# Package ‘AffyCompatible’

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**Title** Affymetrix GeneChip software compatibility  
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**Imports** Biostrings  
**Description** This package provides an interface to Affymetrix chip annotation and sample attribute files. The package allows an easy way for users to download and manage local data bases of Affymetrix NetAffx annotation files. The package also provides access to GeneChip Operating System (GCOS) and GeneChip Command Console (AGCC)-compatible sample annotation files.  
**License** Artistic-2.0  
**biocViews** Infrastructure, Microarray, OneChannel  
**NeedsCompilation** no

**R topics documented:**

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AffyCompatible-package

Affymetrix chip annotation and sample attribute management

Description

This package manages Affymetrix NetAffx annotation files, and parses MAGE and ARR sample attribute files into R data structures.

NetAffx provides a way to manage the diverse annotation files provided by Affymetrix for their arrays.

ARR files provide attribute information about samples used in an experiment. These files are created, for instance, by the GeneChip Command Console or compliant applications, or MAGE files also provide information about samples. Support in this package is for MAGE produced by Affymetrix GCOS compliant applications, and emphasizes sample description and processing.

Details

Package details are available in the DESCRIPTION file of the package, or with the R command packageDescription("AffyCompatible")

Overviews of how to use the functionality of this package are available in the package vignettes. See vignette(package="AffyCompatible").

Author(s)

Written by Martin Morgan.
Maintainer: Martin Morgan <martin.t.morgan@gmail.com>

accessors

Access NetAffxResource-class content

Description

These functions exist to access the information represented in objects of \linkS4class{NetAffxResource} and related classes.

Usage

\code{annotationsFile(x)}
\code{directory(x)}
\code{password(x)}
\code{user(x)}

Arguments

\item{x} An object for which the accessor is defined.
Value

See, e.g., help('directory,NetAffxResource-method') for values returned by specific methods.

Author(s)

Martin Morgan

See Also

NetAffxResource

Description

The classes AffyCompatible, DTTCompatibility, ARRCompatibility, and NetAffxCompatibility define the overall class hierarchy in this package. Information about these classes is not usually relevant to the user.

Objects from the Class

These are virtual classes: no objects may be created from them.

Methods

show signature(object = "AffyCompatible"): for each slot, provide the slot name, and then invoke show for the slot content.

Author(s)

Martin Morgan

Examples

showClass(getClass("NetAffxCompatibility", where=getNamespace("AffyCompatible")))
Internal-class  

(Internal) Represent 'typed associations' from XML documents

Description

This internal class represents 'typed associates' (vectors of identically-typed objects) that appear as vectors to the R user.

Objects from the Class

Objects are created internally, during XML document parsing.

Slots

.Data: Object of class "list" containg the association objects
.extends: Object of class "character" and length 1 describing the class each element in .Data must extend

Extends

Class "list", from data part. Class "vector", by class "list", distance 2.

Methods

[ signature(x = ".TypedAssociation", i = "numeric", j = "missing"): Subset the typed association, returning a typed association with elements i.
[ signature(x = ".TypedAssociation", i = "ANY", j = "ANY"): This method is present to stop access to subsetting methods for class list; it has no user-visible functionality.
.show signature(object = ".TypedAssociation"): Compactly display the typed associate, e.g., for .extneds=Foo and length 5, display Foo(5).

Author(s)

Martin Morgan

NetAffxResource  

Create and access a NetAffxResource database

Description

Use this function to create and access a NetAffxResource database.

Usage

NetAffxResource(user = character(0),
password = character(0),
affxLicense = "FHCRC0607",
directory = tempdir(), ...)
Arguments

user
Length 1 character vector containing the Affymetrix user name authorized to
access the NetAffx resource.

password
Length 1 character vector containing the Affymetrix password of the user.

affxLicence
Length 1 character vector containing the Affymetrix licence (typically application
specific, i.e., the specified licence covers AffyCompatible).

directory
(Optional) length 1 character vector providing the full path to the local directory
where the NetAffx database and files will be managed. Defaults to a session-
specific temporary directory.

... Additional arguments, not currently used.

Details

NetAffxResource creates a NetAffxResource object that manages a data base of NetAffx re-
sources. The data base is located on the user file system as indicated by the directory argument.
It is populated when the user requests specific files.

Users should provide a directory argument, so that the data base can be reused across sessions.
This means that large files are only downloaded once.

Additional details are provided in the vignette accompanying this package.

Value

NetAffxResource.

Author(s)

Martin Morgan

See Also

NetAffxResource. The vignette ‘Annotations with NetAffx’.
Slots

user: Object of class "character" containing the full user name (typically an email address) obtained when the user registers with Affymetrix.

password: Object of class "character" containing the password associated with the Affymetrix user name. The password is entered and stored in plain text, and should not be considered secure within Bioconductor.

affxLicence: Object of class "character" containing the licence, obtained from Affymetrix, for retrieving NetAffx annotations. The licence is usually software specific (e.g., for the Affy-Compatible package of Bioconductor). Users will not usually change the default value.

directory: Object of class "character", containing the local directory path where the NetAffx data base and annotation files will reside.

annotationsFile: Object of class "character" containing the file name of the NetAffx data base. Users will not usually change the default value.

affxUrl: Object of class "character" containing the URL used to download the NetAffx annotations file. Users will not usually change the default value.

Extends


Methods

[[ signature(x = "NetAffxResource", i = "numeric", j = "missing")

[[ signature(x = "NetAffxResource", i = "character", j = "missing"): Retrieve an object representing all NetAffx annotations available for an array. The argument i may be a numeric index or character string corresponding to an array name returned by names(x).

[[ signature(x = "NetAffxResource", i = "numeric", j = "numeric")

[[ signature(x = "NetAffxResource", i = "character", j = "numeric")

[[ signature(x = "NetAffxResource", i = "numeric", j = "character")

[[ signature(x = "NetAffxResource", i = "character", j = "character"): Retrieve an object representing a specific annotation for an array. The argument i may be a numeric index or character string corresponding to an array name returned by names(x). The argument i may be a numeric index or character string corresponding to an annotation returned by description(x[[i]]).

affxLicence signature(x = "NetAffxResource"): the character string representation of the licence used to access the NetAffx site.

affxUrl signature(x = "NetAffxResource"): the url used to access the NetAffx site.

annotationsFile signature(x = "NetAffxResource"): the file name of NetAffx data base, as stored on the local disk of the user.

directory signature(x = "NetAffxResource"): the directory in which the NetAffx data base and annotation files are stored on the local disk of the user.

names signature(x = "NetAffxResource"): the names of the arrays for which annotations are available.

password signature(x = "NetAffxResource"): The password associated with the user name obtained when the user registered with Affymetrix. The password is entered and stored as plain text, and is not secure.
readAnnotation  signature(netAffxResource = "NetAffxResource", array = "numeric", annotation = "numeric", ...)
readAnnotation  signature(netAffxResource = "NetAffxResource", array = "numeric", annotation = "character", ...)
readAnnotation  signature(netAffxResource = "NetAffxResource", array = "character", annotation = "numeric", ...)
readAnnotation  signature(netAffxResource = "NetAffxResource", array = "character", annotation = "character", ...)
readAnnotation  signature(netAffxResource = "NetAffxResource", array = "missing", annotation = "AffxAnnotation", ...)

Read a specific annotation file as an R object. for the first four methods, array, if present, indexes or names the array while annotation indexes or names the annotation. All methods also accept content = "logical" to indicate whether the content of the file should be returned if possible (content=TRUE, default) or only the path to the local file (content=FALSE) and update = "logical" indicating whether the file should be read from disk if available (update=FALSE, default) or retrieved from the NetAffx web site (update=TRUE). readAnnotation parses CSV, Tabular, and PSI files to data frames, and reads FASTA files to a list of description / sequence pairs (see Biostrings::readFASTA).

The ... argument is passed to corresponding read functions. CSV files are parsed using read.csv(conn, ...), Tabular files with read.delim(conn, ...), PSI files with read.delim(conn, header=FALSE, skip=1, sep="\t", ...), and FASTA with readFASTA(conn, ...).

show  signature(object = "NetAffxResource"): compactly show the NetAffxResource object.

user  signature(x = "NetAffxResource"): The user name (typically email address) obtained when the user registers with the Affymetrix web site.

Author(s)
Martin Morgan <mtmorgan@fhcrc.org>

See Also

.Rprofile for ways to automatically set variables (such as password, and directory) for each session.

Examples

## password must be obtained by the user
rsrc <- NetAffxResource(user="mtmorgan@fhcrc.org", password=password)
head(names(rsrc))

affxDescription(rsrc[["Bovine"]])

## paradigm to display all elements of 'annotation'
sapply(affxAnnotation(rsrc[["Bovine"]]), force)

## obtain and read a single annotation
anno <- rsrc[["Porcine", "Annotations, CSV format"]]
df <- readAnnotation(rsrc, annotation=anno)
**readArr**

Read ARR sample attribute files

**Description**

This function reads the content of Affymetrix ARR sample attribute files created by GeneChip(R) Command Console. Objects are represented as R classes. Navigation and extraction of data are described in the vignette ‘Retrieving MAGE and ARR sample attributes’.

**Usage**

`readArr(fls, ...)`

**Arguments**

- `fls`: A character vector containing the paths to files to be read.
- `...`: Additional arguments, currently unused.

**Value**

An object or list of objects of class `ArrayFileSet`, depending on whether one or several file paths are provided.

**Author(s)**

Martin Morgan

**See Also**

The vignette ‘Retrieving MAGE and ARR sample attributes’ for detailed illustration of use. `xclass` and `readXml` for advanced access methods.

**Examples**

```r
dir <- system.file("extdata", "ARR", package="AffyCompatible")
fls <- list.files(dir, full=TRUE)
readArr(fls[[1]])
readArr(fls)
```

---

**readMage**

Read DTT (MAGE) sample attribute files

**Description**

This function reads the content of Affymetrix DTT (MAGE) sample attribute files created by GCOS. Objects are represented as R classes. Navigation and extraction of data are described in the vignette ‘Retrieving MAGE and ARR sample attributes’.

**Usage**

`readMage(fls, ...)`

**Description**

This function reads the content of Affymetrix DTT (MAGE) sample attribute files created by GCOS. Objects are represented as R classes. Navigation and extraction of data are described in the vignette ‘Retrieving MAGE and ARR sample attributes’.

**Usage**

`readMage(fls, ...)`
readNetAffx

Arguments

  fls  A character vector containing the paths to files to be read.
  ...  Additional arguments, currently unused.

Value

  An object or list of objects of class ArrayFileSet, depending on whether one or several file paths are provided.

Author(s)

  Martin Morgan

See Also

  The vignette ‘Retrieving MAGE and ARR sample attributes’ for detailed illustration of use.
  xclass and readXml for advanced access methods.

Examples

  dir <- system.file("extdata", "DTT", package="AffyCompatible")
  fls <- list.files(dir, full=TRUE)
  basename(fls)
  readArr(fls[[1]])
readXml

(Advanced) Read XML files of Affymetrix sample attributes or annotation

Description
This function reads the content of Affymetrix DTT (MAGE) or ARR sample files, or AffxNetAffx-AnnotFile array annotation files, return an internal representation of the underlying XML. The return value can be used with xclass to rapidly create R objects representing deeply nested nodes of the document. The return value can also be used with xpathApply in the XML package for access to character-based representation of the data.

Usage
readXml(f1, ...)

Arguments
f1 A length-1 character vector giving the full path to the file to be parsed.
... Additional arguments, passed to xmlTreeParse.

Value
An object of class XMLInternalDocument.

Author(s)
Martin Morgan

See Also
The vignettes ‘Retrieving MAGE and ARR sample attributes’ and ‘Annotation retrieval with NetAffxResource’ for detailed illustration of use.

Examples
mageDir <- system.file("extdata", "DTT", package="AffyCompatible")
mageFiles <- list.files(mageDir, full=TRUE)
x <- readXml(mageFiles[[1]])
xclass(x, "/MeauredBioAssay"[1])
**xclass**

(Advanced) Construct R objects from XML document queries

**Description**

This function takes an xml object, created from `readXml`, and an xpath query referencing an element of the document, and returns an R object representing the element.

The xpath query must retrieve an element, not an attribute.

**Usage**

```r
xclass(doc, xpathq, prefix = character(0))
```

**Arguments**

- `doc`: An `XMLInternalDocument` retrieved using `readXml`.
- `xpathq`: A length-1 character string representing an xpath query into the document.
- `prefix`: A prefix used to map, when necessary, between the XML class name and the corresponding R class. For NetAffx-based classes, the prefix is `Affx`; no prefix is required for DTT or ARR documents.

**Value**

An R object corresponding to the class(es) referenced by the xpath query.

**Author(s)**

Martin Morgan

**References**

[http://www.w3.org/TR/xpath](http://www.w3.org/TR/xpath) provides a very useful description of xpath. Additional references are in the vignette ‘Retrieving MAGE and ARR sample attributes’.

**See Also**

The vignettes ‘Retrieving MAGE and ARR sample attributes’ and ‘Annotation retrieval with NetAffxResource’ for detailed illustration of use.

`readXml` for appropriately reading XML documents.

**Examples**

```r
example(readXml)
```
xmlValue.XMLAttributeValue

Additional functions defined in AffyCompatible

Description

This page documents additional, miscellaneous, functions defined by AffyCompatible

Usage

```r
## S3 method for class 'XMLAttributeValue'
xmlValue(x, ignoreComments = FALSE, recursive = TRUE,
         encoding=XML:::CE_NATIVE, trim=FALSE)
```

Arguments

- `x`: An object of class `XMLAttributeValue`
- `ignoreComments`: Logical; ignored by the `xmlValue.XMLAttributeValue` method
- `recursive`: ignored
- `encoding`: File encoding
- `trim`: Remove trailing whitespace? Ignored by this method

Value

A character vector (usually length 1) containing the character representation of the XML attribute.

zzz-ARRCompatibility-class

(Auto-generated) classes and methods for navigating ARR sample attributes.

Description

These classes and methods facilitate navigation of the Affymetrix ARR sample attribute files. ARR files are generated by the Affymetrix AGCC (GeneChip(R) Command Console) application. Specifically, the classes are R representations of the Affymetrix classes defined in ArraySetAndTemplate-File.dtd. The 'show' methods for these classes indicate how objects are to be accessed; details are in the 'Retrieving MAGE and ARR sample attributes' vignette.

Objects from the Class

Objects are created internally, by parsing XML retrieved from ARR, and are not created directly by the user.

Slots

Objects have a variety of slots. To discover slot names and content type, see the `slotNames` portion of the example, below.
zzz-DTTCompatibility-class

Extends

Class "ARRCompatibility", directly. Class "AffyCompatible", by class "ARRCompatibility", distance 2.

Methods

'Accessor' methods are defined on auto-generated classes to access slot content.

Accessors are apparent from displaying the object; each line of the display is of the form accessor: content. To retrieve the content of an instance object, invoke accessor(object).

Some objects contain several instances of another object. These 'typed associations' are represented by the .TypedAssociation class, and are navigated or subset as one would a standard R vector, e.g., using [, [,[]. A useful paradigm for displaying all instances is illustrated in the vignette.

Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

See Also

Vignette ‘Retrieving MAGE and ARR sample attributes’.

Examples

```r
## defined and auto-generated classes
names(slot(getClass("ARRCompatibility",
    where=getNamespace("AffyCompatible")),
    "subclasses"))
```

zzz-DTTCompatibility-class

(Auto-generated) classes and methods for navigating DTT sample attributes.

Description

These classes and methods facilitate navigation of the Affymetrix DTT sample attribute files. DTT files are generated by the Affymetrix GCOS application. Specifically, the classes are R representations of the Affymetrix classes defined in MAGE-ML.dtd. The 'show' methods for these classes indicate how objects are to be accessed; details are in the 'Retrieving MAGE and ARR sample attributes' vignette.

Objects from the Class

Objects are created internally, by parsing XML retrieved from ARR, and are not created directly by the user.

Slots

Objects have a variety of slots. To discover slot names and content type, see the slotNames portion of the example, below.
zzz-NetAffxCompatibility-class

**Description**

These classes and methods facilitate navigation of the NetAffx resource data base. They are R representations of the Affymetrix classes defined in NetAffxAnnotFileList.dtd. The 'show' methods for these classes indicate how objects are to be accessed; details are in the 'Annotations with NetAffx' vignette.

The auto-generated classes are discoverable as indicated in the example below.

**Objects from the Class**

Objects are created internally, by parsing XML retrieved from the local NetAffx data base or from the Affymetrix web site.

**Slots**

Objects have a variety of slots. To discover slot names and content type, see the `slotNames` portion of the example, below.

---

**Extends**

Class "DTTCompatibility", directly. Class "AffyCompatible", by class "DTTCompatibility", distance 2.

**Methods**

'Accessor' methods are defined on auto-generated classes to access slot content.

Accessors are apparent from displaying the object; each line of the display is of the form accessor: content.

To retrieve the content of an instance object, invoke accessor(object).

Some objects contain several instances of another object. These 'typed associations' are represented by the `.TypedAssociation` class, and are navigated or subset as one would a standard R vector, e.g., using [, [. A useful paradigm for displaying all instances is illustrated in the vignette.

**Author(s)**

Martin Morgan <mtmorgan@fhcrc.org>

**See Also**

Vignette 'Retrieving MAGE and ARR sample attributes'.

**Examples**

```r
## defined and auto-generated classes
names(slot(getClass("DTTCompatibility",
    where=getNamespace("AffyCompatible"),
    "subclasses"))
```

---

zzz-NetAffxCompatibility-class

(Auto-generated) classes and methods for navigating NetAffx resources
### zzz-NetAffxCompatibility-class

#### Extends


#### Methods

'Read' methods are defined on auto-generated classes to access slot content.

Accessors are apparent from displaying the object; each line of the display is of the form accessor: content.

To retrieve the content of an instance object, invoke accessor(object).

Some objects contain several instances of another object. These 'typed associations' are represented by the .TypedAssociation class, and are navigated or subset as one would a standard R vector, e.g., using [, [[]. A useful paradigm for displaying all instances is illustrated on the NetAffxResource page.

#### Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

#### See Also


NetAffxResource for creating and managing the NetAffx data base.

NetAffxResource for navigating the data base.

#### Examples

```r
## defined and auto-generated classes
getClass("NetAffxCompatibility", where=getNamespace("AffyCompatible"))

## slots of an auto-generated class
getSlots(getClass("AffxNetAffxAnnotFileList", where=getNamespace("AffyCompatible")))

## Not run:
example("NetAffxrResource-class")

## End(Not run)
```
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