Package 'ExpressionAtlas'

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Title Download datasets from EMBL-EBI Expression Atlas

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 (>= 4.2.0), methods, Biobase, SummarizedExperiment, limma,
S4Vectors, xml2, RCurl, jsonlite, BiocStyle

Imports utils, XML, httr

Suggests knitr, testthat, rmarkdown

VignetteBuilder knitr

Collate functions.R

License GPL (>= 3)

LazyLoad yes

NeedsCompilation no

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Contents

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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.

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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 results 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/BioStudies experiment accessions, and returns a list containing these objects.

Usage

```
getAtlasData( experimentAccessions )
```

Arguments

experimentAccessions

         Vector of ArrayExpress/BioStudies accessions for experiments to be downloaded.

Value

A list with one entry per experiment summary SimpleList object. Entries are named using the ArrayExpres/BioStudies 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: pre-proc(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" ]]
```

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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 results 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.

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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/BioStudies accessions, the species, experiment types, and titles of Expression Atlas experiments matching the query.

Examples

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

# Download data for first experiment found.
if ( nrow( atlasRes ) == 1 ) {
    atlasData <- getAtlasData( atlasRes$Accession )
} else {
    atlasData <- getAtlasData( atlasRes$Accession[1] )
}
```

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