ArrayExpress

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R topics documented:

`ArrayExpress` *R objects from ArrayExpress database*

Description

`ArrayExpress` produces an `AffyBatch`, an `ExpressionSet` or a `NChannelSet` from a raw dataset from the ArrayExpress database. `ArrayExpress` needs an Internet connection.

Usage

```
ArrayExpress(input, path = ".", save = FALSE, rawcol = NULL)
```

Arguments

`input`	an ArrayExpress identifier. The function currently covers 96% of the raw data sets of the database.
`path`	the name of the directory in which the files downloaded on the ArrayExpress repository will be extracted. The default is the current directory.
`save`	if TRUE, the files downloaded from the database will not be deleted from path after executing the function.
`rawcol`	by default, for the raw data, the columns are automatically selected according to the scanner type. If the scanner is unknown or if the user wants to use different columns than the default, the argument 'rawcol' can be set. For two colour arrays it must be a list with the fields 'R', 'G', 'Rb' and 'Gb' giving the column names to be used for red and green foreground and background. For one colour arrays, it must be a character string with the column name to be used. These column names must correspond to existing column names of the expression files.

Value

The output is an object of class AffyBatch or ExpressionSet or NChannelSet with the raw expression values in the assayData of the object, the information contained in the .sdrf file in the phenoData, the adf file in the featureData and the idf file content in the experimentData.

If several array designs are used in the data set, the output is a list with an object for each array design.

Author(s)

Audrey Kauffmann Maintainer: <audrey@ebi.ac.uk>

See Also

queryAE, getAE, magetab2bioc, getcolproc, procset

Examples

```
ETABM25.affybatch = ArrayExpress(input = "E-TABM-25")
print(ETABM25.affybatch)
sampleNames(ETABM25.affybatch)
colnames(pData(ETABM25.affybatch))
```

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extract.zip *Unzip archives in a specified directory*

Description

extract.zip extracts the files from a .zip archive in a specific directory.

Usage

```
extract.zip(file, extract_path = dirname(file))
```

Arguments

file	A file name.
extract_path	A path to define where the files are to be extracted.

Value

Success is indicated by returning the directory in which the files have been extracted. If it fails, it returns an empty character string.

Author(s)

Audrey Kauffmann Maintainer: <audrey@ebi.ac.uk>

getAE *Download MAGE-TAB files from ArrayExpress in a specified directory*

Description

getAE downloads and extracts the MAGE-TAB files from an ArrayExpress dataset.

Usage

```
getAE(input, path = ".", type = "full", extract = TRUE)
```

Arguments

input	is an ArrayExpress identifier.
path	is the name of the directory in which the files downloaded on the ArrayExpress repository will be extracted.
type	can be 'raw' to download and extract only the raw data, 'processed' to download and extract only the processed data or 'full' to have both raw and processed data.
extract	if FALSE, the files are not extracted from the zip archive.

Value

A list with the names of the files that have been downloaded and extracted.

Author(s)

Audrey Kauffmann Maintainer: <audrey@ebi.ac.uk>

See Also

magetab2bioc, getcolproc

Examples

```
mexp1422 = getAE("E-MEXP-1422", type = "full")

## Build a an ExpressionSet from the raw data
MEXP1422raw = magetab2bioc(files = mexp1422)

## Build a an ExpressionSet from the processed data
cnames = getcolproc(mexp1422)
MEXP1422proc = procset(mexp1422, cnames[2])
```

getcolproc — *Return the possible column names to from processed MAGE-TAB files*

Description

getcolproc extracts the column names from processed MAGE-TAB and return them. The output is needed to call the function procset.

Usage

```
getcolproc(files)
```

Arguments

files	A list as given from getAE function. Containing the following elements:
	procfile procfile is the name of the processed MAGE-TAB file to be read.
	path is the name of the directory where to find this file.

Author(s)

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See Also

queryAE, getAE, procset

Examples

```
# An example can be found in the help of the getAE function.
```

magetab2bioc — *Convert MAGE-TAB files from raw data into a Bioconductor object*

Description

magetab2bioc converts local MAGE-TAB files into a AffyBatch, an ExpressionSet or a NChannelSet.

Usage

```
magetab2bioc(files, rawcol = NULL)
```

Arguments

files	A list as given from getAE function. Containing the following elements: **rawfiles** all the expression files to use to create the object. The content of the raw.zip MAGE-TAB file. **sdrf** the name of the sdrf file from MAGE-TAB. **idf** the name of the idf file from MAGE-TAB. **adf** the name of the adf file from MAGE-TAB. **path** is the name of the directory containing these files.
rawcol	by default, the columns are automatically selected according to the scanner type. If the scanner is unknown or if the user wants to use different columns than the default, the argument 'rawcol' can be set. For two colour arrays it must be a list with the fields 'R', 'G', 'Rb' and 'Gb' giving the column names to be used for red and green foreground and background. For one colour arrays, it must be a character string with the column name to be used. These column names must correspond to existing column names of the expression files.

Value

An object of class AffyBatch, ExpressionSet or NChannelSet with the raw expression values in the 'assayData' of the object, the information contained in the sdrf file in the 'phenoData', the adf file content in the 'featureData' and the idf file content in the 'experimentData'.

If several array designs are used in the dataset, the output is a list with an object for each array design.

Author(s)

Audrey Kauffmann Maintainer: <audrey@ebi.ac.uk>

See Also

queryAE, getAE

Examples

```
# An example can be found in the help of the getAE function.
```

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procset *Convert processed MAGE-TAB files into a Bioconductor object*

Description

procset converts local MAGE-TAB files into an ExpressionSet.

Usage

```
procset(files, procol)
```

Arguments

files	is the list with the names of the processed, the sdrf, the adf and the idf files and the path of the data as given by getAE.
procol	the name of the column to be extracted from the file. Obtained using getcolproc.

Author(s)

Audrey Kauffmann Maintainer: <audrey@ebi.ac.uk>

See Also

queryAE, getAE, getcolproc

Examples

```
# An example can be found in the help of the getAE function.
```

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queryAE *XML query of the ArrayExpress repository*

Description

queryAE queries the ArrayExpress database with keywords and give a dataframe with ArrayExpress identifiers and related information, as an output.

Usage

```
queryAE(keywords = NULL, species = NULL)
```

Arguments

keywords	the keyword(s) of interest. To use several words, they must be separated by a "+" as shown in the examples.
species	the specie(s) of interest.

Value

A dataframe with all the ArrayExpress dataset identifiers which correspond to the query in the first column. The following columns contain information about these datasets, such as the number of raw files, the number of data processed, the release date on the database, the pubmed ID, the species, the experiment design and the experimental factors.

Author(s)

Audrey Kauffmann Maintainer: <audrey@ebi.ac.uk>

See Also

ArrayExpress, getAE

Examples

```
## To retrieve all the identifiers of pneumonia data sets
pneumo = queryAE(keywords = "pneumonia")

## To retrieve all the identifiers of pneumonia data sets studied in human
pneumoHS = queryAE(keywords = "pneumonia", species = "homo+sapiens")
```

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