Package 'Risa'

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Title Converting experimental metadata from ISA-tab into Bioconductor
data structures

Author

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Depends R (>= 2.0.9), Biobase (>= 2.4.0), methods, Rcpp (>= 0.9.13),
biocViews, affy

Imports xcms

Suggests faahKO (>= 1.2.11)

Description The Investigation / Study / Assay (ISA) tab-delimited
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, spanning from traditional approaches to high-throughput
techniques. Risa allows to access metadata/data in ISA-Tab format and
build Bioconductor data structures. Currently, data generated from microarray,
flow cytometry and metabolomics-based (i.e. mass spectrometry) assays are supported.
The package is extendable and efforts are undergoing to support metadata associated to pro-
teomics assays.

License LGPL

biocViews Annotation, DataImport, MassSpectrometry

URL http://www.isa-tools.org/

BugReports https://github.com/ISA-tools/Risa/issues

git_url https://git.bioconductor.org/packages/Risa

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Date/Publication 2022-04-12

R **topics documented:**

AssayTab-class   *Class* "AssayTab", *a class for maintaing the information of AssayTab*

Description

This class maintains information from an AssayTab dataset, including an investigation file, one or more study files, and one or more assay files for each study file.

Objects from the Class

Objects can be created by calls of the form new("AssayTab",...).

Slots

path Object of class "character", it represents the path of the ISA-Tab dataset to which this AssayTab belongs

study.filename Object of class "character" with the filename of the study to which this assay belongs to.

study.identifier Object of class "character" with the identifier of the study to which this assay belongs to.

assay.filename Object of class "character" with the filename of the assay.

assay.file Object of class "data.frame" with the contents of the assay file.

assay.technology.type Object of class "character" with the technology type of this assay.

assay.measurement.type Object of class "character" with the measurement type of this assay.

assay.names Object of class "data.frame" with the assay names for this assay file.

data.filenames Object of class "data.frame" with the data filenames.

Methods

[signature(x = "AssayTab"): ...

getAssayRawDataFilenames signature(.Object = "AssayTab",full.path="logical"): returns the raw data filenames for this assay

Author(s)

Alejandra Gonzalez-Beltran, <isatools@googlegroups.com>

See Also

ISATab-class,ISATab-methods,

Examples

```
showClass("AssayTab")
showClass("MSAssayTab")
showClass("MicroarrayAssayTab")
showClass("SeqAssayTab")
showClass("NMRAssayTab")
```

---

getAnnotatedDataFrameAssay

Retrieves an AnnotatedDataFrameAssay.

Description

Retrieves an AnnotatedDataFrameAssay.

Usage

```
getAnnotatedDataFrameAssay(isa, assay.filename)
```

Arguments

isa   An object of the ISAtab-class.

assay.filename

Value

An annotated data frame.

Author(s)

Alejandra Gonzalez-Beltran

See Also

`ISATab-class`, `AnnotatedDataFrame`

Examples

```
faahkoISAzip <- system.file("extdata","faahKO-metadata.zip", package="Risa")
faahkoISA <- readISAtab(zipfile = faahkoISAzip, path = file.path(system.file("extdata", package="Risa"),"faahkoI
faahkoADF <- getAnnotatedDataFrameAssay(faahkoISA, faahkoISA@assay.filenames[[1]])
str(faahkoADF)


armstrongISAzip <- system.file("extdata","ARMSTRONG-S-3-metadata.zip", package="Risa")
armstrongISA <- readISAtab(zipfile = armstrongISAzip, path = file.path(system.file("extdata", package="Risa"),"a
armstrongADF <- getAnnotatedDataFrameAssay(armstrongISA, armstrongISA@assay.filenames[[1]])
str(armstrongADF)
```

---

getAssayRawDataFilenames-methods

~~ Methods for Function getAssayRawDataFilenames *in Package*
Risa *~~*

Description

~~ Methods for function `getAssayRawDataFilenames` in package **Risa** ~~ They retrieve the raw data files for a particular assay type.

Methods

`signature(.Object = "AssayTab", full.path = "logical")` Retrieves the raw data filenames for a generic assay.

`signature(.Object = "MicroarrayAssayTab", full.path = "logical")` Retrieves the raw data filenames for an assay whose technology type is DNA microarray.

`signature(.Object = "MSAssayTab", full.path = "logical")` Retrieves the raw data filenames for an assay whose technology type is mass spectrometry. These data filenames correspond to those specified in the column 'Raw Spectral Data File'.

`signature(.Object = "NMRAssayTab", full.path = "logical")` Retrieves the raw data filenames for an assay whose technology type is NMR spectroscopy.

`signature(.Object = "SeqAssayTab", full.path = "logical")` Retrieves the raw data filenames for an assay whose technology type is nucleotide sequencing.

---

getExpressionSet   *Retrieves an ExpressionSet for a DNA microarray assay.*

Description

Retrieves an ExpressionSet for a DNA microarray assay.

Usage

```
getExpressionSet(isa, assay.filename)
```

Arguments

isa   An object from the ISATab-class.

assay.filename A character vector with the assay filename of the microarray assay.

Value

It returns an ExpressionSet.

Author(s)

Alejandra Gonzalez-Beltran

References

affy

See Also

ISATab-class

Examples

```
data.dir <- system.file("extdata", package="Risa")
isazip <- system.file("extdata","ARMSTRONG-S-3-metadata.zip", package="Risa")
path <- file.path(data.dir,"ARMSTRONG_ISA")
isa <- readISAtab(zipfile = isazip, path = path, verbose =TRUE)
path <- file.path(data.dir,"ARMSTRONG_ISA/")

cel.files <- c("GSM510377_SA2006121413.CEL", "GSM510378_SA2006121414.CEL", "GSM510379_SA2006121415.CEL", "GSM510
            "GSM510381_SA2006121417.CEL", "GSM510382_SA2006121418.CEL","GSM510383_SA2006121419.CEL","GSM510384_S
            "GSM510385_SA2006121421.CEL","GSM510386_SA2006121427.CEL", "GSM510387_SA2006121428.CEL", "GSM510388_
            "GSM510389_SA2006121440.CEL","GSM510390_SA2006121441.CEL", "GSM510391_SA2006121442.CEL")

base.url <- "http://perdera.sph.harvard.edu/biidata/microarray/study_ARMSTRONG-S-3_3Zd4KeJNJ7/raw_data/"

###########download all the cel files - this is commented out, uncomment the following two lines if you want to buil
#lapply(cel.files, function(x) download.file(paste(base.url, x, sep=""), destfile=paste(path, x, sep="")))
```

```
#getExpressionSet(isa, isa@assay.filenames[[1]])
```

---

getMIAMEMetadata   *Retrieves the MIAME information about a microarray experiment*

Description

If the assay.filename uses the microarray technology, it retrieves an object of the class MIAME with the minimum information about the experiment. Otherwise, it outputs a message indicating that the method is not valid for assays not using the microarray technology.

Usage

```
getMIAMEMetadata(isa, assay.filename)
```

Arguments

isa   An object of the ISAtab-class.

assay.filename A string indicating the name of an assay file. It must correspond to a microarray-
                based assay for the function to return a valid value.

Value

It retrieves an object from the MIAME class or an error message.

Author(s)

Alejandra Gonzalez-Beltran

See Also

isMicroarrayAssay

Examples

```
armstrongISAzip <- system.file("extdata","ARMSTRONG-S-3-metadata.zip", package="Risa")
armstrongISA <- readISAtab(zipfile = armstrongISAzip, path = file.path(system.file("extdata", package="Risa"),"a
assay.filename <- armstrongISA@assay.filenames[[1]]
miame <- getMIAMEMetadata(armstrongISA, assay.filename)
str(miame)
```

`getMicroarrayAssayFilenames`

Listing filenames of microarray-based asssay from an ISAtab dataset.

Description

Retrieves the list of asssay filenames in an ISAtab dataset, which correspond to microarray-based assays.

Usage

```
getMicroarrayAssayFilenames(isa)
```

Arguments

isa   An object of the `ISAtab-class`.

Value

a list of assay filenames

Author(s)

Alejandra Gonzalez-Beltran

See Also

`isMicroarrayAssay`

Examples

```
armstrongISAzip <- system.file("extdata","ARMSTRONG-S-3-metadata.zip", package="Risa")
armstrongISA <- readISAtab(zipfile = armstrongISAzip, path = file.path(system.file("extdata", package="Risa"),"ar
getMicroarrayAssayFilenames(armstrongISA)
```

`getMSAssayFilenames`   *Retrieves a vector with the assay filenames corresponding to mass spectrometry.*

Description

Given an object from the ISAtab-class, this method retrieves a vector with the assay filenames corresponding to mass spectrometry (identified by having a column called 'Raw Spectral Data File'.

Usage

```
getMSAssayFilenames(isa)
```

Arguments

isa   an object from the ISAtab class

Value

A character vector with the assay filenames corresponding to mass spectrometry.

Author(s)

Alejandra Gonzalez-Beltran

Examples

```
data.dir <- system.file("extdata", package="Risa")
isazip <- system.file("extdata","faahKO-metadata.zip", package="Risa")
faahkoISA <- readISAtab(zipfile = isazip, path = file.path(data.dir,"faahKOISA"), verbose =TRUE)
ms.assay.filenames <- getMSAssayFilenames(faahkoISA)
```

---

getRawDataFilenames-methods

> ~~ *Methods for Function* getRawDataFilenames *in Package* **Risa** ~~

Description

~~ Methods for function getRawDataFilenames in package **Risa** ~~\ To retrieve the raw data filenames in the ISATab dataset.

Methods:

signature(.Object = "ISATab", full.path = "logical") Retrieves the raw data filenames in the ISATab dataset given an object from the ISATab-class and a boolean value indicating if the filenames are retrieved with their full path or not.

---

getStudyFilename   *Retrieves the study filename to which an assay.filename corresponds.*

Description

Retrieves the study filename to which an assay.filename corresponds.

Usage

```
getStudyFilename(isa, assay.filename)
```

Arguments

isa   an object from the `ISATab-class`.

`assay.filename` a string with the filename of an assay

Value

a string with the study filename.

Author(s)

Alejandra Gonzalez-Beltran

See Also

`ISATab-class`

Examples

```
faahkoISA <- readISAtab(find.package("faahKO"))
getStudyFilename(faahkoISA, faahkoISA@assay.filenames[[1]])
```

`ISATab-class`   *Class* `"ISATab"`*, a class for maintaing ISATab information*

Description

This class maintains information from an ISATab dataset, including an investigation file, one or more study files, and one or more assay files for each study file.

Objects from the Class

Objects can be created by calls of the form `new("ISATab",...)`.

Slots

`path:` Object of class `"character"`, it represents the path of the ISA-Tab dataset

`investigation.filename:` Object of class `"character"`, it represents the name of the Investigation file

`investigation.file:` Object of class `"data.frame"`, it is a data frame with the contents of the Investigation file

`investigation.identifier:` Object of class `"character"`, it is a string with the identifier for the investigation

`study.identifiers:` Object of class `"character"`, it is the list of study identifiers

`study.titles:` Object of class `"character"`, it is the list of study titles

`study.descriptions:` Object of class `"character"`, it is the list of study descriptions

study.contacts: Object of class "character", it is the list of study contacts

study.contacts.affiliations: Object of class "character", it is the list of affiliations of the
    study contacts

study.filenames: Object of class "character", the names of the study files

study.files: Object of class "list", a list of data frames wiht the contents of the study files

assay.filenames: Object of class "character", the names of the assay files

assay.filenames.per.study: Object of class "list", the names of the assay files according to
    the study they belong to

assay.files: Object of class "list", a list of data frames with the contents of the assay files

assay.files.per.study: Object of class "list", a list of data frames with the contents of the
    assay files divided per study they belong to

assay.names: Object of class "list", which is a list of data frames, containing, per each assay
    file, the column of the assay file corresponding to the "Assay Name"

assay.technology.types: Object of class "character", a list with the technology types corre-
    sponding to each assay

assay.measurement.types: Object of class "character", a list with the names of the data files

data.filenames: Object of class "list", a list with the names of the samples

samples: Object of class "character"

samples.per.study: Object of class "list",

samples.per.assay.filename: Object of class "list",the samples classified according to the
    assay filename they belong to

assay.filenames.per.sample: Object of class "list", where each element is a list of assay file
    names per each sample name

sample.to.rawdatafile: Object of class "list", a list of data frames with samples associated
    with raw data files

sample.to.assayname: Object of class "list", maintains the association between samples and
    assay names

rawdatafile.to.sample: Object of class "list", mantains the association raw data file and sam-
    ples

assayname.to.sample: Object of class "list", mantains the associations between assay names
    and samples

factors: Object of class "list", which contains R 'factor' objects for each of the studies (with
    factor names and factor levels).

treatments: Object of class "list" of data frames with the combination of factor values, per
    study file, or a factor object, if there is a single study

groups: Object of class "list", with one element per study file, and each element is a list of the
    samples for the corresponding treatment

assay.tabs: Object of class "list", where each element is an object of the class AssayTab or its
    specialisations (MSAssayTab or MicroarrayAssayTab), representing the information of each
    of the assay files in the investigation.

Methods

[signature(x = "ISATab"): ...

getRawDataFilenames signature(.Object="ISATab",full.path=TRUE): get the raw data filenames for all the assays in the ISATab dataset

Note

No notes yet.

Author(s)

Alejandra Gonzalez-Beltran, <isatools@googlegroups.com>

References

Risa is a component of the ISA software infrastructure <http://isa-tools.org/>. 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>.

See Also

ISATab-methods

Examples

showClass("ISATab")

---

isMicroarrayAssay   *Determines if an assay is microarray-based or not.*

Description

Retrieves a boolean value indicating wether the assay filename given as parameter corresponds to a microarray-based assay or not.

Usage

isMicroarrayAssay(isa, assay.filename)

Arguments

isa   An object of the ISAtab-class.

assay.filename A string indicating the name of an assay file. It must correspond to a microarray-based assay for the function to return a valid value.

Value

Retrieves a boolean value.

Author(s)

Alejandra Gonzalez-Beltran

See Also

getMIAMEMetadata

Examples

```
data.dir <- system.file("extdata", package="Risa")
isazip <- system.file("extdata","ARMSTRONG-S-3-metadata.zip", package="Risa")
isa <- readISAtab(zipfile = isazip, path = file.path(data.dir,"ARMSTRONG_ISA"), verbose =TRUE)

assay.filename <- isa@assay.filenames[[1]]
isMicroarrayAssay(isa, assay.filename)
```

---

isMSAssay	*Indicates if an assay filename corresponds to a mass spectrometry assay.*

Description

Indicates if an assay filename corresponds to a mass spectrometry assay.

Usage

```
isMSAssay(isa, assay.filename)
```

Arguments

isa   an object from the ISAtab-class.
assay.filename the filename of an assay file

Value

It retrieves a boolean value indicating wether the assay is a mass spectrometry assay or not.

Author(s)

Alejandra Gonzalez-Beltran

Examples

```
faahkoISA = readISAtab(find.package("faahKO"))
assay.filename <- faahkoISA["assay.filenames"][[1]]
isMSAssay(faahkoISA, assay.filename)
```

---

processAssayXcmsSet   *Build an xcmsSet object given a mass spectrometry assay and considering all factors defined*

Description

processAssayXcmsSet retrieves an xcmsSet object given and ISA-tab object and one of its assay filenames.

Usage

```
processAssayXcmsSet(isa, assay.filename, ...)
```

Arguments

isa	an ISA object, as retrieved by the function readISAtab
assay.filename	a boolean indicating to show messages for the different steps, if TRUE, or not to show them, if FALSE
...	extra arguments that can be pass down to the xcmsSet function from the xcms package

Value

the xcmsSet object built from the assay metadata, considering all the factors defined, and data files

Author(s)

Steffen Neumann, Alejandra Gonzalez-Beltran / Maintainer: Alejandra Gonzalez-Beltran <isatools@googlegroups.com>

See Also

readISAtab

Examples

```
faahkoISA = readISAtab(find.package("faahKO"))
assay.filename <- faahkoISA["assay.filenames"][[1]]
xset = processAssayXcmsSet(faahkoISA, assay.filename)
```

---

processAssayXcmsSet.1factor

*Build an xcmsSet object given a mass spectrometry assay and consid-
ering the first factor defined*

Description

processAssayXcmsSet.1factor retrieves an xcmsSet object given and ISA-tab object and one of
its assay filenames.

Usage

```
processAssayXcmsSet.1factor(isa, assay.filename, ...)
```

Arguments

isa	an ISA object, as retrieved by the function readISAtab
assay.filename	a boolean indicating to show messages for the different steps, if TRUE, or not to show them, if FALSE
...	extra arguments that can be pass down to the xcmsSet function from the xcms package

Value

the xcmsSet object built from the assay metadata, considering all the factors defined, and data files

Author(s)

Alejandra Gonzalez-Beltran / Maintainer: Alejandra Gonzalez-Beltran <isatools@googlegroups.com>

See Also

readISAtab

Examples

```
faahkoISA = readISAtab(find.package("faahKO"))
assay.filename <- faahkoISA["assay.filenames"][[1]]
xset = processAssayXcmsSet.1factor(faahkoISA, assay.filename)
```

---

readISAtab *Reads an ISAtab dataset into an R object.*

Description

Reads an ISAtab dataset given as a zip file or as a set of files in a specific folder, and builds an object from the ISAtab class.

Usage

```
readISAtab(path = getwd(), zipfile = NULL, verbose = FALSE)
```

Arguments

path	the name of the directory in which the ISAtab files are located (if the parameter zipfile is not provided or if it is equal to NULL), or the name of the directory where the zip file will be extracted (if the parameter zipfile is not NULL.) The default is the working directory.
zipfile	a zip archive containing ISAtab files. The default value is NULL.
verbose	a boolean indicating to show messages for the different steps, if TRUE, or not to show them, if FALSE

Value

The result is an object from the ISAtab class.

Author(s)

Alejandra Gonzalez-Beltran, Audrey Kauffmann / Maintainer: Alejandra Gonzalez-Beltran, ISA Team <isatools@googlegroups.com>

Examples

```
## Example for mass spectrometry dataset
  temp = tempdir()
 datafiles = c(file.path(system.file("cdf/KO", package="faahKO"), grep("CDF",dir(system.file("cdf/KO", package
  file.copy(datafiles, temp, recursive=TRUE)
 isafiles = file.path(system.file(package="faahKO"), grep("txt",dir(system.file(package="faahKO")),value=TRUE
  file.copy(isafiles, temp, recursive=TRUE)
  isaObject1 = readISAtab(path = temp)

## Example of readISAtab for a mass spectrometry experiment
 isazip <- system.file("extdata","faahKO-metadata.zip", package="Risa")
 isaObject2 <- readISAtab(zipfile = isazip, path = file.path(system.file("extdata", package="Risa"),"ISAexample")
```

Risa   *Risa package overview*

Description

The Risa package builds R objects from ISA-tab format files and it is a component of the ISA software infrastructure (see <http://isa-tools.org/>). ISA stands for Investigation, Study, Assay and the infrastructure revolves around the ISA-Tab format, which supports descriptions of biological experiments, with focus but not limited to high-throughput experiments. The format is supported by a series of open-source tools (all available in There is a growing international user community of the ISA infrastructure, featured in the ISA commons website (<http://isacommons.org>).

The source code and latest version of the Risa package 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>.

The function readISAtab reads ISA-tab files from a local zip archive or from a local folder.

The package also contains methods to save the ISA-tab files and to update the metadata after analysis. For mass spectrometry assays, the package includes several methods to build necessary object for processing using the xcms package (available in Bioconductor).

There are also functions to deal with DNA microarray-based assays, such as building an ExpressionSet object, relying on the affy package (available in Bioconductor)

In addition, there is a function called suggestBiocPackage that, given an object from the ISAtab-class - i.e. an ISAtab dataset - it will retrieve a list of potentially useful packages from Bioconductor, according to the assays measurement and technology types. This functionality is based on the annotations provided by the BiocViews.

The Risa package bridges the ISA metadata with analysis pipelines in R, and this is the reason of its name: R + ISA = Risa. Anecdotically, we note that Risa is the Pleasure Planet in Star Trek (see <http://en.memory-alpha.org/wiki/Risa>) and that 'Risa' means laughter in Spanish.

Author(s)

Alejandra Gonzalez-Beltran, Steffen Neumann, Audrey Kauffmann, Gabriella Rustici, Philippe Rocca-Serra, Eamonn Maguire, Susanna-Asunta Sansone. Maintainer: Alejandra Gonzalez-Beltran <isatools@googlegroups.com>

See Also

readISAtab, processAssayXcmsSet, updateAssayMetadata, write.ISAtab

Examples

```
  ## Example of readISAtab for a mass spectrometry experiment from a zip file
  isazip = system.file("extdata","faahKO-metadata.zip", package="Risa")
isaset = readISAtab(zipfile = isazip, path = file.path(system.file("extdata", package="Risa"),"ISAexample"), v

  require("faahKO")
  ## Example of readISAtab for mass spectrometry data
```

```
    temp = tempdir()
  datafiles = c(file.path(system.file("cdf/KO", package="faahKO"), grep("CDF",dir(system.file("cdf/KO", package
    file.copy(datafiles, temp, recursive=TRUE)
  isafiles = file.path(system.file(package="faahKO"), grep("txt",dir(system.file(package="faahKO")),value=TRUE
    file.copy(isafiles, temp, recursive=TRUE)
    isatab.object = readISAtab(path = temp)
```

---

suggestBiocPackage   *Suggest Bioconductor pacakges*

Description

Suggest a list of packages available in Bioconductor, which may be useful for processing the assay
according to its technology and measurement types.

Usage

```
suggestBiocPackage(isa,bioc.version)
```

Arguments

isa   An ISAtab-class object.

bioc.version   The version number of Bioconductor to be considered as the source of the
                pacakges for suggestions.

Author(s)

Alejandra Gonzalez-Beltran

---

updateAssayMetadata   *Update metadata into the assay file*

Description

updateAssayMetadata Updates metadata into a particular assay file. See an example of use for a
metabolite dataset at <https://github.com/sneumann/mtbls2>.

Usage

```
updateAssayMetadata(isa, assay.filename, col.name, values)
```

Arguments

`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)

Value

The updated ISA-Tab object.

Author(s)

Alejandra Gonzalez-Beltran / Maintainer: Alejandra Gonzalez-Beltran, ISA Team <isatools@googlegroups.com>

See Also

readISAtab, <https://github.com/sneumann/mtbls2>

Examples

```
### This example shows how to add values to the column "Derived Spectral Data File", assuming that the results are s
faahkoISA = readISAtab(find.package("faahKO"))
assay.filename <- faahkoISA["assay.filenames"][[1]]
updateAssayMetadata(faahkoISA, assay.filename,"Derived Spectral Data File","faahkoDSDF.txt" )
```

---

write.assay.file	*Write an Assay File from the ISA-Tab dataset*

Description

`write.assay.file` writes a specific assay file from the ISA-tab dataset into disk.

Usage

```
write.assay.file(isa, assay.filename, path = getwd())
```

Arguments

`isa`	the ISA-Tab object (as retrieved by the readISAtab function)
`assay.filename`	the name of the assay file to be written to disk
`path`	the output path in which the study file is going to be written, by default is the working directory

Author(s)

Alejandra Gonzalez-Beltran / Maintainer: Alejandra Gonzalez-Beltran, ISA Team <isatools@googlegroups.com>

See Also

`write.ISAtab,write.investigation.file, write.study.file, readISAtab`

Examples

```
### Example of writing the study file of faahKO ISA-Tab dataset into the temp directory
 faahkoISA <- readISAtab(find.package("faahKO"))
 temp = tempdir()
 write.assay.file(faahkoISA, faahkoISA["assay.filenames"][[1]], temp)
```

`write.investigation.file`

Writes the Investigation File of an ISA-Tab dataset

Description

`write.investigation.file` reads a ISA-tab file.

Usage

```
write.investigation.file(isa, path = getwd())
```

Arguments

isa	the ISA-Tab object (as retrieved by the readISAtab function)
path	the output path in which the study file is going to be written, by default is the working directory

Author(s)

Alejandra Gonzalez-Beltran / Maintainer: Alejandra Gonzalez-Beltran, ISA Team <isatools@googlegroups.com>

See Also

`write.ISAtab, write.study.file, write.assay.file, readISAtab`

Examples

```
### Example of writing the study file of faahKO ISA-Tab dataset into the temp director
 faahkoISA <- readISAtab(find.package("faahKO"))
 temp = tempdir()
 write.investigation.file(faahkoISA, temp)
```

---

write.ISAtab   *Write an ISA-Tab dataset*

Description

`write.ISAtab` writes a ISA-Tab dataset.

Usage

```
write.ISAtab(isa, path = getwd())
```

Arguments

isa   the ISA-Tab object as built with the function `readISAtab`.

path   the directory where the files are going to be written, by default is the working
               directory

Author(s)

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See Also

`write.investigation.file`, `write.study.file`, `write.assay.file`, `readISAtab`

Examples

```
  ### Example of writing the study file of faahKO ISA-Tab dataset into the temp director
   data.dir <- system.file("extdata", package="Risa")
   isazip <- system.file("extdata","faahKO-metadata.zip", package="Risa")
  faahkoISA <- readISAtab(zipfile = isazip, path = file.path(data.dir,"faahKOISA"), verbose =TRUE)
   temp = tempdir()
   write.ISAtab(faahkoISA, temp)
```

---

write.study.file   *Write a Study File of an ISA-Tab dataset*

Description

`write.study.file` writes a specific Study file from the ISA-tab dataset.

Usage

```
write.study.file(isa, study.filename, path = getwd())
```

Arguments

`isa`	the ISA-Tab object (as retrieved by the readISAtab function)
`study.filename`	the name of the study file to be written to disk
`path`	the output path in which the study file is going to be written, by default is the working directory

Author(s)

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See Also

`write.study.file`, `write.ISAtab`, `readISAtab`

Examples

```
### Example of writing the study file of faahKO ISA-Tab dataset into the temp director
faahkoISA <- readISAtab(find.package("faahKO"))
temp = tempdir()
write.study.file(faahkoISA, faahkoISA["study.filenames"][[1]], temp)
```

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