affyio

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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>

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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 INTEN-
SITY 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.outli
```

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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