

# affyio

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check.cdf.type	<i>CDF file format function</i>
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## 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
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## 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>

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

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### 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)

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

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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

<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 <a href="#">logical</a> . 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>

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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(filenamees, cdfInfo, rm.mask=FALSE, rm.outliers)
```

**Arguments**

<code>filenamees</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 <code>logical</code> . Return these probes as NA if there are in the [MASK] section of the CEL file
<code>rm.outliers</code>	a <code>logical</code> . Return these probes as NA if there are in the [OUTLIERS] section of the CEL file
<code>rm.extra</code>	a <code>logical</code> . Return these probes as NA if there are in the [OUTLIERS] section of the CEL file
<code>verbose</code>	a <code>logical</code> . 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)**

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

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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)**

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

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