

Risa: Building R objects from local ISA-Tab files

Alejandra Gonzalez-Beltran and Steffen Neumann and Audrey Kauffmann
and Gabriella Rustici and Philippe Rocca-Serra and Eamonn Maguire
and Susanna-Asunta Sansone
isatools@googlegroups.com

October 1, 2012

1 Introduction

The Risa package is part of the ISA infrastructure software suite (<http://isa-tools.org>). It provides functionality to read ISA-Tab datasets, described in the following section. The source code and latest version can be found in the GitHub repository <https://github.com/ISA-tools/Risa>. Please, submit all 'bugs' and feature requests through <https://github.com/ISA-tools/Risa/issues>.

2 ISA-Tab format

The Investigation / Study / Assay (ISA) Tab-delimited (Tab) format is a general purpose framework with which to collect and communicate complex metadata (i.e. sample characteristics, technologies used, type of measurements made) from experiments employing a combination of technologies (<http://isa-tools.org>). In particular, ISA-Tab has been developed for - but not limited to - experiments using genomics, transcriptomics, proteomics or metabol/nomics techniques (the 'omics').

ISA-Tab uses three types of file to capture the experimental metadata:

- *Investigation file*
- *Study file*
- *Assay file* (with associated data files).

The Investigation file contains an overall description of an experiment while all experimental steps are described in the Study and in the Assay file(s). For each Investigation file there may be one or more Study files; for each Study file there may be one or more Assay files.

2.1 Investigation file

In this file, information is reported on a per-column basis and the fields are organized and divided in sections. The Investigation file is intended to meet three needs:

- to define key entities, such as factors, protocols, parameters, which may be referenced in the other files;
- to relate Assay files to Study files; and optionally,
- to relate each Study file to an Investigation (when two or more Study files need to be grouped). The declarative sections cover general information such as contacts, protocols and equipment, and also - where applicable - the description of terminologies (controlled vocabularies or ontologies) and other annotation resources that were used.

2.2 Study file

In this file, information is structured on a per-row basis with the first row being used for column headers. The Study file contains contextualizing information for one or more assays, for example; the subjects studied; their source(s); the sampling methodology; their characteristics; and any treatments or manipulations performed to prepare the specimens.

2.3 Assay file

In this file, as for the Study file, fields are organized on a per-row basis with the first row being used for column headers. The Assay file represents a portion of the experimental graph (i.e., one part of the overall structure of the workflow); each Assay file must contain assays of the same type, defined by the type of measurement (i.e. gene expression) and the technology employed (i.e. DNA microarray). Assay-related information includes protocols, additional information relating to the execution of those protocols and references to data files (whether raw or processed).

For easy transfer, ISA-Tab files and associated data files can be packaged into an ISArchive, using a standalone Java application named ISAcreator (<http://isatab.sourceforge.net>). In order to facilitate identification of ISA-Tab components in an ISArchive, specific extensions have been created as follows:

- *i_iname.txt* for identifying the Investigation file
- *s_sname.txt* for identifying Study file (s)
- *a_aname.txt* for identifying Assay file (s)

where 'iname', 'sname', 'aname' are the user-given names for the investigation, study/ies, assay(s), respectively.

3 The Risa package

The Risa package is used to build R objects from an ISA archive or dataset. The output is a list of objects containing, for example, the investigation, studies and assays filenames, the contents of their files, the list of samples, among other things.

These objects can then be used by downstream Bioconductor packages for data analysis and visualization (i.e. xcms). The package currently includes the function `processAssayXcmsSet` that, for a specific mass spectrometry assay, builds an `xcmsSet` object.

3.1 Building an R object from a local ISA dataset

If you have your own ISA archive, you can use the function `readISAtab` to convert it into an R object. The arguments for the function `readISAtab` are:

- `path` the name of the directory containing ISAtab files. The default is the working directory.
- `verbose` a boolean indicating to show messages for the different steps, if TRUE, or not to show them, if FALSE

As an example, we can use the *faahKO* dataset, whose version 1.2.11 contains an ISA dataset describing the experiment. First, it is required to load the *Risa* package, and the *faahKO* package must have been installed.

```
> library(Risa)
> require(faahKO)
```

Then, we read the ISA-Tab data set from the *faahKO* package:

```
> faahkoISA <- readISAtab(find.package("faahKO"))
```

The object `faahkoISA` belongs to the *ISAtab* class, and contains the following elements:

- `path` - the path of the ISA-Tab dataset,
- `investigation.filename` - the name of the Investigation file
- `investigation.file` - a data frame with the contents of the Investigation file
- `study.identifiers` - the list of study identifiers
- `study filenames` - the names of the study files
- `study.files` - a list of data frames with the contents of the study files
- `assay filenames` - the names of the assay files
- `assay filenames.per.study` - the names of the assay files according to the study they belong to
- `assay.files` - a list of data frames with the contents of the assay files
- `assay.files.per.study` - a list of data frames with the contents of the assay files divided per study they belong to
- `assay.technology.types` - a list with the technology types corresponding to each assay
- `assay.measurement.types` - a list with the measurement types corresponding to each assay
- `data filenames` - a list with the names of the data files
- `samples` - a list with the names of the samples
- `samples.per.assay.filename` - the samples classified according to the assay filename they belong to
- `assay filenames.per.sample` - the names of the assay files classified per sample name
- `sample.to.rawdatafile` - the association between samples and raw data files
- `sample.to.assayname` - the association between samples and assay names
- `rawdatafile.to.sample` - the association between raw data files and samples
- `assayname.to.sample` - the association between assay names and samples

Additionally, the ISA dataset could be compressed in a .zip file. If that is the case, the function `readISAtab` can be used, passing the `zipfile` as parameter. The only condition is that the ISA-Tab files are contained directly into the zip file, i.e. not inside additional folders.

In this case, the parameters for the function `readISAtab` will be:

- `zipfile` a zip archive containing ISAtab files.
- `path` the name of the directory in which the files from the zip archive will be extracted. The default is the working directory.
- `verbose` a boolean indicating to show messages for the different steps, if TRUE, or not to show them, if FALSE

Building `xcmsSet` for mass spectrometry assays

The function `processAssayXcmsSet` allows to build an `xcmsSet` (object defined in the `xcms` package) from the information in an assay file.

The parameters for this function are:

- `isa`: an ISA object, as retrieved by the function `readISAtab`
- `assay.filename` the name of the assay file with information about the relevant assay
- ... extra arguments that can be passed down to the `xcmsSet` function from the `xcms` package

Using the `faahKO` package as an example, we select the name of assay file, and use the `processAssayXcmsSet` to build a object of type `xcmsSet`:

```
> assay.filename <- faahkoISA["assay.names"][1]
> faahkoXset <- processAssayXcmsSet(faahkoISA, assay.filename)

ko15: 250:38 300:103 350:226 400:338 450:431 500:529 550:674 600:847
ko16: 250:43 300:128 350:275 400:394 450:500 500:637 550:835 600:1027
ko18: 250:25 300:93 350:227 400:337 450:411 500:498 550:640 600:758
ko19: 250:19 300:67 350:169 400:258 450:301 500:373 550:488 600:580
ko21: 250:24 300:60 350:166 400:254 450:315 500:391 550:501 600:582
ko22: 250:31 300:71 350:183 400:280 450:338 500:422 550:532 600:604
wt15: 250:41 300:105 350:212 400:319 450:416 500:533 550:684 600:838
wt16: 250:27 300:107 350:232 400:347 450:440 500:549 550:712 600:905
wt18: 250:24 300:87 350:200 400:293 450:351 500:426 550:548 600:661
wt19: 250:22 300:65 350:161 400:243 450:293 500:358 550:483 600:561
wt21: 250:28 300:69 350:157 400:229 450:282 500:364 550:493 600:592
wt22: 250:30 300:81 350:188 400:280 450:356 500:473 550:618 600:765
```

Augmenting the ISA-Tab dataset after analysis

The `Risa` package also provides the functionality to augment the original ISA-Tab dataset with more information after analysis.

The function `updateAssayMetadata` allows to modify the metadata in a particular assay file. The arguments are:

- `isa` An `isatab` object, as retrieved by the `readISAtab` function.
- `assay.filename` the filename of the assay file to be augmented/modified
- `col.name` the name of the column of the assay file to be modified
- `values` the values to be added to the column of the assay file: it could be a single value, and in this case the value is repeated across the column, or it could be a list of values (whose length must match the number of rows of the assay file)

To continue with our example using the `faahKO` data package, we will assume that the results of analysis are stored in the file `faahkoDSDF.txt`. Then, we will update the ISA-Tab dataset adding the result file into the 'Derived Spectral Data File' column of the assay file.

```
> updateAssayMetadata(faahkoISA, assay.filename, "Derived Spectral Data File", "faahkoDSDF.txt" )
```

```
An object of class "ISAtab"
```

```
Slot "path":
```

```
[1] "/loc/home/biocbuild/bbs-2.11-bioc/R/library/faahKO"
```

Slot "investigation.filename":
[1] "i_Investigation.txt"

Slot "investigation.file":

```

V1
1          ONTOLOGY SOURCE REFERENCE
2              Term Source Name
3              Term Source File
4              Term Source Version
5              Term Source Description
6          INVESTIGATION
7              Investigation Identifier
8              Investigation Title
9              Investigation Description
10             Investigation Submission Date
11             Investigation Public Release Date
12             Comment [Created with configuration]
13             Comment [Last Opened With Configuration]
14          INVESTIGATION PUBLICATIONS
15             Investigation PubMed ID
16             Investigation Publication DOI
17             Investigation Publication Author List
18             Investigation Publication Title
19             Investigation Publication Status
20 Investigation Publication Status Term Accession Number
21     Investigation Publication Status Term Source REF
22             INVESTIGATION CONTACTS
23             Investigation Person Last Name
24             Investigation Person First Name
25             Investigation Person Mid Initials
26             Investigation Person Email
27             Investigation Person Phone
28             Investigation Person Fax
29             Investigation Person Address
30             Investigation Person Affiliation
31             Investigation Person Roles
32     Investigation Person Roles Term Accession Number
33     Investigation Person Roles Term Source REF
34             STUDY
35             Study Identifier
36             Study Title
37             Study Description
38             Study Submission Date
39             Study Public Release Date
40             Study File Name
41             STUDY DESIGN DESCRIPTORS
42             Study Design Type
43     Study Design Type Term Accession Number
44     Study Design Type Term Source REF
45             STUDY PUBLICATIONS
46             Study PubMed ID
47             Study Publication DOI
48             Study Publication Author List
```

49 Study Publication Title
 50 Study Publication Status
 51 Study Publication Status Term Accession Number
 52 Study Publication Status Term Source REF
 53 STUDY FACTORS
 54 Study Factor Name
 55 Study Factor Type
 56 Study Factor Type Term Accession Number
 57 Study Factor Type Term Source REF
 58 STUDY ASSAYS
 59 Study Assay Measurement Type
 60 Study Assay Measurement Type Term Source REF
 61 Study Assay Measurement Type Term Accession Number
 62 Study Assay Technology Type
 63 Study Assay Technology Type Term Source REF
 64 Study Assay Technology Type Term Accession Number
 65 Study Assay Technology Platform
 66 Study Assay File Name
 67 STUDY PROTOCOLS
 68 Study Protocol Name
 69 Study Protocol Type
 70 Study Protocol Type Term Accession Number
 71 Study Protocol Type Term Source REF
 72 Study Protocol Description
 73 Study Protocol URI
 74 Study Protocol Version
 75 Study Protocol Parameters Name
 76 Study Protocol Parameters Name Term Accession Number
 77 Study Protocol Parameters Name Term Source REF
 78 Study Protocol Components Name
 79 Study Protocol Components Type
 80 Study Protocol Components Type Term Accession Number
 81 Study Protocol Components Type Term Source REF
 82 STUDY CONTACTS
 83 Study Person Last Name
 84 Study Person First Name
 85 Study Person Mid Initials
 86 Study Person Email
 87 Study Person Phone
 88 Study Person Fax
 89 Study Person Address
 90 Study Person Affiliation
 91 Study Person Roles
 92 Study Person Roles Term Accession Number
 93 Study Person Roles Term Source REF

1
 2
 3
 4
 5
 6
 7
 8

9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36

37 Enzymes regulate biological processes through the conversion of specific substrates to product

38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62

63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22

23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71

72 A 2:1:1 CHCl₃/MeOH/1% NaCl solution (8 mL per brain and 4 mL per spinal cord in 8 mL vials) wa

73
74
75
76

77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36

37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71

72 LC-MS analysis was performed using an Agilent 1100 LC-MSD SL instrument. For the LC analysis,

73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90

91
92
93

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50

51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
1
2
3
4
5
6
7
8
9
10

The analysis of the resulting total ion chromatogram was performed manually by generating extr

V6

V7

PATO

EFO

v 1.26

Phenotypic qualities (properties) ArrayExpress Experimental Factor Ontology

11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64

65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93

labeling
labeling

V8
1 NA
2 NA
3 NA
4 NA
5 NA
6 NA
7 NA
8 NA
9 NA
10 NA
11 NA
12 NA
13 NA
14 NA
15 NA
16 NA
17 NA
18 NA
19 NA
20 NA
21 NA
22 NA
23 NA
24 NA

25 NA
26 NA
27 NA
28 NA
29 NA
30 NA
31 NA
32 NA
33 NA
34 NA
35 NA
36 NA
37 NA
38 NA
39 NA
40 NA
41 NA
42 NA
43 NA
44 NA
45 NA
46 NA
47 NA
48 NA
49 NA
50 NA
51 NA
52 NA
53 NA
54 NA
55 NA
56 NA
57 NA
58 NA
59 NA
60 NA
61 NA
62 NA
63 NA
64 NA
65 NA
66 NA
67 NA
68 NA
69 NA
70 NA
71 NA
72 NA
73 NA
74 NA
75 NA
76 NA
77 NA
78 NA

79 NA
 80 NA
 81 NA
 82 NA
 83 NA
 84 NA
 85 NA
 86 NA
 87 NA
 88 NA
 89 NA
 90 NA
 91 NA
 92 NA
 93 NA

Slot "study.identifiers":

[1] Global metabolite profiling of faah(-/-) mice
 24 Levels: 10.1021/bi0480335 15533037 16/11/2004 1796 ... v 1.26

Slot "study.fileNames":

Global metabolite profiling of faah(-/-) mice
 "s_Proteomic profiling of yeast TFs.txt"

Slot "study.files":

\$`Global metabolite profiling of faah(-/-) mice`

	Source Name	Characteristics[NEWT:Organism LC]	Term	Source	REF
1	Saghantelian_1	Mus musculus (Mouse)			NEWT
2	Saghantelian_2	Mus musculus (Mouse)			NEWT
3	Saghantelian_3	Mus musculus (Mouse)			NEWT
4	Saghantelian_4	Mus musculus (Mouse)			NEWT
5	Saghantelian_5	Mus musculus (Mouse)			NEWT
6	Saghantelian_6	Mus musculus (Mouse)			NEWT
7	Saghantelian_7	Mus musculus (Mouse)			NEWT
8	Saghantelian_8	Mus musculus (Mouse)			NEWT
9	Saghantelian_9	Mus musculus (Mouse)			NEWT
10	Saghantelian_10	Mus musculus (Mouse)			NEWT
11	Saghantelian_11	Mus musculus (Mouse)			NEWT
12	Saghantelian_12	Mus musculus (Mouse)			NEWT

	Term	Accession	Number	Characteristics[tissue]	Term	Source	REF
1			10090	spinal cord			MA
2			10090	spinal cord			MA
3			10090	spinal cord			MA
4			10090	spinal cord			MA
5			10090	spinal cord			MA
6			10090	spinal cord			MA
7			10090	spinal cord			MA
8			10090	spinal cord			MA
9			10090	spinal cord			MA
10			10090	spinal cord			MA
11			10090	spinal cord			MA
12			10090	spinal cord			MA

	Term	Accession	Number	Protocol	REF	Sample	Name	Factor	Value[Genotype]
1			216	sample collection			K01		K0

2	216 sample collection	K02	KO
3	216 sample collection	K03	KO
4	216 sample collection	K04	KO
5	216 sample collection	K05	KO
6	216 sample collection	K06	KO
7	216 sample collection	WT1	WT
8	216 sample collection	WT2	WT
9	216 sample collection	WT3	WT
10	216 sample collection	WT4	WT
11	216 sample collection	WT5	WT
12	216 sample collection	WT6	WT

	Term	Source	REF	Term	Accession	Number
1			NA			NA
2			NA			NA
3			NA			NA
4			NA			NA
5			NA			NA
6			NA			NA
7			NA			NA
8			NA			NA
9			NA			NA
10			NA			NA
11			NA			NA
12			NA			NA

Slot "assay_filenames":

```
V2
"a_metabolite.txt"
```

Slot "assay_filenames.per.study":

```
$`Global metabolite profiling of faah(-/-) mice`
$`Global metabolite profiling of faah(-/-) mice`[[1]]
[1] "a_metabolite.txt"
```

Slot "assay_files":

```
$a_metabolite.txt
Sample Name Protocol REF Extract Name Protocol REF Labeled Extract Name
1 K01 extraction K01 labeling NA
2 K02 extraction K02 labeling NA
3 K03 extraction K03 labeling NA
4 K04 extraction K04 labeling NA
5 K05 extraction K05 labeling NA
6 K06 extraction K06 labeling NA
7 WT1 extraction WT1 labeling NA
8 WT2 extraction WT2 labeling NA
9 WT3 extraction WT3 labeling NA
10 WT4 extraction WT4 labeling NA
11 WT5 extraction WT5 labeling NA
12 WT6 extraction WT6 labeling NA
Label Term Source REF Term Accession Number Protocol REF
1 NA NA NA mass spectrometry
```

2	NA	NA	NA	mass spectrometry
3	NA	NA	NA	mass spectrometry
4	NA	NA	NA	mass spectrometry
5	NA	NA	NA	mass spectrometry
6	NA	NA	NA	mass spectrometry
7	NA	NA	NA	mass spectrometry
8	NA	NA	NA	mass spectrometry
9	NA	NA	NA	mass spectrometry
10	NA	NA	NA	mass spectrometry
11	NA	NA	NA	mass spectrometry
12	NA	NA	NA	mass spectrometry

	Parameter Value[instrument]	Term	Source	REF	Term	Accession Number
1	Agilent 1100 LC-MSD SL			NA		NA
2	Agilent 1100 LC-MSD SL			NA		NA
3	Agilent 1100 LC-MSD SL			NA		NA
4	Agilent 1100 LC-MSD SL			NA		NA
5	Agilent 1100 LC-MSD SL			NA		NA
6	Agilent 1100 LC-MSD SL			NA		NA
7	Agilent 1100 LC-MSD SL			NA		NA
8	Agilent 1100 LC-MSD SL			NA		NA
9	Agilent 1100 LC-MSD SL			NA		NA
10	Agilent 1100 LC-MSD SL			NA		NA
11	Agilent 1100 LC-MSD SL			NA		NA
12	Agilent 1100 LC-MSD SL			NA		NA

	Parameter Value[ion source]	Term	Source	REF	Term	Accession Number
1	electrospray ionization			MS		1000073
2	electrospray ionization			MS		1000073
3	electrospray ionization			MS		1000073
4	electrospray ionization			MS		1000073
5	electrospray ionization			MS		1000073
6	electrospray ionization			MS		1000073
7	electrospray ionization			MS		1000073
8	electrospray ionization			MS		1000073
9	electrospray ionization			MS		1000073
10	electrospray ionization			MS		1000073
11	electrospray ionization			MS		1000073
12	electrospray ionization			MS		1000073

	Parameter Value[detector]	Term	Source	REF	Term	Accession Number
1		NA		NA		NA
2		NA		NA		NA
3		NA		NA		NA
4		NA		NA		NA
5		NA		NA		NA
6		NA		NA		NA
7		NA		NA		NA
8		NA		NA		NA
9		NA		NA		NA
10		NA		NA		NA
11		NA		NA		NA
12		NA		NA		NA

	Parameter Value[ionization mode]	Term	Source	REF	Term	Accession Number
1	positive mode			NA		NA
2	positive mode			NA		NA
3	positive mode			NA		NA

4	positive mode	NA	NA
5	positive mode	NA	NA
6	positive mode	NA	NA
7	positive mode	NA	NA
8	positive mode	NA	NA
9	positive mode	NA	NA
10	positive mode	NA	NA
11	positive mode	NA	NA
12	positive mode	NA	NA

	MS Assay Name	Raw Spectral Data File	Protocol	REF	Normalization Name
1	lc-ms-1	./cdf/KO/ko15.CDF		NA	NA
2	lc-ms-2	./cdf/KO/ko16.CDF		NA	NA
3	lc-ms-3	./cdf/KO/ko18.CDF		NA	NA
4	lc-ms-4	./cdf/KO/ko19.CDF		NA	NA
5	lc-ms-5	./cdf/KO/ko21.CDF		NA	NA
6	lc-ms-6	./cdf/KO/ko22.CDF		NA	NA
7	lc-ms-7	./cdf/WT/wt15.CDF		NA	NA
8	lc-ms-8	./cdf/WT/wt16.CDF		NA	NA
9	lc-ms-9	./cdf/WT/wt18.CDF		NA	NA
10	lc-ms-10	./cdf/WT/wt19.CDF		NA	NA
11	lc-ms-11	./cdf/WT/wt21.CDF		NA	NA
12	lc-ms-12	./cdf/WT/wt22.CDF		NA	NA

	Data Transformation Name	Derived Spectral Data File	Factor Value[Genotype]
1	NA	faahkoDSDF.txt	KO
2	NA	faahkoDSDF.txt	KO
3	NA	faahkoDSDF.txt	KO
4	NA	faahkoDSDF.txt	KO
5	NA	faahkoDSDF.txt	KO
6	NA	faahkoDSDF.txt	KO
7	NA	faahkoDSDF.txt	WT
8	NA	faahkoDSDF.txt	WT
9	NA	faahkoDSDF.txt	WT
10	NA	faahkoDSDF.txt	WT
11	NA	faahkoDSDF.txt	WT
12	NA	faahkoDSDF.txt	WT

	Term Source	REF	Term Accession Number
1	NA		NA
2	NA		NA
3	NA		NA
4	NA		NA
5	NA		NA
6	NA		NA
7	NA		NA
8	NA		NA
9	NA		NA
10	NA		NA
11	NA		NA
12	NA		NA

Slot "assay.files.per.study":
list()

Slot "assay.technology.types":

[1] "mass spectrometry"

Slot "assay.measurement.types":

[1] "metabolite profiling"

Slot "data.filenames":

\$a_metabolite.txt

	Raw Spectral Data File	Derived Spectral Data File
1	./cdf/KO/ko15.CDF	faahkoDSDF.txt
2	./cdf/KO/ko16.CDF	faahkoDSDF.txt
3	./cdf/KO/ko18.CDF	faahkoDSDF.txt
4	./cdf/KO/ko19.CDF	faahkoDSDF.txt
5	./cdf/KO/ko21.CDF	faahkoDSDF.txt
6	./cdf/KO/ko22.CDF	faahkoDSDF.txt
7	./cdf/WT/wt15.CDF	faahkoDSDF.txt
8	./cdf/WT/wt16.CDF	faahkoDSDF.txt
9	./cdf/WT/wt18.CDF	faahkoDSDF.txt
10	./cdf/WT/wt19.CDF	faahkoDSDF.txt
11	./cdf/WT/wt21.CDF	faahkoDSDF.txt
12	./cdf/WT/wt22.CDF	faahkoDSDF.txt

Slot "samples":

Global metabolite profiling of faah(-/-) mice1
"K01"
Global metabolite profiling of faah(-/-) mice2
"K02"
Global metabolite profiling of faah(-/-) mice3
"K03"
Global metabolite profiling of faah(-/-) mice4
"K04"
Global metabolite profiling of faah(-/-) mice5
"K05"
Global metabolite profiling of faah(-/-) mice6
"K06"
Global metabolite profiling of faah(-/-) mice7
"WT1"
Global metabolite profiling of faah(-/-) mice8
"WT2"
Global metabolite profiling of faah(-/-) mice9
"WT3"
Global metabolite profiling of faah(-/-) mice10
"WT4"
Global metabolite profiling of faah(-/-) mice11
"WT5"
Global metabolite profiling of faah(-/-) mice12
"WT6"

Slot "samples.per.study":

\$`Global metabolite profiling of faah(-/-) mice`

[1] "K01" "K02" "K03" "K04" "K05" "K06" "WT1" "WT2" "WT3" "WT4" "WT5" "WT6"

Slot "samples.per.assay.filename":

```
$a_metabolite.txt
[1] "K01" "K02" "K03" "K04" "K05" "K06" "WT1" "WT2" "WT3" "WT4" "WT5" "WT6"
```

```
Slot "assay_filenames_per_sample":
[1] "a_metabolite.txt" "a_metabolite.txt" "a_metabolite.txt" "a_metabolite.txt"
[5] "a_metabolite.txt" "a_metabolite.txt" "a_metabolite.txt" "a_metabolite.txt"
[9] "a_metabolite.txt" "a_metabolite.txt" "a_metabolite.txt" "a_metabolite.txt"
```

```
Slot "sample_to_rawdatafile":
[[1]]
  Sample Name Raw Spectral Data File
1          K01      ./cdf/K0/ko15.CDF
2          K02      ./cdf/K0/ko16.CDF
3          K03      ./cdf/K0/ko18.CDF
4          K04      ./cdf/K0/ko19.CDF
5          K05      ./cdf/K0/ko21.CDF
6          K06      ./cdf/K0/ko22.CDF
7          WT1      ./cdf/WT/wt15.CDF
8          WT2      ./cdf/WT/wt16.CDF
9          WT3      ./cdf/WT/wt18.CDF
10         WT4      ./cdf/WT/wt19.CDF
11         WT5      ./cdf/WT/wt21.CDF
12         WT6      ./cdf/WT/wt22.CDF
```

```
Slot "sample_to_assayname":
[[1]]
  Sample Name MS Assay Name
1          K01      lc-ms-1
2          K02      lc-ms-2
3          K03      lc-ms-3
4          K04      lc-ms-4
5          K05      lc-ms-5
6          K06      lc-ms-6
7          WT1      lc-ms-7
8          WT2      lc-ms-8
9          WT3      lc-ms-9
10         WT4      lc-ms-10
11         WT5      lc-ms-11
12         WT6      lc-ms-12
```

```
Slot "rawdatafile_to_sample":
[[1]]
  Raw Spectral Data File Sample Name
1      ./cdf/K0/ko15.CDF      K01
2      ./cdf/K0/ko16.CDF      K02
3      ./cdf/K0/ko18.CDF      K03
4      ./cdf/K0/ko19.CDF      K04
5      ./cdf/K0/ko21.CDF      K05
6      ./cdf/K0/ko22.CDF      K06
7      ./cdf/WT/wt15.CDF      WT1
8      ./cdf/WT/wt16.CDF      WT2
```

```

9      ./cdf/WT/wt18.CDF      WT3
10     ./cdf/WT/wt19.CDF      WT4
11     ./cdf/WT/wt21.CDF      WT5
12     ./cdf/WT/wt22.CDF      WT6

```

Slot "assayname.to.sample":

```

[[1]]
  MS Assay Name Sample Name
1      lc-ms-1      K01
2      lc-ms-10     WT4
3      lc-ms-11     WT5
4      lc-ms-12     WT6
5      lc-ms-2      K02
6      lc-ms-3      K03
7      lc-ms-4      K04
8      lc-ms-5      K05
9      lc-ms-6      K06
10     lc-ms-7      WT1
11     lc-ms-8      WT2
12     lc-ms-9      WT3

```

For an example for a real use case, please refer to <https://github.com/sneumann/mtbls2/>.

Writing ISA-Tab datasets

The Risa package offers functions to write the whole ISA-Tab dataset or part of it back to disk. These functions are `write.ISAtab`, `write.investigation.file`, `write.study.file`, `write.assay.file`.

So, after updating the assay file as indicated above, we can save it back to disk, using the following command:

```

> temp = tempdir()
> write.ISAtab(faahkoISA, temp)
> #write.assay.file(faahkoISA, assay.filename, temp)

```

Session Info

```

> toLatex(sessionInfo())

```

- R version 2.15.1 (2012-06-22), x86_64-unknown-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=C, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: Biobase 2.18.0, BiocGenerics 0.4.0, Rcpp 0.9.14, Risa 1.0.0, faahKO 1.2.11, mzR 1.4.0, xcms 1.34.0
- Loaded via a namespace (and not attached): codetools 0.2-8, tools 2.15.1

Further information

For further information about the ISA software infrastructure, please visit our website <http://isa-tools.org>.