Package ‘ExpressionAtlas’

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Title Download datasets from EMBL-EBI Expression Atlas

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Description This package is for searching for datasets in EMBL-EBI Expression Atlas, and downloading them into R for further analysis. Each Expression Atlas dataset is represented as a SimpleList object with one element per platform. Sequencing data is contained in a SummarizedExperiment object, while microarray data is contained in an ExpressionSet or MAList object.

biocViews ExpressionData, ExperimentData, SequencingData, MicroarrayData, ArrayExpress

Depends R (>= 4.1.1), methods, Biobase, SummarizedExperiment, limma, S4Vectors, xml2

Imports utils, XML, httr

Suggests knitr, testthat, rmarkdown

VignetteBuilder knitr

Collate functions.R

License GPL (>= 3)

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NeedsCompilation no

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R topics documented:

`allExps` *A SimpleList containing some dummy Expression Atlas datasets*

Description

This is a SimpleList object containing dummy data from some Expression Atlas experiments, to demonstrate a typical example of the reesults of using the `getAtlasData()` function. The dummy data objects only contain the first 10 rows of the real data, to save disk space. To get the real data, download it using `getAtlasData()`.

Usage

```
data( "allExps" )
```

Value

A SimpleList with one element per Expression Atlas dataset.

`atlasRes` *A DataFrame listing some Expression Atlas experiments*

Description

This is a DataFrame object listing some Expression Atlas experiments, to demonstrate a typical example of the reesults of using the `searchAtlasExperiments()` function.

Usage

```
data( "atlasRes" )
```

Value

A DataFrame with one row per Expression Atlas dataset.

`getAtlasData` *Download data from multiple Expression Atlas experiments*

Description

This function downloads Expression Atlas experiment summary SimpleList objects based on a vector of ArrayExpress experiment accessions, and returns a list containing these objects.

Usage

```
getAtlasData( experimentAccessions )
```

Arguments

`experimentAccessions`	Vector of ArrayExpress accessions for experiments to be downloaded.

Value

A list with one entry per experiment summary SimpleList object. Entries are named using the ArrayExpres accession of the respective experiment.

Examples

```
# Download some Expression Atlas data into a list.
myExperimentSummaries <- getAtlasData(
    c(
        "E-GEOD-11175",
        "E-MTAB-3007",
        "E-GEOD-21070"
    )
)
```

`getAtlasExperiment` *Download data for an Expression Atlas experiment*

Description

This function downloads and returns a SimpleList object representing a single Expression Atlas experiment, based on the ArrayExpress accession of the experiment.

Usage

```
getAtlasExperiment( experimentAccession )
```

Arguments

`experimentAccession`	ArrayExpress experiment accession e.g. "E-GEOD-11175"

Value

A SimpleList object representing a single Expression Atlas experiment. The SimpleList contains one entry per platform used in the experiment. For sequencing experiments, there is a single entry in the list. For microarray experiments, there is one entry per array design used. Currently Expression Atlas does not support multi-technology (e.g. microarray and RNA-seq) experiments.

For a single-channel microarray experiment, each entry of the list is an ExpressionSet object. For a sequencing experiment, the single entry is a SummarizedExperiment object. Please refer to the relevant documentation on these classes for more information about them.

RNA-seq data

Each SummarizedExperiment object contains the following:

- Matrix of raw counts (not normalized), in the assays slot, in a counts element.
- Sample annotations, in the colData slot.
- Brief outline of methods, from QC of FASTQ files to production of raw counts, in the exptData slot.

Single-channel microarray data

Each ExpressionSet object contains the following:

- Matrix of normalized intensity values, in the assayData, accessed via: exprs(expressionSet)
- Sample annotations, in the phenoData, accessed via: pData(expressionSet)
- Brief outline of normalization method applied, in the experimentData slot, accessed via: preproc(experimentData(expressionSet))

Examples

```
# Download the experiment summary for E-GEOD-11175
geod11175 <- getAtlasExperiment( "E-GEOD-11175" )

# See the entries available (in this case array design accessions)
names( geod11175 )
# Prints out the following:
# [1] "A-AFFY-126"

# Get the only ExpressionSet object from this experiment.
eset <- geod11175[[ "A-AFFY-126" ]]
```

`rnaseqExps` *A SimpleList containing a dummy RNA-seq Expression Atlas dataset*

Description

This is a SimpleList object containing dummy data from an RNA-seq Expression Atlas experiment, to demonstrate a typical example of the reesults of using the `getAtlasData()` function for a subset of results obtained using `searchAtlasExperiments`. This object contains the first 10 rows of the original data, to save disk space. To get the full dataset, download it using `getAtlasData()`.

Usage

```
data( "rnaseqExps" )
```

Value

A SimpleList with one element per Expression Atlas dataset.

`searchAtlasExperiments` *Search for Expression Atlas experiments*

Description

This function accepts a vector of sample properties, and optionally a species name, and then searches for matching Expression Atlas experiments.

Usage

```
searchAtlasExperiments( properties, species = NULL )
```

Arguments

`properties`	Character vector of sample properties to search Atlas for. These can be biological characteristics, experimental treatments, etc.
`species`	Optional. The name of a species to limit results to. If not provided, search is performed across all species in Expression Atlas.

Value

A DataFrame containing the ArrayExpress accessions, the species, experiment types, and titles of Expression Atlas experiments matching the query.

Examples

```
# Search for experiments on salt in rice.
atlasRes <- searchAtlasExperiments( properties = "salt", species = "rice"  )

# Download data for all experiments found.
atlasData <- getAtlasData( atlasRes$Accession )
```

Index