Package ‘affyio’

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Title Tools for parsing Affymetrix data files

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Depends R (>= 2.6.0)

Imports zlibbioc

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)

biocViews Microarray, DataImport, Infrastructure

LazyLoad yes

R topics documented:

`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)

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`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)

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`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)

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`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)

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`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

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