Package 'affyio'

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Title Tools for parsing Affymetrix data files

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Depends R (>= 2.6.0)

Imports methods

Description Routines for parsing Affymetrix data files based upon file format information. Primary focus is on accessing the CEL and CDF file formats.

License LGPL (>= 2)

URL https://github.com/bmbolstad/affyio

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affyio internal functions

Internal affyio functions

Description

Internal affyio functions

Details

These are not normally meant to be called by the user and/or are undergoing testing

check.cdf.type

CDF file format function

Description

This function returns a text string giving the file format for the supplied filename

Usage

```
check.cdf.type(filename)
```

Arguments

filename	fullpath to a cdf file

Value

Returns a string which is currently one of:

text	the cdf file is of the text format
xda	the cdf file is of the binary format used in GCOS
unknown	the parser can not handle this format or does not recognize this file as a CDF file

Author(s)

B. M. Bolstad <bmb@bmbolstad.com>

get.celfile.dates *Extract Dates from CEL files*

Description

This function reads the header information for a series of CEL files then extracts and returns the dates.

Usage

```
get.celfile.dates(filenames, ...)
```

Arguments

filenames	a vector of characters with the CEL filenames. May be fully pathed.
...	further arguments passed on to read.celfile.header.

Details

The function uses read.celfile.header to read in the header of each file. The ScanDate component is then parsed to extract the date. Note that an assumption is made about the format. Namely, that dates are in the Y-m-d or m/d/y format.

Value

A vector of class Date with one date for each celfile.

Author(s)

Rafael A. Irizarry <rafa@jimmy.harvard.edu>

See Also

See Also as read.celfile.header.

internal functions *Internal affyio functions*

Description

Internal affyio functions

Details

These are not to be called directly by a user. They support the affy package

read.cdffile.list *Read CDF file into an R list*

Description

This function reads the entire contents of a cdf file into an R list structure

Usage

```
read.cdffile.list(filename, cdf.path = getwd())
```

Arguments

filename	name of CDF file
cdf.path	path to cdf file

Details

Note that this function can be very memory intensive with large CDF files.

Value

returns a list structure. The exact contents may vary depending on the file format of the cdf file (see check.cdf.type)

Author(s)

B. M. Bolstad <bmb@bmbolstad.com>

read.celfile *Read a CEL file into an R list*

Description

This function reads the entire contents of a CEL file into an R list structure

Usage

```
read.celfile(filename,intensity.means.only=FALSE)
```

Arguments

filename	name of CEL file
intensity.means.only	If TRUE then read on only the MEAN section in INTENSITY

Details

The list has four main items. HEADER, INTENSITY, MASKS, OUTLIERS. Note that INTENSITY is a list of three vectors MEAN, STDEV, NPIXELS. HEADER is also a list. Both of MASKS and OUTLIERS are matrices.

Value

returns a `list` structure. The exact contents may vary depending on the file format of the CEL file

Author(s)

B. M. Bolstad <bmb@bmbolstad.com>

`read.celfile.header` *Read header information from cel file*

Description

This function reads some of the header information (appears before probe intensity data) from the supplied cel file.

Usage

```
read.celfile.header(filename,info=c("basic","full"),verbose=FALSE)
```

Arguments

`filename`	name of CEL file. May be fully pathed
`info`	A string. `basic` returns the dimensions of the chip and the name of the CDF file used when the CEL file was produced. `full` returns more information in greater detail.
`verbose`	a `logical`. When true the parsing routine prints more information, typically useful for debugging.

Value

A `list` data structure.

Author(s)

B. M. Bolstad <bmb@bmbolstad.com>

`read.celfile.probeintensity.matrices` *Read PM or MM from CEL file into matrices*

Description

This function reads PM, MM or both types of intensities into matrices. These matrices have all the probes for a probeset in adjacent rows

Usage

```
read.celfile.probeintensity.matrices(filenames, cdfInfo, rm.mask=FALSE, rm.outliers=FALSE, rm.extra=F
```

Arguments

`filenames`	a character vector of filenames
`cdfInfo`	a list with items giving PM and MM locations for desired probesets. In same structure as returned by `make.cdf.package`
`rm.mask`	a `logical`. Return these probes as NA if there are in the [MASK] section of the CEL file
`rm.outliers`	a `logical`. Return these probes as NA if there are in the [OUTLIERS] section of the CEL file
.	
`rm.extra`	a `logical`. Return these probes as NA if there are in the [OUTLIERS] section of the CEL file
.	
`verbose`	a `logical`. When true the parsing routine prints more information, typically useful for debugging.
`which`	a string specifing which probe type to return

Value

returns a `list` of `matrix` items. One matrix contains PM probe intensities, with probes in rows and arrays in columns

Author(s)

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