

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:

<code>text</code>	the cdf file is of the text format
<code>xda</code>	the cdf file is of the binary format used in GCOS
<code>unknown</code>	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>

`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

<code>filename</code>	name of CDF file
<code>cdf.path</code>	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

<code>filename</code>	name of CEL file
<code>intensity.means.only</code>	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

<code>filename</code>	name of CEL file. May be fully pathed
<code>info</code>	A string. <code>basic</code> returns the dimensions of the chip and the name of the CDF file used when the CEL file was produced. <code>full</code> returns more information in greater detail.
<code>verbose</code>	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(filenamees, cdfInfo, rm.mask=FALSE, rm.outli
```

Arguments

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