

# Risa: Building R objects from local ISA-Tab files

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May 4, 2016

## 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 `xcmsSets` 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)

250:38 300:103 350:226 400:338 450:431 500:529 550:674 600:847
250:43 300:128 350:275 400:394 450:500 500:637 550:835 600:1027
250:25 300:93 350:227 400:337 450:411 500:498 550:640 600:758
250:19 300:67 350:169 400:258 450:301 500:373 550:488 600:580
250:24 300:60 350:166 400:254 450:315 500:391 550:501 600:582
250:31 300:71 350:183 400:280 450:338 500:422 550:532 600:604
250:41 300:105 350:212 400:319 450:416 500:533 550:684 600:838
250:27 300:107 350:232 400:347 450:440 500:549 550:712 600:905
250:24 300:87 350:200 400:293 450:351 500:426 550:548 600:661
250:22 300:65 350:161 400:243 450:293 500:358 550:483 600:561
250:28 300:69 350:157 400:229 450:282 500:364 550:493 600:592
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] "/home/biocbuild/bbs-3.3-bioc/R/library/faahKO"
```

Slot "investigation.filename":  
[1] "i\_Investigation.txt"

Slot "investigation.file":

```

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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
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30             Investigation Person Affiliation
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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
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41             STUDY DESIGN DESCRIPTORS
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47             Study Publication DOI
48             Study Publication Author List
```

49 Study Publication Title  
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 51 Study Publication Status Term Accession Number  
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 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  
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 70 Study Protocol Type Term Accession Number  
 71 Study Protocol Type Term Source REF  
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 83 Study Person Last Name  
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72 LC-MS analysis was performed using an Agilent 1100 LC-MSD SL instrument. For the LC analysis,

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Slot "investigation.identifier":  
[1] ""

Slot "study.identifiers":  
[1] "Global metabolite profiling of faah(-/-) mice"

Slot "study.titles":  
[1] "Global metabolite profiling of faah(-/-) mice"

Slot "study.descriptions":  
[1] "Enzymes regulate biological processes through the conversion of specific substrates to products"

Slot "study.contacts":  
[1] " "

Slot "study.contacts.affiliations":  
[1] ""

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		
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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		KO
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			
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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
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	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":

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

\$`Global metabolite profiling of faah(-/-) mice`[[1]]

	Sample Name	Protocol	REF	Extract Name	Protocol	REF	Labeled Extract Name
1	KO1	extraction		KO1	labeling		NA
2	KO2	extraction		KO2	labeling		NA
3	KO3	extraction		KO3	labeling		NA
4	KO4	extraction		KO4	labeling		NA
5	KO5	extraction		KO5	labeling		NA
6	KO6	extraction		KO6	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	NA	NA	NA
2	NA	NA	NA	NA	NA	NA
3	NA	NA	NA	NA	NA	NA
4	NA	NA	NA	NA	NA	NA
5	NA	NA	NA	NA	NA	NA
6	NA	NA	NA	NA	NA	NA
7	NA	NA	NA	NA	NA	NA
8	NA	NA	NA	NA	NA	NA
9	NA	NA	NA	NA	NA	NA
10	NA	NA	NA	NA	NA	NA
11	NA	NA	NA	NA	NA	NA
12	NA	NA	NA	NA	NA	NA

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

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

	Data Transformation Name	Derived Spectral Data File	Factor Value[Genotype]
1	NA	NA	KO
2	NA	NA	KO
3	NA	NA	KO

4	NA	NA	KO
5	NA	NA	KO
6	NA	NA	KO
7	NA	NA	WT
8	NA	NA	WT
9	NA	NA	WT
10	NA	NA	WT
11	NA	NA	WT
12	NA	NA	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.names":

\$a\_metabolite.txt

	MS Assay Name
1	lc-ms-1
2	lc-ms-2
3	lc-ms-3
4	lc-ms-4
5	lc-ms-5
6	lc-ms-6
7	lc-ms-7
8	lc-ms-8
9	lc-ms-9
10	lc-ms-10
11	lc-ms-11
12	lc-ms-12

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	faahkoSDF.txt
2	./cdf/KO/ko16.CDF	faahkoSDF.txt
3	./cdf/KO/ko18.CDF	faahkoSDF.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":

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

```
$_metabolite.txt
```

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

Slot "assay\_filenames.per.sample":

```
[[1]]
```

```
[[1]][[1]]
```

```
[1] "a_metabolite.txt"
```

```
[[2]]
```

```
[[2]][[1]]
```

```
[1] "a_metabolite.txt"
```

```
[[3]]
```

```
[[3]][[1]]
```

```
[1] "a_metabolite.txt"
```

```
[[4]]
```

```
[[4]][[1]]
```

```
[1] "a_metabolite.txt"
```

```
[[5]]
```

```
[[5]][[1]]
```

```
[1] "a_metabolite.txt"
```

```
[[6]]
```

```
[[6]][[1]]
```

```
[1] "a_metabolite.txt"
```



```
[[7]]
[[7]][[1]]
[1] "a_metabolite.txt"
```

```
[[8]]
[[8]][[1]]
[1] "a_metabolite.txt"
```

```
[[9]]
[[9]][[1]]
[1] "a_metabolite.txt"
```

```
[[10]]
[[10]][[1]]
[1] "a_metabolite.txt"
```

```
[[11]]
[[11]][[1]]
[1] "a_metabolite.txt"
```

```
[[12]]
[[12]][[1]]
[1] "a_metabolite.txt"
```

Slot "sample.to.rawdatafile":

```
[[1]]
  Sample Name Raw Spectral Data File
1          KO1      ./cdf/KO/ko15.CDF
2          KO2      ./cdf/KO/ko16.CDF
3          KO3      ./cdf/KO/ko18.CDF
4          KO4      ./cdf/KO/ko19.CDF
5          KO5      ./cdf/KO/ko21.CDF
6          KO6      ./cdf/KO/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          KO1      lc-ms-1
2          KO2      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/KO/ko15.CDF	K01
2	./cdf/KO/ko16.CDF	K02
3	./cdf/KO/ko18.CDF	K03
4	./cdf/KO/ko19.CDF	K04
5	./cdf/KO/ko21.CDF	K05
6	./cdf/KO/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

Slot "factors":

[[1]]

[[1]]\$`Factor Value[Genotype]`

[1] KO KO KO KO KO KO WT WT WT WT WT WT

Levels: KO WT

```
Slot "treatments":
$`Factor Value[Genotype]`
[1] KO WT
Levels: KO WT
```

```
Slot "groups":
[[1]]
[[1]][[1]]
[1] "K01" "K02" "K03" "K04" "K05" "K06"

[[1]][[2]]
[1] "WT1" "WT2" "WT3" "WT4" "WT5" "WT6"
```

```
Slot "assay.tabs":
[[1]]
An object of class "MSAssayTab"
Slot "path":
[1] "/home/biocbuild/bbs-3.3-bioc/R/library/faahKO"
```

```
Slot "study.filename":
[1] "s_Proteomic profiling of yeast TFs.txt"
```

```
Slot "study.identifier":
[1] "Global metabolite profiling of faah(-/-) mice"
```

```
Slot "assay.filename":
[1] "a_metabolite.txt"
```

```
Slot "assay.file":
  Sample Name Protocol REF Extract Name Protocol REF Labeled Extract Name
1          KO1  extraction          KO1  labeling          NA
2          KO2  extraction          KO2  labeling          NA
3          KO3  extraction          KO3  labeling          NA
4          KO4  extraction          KO4  labeling          NA
5          KO5  extraction          KO5  labeling          NA
6          KO6  extraction          KO6  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      NA mass spectrometry
2     NA      NA      NA      NA mass spectrometry
3     NA      NA      NA      NA mass spectrometry
4     NA      NA      NA      NA mass spectrometry
5     NA      NA      NA      NA mass spectrometry
6     NA      NA      NA      NA mass spectrometry
7     NA      NA      NA      NA mass spectrometry
8     NA      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	NA	KO
2	NA	NA	KO
3	NA	NA	KO
4	NA	NA	KO
5	NA	NA	KO
6	NA	NA	KO
7	NA	NA	WT
8	NA	NA	WT
9	NA	NA	WT
10	NA	NA	WT
11	NA	NA	WT
12	NA	NA	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.technology.type":  
 [1] "mass spectrometry"

Slot "assay.measurement.type":  
 [1] "metabolite profiling"

Slot "assay.names":  
 MS Assay Name  
 1 lc-ms-1  
 2 lc-ms-2  
 3 lc-ms-3  
 4 lc-ms-4

```

5      lc-ms-5
6      lc-ms-6
7      lc-ms-7
8      lc-ms-8
9      lc-ms-9
10     lc-ms-10
11     lc-ms-11
12     lc-ms-12

```

Slot "data.fileNames":

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

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 3.3.0 (2016-05-03), x86\_64-pc-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=en\_US.UTF-8, 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, parallel, stats, utils
- Other packages: Biobase 2.32.0, BiocGenerics 0.18.0, ProtGenerics 1.4.0, Rcpp 0.12.4.5, Risa 1.14.0, affy 1.50.0, biocViews 1.40.0, faahKO 1.11.0, mzR 2.6.0, xcms 1.48.0

- Loaded via a namespace (and not attached): BiocInstaller 1.22.1, RBGL 1.48.0, RColorBrewer 1.1-2, RCurl 1.95-4.8, RUnit 0.4.31, XML 3.98-1.4, affyio 1.42.0, bitops 1.0-6, codetools 0.2-14, graph 1.50.0, grid 3.3.0, knitr 1.12.3, lattice 0.20-33, preprocessCore 1.34.0, stats4 3.3.0, tools 3.3.0, zlibbioc 1.18.0

## Further information

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