CHEBI:30860	C4H6O4	C(CC(=O)O)C(=O)O	InChI=1S/C4H6O4/c...	methylmalonate	[1.22 .. 1.26]	d 1.255
				unknown_s_1.27	[1.26 .. 1.32]	s 1.27
CHEBI:28358	C3H6O3	CC(C(=O)O)O	InChI=1S/C3H6O3/c...	lactate	[1.32 .. 1.35]	d 1.335
				unknown_s_1.35	[1.35 .. 1.38]	s 1.35
CHEBI:50129	C4H8O3	C(CC(=O)[O-])CO	InChI=1S/C4H8O3/c...	a-hydroxyisobutyrate	[1.35 .. 1.38]	s 1.36
					[1.38 .. 1.43]	
					[1.43 .. 1.47]	
CHEBI:16449	C3H7NO2	CCOC(=O)N	InChI=1S/C3H7NO2/...	alanine	[1.47 .. 1.50]	d 1.485
					[1.50 .. 1.55]	
CHEBI:64390	C8H15NO3	CC(C)C(C(=O)OC)NC(...	InChI=1S/C8H15NO3...	n-caproylglycine	[1.55 .. 1.60]	
					[1.60 .. 1.63]	
CID638154	C8H15NO3	CC(C)C(C(=O)OC)NC(...	InChI=1S/C8H15NO3...	methyl N-acetylvalinate	[1.63 .. 1.65]	
					[1.65 .. 1.70]	
CHEBI:25017	C6H13NO2	CC(C)CC(C(=O)O)N	InChI=1S/C6H13NO2...	leucine	[1.70 .. 1.76]	m 1.71
CHEBI:25094	C6H14N2O2	CC(CCCN)(C(=O)O)N	InChI=1S/C6H14N2O...	lysine	[1.70 .. 1.76]	m 1.73
					[1.76 .. 1.81]	
CHEBI:18257	C5H12N2O2	C(CC(C(=O)O)N)CN	InChI=1S/C5H12N2O...	ornithine	[1.81 .. 1.87]	m 1.81
CHEBI:66922	C6H12N3O3	C(CC(C(=O)[O-])N)CN...	InChI=1S/C6H13N3O...	citrullinate	[1.81 .. 1.87]	m 1.88

ISA ecosystem





MetabolomeXchange.org

- Network of repositories (EU/US/...)
- Metadata exchange, storage & search

142 datasets (08.09.2014)

EBI - MetaboLights	58
Metabolomics Workbench	45
Metabolomic Repository Bordeaux	25
Golm Metabolome Database	14

The screenshot shows the website's header with navigation tabs for Home, Search, and API. Below the header, there is a 'Latest datasets' section with three entries:

- NMR-based Blood Metabolic Profiles of Rats Exposed to Different Levels of Short Term Caloric Restriction** by Gustav Nestor. Source: EBI - MetaboLights, Fri, 05 Sep 2014, MTBLS114. Includes a quote: "Caloric restriction increases life-span of a number of different organisms including mammalian species such as dogs and rats..."
- Wax ester and lipophilic compound profiling of Euglena gracilis by gas chromatography-mass spectrometry: toward understanding of anoxia wax ester fermentation** by Takeshi Furuhashi. Source: EBI - MetaboLights, Thu, 04 Sep 2014, MTBLS113. Includes a quote: "In this study, we established a profiling method for wax esters and lipophilic compounds in Euglena using gas chromatography-mass spectrometry (GC-MS)..."
- A metabolomics approach to unravel the regulating role of phytohormones towards carotenoid metabolism in tomato fruit. (Zeaxanthin metabolism)** by Li Jiyun, Yan, Hui, et al. Source: EBI - MetaboLights, Sun, 31 Aug 2014, MTBLS107.

On the right side of the screenshot, there is a summary box for '142 datasets' with a breakdown: EBI - MetaboLights (58), Metabolomics Workbench (45), Metabolomic Repository Bordeaux (25), and Golm Metabolome Database (14). Below this is a search bar with a 'go' button and a list of search results including '1-O-oleoyl-sn-glycero-3-phosphocholine', '2'-O-methylinosine', '2,3-dihydroxybenzenesulfonic acid', and '2-hydroxy-'.





MetabolomeXchange.org

- No actual data: Link back to repo

EBI - MetaboLights dataset



Comparative LC/MS-based profiling of silver nitrate-treated *Arabidopsis thaliana* leaves of wild-type and *cyp79B2 cyp79B3* double knockout plants

by Steffen Neumann

EBI - MetaboLights

Tue, 22 May 2012

MTBLS2

"Indole-3-acetaldoxime (IAOx) represents an early intermediate of the biosynthesis of a variety of indolic secondary metabolites including the phytoanticipin indol-3-ylmethyl glucosinolate and the phytoalexin camalexin (3-thiazol-2'-yl-indole). Arabidopsis thaliana cyp79B2 cyp79B3 double knockout plants are completely impaired in the conversion of tryptophan to indole-3-acetaldoxime and do not accumulate IAOx-derived metabolites any longer. Consequently, comparative analysis of wild-type and cyp79B2 cyp79B3 plant lines has the potential to explore the complete range of IAOx-derived indolic secondary metabolites."

<http://www.ebi.ac.uk/metabollights/MTBLS2>

Analysis: Mass spectrometry

Platform: MicrOTOF-Q II ESI TOF (Bruker)

Organism: *Arabidopsis thaliana* (thale cress)

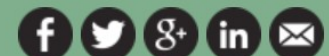
EBI - MetaboLights

MetaboLights is a database for Metabolomics experiments and derived information. The database is cross-species, cross-technique and covers metabolite structures and their reference spectra as well as their biological roles, locations and concentrations, and experimental data from metabolic experiments.

[read more...](#)



This project is funded through European Commission COSMOS Grant EC312941





MetabolomeXchange.org

- API to integrate into software and websites
- Push and Pull between data consumers and data providers

GET :: /api/dataset/search/@in/@for

Find all datasets where @for is found in @in. The @in value is case insensitive.

All datasets submitted by Reza (max 2)

cURL: `curl -i http://metabolomexchange.org/api/dataset/search/submitter/Reza/?limit=2`

```
[
  {
    "accession": "MTBLS3",
    "url": "http://www.ebi.ac.uk/metabolights/MTBLS3",
    "title": "A metabolomic strategy defines the regulation of lipid content and global metabolism in Caenorhabditis elegans",
    "description": "Caenorhabditis elegans provides a genetically tractable model organism to study metabolism and how regulation is perturbed to produce the complex phenotype of obesity. C. elegans including the delta-9 desaturases expressed by fat-5, fat-6 and fat-7. They regulate the biosynthesis of lipids including phospholipids, triglycerides and cholesteryl esters. Gas chromatography-mass spectrometry define the metabolome of all the possible knock-outs for the delta 9 desaturases, including fat-5, fat-6 and fat-7, both expressing steroyl-CoA desaturases. The metabolomic changes extend to all delta 9 desaturases have on regulating global metabolism and highlighting how comprehensive metabolite analysis using mass spectrometry used dyes for fat staining. The propagation of metabolic changes across the network of metabolites places C.elegans into a catabolic state compared with wildtype controls.",
    "date": "1329177600",
    "submitter": "Reza Salek",
    "meta": {
      "analysis": "mass spectrometry",
      "platform": "DSQ II Single Quadrupole GC/MS (Thermo Scientific)",
      "organism": "Caenorhabditis elegans",
      "metabolites": [
        "tyrosine",
        "ornithine",
        "L-histidine zwitterion",
      ]
    }
  }
]
```





Granularity of metadata

- There can be too little and too much metadata
 - Too little: meaningless data dump
 - Too much: over-engineered database, problematic User Acceptance
- Future: Text-Mining the MetaData ?
 - Automatic RDF extraction as suggestion during submission
- Different granularity for in-house “LIMS” and published data-sets ?





Ontologies

- Controlled vocabulary/ies
- Relationships: e.g.
`is_a`, `contained_in`, `tributary_of`
- Different formats (OWL, OBO)
- Online queries: www.ebi.ac.uk/ols
or <http://bioportal.bioontology.org/>
- Centrally or community maintained





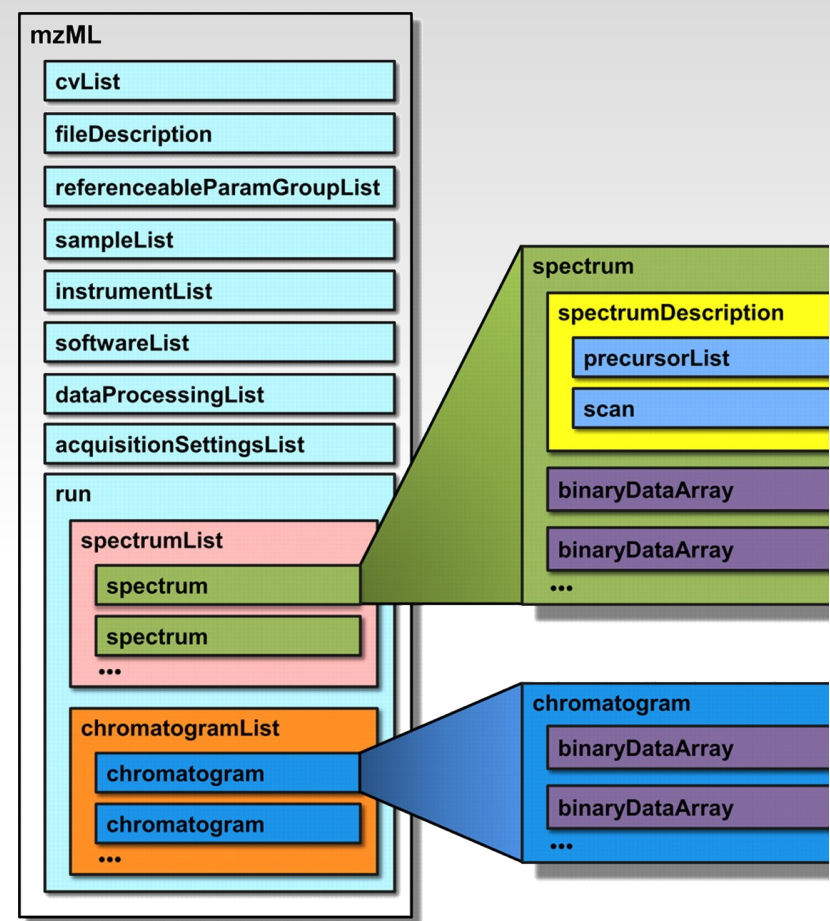
Change gears: low-level data standards

- Standardised Metadata allows to compare and integrate knowledge between Experiments
- Proprietary data formats:
*.d (Bruker) or *.RAW (Waters) or ...
- Standardised (raw) data formats allow to mix-and-match software and workflow pipelines
- Open Formats: well documented, I/O and parsing available for Java, R, Matlab, ...

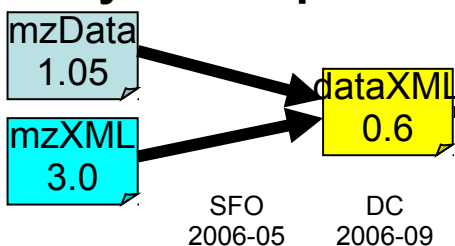


Example: mzML

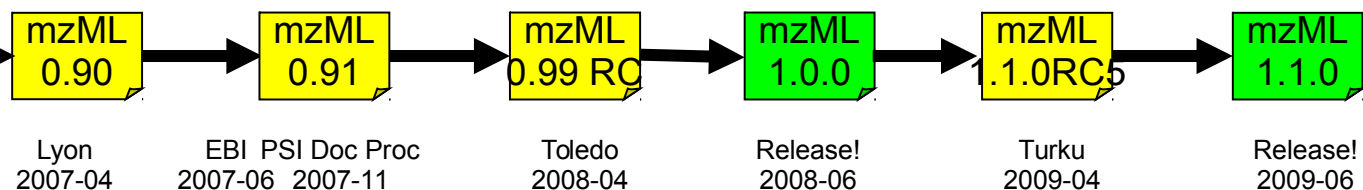
- mzData and mzXML flawed: too little/much structure
- Joint open development
- ABI, Bruker, Waters, Thermo, ...
- Implementations: jmzML, mzR, OpenMS, pymzML, proteowizard, ...



Early Development



Final Development





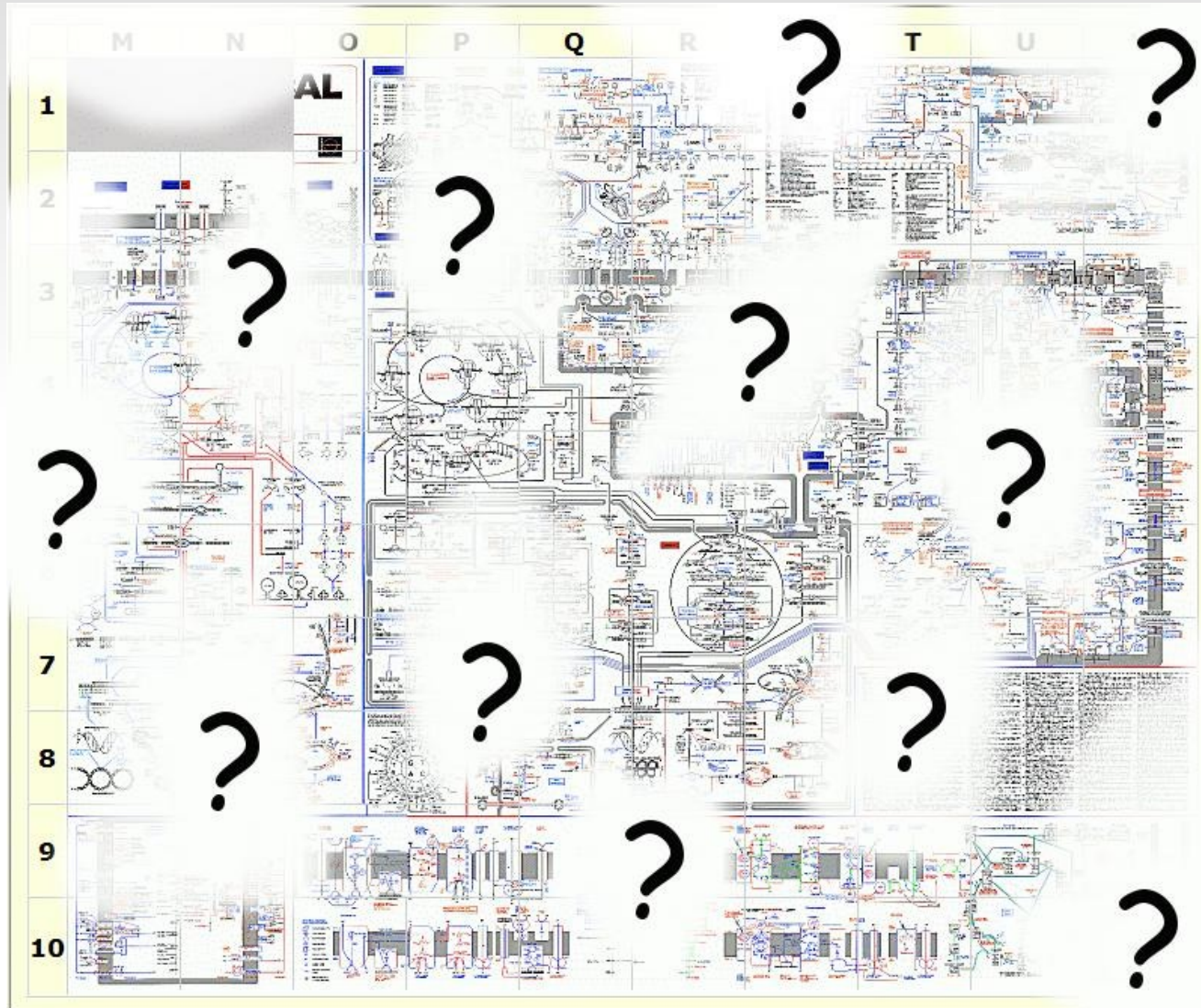
Acknowledgements

Many:

- Eawag (Emma, Michele, Heinz, Juliane, ...)
- EBI Metabolights team Hinxton
- ISA team Oxford
- COSMOS project members
- IPB Halle team



Questions ?

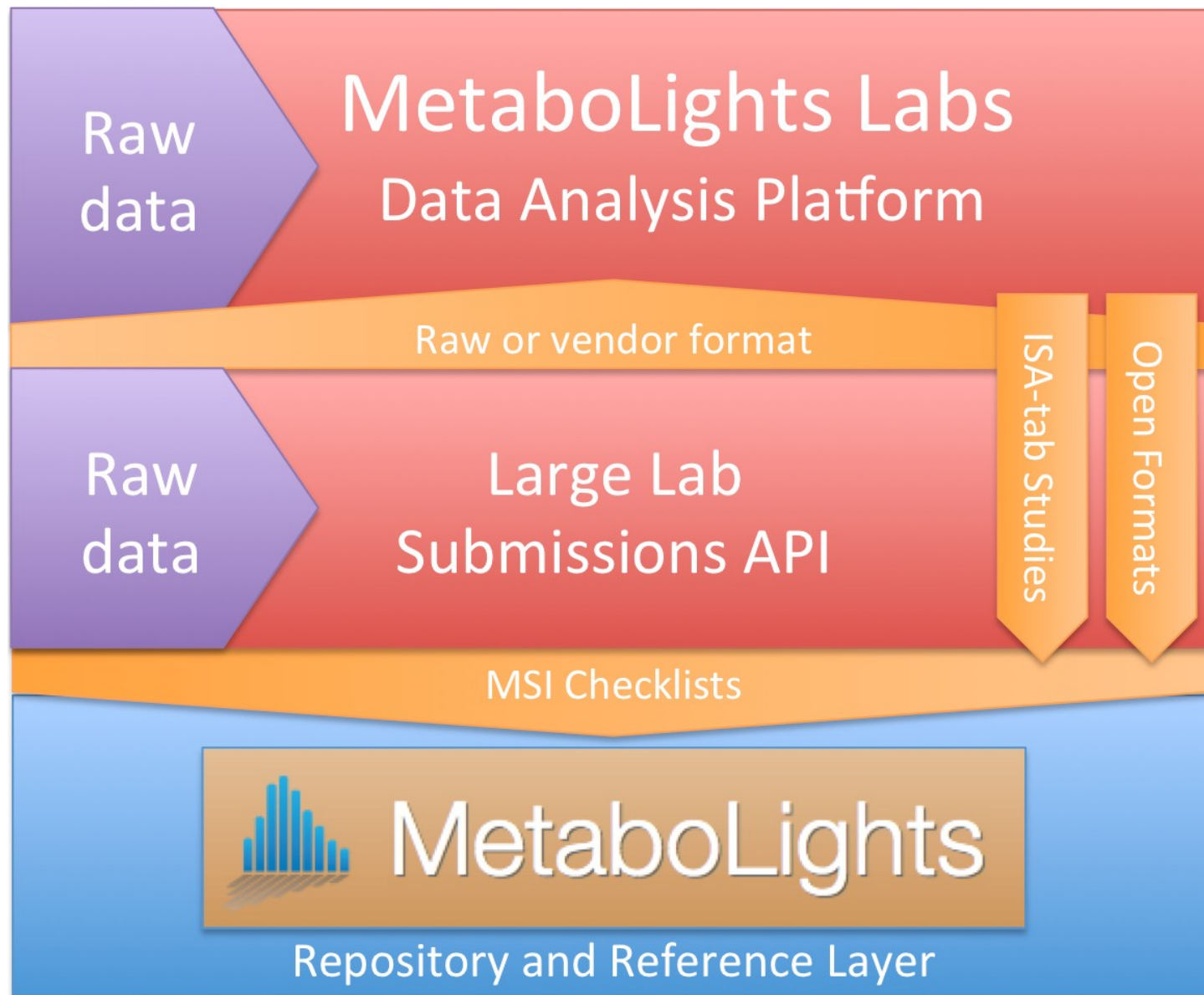




**Only supplemental slides
beyond this point**



MetaboLights – What are we working on



MetaboLights – Analysis

MetaboLights > MetaboAnalyst

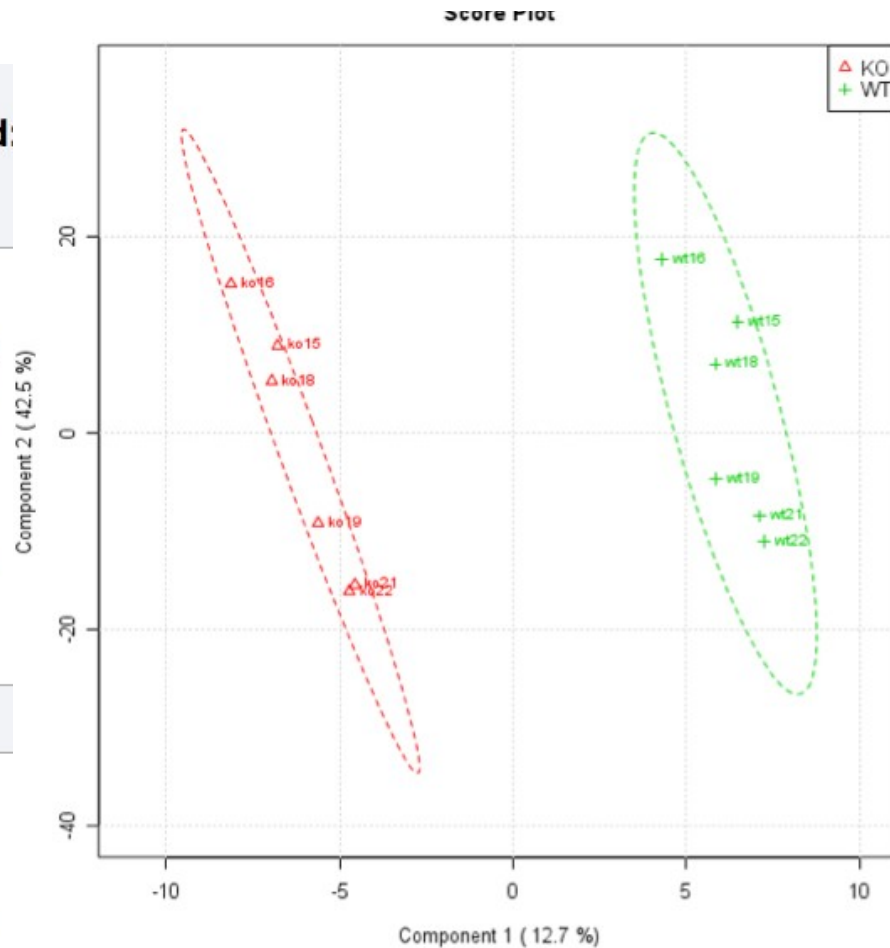
Please choose a functional module to proceed:

➔ Statistical Analysis

This module offers various commonly used statistical and machine learning methods from t-tests, ANOVA to PCA and PLS-DA. It also provides clustering and visualization such as dendrogram, heatmap, K-means, as well as classification based on random forests and SVM.

➔ Pathway Analysis

This module supports pathway analysis (including pathway enrichment analysis and pathway topology



MetaboLights – What more are we working on

- Tools integration, R focus (MetaboAnalyst, rISA, MetFrag, BATMAN)
- Online creation and edit of studies
- Extensive international data exchange
- Considering “Community Portals” on top of MetaboLights
 - Branded for each community
 - Bespoke curation and submission templates
 - Data exchange
 - Linking community resources



License: rights+obligations

- Creative Commons: Family of licenses
 - By Attribution (BY): Obligation to cite the origin
 - Share Alike (SA): Derived must be CC-SA as well
The “viral” license, it spreads!
 - No Derivatives: Redistribution only unchanged
 - NC (Non Commercial): problematic definition
 - And (almost) combinations thereof
- And many other: opendatacommons.org/licenses
- No license is the worst choice, because the “default rights/obligations” differ across legislations



MetaboLights – The team



Kenneth Haug



Pablo Conesa



Kalai Jayaseelan

Software development



Reza Salek



Mark Williams



Namrata Kale

Curation



Christoph Steinbeck

PIs



Jules Griffin (UC/MRC)

Previous: Paula de Matos, Mark Rijnbeek, Tejasvi Mahendraker



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LinkedIn

Twitter



Eamonn Maguire

Lead Software Engineer

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Figshare

GitHub

LinkedIn

Twitter



Alejandra Gonzalez-Beltran

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GitHub

LinkedIn

Twitter

funding



2012-2015, latest funding stream for metabolomics standards from the EU COSMOS.

2012-2015, travel funds for a UK-China partnership on harmonization of data curation from the BBSRC, a collaboration with TGAC and BGI/GigaScience

2012-2015, more funding for ISA project from the BBSRC MGportal project, a collaboration with the EMBL-EBI.

2011-2014, the ISA project has received another new funding stream from BBSRC and NERC.

2010-2013, the ISA project has received new funding stream from BBSRC and NERC.

2007-2010, the ISA project has been mainly supported by funds from the EU IP CarcinoGenomics, with contribution from EU NoE NuGO, NERC-NEBC, BBSRC and EMBL-EBI.

