

# affxparser

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1. Dictionary	<i>1. Dictionary</i>
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## Description

This part describes non-obvious terms used in this package.

**affxparser** The name of this package.

**API** Application program interface, which describes the functional interface of underlying methods.

**block** (aka group).

**BPMAP** A file format containing information related to the design of the tiling arrays.

**Calvin** A special binary file format.

**CDF** A file format: chip definition file.

**CEL** A file format: cell intensity file.

**cell** (aka feature) A probe.

**cell index** An integer that identifies a probe uniquely.

**chip** An array.

**chip type** An identifier specifying a chip design uniquely, e.g. "Mapping50K\_Xba240".

**DAT** A file format: contains pixel intensity values collected from an Affymetrix GeneArray scanner.

**feature** A probe.

**Fusion SDK** Open-source software development kit (SDK) provided by Affymetrix to access their data files.

**group** (aka block) Defines a unique subset of the cells in a unit. Expression arrays typically only have one group per unit, whereas SNP arrays have either two or four groups per unit, one for each of the two allele times possibly repeated for both strands.

**MM** Mismatch-match, e.g. MM probe.

**TPMAP** A file format storing the relationship between (PM,MM) pairs (or PM probes) and positions on a set of sequences.

**QC** Quality control, e.g. QC probes and QC probe sets.

**unit** A probeset.

**XDA** A file format, aka as the binary file format.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## 2. Cell coordinates and cell indices

### 2. Cell coordinates and cell indices

### Description

This part describes how Affymetrix *cells*, also known as *probes* or *features*, are addressed.

### Cell coordinates

In Affymetrix data files, cells are uniquely identified by their *cell coordinates*, i.e.  $(x, y)$ . For an array with  $N * K$  cells in  $N$  rows and  $K$  columns, the  $x$  coordinate is an integer in  $[0, K - 1]$ , and the  $y$  coordinate is an integer in  $[0, N - 1]$ . The cell in the upper-left corner has coordinate  $(x, y) = (0, 0)$  and the one in the lower-right corner  $(x, y) = (K - 1, N - 1)$ .

### Cell indices and cell-index offsets

To simplify addressing of cells, a coordinate-to-index function is used so that each cell can be addressed using a single integer instead (of two). Affymetrix defines the *cell index*,  $i$ , of cell  $(x, y)$  as

$$i = K * y + x + 1,$$

where one is added to give indices in  $[1, N * K]$ . Continuing, the above definition means that cells are ordered row by row, that is from left to right and from top to bottom, starting at the upper-left corner. For example, with a chip layout  $(N, K) = (1600, 1600)$  the cell at  $(x, y) = (0, 0)$  has index  $i=1$ , and the cell at  $(x, y) = (1599, 1599)$  has index  $i = 2560000$ . A cell at  $(x, y) = (1498, 3)$  has index  $i = 6299$ .

Given the cell index  $i$ , the coordinate  $(x, y)$  can be calculated as

$$y = \text{floor}((i - 1)/K)$$

$$x = (i - 1) - K * y.$$

Continuing the above example, the coordinate for cell  $i = 1$  is found to be  $(x, y) = (0, 0)$ , for cell  $i = 2560000$  it is  $(x, y) = (1599, 1599)$ , for cell  $i = 6299$  it is  $(x, y) = (1498, 3)$ .

Although not needed to use the methods in this package, to get the cell indices for the cell coordinates or vice versa, see `xy2indices` and `indices2xy()` in the **affy** package.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

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9. Advanced - Cell-index maps for reading and writing  
 9. Advanced - Cell-index maps for reading and writing

---

**Description**

This part defines read and write maps that can be used to remap cell indices before reading and writing data from and to file, respectively.

This package provides methods to create read and write (cell-index) maps from Affymetrix CDF files. These can be used to store the cell data in an optimal order so that when data is read it is read in contiguous blocks, which is faster.

In addition to this, read maps may also be used to read CEL files that have been "reshuffled" by other software. For instance, the dChip software (<http://www.dchip.org/>) rotates Affymetrix Exon, Tiling and Mapping 500K data. See example below how to read such data "unrotated".

For more details how cell indices are defined, see [2. Cell coordinates and cell indices](#).

**Motivation**

When reading data from file, it is faster to read the data in the order that it is stored compared with, say, in a random order. The main reason for this is that the read arm of the harddrive has to move more if data is not read consecutively. Same applies when writing data to file. The read and write cache of the file system may compensate a bit for this, but not completely.

In Affymetrix CEL files, cell data is stored in order of cell indices. Moreover, (except for a few early chip types) Affymetrix randomizes the locations of the cells such that cells in the same unit (probeset) are scattered across the array. Thus, when reading CEL data arranged by units using for instance `readCelUnits()`, the order of the cells requested is both random and scattered.

Since CEL data is often queried unit by unit (except for some probe-level normalization methods), one can improve the speed of reading data by saving data such that cells in the same unit are stored together. A *write map* is used to remap cell indices to file indices. When later reading that data back, a *read map* is used to remap file indices to cell indices. Read and write maps are described next.

**Definition of read and write maps**

Consider cell indices  $i = 1, 2, \dots, N * K$  and file indices  $j = 1, 2, \dots, N * K$ . A *read map* is then a *bijective* (one-to-one) function  $h()$  such that

$$i = h(j),$$

and the corresponding *write map* is the inverse function  $h^{-1}()$  such that

$$j = h^{-1}(i).$$

Since the mapping is required to be bijective, it holds that  $i = h(h^{-1}(i))$  and that  $j = h^{-1}(h(j))$ . For example, consider the "reversing" read map function  $h(j) = N * K - j + 1$ . The write map function is  $h^{-1}(i) = N * K - i + 1$ . To verify the bijective property of this map, we see that  $h(h^{-1}(i)) = h(N * K - i + 1) = N * K - (N * K - i + 1) + 1 = i$  as well as  $h^{-1}(h(j)) = h^{-1}(N * K - j + 1) = N * K - (N * K - j + 1) + 1 = j$ .

### Read and write maps in R

In this package, read and write maps are represented as `integer vectors` of length  $N * K$  with *unique* elements in  $\{1, 2, \dots, N * K\}$ . Consider cell and file indices as in previous section.

For example, the "reversing" read map in previous section can be represented as

```
readMap <- (N*K) : 1
```

Given a `vector` `j` of file indices, the cell indices are the obtained as `i = readMap[j]`. The corresponding write map is

```
writeMap <- (N*K) : 1
```

and given a `vector` `i` of cell indices, the file indices are the obtained as `j = writeMap[i]`.

Note also that the bijective property holds for this mapping, that is `i == readMap[writeMap[i]]` and `i == writeMap[readMap[i]]` are both `TRUE`.

Because the mapping is bijective, the write map can be calculated from the read map by:

```
writeMap <- order(readMap)
```

and vice versa:

```
readMap <- order(writeMap)
```

Note, the `invertMap()` method is much faster than `order()`.

Since most algorithms for Affymetrix data are based on probeset (unit) models, it is natural to read data unit by unit. Thus, to optimize the speed, cells should be stored in contiguous blocks of units. The methods `readCdfUnitsWriteMap()` can be used to generate a *write map* from a CDF file such that if the units are read in order, `readCelUnits()` will read the cells data in order. Example:

```
Find any CDF file
cdfFile <- findCdf()

# Get the order of cell indices
indices <- readCdfCellIndices(cdfFile)
indices <- unlist(indices, use.names=FALSE)

# Get an optimal write map for the CDF file
writeMap <- readCdfUnitsWriteMap(cdfFile)

# Get the read map
readMap <- invertMap(writeMap)

# Validate correctness
indices2 <- readMap[indices] # == 1, 2, 3, ..., N*K
```

*Warning*, do not misunderstand this example. It can not be used improve the reading speed of default CEL files. For this, the data in the CEL files has to be rearranged (by the corresponding write map).

### Reading rotated CEL files

It might be that a CEL file was rotated by another software, e.g. the dChip software rotates Affymetrix Exon, Tiling and Mapping 500K arrays 90 degrees clockwise, which remains rotated when exported as CEL files. To read such data in a non-rotated way, a read map can be used to "unrotate" the data. The 90-degree clockwise rotation that dChip effectly uses to store such data is explained by:

```
h <- readCdfHeader(cdfFile)
# (x,y) chip layout rotated 90 degrees clockwise
nrow <- h$cols
ncol <- h$rows
y <- (nrow-1):0
x <- rep(1:ncol, each=nrow)
writeMap <- as.vector(y*ncol + x)
```

Thus, to read this data "unrotated", use the following read map:

```
readMap <- invertMap(writeMap)
data <- readCel(ceFile, indices=1:10, readMap=readMap)
```

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

affxparser-package *Package affxparser*

---

### Description

The **affxparser** package provides methods for fast and memory efficient parsing of Affymetrix files [1] using the Affymetrix' Fusion SDK [2]. Both traditional ASCII- and binary (XDA)-based files are supported, as well as Affymetrix future binary format "Calvin". The efficiency of the parsing is dependent on whether a specific file is binary or ASCII.

Currently, there are methods for reading chip definition file (CDF) and a cell intensity file (CEL). These files can be read either in full or in part. For example, probe signals from a few probesets can be extracted very quickly from a set of CEL files into a convenient list structure.

### Requirements

This package requires only a standard R installation, that is, it works independently of other CRAN and Bioconductor packages.

### To get started

To get started, see:

1. `readCelUnits()` - reads one or several Affymetrix CEL file probeset by probeset.
2. `readCel()` - reads an Affymetrix CEL file. by probe.
3. `readCdf()` - reads an Affymetrix CDF file. by probe.
4. `readCdfUnits()` - reads an Affymetrix CDF file unit by unit.

5. `readCdfCellIndices()` - Like `readCdfUnits()`, but returns cell indices only, which is often enough to read CEL files unit by unit.
6. `applyCdfGroups()` - Re-arranges a CDF structure.
7. `findCdf()` - Locates an Affymetrix CDF file by chip type. This page also describes how to setup default search path for CDF files.

### Setting up the CDF search path

Some of the functions in this package search for CDF files automatically by scanning certain directories. To add directories to the default search path, see instructions in `findCdf()`.

### Future Work

Other Affymetrix files can be parsed using the Fusion SDK. Given sufficient interest we will implement this, e.g. DAT files (image files).

### Running examples

In order to run the examples, data files must exist in the current directory. Otherwise, the example scripts will do nothing. Most of the examples requires a CDF file or a CEL file, or both. Make sure the CDF file is of the same chip type as the CEL file.

Affymetrix provides data sets of different types at <http://www.affymetrix.com/support/datasets.affx> that can be used. There are both small and very large data sets available.

### Technical details

This package implements an interface to the Fusion SDK from Affymetrix.com. This SDK (software development kit) is an open source library used for parsing the various file formats used by the Affymetrix platform.

The intention is to provide interfaces to most if not all file formats which may be parsed using Fusion.

The SDK supports parsing of all the different versions of a specific fileformat. This means that ASCII, binary as well as the new binary format (codename Calvin) used by Affymetrix is supported through a single API. We also expect any future changes to the file formats to be reflected in the SDK, and subsequently in this package.

However, as the current Fusion SDK does not support compressed files, neither does **affxparser**. This is in contrast to some of the existing code in **affy** and relatives (see below for links).

In general we aim to provide functions returning all information in the respective files. Currently it seems that future Affymetrix chip designs may consist of so many features that returning all information will lead to an unnecessary overhead in the case a user only wants access to a subset. We have tried to make this possible.

For older files, certain entries in the files have been removed from newer specifications, and the SDK does not provide utilities for reading these entries. This includes e.g. the FEAT column of CDF files.

Currently the package as well as the Fusion SDK is in beta stage. Bugs may be related to either codebase. We are very interested in users being unable to compile/parse files using this library - this includes users with custom chip designs.

In addition, since we aim to return all information stored in the file (and accessible using the Fusion SDK) we would like reports from users being unable to do that.

The efficiency of the underlying code may vary with the version of the file being parsed. For example, we currently report the number of outliers present in a CEL file when reading the header

of the file using `readCelHeader`. In order to obtain this information from text based CEL files (version 2), the entire file needs to be read into memory. With version 3 of the file format, this information is stored in the header.

With the introduction of the Fusion SDK (and the next version of their file formats) Affymetrix has made it possible to use multibyte character sets. This implies that character information may be inaccessible if the compiler used to compile the C++ code does not support multibyte character sets (specifically we require that the R installation has defined the macro `SUPPORT_MCBS` in the `Rconfig.h` header file). For example GCC needs to be version 3.4 or greater on Solaris.

In the `info` subdirectory of the package installation, information regarding changes to the Fusion SDK is stored, e.g.

```
pathname <- system.file("info/README", package="affxparser")
file.show(pathname)
```

### Acknowledgments

We would like to thanks Ken Simpson (WEHI, Melbourne) and Seth Falcon (FHCRC, Seattle) for feedback and code contributions.

### License

The releases of this package is licensed under LGPL version 2.1 or newer. This applies also to the Fusion SDK.

### Author(s)

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### References

- [1] Affymetrix Inc, Affymetrix GCOS 1.x compatible file formats, April, 2006. <http://www.affymetrix.com/support/developer/>
- [2] Affymetrix Inc, Fusion Software Developers Kit (SDK), 2006. <http://www.affymetrix.com/support/developer/fusion/>

---

applyCdfGroups

*Applies a function over the groups in a CDF structure*

---

### Description

Applies a function over the groups in a CDF structure.

### Usage

```
applyCdfGroups(cdf, fcn, ...)
```



**Arguments**

<code>cdf</code>	A CDF <code>list</code> structure.
<code>fcn</code>	A <code>function</code> that takes a <code>list</code> structure of group elements and returns an updated <code>list</code> of groups.
<code>...</code>	Arguments passed to the <code>fcn</code> function.

**Value**

Returns an updated CDF `list` structure.

**Pre-defined restructuring functions**

- Generic:
- `cdfGetFields()` - Gets a subset of groups fields in a CDF structure.
  - `cdfGetGroups()` - Gets a subset of groups in a CDF structure.
  - `cdfOrderBy()` - Orders the fields according to the value of another field in the same CDF group.
  - `cdfOrderColumnsBy()` - Orders the columns of fields according to the values in a certain row of another field in the same CDF group.
- Designed for SNP arrays:
- `cdfAddBaseMmCounts()` - Adds the number of allele A and allele B mismatching nucleotides of the probes in a CDF structure.
  - `cdfAddProbeOffsets()` - Adds probe offsets to the groups in a CDF structure.
  - `cdfGtypeCelToPQ()` - Function to immitate Affymetrix' `gtype_cel_to_pq` software.
  - `cdfMergeAlleles()` - Function to join CDF allele A and allele B groups strand by strand.
  - `cdfMergeStrands()` - Function to join CDF groups with the same names.

We appreciate contributions.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

cdfFile <- findCdf("Mapping10K_Xbal31")

# Identify the unit index from the unit name
unitName <- "SNP_A-1509436"
unit <- which(readCdfUnitNames(cdfFile) == unitName)

# Read the CDF file
cdf0 <- readCdfUnits(cdfFile, units=unit, stratifyBy="pmmm", readType=FALSE, readDirectio
cat("Default CDF structure:\n")
print(cdf0)

# -----
# Tabulate the information in each group
# -----
```

```

cdf <- readCdfUnits(cdfFile, units=unit)
cdf <- applyCdfGroups(cdf, lapply, as.data.frame)
print(cdf)

# -----
# Infer the (true or the relative) offset for probe quartets.
# -----
cdf <- applyCdfGroups(cdf, cdfAddProbeOffsets)
cat("Probe offsets:\n")
print(cdf)

# -----
# Identify the number of nucleotides that mismatch the
# allele A and the allele B sequences, respectively.
# -----
cdf <- applyCdfGroups(cdf, cdfAddBaseMmCounts)
cat("Allele A & B target sequence mismatch counts:\n")
print(cdf)

# -----
# Combine the signals from the sense and the anti-sense
# strands in a SNP CEL files.
# -----
# First, join the strands in the CDF structure.
cdf <- applyCdfGroups(cdf, cdfMergeStrands)
cat("Joined CDF structure:\n")
print(cdf)

# -----
# Rearrange values of group fields into quartets. This
# requires that the values are already arranged as PMs and MMs.
# -----
cdf <- applyCdfGroups(cdf, cdfMergeAlleles)
cat("Probe quartets:\n")
print(cdf)

# -----
# Get the x and y cell locations (note, zero-based)
# -----
x <- unlist(applyCdfGroups(cdf, cdfGetFields, "x"), use.names=FALSE)
y <- unlist(applyCdfGroups(cdf, cdfGetFields, "y"), use.names=FALSE)

# Validate
ncol <- readCdfHeader(cdfFile)$cols
cells <- as.integer(y*ncol+x+1)
cells <- sort(cells)

cells0 <- readCdfCellIndices(cdfFile, units=unit)
cells0 <- unlist(cells0, use.names=FALSE)
cells0 <- sort(cells0)

stopifnot(identical(cells0, cells))

#####
} # STOP #
#####

```

---

`cdfAddBaseMmCounts` *Adds the number of allele A and allele B mismatching nucleotides of the probes in a CDF structure*

---

### Description

Adds the number of allele A and allele B mismatching nucleotides of the probes in a CDF structure.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

Identifies the number of nucleotides (bases) in probe sequences that mismatch the the target sequence for allele A and the allele B, as used by [1].

### Usage

```
cdfAddBaseMmCounts(groups, ...)
```

### Arguments

<code>groups</code>	A <code>list</code> structure with groups. Each group must contain the fields <code>tbase</code> , <code>pbase</code> , and <code>offset</code> (from <code>cdfAddProbeOffsets()</code> ).
<code>...</code>	Not used.

### Details

Note that the above counts can be inferred from the CDF structure alone, i.e. no sequence information is required. Consider a probe group interrogating allele A. First, all PM probes matches the allele A target sequence perfectly regardless of shift. Moreover, all these PM probes mismatch the allele B target sequence at exactly one position. Second, all MM probes mismatches the allele A sequence at exactly one position. This is also true for the allele B sequence, *except* for an MM probe with zero offset, which only mismatch at one (the middle) position. For a probe group interrogating allele B, the same rules applies with labels A and B swapped. In summary, the mismatch counts for PM probes can take values 0 and 1, and for MM probes they can take values 0, 1, and 2.

### Value

Returns a `list` structure with the same number of groups as the `groups` argument. To each group, two fields is added:

<code>mmACount</code>	The number of nucleotides in the probe sequence that mismatches the target sequence of allele A.
<code>mmBCount</code>	The number of nucleotides in the probe sequence that mismatches the target sequence of allele B.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## References

- [1] LaFramboise T, Weir BA, Zhao X, Beroukhim R, Li C, Harrington D, Sellers WR, and Meyerson M. *Allele-specific amplification in cancer revealed by SNP array analysis*, PLoS Computational Biology, Nov 2005, Volume 1, Issue 6, e65.
- [2] Affymetrix, *Understanding Genotyping Probe Set Structure*, 2005. [http://www.affymetrix.com/support/developer/whitepapers/genotyping\\_probe\\_set\\_structure.affx](http://www.affymetrix.com/support/developer/whitepapers/genotyping_probe_set_structure.affx)

## See Also

To add required probe offsets, `cdfAddProbeOffsets()`. `applyCdfGroups()`.

---

`cdfAddPlasqTypes`     *Adds the PLASQ types for the probes in a CDF structure*

---

## Description

Adds the PLASQ types for the probes in a CDF structure.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

## Usage

```
cdfAddPlasqTypes(groups, ...)
```

## Arguments

<code>groups</code>	A <code>list</code> structure with groups. Each group must contain the fields <code>tbase</code> , <code>pbase</code> , and <code>expos</code> .
<code>...</code>	Not used.

## Details

This function identifies the number of nucleotides (bases) in probe sequences that mismatch the target sequence for allele A and the allele B, as used by PLASQ [1], and adds an integer [0,15] interpreted as one of 16 probe types. In PLASQ these probe types are referred to as: 0=MMoBR, 1=MMoBF, 2=MMcBR, 3=MMcBF, 4=MMoAR, 5=MMoAF, 6=MMcAR, 7=MMcAF, 8=PMoBR, 9=PMoBF, 10=PMcBR, 11=PMcBF, 12=PMoAR, 13=PMoAF, 14=PMcAR, 15=PMcAF.

Pseudo rule for finding out the probe-type value:

- PM/MM: For MMs add 0, for PMs add 8.
- A/B: For Bs add 0, for As add 4.
- o/c: For shifted (o) add 0, for centered (c) add 2.
- R/F: For antisense (R) add 0, for sense (F) add 1.

Example: (PM,A,c,R) = 8 + 4 + 2 + 0 = 14 (=PMcAR)

**Value**

Returns a `list` structure with the same number of groups as the `groups` argument. To each group, one field is added:

`plasqType`     A `vector` of `integers` in `[0,15]`.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

[1] LaFramboise T, Weir BA, Zhao X, Beroukhim R, Li C, Harrington D, Sellers WR, and Meyer-son M. *Allele-specific amplification in cancer revealed by SNP array analysis*, PLoS Computational Biology, Nov 2005, Volume 1, Issue 6, e65.

---

`cdfAddProbeOffsets` *Adds probe offsets to the groups in a CDF structure*

---

**Description**

Adds probe offsets to the groups in a CDF structure.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

**Usage**

```
cdfAddProbeOffsets(groups, ...)
```

**Arguments**

<code>groups</code>	A <code>list</code> structure with groups. Each group must contain the fields <code>tbase</code> , and <code>expos</code> .
<code>...</code>	Not used.

**Value**

Returns a `list` structure with half the number of groups as the `groups` argument (since allele A and allele B groups have been joined).

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

[1] Affymetrix, *Understanding Genotyping Probe Set Structure*, 2005. [http://www.affymetrix.com/support/developer/whitepapers/genotyping\\_probe\\_set\\_structure.affx](http://www.affymetrix.com/support/developer/whitepapers/genotyping_probe_set_structure.affx)

**See Also**

[applyCdfGroups\(\)](#).

---

cdfGetFields

*Gets a subset of groups fields in a CDF structure*

---

**Description**

Gets a subset of groups fields in a CDF structure.

This [function](#) is design to be used with [applyCdfGroups\(\)](#) on an Affymetrix Mapping (SNP) CDF [list](#) structure.

**Usage**

```
cdfGetFields(groups, fields, ...)
```

**Arguments**

<code>groups</code>	A <a href="#">list</a> of groups.
<code>fields</code>	A <a href="#">character vector</a> of names of fields to be returned.
<code>...</code>	Not used.

**Details**

Note that an error is *not* generated for missing fields. Instead the field is returned with value [NA](#). The reason for this is that it is much faster.

**Value**

Returns a [list](#) structure of groups.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[applyCdfGroups\(\)](#).

---

cdfGetGroups	<i>Gets a subset of groups in a CDF structure</i>
--------------	---

---

**Description**

Gets a subset of groups in a CDF structure.

This [function](#) is design to be used with [applyCdfGroups\(\)](#) on an Affymetrix Mapping (SNP) CDF [list](#) structure.

**Usage**

```
cdfGetGroups(groups, which, ...)
```

**Arguments**

groups	A <a href="#">list</a> of groups.
which	An <a href="#">integer</a> or <a href="#">character vector</a> of groups be returned.
...	Not used.

**Value**

Returns a [list](#) structure of groups.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[applyCdfGroups\(\)](#).

---

cdfGtypeCelToPQ	<i>Function to immitate Affymetrix' gtype_cel_to_pq software</i>
-----------------	--

---

**Description**

Function to immitate Affymetrix' gtype\_cel\_to\_pq software.

This [function](#) is design to be used with [applyCdfGroups\(\)](#) on an Affymetrix Mapping (SNP) CDF [list](#) structure.

**Usage**

```
cdfGtypeCelToPQ(groups, ...)
```

**Arguments**

groups	A <a href="#">list</a> structure with groups.
...	Not used.

**Value**

Returns a `list` structure with a single group. The fields in this groups are in turn vectors (all of equal length) where the elements are stored as subsequent quartets (PMA, MMA, PMB, MMB) with all forward-strand quartets first followed by all reverse-strand quartets.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

[1] Affymetrix, *Understanding Genotyping Probe Set Structure*, 2005. [http://www.affymetrix.com/support/developer/whitepapers/genotyping\\_probe\\_set\\_structure.affx](http://www.affymetrix.com/support/developer/whitepapers/genotyping_probe_set_structure.affx)

**See Also**

`applyCdfGroups()`.

---

`cdfHeaderToCelHeader`

*Creates a valid CEL header from a CDF header*

---

**Description**

Creates a valid CEL header from a CDF header.

**Usage**

```
cdfHeaderToCelHeader(cdfHeader, sampleName="noname", date=Sys.time(), ..., version)
```

**Arguments**

<code>cdfHeader</code>	A CDF <code>list</code> structure.
<code>sampleName</code>	The name of the sample to be added to the CEL header.
<code>date</code>	The (scan) date to be added to the CEL header.
<code>...</code>	Not used.
<code>version</code>	The file-format version of the generated CEL file. Currently only version 4 is supported.

**Value**

Returns a CDF `list` structure.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)



---

`cdfMergeAlleles`      *Function to join CDF allele A and allele B groups strand by strand*

---

### Description

Function to join CDF allele A and allele B groups strand by strand.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

### Usage

```
cdfMergeAlleles(groups, compReverseBases=FALSE, collapse="", ...)
```

### Arguments

<code>groups</code>	A <code>list</code> structure with groups.
<code>compReverseBases</code>	If <code>TRUE</code> , the group names, which typically are names for bases, are turned into their complementary bases for the reverse strand.
<code>collapse</code>	The <code>character</code> string used to collapse the allele A and the allele B group names.
<code>...</code>	Not used.

### Details

Allele A and allele B are merged into a `matrix` where first row hold the elements for allele A and the second elements for allele B.

### Value

Returns a `list` structure with the two groups `forward` and `reverse`, if the latter exists.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### References

[1] Affymetrix, *Understanding Genotyping Probe Set Structure*, 2005. [http://www.affymetrix.com/support/developer/whitepapers/genotyping\\_probe\\_set\\_structure.affx](http://www.affymetrix.com/support/developer/whitepapers/genotyping_probe_set_structure.affx)

### See Also

`applyCdfGroups()`.

---

`cdfMergeStrands`      *Function to join CDF groups with the same names*

---

### Description

Function to join CDF groups with the same names.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

This can be used to join the sense and anti-sense groups of the same allele in SNP arrays.

### Usage

```
cdfMergeStrands(groups, ...)
```

### Arguments

<code>groups</code>	A <code>list</code> structure with groups.
<code>...</code>	Not used.

### Details

If a unit has two strands, they are merged such that the elements for the second strand are concatenated to the end of the elements of first strand (This is done seperately for the two alleles).

### Value

Returns a `list` structure with only two groups.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### References

[1] Affymetrix, *Understanding Genotyping Probe Set Structure*, 2005. [http://www.affymetrix.com/support/developer/whitepapers/genotyping\\_probe\\_set\\_structure.affx](http://www.affymetrix.com/support/developer/whitepapers/genotyping_probe_set_structure.affx)

### See Also

`applyCdfGroups()`.

---

`cdfMergeToQuartets` *Function to re-arrange CDF groups values in quartets*

---

### Description

Function to re-arrange CDF groups values in quartets.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

Note, this requires that the group values have already been arranged in PMs and MMs.

### Usage

```
cdfMergeToQuartets(groups, ...)
```

### Arguments

<code>groups</code>	A <code>list</code> structure with groups.
<code>...</code>	Not used.

### Value

Returns a `list` structure with the two groups forward and reverse, if the latter exists.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### References

[1] Affymetrix, *Understanding Genotyping Probe Set Structure*, 2005. [http://www.affymetrix.com/support/developer/whitepapers/genotyping\\_probe\\_set\\_structure.affx](http://www.affymetrix.com/support/developer/whitepapers/genotyping_probe_set_structure.affx)

### See Also

[applyCdfGroups\(\)](#).

---

`cdfOrderBy` *Orders the fields according to the value of another field in the same CDF group*

---

### Description

Orders the fields according to the value of another field in the same CDF group.

This `function` is design to be used with `applyCdfGroups()` on an Affymetrix Mapping (SNP) CDF `list` structure.

**Usage**

```
cdfOrderBy(groups, field, ...)
```

**Arguments**

groups	A <a href="#">list</a> of groups.
field	The field whose values are used to order the other fields.
...	Optional arguments passed <a href="#">order()</a> .

**Value**

Returns a [list](#) structure of groups.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[cdfOrderColumnsBy\(\)](#). [applyCdfGroups\(\)](#).

---

`cdfOrderColumnsBy` *Orders the columns of fields according to the values in a certain row of another field in the same CDF group*

---

**Description**

Orders the columns of fields according to the values in a certain row of another field in the same CDF group. Note that this method requires that the group fields are matrices.

This [function](#) is design to be used with [applyCdfGroups\(\)](#) on an Affymetrix Mapping (SNP) CDF [list](#) structure.

**Usage**

```
cdfOrderColumnsBy(groups, field, row=1, ...)
```

**Arguments**

groups	A <a href="#">list</a> of groups.
field	The field whose values in row <code>row</code> are used to order the other fields.
row	The row of the above field to be used to find the order.
...	Optional arguments passed <a href="#">order()</a> .

**Value**

Returns a [list](#) structure of groups.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[cdfOrderBy\(\). applyCdfGroups\(\)](#).

---

compareCdfs

*Compares the contents of two CDF files*

---

**Description**

Compares the contents of two CDF files.

**Usage**

```
compareCdfs(pathname, other, quick=FALSE, verbose=0, ...)
```

**Arguments**

pathname	The pathname of the first CDF file.
other	The pathname of the seconds CDF file.
quick	If <b>TRUE</b> , only a subset of the units are compared, otherwise all units are compared.
verbose	An <b>integer</b> . The larger the more details are printed.
...	Not used.

**Details**

The comparison is done with an upper-limit memory usage, regardless of the size of the CDFs.

**Value**

Returns **TRUE** if the two CDF are equal, otherwise **FALSE**. If **FALSE**, the attribute `reason` contains a string explaining what difference was detected, and the attributes `value1` and `value2` contain the two objects/values that differs.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[convertCdf\(\)](#).

---

compareCels	<i>Compares the contents of two CEL files</i>
-------------	---

---

**Description**

Compares the contents of two CEL files.

**Usage**

```
compareCels(pathname, other, readMap=NULL, otherReadMap=NULL, verbose=0, ...)
```

**Arguments**

pathname	The pathname of the first CEL file.
other	The pathname of the seconds CEL file.
readMap	An optional read map for the first CEL file.
otherReadMap	An optional read map for the second CEL file.
verbose	An <i>integer</i> . The larger the more details are printed.
...	Not used.

**Value**

Returns *TRUE* if the two CELs are equal, otherwise *FALSE*. If *FALSE*, the attribute *reason* contains a string explaining what difference was detected, and the attributes *value1* and *value2* contain the two objects/values that differs.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[convertCel\(\)](#).

---

convertCdf	<i>Converts a CDF into the same CDF but with another format</i>
------------	---

---

**Description**

Converts a CDF into the same CDF but with another format. Currently only CDF files in version 4 (binary/XDA) can be written. However, any input format is recognized.

**Usage**

```
convertCdf(filename, outFilename, version="4", force=FALSE, ..., .validate=TRUE,
```

**Arguments**

filename	The pathname of the original CDF file.
outFilename	The pathname of the destination CDF file. If the same as the source file, an exception is thrown.
version	The version of the output file format.
force	If <code>FALSE</code> , and the version of the original CDF is the same as the output version, the new CDF will not be generated, otherwise it will.
...	Not used.
.validate	If <code>TRUE</code> , a consistency test between the generated and the original CDF is performed. Note that the memory overhead for this can be quite large, because two complete CDF structures are kept in memory at the same time.
verbose	If <code>TRUE</code> , extra details are written while processing.

**Value**

Returns (invisibly) `TRUE` if a new CDF was generated, otherwise `FALSE`.

**Benchmarking of ASCII and binary CDFs**

Binary CDFs are much faster to read than ASCII CDFs. Here are some example for reading complete CDFs (the difference is even larger when reading CDFs in subsets):

- HG-U133A (22283 units): ASCII 11.7s (9.3x), binary 1.20s (1x).
- Hu6800 (7129 units): ASCII 3.5s (6.1x), binary 0.57s (1x).

**Confirmed conversions to binary (XDA) CDFs**

The following chip types have been converted using `convertCdf()` and then verified for correctness using `compareCdfs()`: ASCII-to-binary: HG-U133A, Hu6800. Binary-to-binary: Test3.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

See `compareCdfs()` to compare two CDF files. `writeCdf()`.

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

chipType <- "Test3"
cdfFiles <- findCdf(chipType, firstOnly=FALSE)
cdfFiles <- list(
  ASCII=grep("ASCII", cdfFiles, value=TRUE),
  XDA=grep("XDA", cdfFiles, value=TRUE)
)

outFile <- file.path(tempdir(), sprintf("%s.cdf", chipType))
```

```

convertCdf(cdfFiles$ASCII, outFile, verbose=TRUE)

#####
} # STOP #
#####

```

---

convertCel                      *Converts a CEL into the same CEL but with another format*

---

### Description

Converts a CEL into the same CEL but with another format. Currently only CEL files in version 4 (binary/XDA) can be written. However, any input format is recognized.

### Usage

```
convertCel(filename, outFilename, readMap=NULL, writeMap=NULL, version="4", newC
```

### Arguments

filename	The pathname of the original CEL file.
outFilename	The pathname of the destination CEL file. If the same as the source file, an exception is thrown.
readMap	An optional read map for the input CEL file.
writeMap	An optional write map for the output CEL file.
version	The version of the output file format.
newChipType	An optional string for overriding the chip type in the CEL file header.
...	Not used.
.validate	If <b>TRUE</b> , a consistency test between the generated and the original CEL is performed.
verbose	If <b>TRUE</b> , extra details are written while processing.

### Value

Returns (invisibly) **TRUE** if a new CEL was generated, otherwise **FALSE**.

### Benchmarking of ASCII and binary CELs

Binary CELs are much faster to read than ASCII CELs. Here are some example for reading complete CELs (the difference is even larger when reading CELs in subsets):

- To do

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### See Also

[createCel\(\)](#).



**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) {          # START #
#####

# Search for some available Calvin CEL files
path <- system.file("rawData", package="AffymetrixDataTestFiles")
files <- findFiles(pattern=".(cel|CEL)$", path=path, recursive=TRUE, firstOnly=FALSE)
files <- grep("FusionSDK_Test3", files, value=TRUE)
files <- grep("Calvin", files, value=TRUE)
file <- files[1]

outFile <- file.path(tempdir(), gsub("(.|)CEL$", ".XBA.CEL", basename(file)))
if (file.exists(outFile))
  file.remove(outFile)
convertCel(file, outFile, .validate=TRUE)

#####
}          # STOP #
#####
```

---

copyCel

*Copies a CEL file*


---

**Description**

Copies a CEL file.

The file must be a valid CEL file, if not an exception is thrown.

**Usage**

```
copyCel(from, to, overwrite=FALSE, ...)
```

**Arguments**

from	The filename of the CEL file to be copied.
to	The filename of destination file.
overwrite	If <b>FALSE</b> and the destination file already exists, an exception is thrown, otherwise not.
...	Not used.

**Value**

Return **TRUE** if file was successfully copied, otherwise **FALSE**.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[isCelFile\(\)](#).

---

createCel	<i>Creates an empty CEL file</i>
-----------	----------------------------------

---

### Description

Creates an empty CEL file.

### Usage

```
createCel(filename, header, nsubgrids=0, overwrite=FALSE, ..., verbose=FALSE)
```

### Arguments

filename	The filename of the CEL file to be created.
header	A <code>list</code> structure describing the CEL header, similar to the structure returned by <code>readCelHeader()</code> . This header can be of any CEL header version.
overwrite	If <code>FALSE</code> and the file already exists, an exception is thrown, otherwise the file is created.
nsubgrids	The number of subgrids.
...	Not used.
verbose	An <code>integer</code> specifying how much verbose details are outputted.

### Details

Currently only binary (v4) CEL files are supported. The current version of the method does not make use of the Fusion SDK, but its own code to create the CEL file.

### Value

Returns (invisibly) the pathname of the file created.

### Redundant fields in the CEL header

There are a few redundant fields in the CEL header. To make sure the CEL header is consistent, redundant fields are cleared and regenerated. For instance, the field for the total number of cells is calculated from the number of cell rows and columns.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### Examples

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

# Search for first available ASCII CEL file
path <- system.file("rawData", package="AffymetrixDataTestFiles")
files <- findFiles(pattern=".(cel|CEL)$", path=path, recursive=TRUE, firstOnly=FALSE)
files <- grep("ASCII", files, value=TRUE)
```

```

file <- files[1]

# -----
# Read the CEL header
# -----
hdr <- readCelHeader(file)

# Assert that we found an ASCII CEL file, but any will do
stopifnot(hdr$version == 3)

# -----
# Create a CEL v4 file of the same chip type
# -----
outFile <- file.path(tempdir(), "zzz.CEL")
if (file.exists(outFile))
  file.remove(outFile)
createCel(outFile, hdr, overwrite=TRUE)
str(readCelHeader(outFile))

# Verify correctness by update and re-read a few cells
intensities <- as.double(1:100)
indices <- seq(along=intensities)
updateCel(outFile, indices=indices, intensities=intensities)
value <- readCel(outFile, indices=indices)$intensities
stopifnot(identical(intensities, value))

#####
} # STOP #
#####

```

---

findCdf

*Search for CDF files in multiple directories*


---

## Description

Search for CDF files in multiple directories.

## Usage

```
findCdf(chipType=NULL, paths=NULL, recursive=TRUE, pattern=".[c|C)(d|D)(f|F)$"
```

## Arguments

chipType	A <a href="#">character</a> string of the chip type to search for.
paths	A <a href="#">character vector</a> of paths to be searched. The current directory is always searched at the beginning. If <code>NULL</code> , default paths are searched. For more details, see below.
recursive	If <code>TRUE</code> , directories are searched recursively.
pattern	A regular expression file name pattern to match.
...	Additional arguments passed to <code>findFiles()</code> .

## Details

Note, the current directory is always searched first, but never recursively (unless it is added to the search path explicitly). This provides an easy way to override other files in the search path.

If `paths` is `NULL`, then a set of default paths are searched. The default search path consists:

1. `getOption("AFFX_CDF_PATH")`
2. `Sys.getenv("AFFX_CDF_PATH")`

One of the easiest ways to set system variables for R is to set them in an `.Renviron` file, e.g.

```
# affxparser: Set default CDF path
AFFX_CDF_PATH=${AFFX_CDF_PATH};M:/Affymetrix_2004-100k_trios/cdf
AFFX_CDF_PATH=${AFFX_CDF_PATH};M:/Affymetrix_2005-500k_data/cdf
```

See [Startup](#) for more details.

## Value

Returns a [vector](#) of the full pathnames of the files found.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## See Also

This method is used internally by `readCelUnits()` if the CDF file is not specified.

## Examples

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

# Find a specific CDF file
cdfFile <- findCdf("Mapping10K_Xba131")
print(cdfFile)

# Find the first CDF file (no matter what it is)
cdfFile <- findCdf()
print(cdfFile)

# Find all CDF files in search path and display their headers
cdfFiles <- findCdf(firstOnly=FALSE)
for (cdfFile in cdfFiles) {
  cat("=====\n")
  hdr <- readCdfHeader(cdfFile)
  str(hdr)
}

#####
} # STOP #
#####
```

---

findFiles	<i>Finds one or several files in multiple directories</i>
-----------	---

---

### Description

Finds one or several files in multiple directories.

### Usage

```
findFiles(pattern=NULL, paths=NULL, recursive=FALSE, firstOnly=TRUE, allFiles=TR
```

### Arguments

pattern	A regular expression file name pattern to match.
paths	A <a href="#">character vector</a> of paths to be searched.
recursive	If <b>TRUE</b> , the directory structure is searched breath-first, in lexicographic order.
firstOnly	If <b>TRUE</b> , the method returns as soon as a matching file is found, otherwise not.
allFiles	If <b>FALSE</b> , files and directories starting with a period will be skipped, otherwise not.
...	Arguments passed to <code>list.files()</code> .

### Value

Returns a [vector](#) of the full pathnames of the files found.

### Paths

The `paths` argument may also contain paths specified as semi-colon (";") separated paths, e.g. `"/usr;/usr/bin/;.;"`.

### Windows Shortcut links

If package **R.utils** is available and loaded, Windows Shortcut links (\*.lnk) are recognized and can be used to immitate links to directories elsewhere. For more details, see [filePath](#).

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

---

`invertMap`*Inverts a read or a write map*

---

### Description

Inverts a read or a write map.

### Usage

```
invertMap(map, ...)
```

### Arguments

<code>map</code>	An <i>integer vector</i> .
<code>...</code>	Not used.

### Details

A map is defined to be a *vector* of  $n$  with unique finite values in  $[1, n]$ . Finding the inverse of a map is the same as finding the rank of each element, cf. `order()`. However, this method is much faster, because it utilizes the fact that all values are unique and in  $[1, n]$ . Moreover, for any map it holds that taking the inverse twice will result in the same map.

### Value

Returns an *integer vector*.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### See Also

To generate an optimized write map for a CDF file, see `readCdfUnitsWriteMap()`.

### Examples

```
set.seed(1)

# Simulate a read map for a chip with 2.6 million cells
nbrOfCells <- 2600000
readMap <- sample(nbrOfCells)

# Get the corresponding write map
writeMap <- invertMap(readMap)

# A map inverted twice should be equal itself
stopifnot(identical(invertMap(writeMap), readMap))

# Another example illustrating that the write map is the
# inverse of the read map
idx <- sample(nbrOfCells, size=1000)
stopifnot(identical(writeMap[readMap[idx]], idx))
```

```
# invertMap() is much faster than order()
t1 <- system.time(invertMap(readMap))[3]
cat(sprintf("invertMap() : %5.2fs [ 1.00x]\n", t1))

t2 <- system.time(writeMap2 <- sort.list(readMap, na.last=NA, method="quick"))[3]
cat(sprintf("'quick sort' : %5.2fs [%5.2fx]\n", t2, t2/t1))
stopifnot(identical(writeMap, writeMap2))

t3 <- system.time(writeMap2 <- order(readMap))[3]
cat(sprintf("order() : %5.2fs [%5.2fx]\n", t3, t3/t1))
stopifnot(identical(writeMap, writeMap2))

# Clean up
rm(nbrOfCells, idx, readMap, writeMap, writeMap2)
```

---

isCelFile

*Checks if a file is a CEL file or not*

---

## Description

Checks if a file is a CEL file or not.

## Usage

```
isCelFile(filename, ...)
```

## Arguments

filename	A filename.
...	Not used.

## Value

Returns `TRUE` if a CEL file, otherwise `FALSE`. ASCII (v3), binary (v4;XDA), and binary (CCG v1;Calvin) CEL files are recognized. If file does not exist, an exception is thrown.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## See Also

`readCel()`, `readCelHeader()`, `readCelUnits()`.

---

readBpmap	<i>Parses a Bpmap file</i>
-----------	----------------------------

---

### Description

Parses (parts of) a Bpmap (binary probe mapping) file from Affymetrix.

### Usage

```
readBpmap(filename, seqIndices = NULL, readProbeSeq = TRUE, readSeqInfo
= TRUE, readPMXY = TRUE, readMMXY = TRUE, readStartPos = TRUE,
readCenterPos = FALSE, readStrand = TRUE, readMatchScore = FALSE,
readProbeLength = FALSE, verbose = 0)
```

```
readBpmapHeader(filename)
```

```
readBpmapSeqinfo(filename, seqIndices = NULL, verbose = 0)
```

### Arguments

filename	The filename as a character.
seqIndices	A vector of integers, detailing the indices of the sequences being read. If NULL, the entire file is being read.
readProbeSeq	
readSeqInfo	Do we read the sequence information (a list containing information such as sequence name, number of hits etc.)
readPMXY	Do we read the (x,y) coordinates of the PM-probes.
readMMXY	Do we read the (x,y) coordinates of the MM-probes (only relevant if the file has MM information)
readStartPos	Do we read the start position of the probes.
readCenterPos	Do we return the start position of the probes.
readStrand	Do we return the strand of the hits.
readMatchScore	Do we return the matchscore.
readProbeLength	Do we return the probelength.
verbose	How verbose do we want to be.

### Details

readBpmap reads a BMAP file, which is a binary file containing information about a given probe's location in a sequence. Here sequence means some kind of reference sequence, typically a chromosome or a scaffold. readBpmapHeader reads the header of the BMAP file, and readBpmapSeqinfo reads the sequence info of the sequences (so this function is merely a convenience function).



**Value**

For `readBpmap`: A list of lists, one list for every sequence read. The components of the sequence lists, depends on the argument of the function call. For `readBpmapheader` a list with two components `version` and `numSequences`. For `readBpmapSeqinfo` a list of lists containing the sequence info.

**Author(s)**

Kasper Daniel Hansen <khansen@stat.berkeley.edu>

**See Also**

[tmap2bmap](#) for information on how to write Bpmap files.

---

<code>readCcgHeader</code>	<i>Reads an the header of an Affymetrix Command Console Generic (CCG) file</i>
----------------------------	--

---

**Description**

Reads an the header of an Affymetrix Command Console Generic (CCG) file.

**Usage**

```
readCcgHeader(pathname, verbose=0, .filter=list(fileHeader = TRUE, dataHeader =
```

**Arguments**

<code>pathname</code>	The pathname of the CCG file.
<code>verbose</code>	An <a href="#">integer</a> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.
<code>.filter</code>	A <a href="#">list</a> .
<code>...</code>	Not used.

**Details**

Note, the current implementation of this methods does not utilize the Affymetrix Fusion SDK library. Instead, it is implemented in R from the file format definition [1].

**Value**

A named [list](#) structure consisting of ...

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

[1] Affymetrix Inc, Affymetrix GCOS 1.x compatible file formats, April, 2006. <http://www.affymetrix.com/support/developer/>

**See Also**

[readCcg\(\)](#).

---

readCcg	<i>Reads an Affymetrix Command Console Generic (CCG) Data file</i>
---------	--

---

**Description**

Reads an Affymetrix Command Console Generic (CCG) Data file. The CCG data file format is also known as the Calvin file format.

**Usage**

```
readCcg(pathname, verbose=0, .filter=NULL, ...)
```

**Arguments**

pathname	The pathname of the CCG file.
verbose	An <a href="#">integer</a> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.
.filter	A <a href="#">list</a> .
...	Not used.

**Details**

Note, the current implementation of this methods does not utilize the Affymetrix Fusion SDK library. Instead, it is implemented in R from the file format definition [1].

**Value**

A named [list](#) structure consisting of ...

**About the CCG file format**

A CCG file, consists of a "file header", a "generic data header", and "data" section, as outlined here:

- File Header
- Generic Data Header (for the file)
  1. Generic Data Header (for the files 1st parent)
    - (a) Generic Data Header (for the files 1st parents 1st parent)
    - (b) Generic Data Header (for the files 1st parents 2nd parent)
    - (c) ...
    - (d) Generic Data Header (for the files 1st parents Mth parent)
  2. Generic Data Header (for the files 2nd parent)
  3. ...
  4. Generic Data Header (for the files Nth parent)
- Data
  1. Data Group #1

- (a) Data Set #1
  - Parameters
  - Column definitions
  - Matrix of data
- (b) Data Set #2
- (c) ...
- (d) Data Set #L
- 2. Data Group #2
- 3. ...
- 4. Data Group #K

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**References**

[1] Affymetrix Inc, Affymetrix GCOS 1.x compatible file formats, April, 2006. <http://www.affymetrix.com/support/developer/>

**See Also**

[readCcgHeader\(\)](#). [readCdfUnits\(\)](#).

---

`readCdfCellIndices` *Reads cell indices of units (probesets) in an Affymetrix CDF file*

---

**Description**

Reads cell indices of units (probesets) in an Affymetrix CDF file.

**Usage**

```
readCdfCellIndices(filename, units=NULL, stratifyBy=c("nothing", "pmmm", "pm", "
```

**Arguments**

<code>filename</code>	The filename of the CDF file.
<code>units</code>	An <a href="#">integer vector</a> of unit indices specifying which units to be read. If <code>NULL</code> , all units are read.
<code>stratifyBy</code>	A <a href="#">character</a> string specifying which and how elements in group fields are returned. If "nothing", elements are returned as is, i.e. as <a href="#">vectors</a> . If "pm"/"mm", only elements corresponding to perfect-match (PM) / mismatch (MM) probes are returned (as <a href="#">vectors</a> ). If "pmmm", elements are returned as a matrix where the first row holds elements corresponding to PM probes and the second corresponding to MM probes. Note that in this case, it is assumed that there are equal number of PMs and MMs; if not, an error is generated. Moreover, the PMs and MMs may not even be paired, i.e. there is no guarantee that the two elements in a column corresponds to a PM-MM pair.
<code>verbose</code>	An <a href="#">integer</a> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

**Value**

A named `list` where the names corresponds to the names of the units read. Each unit element of the list is in turn a `list` structure with one element `groups` which in turn is a `list`. Each group element in `groups` is a `list` with a single field named `indices`. Thus, the structure is

```

cdf
+- unit #1
|   +- "groups"
|     +- group #1
|       | +- "indices"
|       | group #2
|       | +- "indices"
|       .
|       +- group #K
|         +- "indices"
+- unit #2
.
+- unit #J

```

This structure is compatible with what `readCdfUnits()` returns.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

`readCdfUnits()`.

---

`readCdfDataFrame`     *Reads units (probesets) from an Affymetrix CDF file*

---

**Description**

Reads units (probesets) from an Affymetrix CDF file. Gets all or a subset of units (probesets).

**Usage**

```
readCdfDataFrame(filename, units=NULL, groups=NULL, cells=NULL, fields=NULL, dro
```

**Arguments**

<code>filename</code>	The filename of the CDF file.
<code>units</code>	An <code>integer vector</code> of unit indices specifying which units to be read. If <code>NULL</code> , all are read.
<code>groups</code>	An <code>integer vector</code> of group indices specifying which groups to be read. If <code>NULL</code> , all are read.
<code>cells</code>	An <code>integer vector</code> of cell indices specifying which cells to be read. If <code>NULL</code> , all are read.

fields	A <a href="#">character vector</a> specifying what fields to read. If <code>NULL</code> , all unit, group and cell fields are returned.
drop	If <code>TRUE</code> and only one field is read, then a <a href="#">vector</a> (rather than a single-column <code>data.frame</code> ) is returned.
verbose	An <a href="#">integer</a> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

**Value**

An  $N \times K$  `data.frame` or a `vector` of length `N`.

**References**

[1] Affymetrix Inc, Affymetrix GCOS 1.x compatible file formats, June 14, 2005. <http://www.affymetrix.com/support/developer/>

**See Also**

For retrieving the CDF as a `list` structure, see `readCdfUnits()`.

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

# Find any CDF file
cdfFile <- findCdf()

units <- 101:120
fields <- c("unit", "unitName", "group", "groupName", "cell")
df <- readCdfDataFrame(cdfFile, units=units, fields=fields)
stopifnot(identical(sort(unique(df$unit)), units))

fields <- c("unit", "unitName", "unitType")
fields <- c(fields, "group", "groupName")
fields <- c(fields, "x", "y", "cell", "pbase", "tbase")
df <- readCdfDataFrame(cdfFile, units=units, fields=fields)
stopifnot(identical(sort(unique(df$unit)), units))

#####
} # STOP #
#####
```

---

`readCdfGroupNames` *Reads group names for a set of units (probesets) in an Affymetrix CDF file*

---

**Description**

Reads group names for a set of units (probesets) in an Affymetrix CDF file.

This is for instance useful for SNP arrays where the nucleotides used for the A and B alleles are the same as the group names.

**Usage**

```
readCdfGroupNames(filename, units=NULL, truncateGroupNames=TRUE, verbose=0)
```

**Arguments**

`filename` The filename of the CDF file.

`units` An *integer vector* of unit indices specifying which units to be read. If `NULL`, all units are read.

`truncateGroupNames` A *logical* variable indicating whether unit names should be stripped from the beginning of group names.

`verbose` An *integer* specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

**Value**

A named *list* structure where the names of the elements are the names of the units read. Each element is a *character vector* with group names for the corresponding unit.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

[readCdfUnits\(\)](#).

---

readCdfHeader	<i>Reads the header associated with an Affymetrix CDF file</i>
---------------	--

---

**Description**

Reads the header of an Affymetrix CDF file using the Fusion SDK.

**Usage**

```
readCdfHeader(filename)
```

**Arguments**

`filename` name of the CDF file.

**Value**

A named list with the following components:

`rows` the number of rows on the chip.

`cols` the number of columns on the chip.

`probesets` the number of probesets on the chip.

`qcprobesets` the number of QC probesets on the chip.

`reference` the reference sequence (this component only exists for resequencing chips).

`chiptype` the type of the chip.

`filename` the name of the cdf file.

**Author(s)**

James Bullard, <bullard@stat.berkeley.edu> and Kasper Daniel Hansen, <khansen@stat.berkeley.edu>

**See Also**

`readCdfUnits()`.

**Examples**

```
for (zzz in 0) {  
  
  # Find any CDF file  
  cdfFile <- findCdf()  
  if (is.null(cdfFile))  
    break  
  
  header <- readCdfHeader(cdfFile)  
  print(header)  
  
} # for (zzz in 0)
```

---

readCdfIsPm

*Checks if cells in a CDF file are perfect-match probes or not*

---

**Description**

Checks if cells in a CDF file are perfect-match probes or not.

**Usage**

```
readCdfIsPm(filename, units=NULL, verbose=0)
```

**Arguments**

filename	The filename of the CDF file.
units	An <i>integer vector</i> of unit indices specifying which units to be read. If <code>NULL</code> , all units are read.
verbose	An <i>integer</i> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

**Value**

A named *list* of named *logical* vectors. The name of the list elements are unit names and the names of the logical vector are group names.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

---

```
readCdfNbrOfCellsPerUnitGroup
```

*Gets the number of cells (probes) that each group of each unit in a CDF file*

---

## Description

Gets the number of cells (probes) that each group of each unit in a CDF file.

## Usage

```
readCdfNbrOfCellsPerUnitGroup(filename, units=NULL, verbose=0)
```

## Arguments

filename	The filename of the CDF file.
units	An <i>integer vector</i> of unit indices specifying which units to be read. If <i>NULL</i> , all units are read.
verbose	An <i>integer</i> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

## Value

A named *list* of named *integer* vectors. The name of the list elements are unit names and the names of the integer vector are group names.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## Examples

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

cdfFile <- findCdf("Mapping10K_Xba131")

groups <- readCdfNbrOfCellsPerUnitGroup(cdfFile)

# Number of units read
print(length(groups))
## 11564

# Details on two units
print(groups[56:57])
## $`SNP_A-1516438`
## SNP_A-1516438C SNP_A-1516438T SNP_A-1516438C SNP_A-1516438T
## 10 10 10 10
##
## $`SNP_A-1508602`
## SNP_A-1508602A SNP_A-1508602G SNP_A-1508602A SNP_A-1508602G
## 10 10 10 10
```



```

# Number of groups with different number of cells
print(table(unlist(groups)))
##      10      60
## 46240      4

# Number of cells per unit
nbrOfCellsPerUnit <- unlist(lapply(groups, FUN=sum))
print(table(nbrOfCellsPerUnit))
nbrOfCellsPerUnit
##      40      60
## 11560      4

# Number of groups per unit
nbrOfGroupsPerUnit <- unlist(lapply(groups, FUN=length))

# Details on a few units
print(nbrOfGroupsPerUnit[20:30])
## SNP_A-1512666 SNP_A-1512740 SNP_A-1512132 SNP_A-1516082 SNP_A-1511962
##           4           4           4           4           4
## SNP_A-1515637 SNP_A-1515878 SNP_A-1518789 SNP_A-1518296 SNP_A-1519701
##           4           4           4           4           4
## SNP_A-1511743
##           4

# Number of units for each unique number of groups
print(table(nbrOfGroupsPerUnit))
## nbrOfGroupsPerUnit
##      1      4
##      4 11560

x <- list()
for (size in unique(nbrOfGroupsPerUnit)) {
  subset <- groups[nbrOfGroupsPerUnit==size]
  t <- matrix(unlist(subset), nrow=size)
  colnames(t) <- names(subset)
  x[[as.character(size)]] <- t
  rm(subset, t)
}

# Check if there are any quartet units where the number
# of cells in Group 1 & 2 or Group 3 & 4 does not have
# the same number of cells.
# Group 1 & 2
print(sum(x[["4"]][1,]-x[["4"]][2,] != 0))
# 0

# Group 3 & 4
print(sum(x[["4"]][3,]-x[["4"]][4,] != 0))
# 0

#####
} # STOP #
#####

```

---

readCdfQc	<i>Reads the QC units of CDF file</i>
-----------	---------------------------------------

---

**Description**

Reads the QC units of CDF file.

**Usage**

```
readCdfQc(filename, units = NULL, verbose = 0)
```

**Arguments**

filename	name of the CDF file.
units	The QC unit indices as a vector of integers. NULL indicates that all units should be read.
verbose	how verbose should the output be. 0 means no output, with higher numbers being more verbose.

**Value**

A list with one component for each QC unit.

**Author(s)**

Kasper Daniel Hansen, (khansen@stat.berkeley.edu)

**See Also**

[readCdf\(\)](#).

---

readCdf	<i>Parsing a CDF file using Affymetrix Fusion SDK</i>
---------	---

---

**Description**

This function parses a CDF file using the Affymetrix Fusion SDK.

*This function will most likely be replaced by the more general [readCdfUnits\(\)](#) function.*

**Usage**

```
readCdf(filename, units=NULL,
        readXY=TRUE, readBases=TRUE,
        readIndexpos=TRUE, readAtoms=TRUE,
        readUnitType=TRUE, readUnitDirection=TRUE,
        readUnitNumber=TRUE, readUnitAtomNumbers=TRUE,
        readGroupAtomNumbers=TRUE, readGroupDirection=TRUE,
        readIndices=FALSE, readIsPm=FALSE,
        stratifyBy=c("nothing", "pmmm", "pm", "mm"),
        verbose=0)
```

**Arguments**

filename	name of the CDF file.
verbose	how verbose should the output be. 0 means no output, with higher numbers being more verbose.

**Value**

A list with one component for each unit. Every component is again a list with three components

groups	This is again a list with one component for each group (also called block). The information on each group is a list with 5 components, x, y, pbase, tbase, expos.
type	type of the unit.
direction	direction of the unit.

**Note**

This version of the function does not return information on the QC probes. This will be added in a (near) future release. In addition we expect the header to be part of the returned object.

So expect changes to the structure of the value of the function in next release. Please contact the developers for details.

**Author(s)**

James Bullard, <bullard@stat.berkeley.edu> and Kasper Daniel Hansen, <khansen@stat.berkeley.edu>

**See Also**

[readCdfHeader\(\)](#) for getting the header of a CDF file.

---

readCdfUnitNames    *Reads unit (probeset) names from an Affymetrix CDF file*

---

**Description**

Gets the names of all or a subset of units (probesets) in an Affymetrix CDF file. This can be used to get a map between unit names and the internal unit indices used by the CDF file.

**Usage**

```
readCdfUnitNames(filename, units=NULL, verbose=0)
```

**Arguments**

filename	The filename of the CDF file.
units	An <a href="#">integer vector</a> of unit indices specifying which units to be read. If <a href="#">NULL</a> , all units are read.
verbose	An <a href="#">integer</a> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

**Value**

A `character vector` of unit names.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

`readCdfUnits()`.

**Examples**

```
## Not run: See help(readCdfUnits) for an example
```

---

<code>readCdfUnits</code>	<i>Reads units (probesets) from an Affymetrix CDF file</i>
---------------------------	--

---

**Description**

Reads units (probesets) from an Affymetrix CDF file. Gets all or a subset of units (probesets).

**Usage**

```
readCdfUnits(filename, units=NULL, readXY=TRUE, readBases=TRUE, readExpos=TRUE,
```

**Arguments**

<code>filename</code>	The filename of the CDF file.
<code>units</code>	An <code>integer vector</code> of unit indices specifying which units to be read. If <code>NULL</code> , all units are read.
<code>readXY</code>	If <code>TRUE</code> , cell row and column (x,y) coordinates are retrieved, otherwise not.
<code>readBases</code>	If <code>TRUE</code> , cell P and T bases are retrieved, otherwise not.
<code>readExpos</code>	If <code>TRUE</code> , cell "expos" values are retrieved, otherwise not.
<code>readType</code>	If <code>TRUE</code> , unit types are retrieved, otherwise not.
<code>readDirection</code>	If <code>TRUE</code> , unit <i>and</i> group directions are retrieved, otherwise not.
<code>stratifyBy</code>	A <code>character</code> string specifying which and how elements in group fields are returned. If "nothing", elements are returned as is, i.e. as <code>vectors</code> . If "pm"/"mm", only elements corresponding to perfect-match (PM) / mismatch (MM) probes are returned (as <code>vectors</code> ). If "pmmm", elements are returned as a matrix where the first row holds elements corresponding to PM probes and the second corresponding to MM probes. Note that in this case, it is assumed that there are equal number of PMs and MMs; if not, an error is generated. Moreover, the PMs and MMs may not even be paired, i.e. there is no guarantee that the two elements in a column corresponds to a PM-MM pair.
<code>readIndices</code>	If <code>TRUE</code> , cell indices calculated from the row and column (X,Y) coordinates are retrieved, otherwise not.
<code>verbose</code>	An <code>integer</code> specifying the verbose level. If 0, the file is parsed quietly. The higher numbers, the more details.

**Value**

A named `list` where the names corresponds to the names of the units read. Each element of the list is in turn a `list` structure with three components:

<code>groups</code>	A <code>list</code> with one component for each group (also called block). The information on each group is a <code>list</code> of up to seven components: <code>x</code> , <code>y</code> , <code>pbase</code> , <code>tbase</code> , <code>expos</code> , <code>indices</code> , and <code>direction</code> . All fields but the latter have the same number of values as there are cells in the group. The latter field has only one value indicating the direction for the whole group.
<code>type</code>	An <code>integer</code> specifying the type of the unit, where 1 is "expression", 2 is "genotyping", 3 is "CustomSeq", and 4 "tag".
<code>direction</code>	An <code>integer</code> specifying the direction of the unit, which defines if the probes are interrogating the sense or the anti-sense target, where 0 is "no direction", 1 is "sense", and 2 is "anti-sense".

**Author(s)**

James Bullard, <bullard@stat.berkeley.edu> and Kasper Daniel Hansen, <khansen@stat.berkeley.edu>. Modified by Henrik Bengtsson (<http://www.braju.com/R/>) to read any subset of units and/or subset of parameters, to stratify by PM/MM, and to return cell indices.d

**References**

[1] Affymetrix Inc, Affymetrix GCOS 1.x compatible file formats, June 14, 2005. <http://www.affymetrix.com/support/developer/>

**See Also**

`readCdfCellIndices()`.

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

# Find any CDF file
cdfFile <- findCdf()

# Read all units in a CDF file [~20s => 0.34ms/unit]
cdf0 <- readCdfUnits(cdfFile, readXY=FALSE, readExpos=FALSE)

# Read a subset of units in a CDF file [~6ms => 0.06ms/unit]
units1 <- c(5, 100:109, 34)
cdf1 <- readCdfUnits(cdfFile, units=units1, readXY=FALSE, readExpos=FALSE)
stopifnot(identical(cdf1, cdf0[units1]))
rm(cdf0)

# Create a unit name to index map
names <- readCdfUnitNames(cdfFile)
units2 <- match(names(cdf1), names)
stopifnot(all.equal(units1, units2))
cdf2 <- readCdfUnits(cdfFile, units=units2, readXY=FALSE, readExpos=FALSE)
```

```
stopifnot(identical(cdf1, cdf2))

#####
} # STOP #
#####
```

---

```
readCdfUnitsWriteMap
```

*Generates an Affymetrix cell-index write map from a CDF file*

---

## Description

Generates an Affymetrix cell-index write map from a CDF file.

The purpose of this method is to provide a re-ordering of cell elements such that cells in units (probesets) can be stored in contiguous blocks. When reading cell elements unit by unit, minimal file re-position is required resulting in a faster reading.

Note: At the moment does this package not provide methods to write/reorder CEL files. In the meanwhile, you have to write and re-read using your own file format. That's not too hard using `writeBin()` and `readBin()`.

## Usage

```
readCdfUnitsWriteMap(filename, units=NULL, ..., verbose=FALSE)
```

## Arguments

filename	The pathname of the CDF file.
units	An <i>integer vector</i> of unit indices specifying which units to listed first. All other units are added in order at the end. If <code>NULL</code> , units are in order.
...	Additional arguments passed to <code>readCdfUnits()</code> .
verbose	Either a <i>logical</i> , a <i>numeric</i> , or a <i>Verbose</i> object specifying how much verbose/debug information is written to standard output. If a <i>Verbose</i> object, how detailed the information is is specified by the threshold level of the object. If a <i>numeric</i> , the value is used to set the threshold of a new <i>Verbose</i> object. If <code>TRUE</code> , the threshold is set to -1 (minimal). If <code>FALSE</code> , no output is written (and neither is the <b>R.utils</b> package required).

## Value

A *integer vector* which is a *write* map.

## Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

## See Also

To invert maps, see `invertMap()`. `readCel()` and `readCelUnits()`.

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) {          # START #
#####

# Find any CDF file
cdfFile <- findCdf()

# Create a cell-index map (for writing)
writeMap <- readCdfUnitsWriteMap(cdfFile)

# Inverse map to be used to read cell elements such that, when read
# read unit by unit, they are read much faster.
readMap <- invertMap(writeMap)

# Validate the two maps
stopifnot(identical(readMap[writeMap], 1:length(readMap)))

cat("Summary of the \"randomness\" of the cell indices:\n")
moves <- diff(readMap) - 1
cat(sprintf("Number of unnecessary file re-positioning: %d (%.1f%%)\n",
            sum(moves != 0), 100*sum(moves != 0)/length(moves))),
cat(sprintf("Extra positioning: %.1fGb\n", sum(abs(moves))/1024^3))

smallMoves <- moves[abs(moves) <= 25];
largeMoves <- moves[abs(moves) > 25];
layout(matrix(1:2))
main <- "Non-signed file moves required in unorded file"
hist(smallMoves, nclass=51, main=main, xlab="moves <=25 bytes")
hist(largeMoves, nclass=101, main="", xlab="moves >25 bytes")

# Clean up
layout(1)
rm(cdfFile, readMap, writeMap, moves, smallMoves, largeMoves, main)

#####
}          # STOP #
#####

#####
if (require("AffymetrixDataTestFiles")) {          # START #
#####

# - - - - -
# Function to read Affymetrix probeset annotations
# - - - - -
readAffymetrixProbesetAnnotation <- function(pathname, ...) {
  # Get headers
  header <- scan(pathname, what="character", sep=",", quote="\"",
                 quiet=TRUE, nlines=1);

  # Read only a subset of columns (unique to this example)
  cols <- c("Probe Set ID"="probeSet",
            "Chromosome"="chromosome",
            "Physical Position"="physicalPosition",
```

```

    "dbSNP RS ID"="dbSnpId");

colClasses <- rep("NULL", length(header));
colClasses[header %in% names(cols)] <- "character";

# Read the data (this is what takes time)
df <- read.table(pathname, colClasses=colClasses, header=TRUE, sep=",",
  quote="\\"", na.strings="---", strip.white=TRUE, check.names=FALSE,
  blank.lines.skip=FALSE, fill=FALSE, comment.char="", ...);

# Re-order columns
df <- df[,match(names(cols), colnames(df))];
colnames(df) <- cols;

# Use "Probe Set ID" as rownames. Note that if we use 'row.names=1'
# or similar something goes wrong. /HB 2006-03-06
rownames(df) <- df[[1]];
df <- df[,-1];

# Change types of columns
df[[1]] <- factor(df[[1]], levels=c(1:22,"X","Y",NA), ordered=TRUE);
df[[2]] <- as.integer(df[[2]]);

df;
} # readAffymetrixProbesetAnnotation()

# - - - - -
# Main
# - - - - -
for (zz in 1) {
# Chip to be remapped
chipType <- "Mapping50K_Xba240"

annoFile <- paste(chipType, "_annot.csv", sep="")
cdfFile <- findCdf(chipType)
if (is.null(cdfFile) || !file.exists(annoFile))
  break;

# Read SNP location details
snpInfo <- readAffymetrixProbesetAnnotation(annoFile)

# Order by chromosome and then physical position
o <- order(snpInfo[[1]], snpInfo[[2]])
snpInfo <- snpInfo[o,]
rm(o)

# Read unit names in CDF file
unitNames <- readCdfUnitNames(cdfFile)

# The CDF unit indices sorted by chromosomal position
units <- match(rownames(snpInfo), unitNames)

# ...and cell indices in the same order
writeMap <- readCdfUnitsWriteMap(cdfFile, units=units)

# Inverse map to be used to write cell elements such that, if they

```



```

# later are read unit by unit, they are read in contiguous blocks.
readMap <- invertMap(writeMap)

# Clean up
rm(chipType, annoFile, cdfFile, snpInfo, unitNames, units, readMap, writeMap)

} # for (zz in 1)
#####
} # STOP #
#####

```

---

readCelHeader	<i>Parsing the header of an Affymetrix CEL file</i>
---------------	---

---

### Description

Reads in the header of an Affymetrix CEL file using the Fusion SDK.

### Usage

```
readCelHeader(filename)
```

### Arguments

filename      the name of the CEL file.

### Details

This function returns the header of a CEL file. Affymetrix operates with different versions of this file format. Depending on what version is being read, different information is accessible.

### Value

A named list with components described below. The entries are obtained from the Fusion SDK interface functions. We try to obtain all relevant information from the file.

filename	the name of the cel file.
version	the version of the cel file.
cols	the number of columns on the chip.
rows	the number of rows on the chip.
total	the total number of features on the chip. Usually equal to rows times cols, but since it is a separate attribute in the SDK we decided to include it anyway.
algorithm	the algorithm used to create the CEL file.
parameters	the parameters used in the algorithm. Seems to be semi-colon separated.
chiptype	the type of the chip.
header	the entire header of the CEL file. Only available for non-calvin format files.
cellmargin	a parameter used to generate the CEL file. According to Affymetrix, it designates the number of pixels to ignore around the feature border when calculating the intensity value (the number of pixels ignored are cellmargin divided by 2).

noutliers      the number of features reported as outliers.  
 nmasked        the number of features reported as masked.

### Note

Memory usage: the Fusion SDK allocates memory for the entire CEL file, when the file is accessed. The memory footprint of this function will therefore seem to be (rather) large.

Speed: CEL files of version 2 (standard text files) needs to be completely read in order to report the number of outliers and masked features.

### Author(s)

James Bullard, <bullard@stat.berkeley.edu> and Kasper Daniel Hansen, <khansen@stat.berkeley.edu>

### See Also

[readCel\(\)](#) for reading in the entire CEL file. That function also returns the header. See [affxparserInfo](#) for general comments on the package and the Fusion SDK.

### Examples

```
# Scan current directory for CEL files
files <- list.files(pattern="(.)(c|C)(e|E)(l|L)$")
if (length(files) > 0) {
  header <- readCelHeader(files[1])
  print(header)
  rm(header)
}

# Clean up
rm(files)
```

---

readCellIntensities *Reads the intensities contained in several Affymetrix CEL files*

---

### Description

Reads the intensities of several Affymetrix CEL files (as opposed to `readCel()` which only reads a single file).

### Usage

```
readCellIntensities(filenamees, indices = NULL, ..., verbose = 0)
```

### Arguments

filenamees      the names of the CEL files as a character vector.  
 indices        a vector of which indices should be read. If the argument is NULL all features will be returned.  
 ...            Additional arguments passed to `readCel()`.  
 verbose        an integer: how verbose do we want to be, higher means more verbose.

**Details**

The function will initially allocate a matrix with the same memory footprint as the final object.

**Value**

A matrix with a number of rows equal to the length of the `indices` argument (or the number of features on the entire chip), and a number of columns equal to the number of files. The columns are ordered according to the `filenames` argument.

**Note**

Currently this function builds on `readCel()`, and simply calls this function multiple times. If testing yields sufficient reasons for doing so, it may be re-implemented in C++.

**Author(s)**

James Bullard, [⟨bullard@stat.berkeley.edu⟩](mailto:bullard@stat.berkeley.edu) and Kasper Daniel Hansen, [⟨khansen@stat.berkeley.edu⟩](mailto:khansen@stat.berkeley.edu)

**See Also**

[readCel\(\)](#) for a discussion of a more versatile function, particular with details of the `indices` argument.

**Examples**

```
# Scan current directory for CEL files
files <- list.files(pattern=".[.] (c|C) (e|E) (l|L) $")
if (length(files) >= 2) {
  cel <- readCelIntensities(files[1:2])
  str(cel)
  rm(cel)
}

# Clean up
rm(files)
```

---

readCel

*Reads an Affymetrix CEL file*

---

**Description**

This function reads all or a subset of the data in an Affymetrix CEL file.

**Usage**

```
readCel(filename,
         indices = NULL,
         readHeader = TRUE,
         readXY = FALSE, readIntensities = TRUE,
         readStdvs = FALSE, readPixels = FALSE,
         readOutliers = TRUE, readMasked = TRUE,
         readMap = NULL,
         verbose = 0,
         .checkArgs = TRUE)
```

**Arguments**

filename	the name of the CEL file.
indices	a vector of indices indicating which features to read. If the argument is NULL all features will be returned.
readXY	a logical: will the (x,y) coordinates be returned.
readIntensities	a logical: will the intensities be returned.
readStdvs	a logical: will the standard deviations be returned.
readPixels	a logical: will the number of pixels be returned.
readOutliers	a logical: will the outliers be return.
readMasked	a logical: will the masked features be returned.
readHeader	a logical: will the header of the file be returned.
readMap	A <a href="#">vector</a> remapping cell indices to file indices. If NULL, no mapping is used.
verbose	how verbose do we want to be. 0 is no verbosity, higher numbers mean more verbose output. At the moment the values 0, 1 and 2 are supported.
.checkArgs	If TRUE, the arguments will be validated, otherwise not. <i>Warning: This should only be used if the arguments have been validated elsewhere!</i>

**Value**

A CEL files consists of a *header*, a set of *cell values*, and information about *outliers* and masked cells.

The cell values, which are values extract for each cell (aka feature or probe), are the (x,y) coordinate, intensity and standard deviation estimates, and the number of pixels in the cell. If `readIndices=NULL`, cell values for all cells are returned, Only cell values specified by argument `readIndices` are returned.

This value returns a named list with components described below:

<code>this-is-escaped-codenormal-bracket44bracket-normal</code>	The header of the CEL file. Equivalent to the output from <code>readCelHeader</code> , see the documentation for that function.
<code>x, y</code>	(cell values) Two integer vectors containing the x and y coordinates associated with each feature.
<code>this-is-escaped-codenormal-bracket51bracket-normal</code>	(cell value) A numeric vector containing the intensity associated with each feature.
<code>stdvs</code>	(cell value) A numeric vector containing the standard deviation associated with each feature.
<code>pixels</code>	(cell value) An integer vector containing the number of pixels associated with each feature.
<code>outliers</code>	An integer vector of indices specifying which of the queried cells that are flagged as outliers. Note that there is a difference between <code>outliers=NULL</code> and <code>outliers=integer(0)</code> ; the last case happens when <code>readOutliers=TRUE</code> but there are no outliers.
<code>masked</code>	An integer vector of indices specifying which of the queried cells that are flagged as masked. Note that there is a difference between <code>masked=NULL</code> and <code>masked=integer(0)</code> ; the last case happens when <code>readMasked=TRUE</code> but there are no masked features.

The elements of the cell values are ordered according to argument `indices`. The lengths of the cell-value elements equals the number of cells read.

Which of the above elements that are returned are controlled by the `readNnn` arguments. If `FALSE`, the corresponding element above is `NULL`, e.g. if `readStdvs=FALSE` then `stdvs` is `NULL`.

### Outliers and masked cells

The Affymetrix image analysis software flags cells as outliers and masked. This method does not return these flags, but instead vectors of cell indices listing which cells *of the queried cells* are outliers and masked, respectively. The current community view seems to be that this should be done based on statistical modelling of the actual probe intensities and should be based on the choice of preprocessing algorithm. Most algorithms are only using the intensities from the CEL file.

### Memory usage

The Fusion SDK allocates memory for the entire CEL file, when the file is accessed (but does not actually read the file into memory). Using the `indices` argument will therefore only affect the memory use of the final object (as well as speed), not the memory allocated in the C function used to parse the file. This should be a minor problem however.

### Troubleshooting

It is considered a bug if the file contains information not accessible by this function, please report it.

### Author(s)

James Bullard, <bullard@stat.berkeley.edu> and Kasper Daniel Hansen, <khansen@stat.berkeley.edu>

### See Also

`readCelHeader()` for a description of the header output. Often a user only wants to read the intensities, look at `readCelIntensities()` for a function specialized for that use.

### Examples

```
for (zzz in 0) { # Only so that 'break' can be used

# Scan current directory for CEL files
celFiles <- list.files(pattern=".(c|C)(e|E)(l|L)$")
if (length(celFiles) == 0)
  break;

celFile <- celFiles[1]

# Read a subset of cells
idxs <- c(1:5, 1250:1500, 450:440)
cel <- readCel(celFile, indices=idxs, readOutliers=TRUE)
str(cel)

# Clean up
rm(celFiles, celFile, cel)

} # for (zzz in 0)
```

---

readCelRectangle     *Reads a spatial subset of probe-level data from Affymetrix CEL files*

---

### Description

Reads a spatial subset of probe-level data from Affymetrix CEL files.

### Usage

```
readCelRectangle(filename, xrange=c(0, Inf), yrange=c(0, Inf), ..., asMatrix=TRUE)
```

### Arguments

filename	The pathname of the CEL file.
xrange	A <a href="#">numeric vector</a> of length two giving the left and right coordinates of the cells to be returned.
yrange	A <a href="#">numeric vector</a> of length two giving the top and bottom coordinates of the cells to be returned.
...	Additional arguments passed to <a href="#">readCel()</a> .
asMatrix	If <a href="#">TRUE</a> , the CEL data fields are returned as matrices with element (1,1) corresponding to cell (xrange[1],yrange[1]).

### Value

A named [list](#) CEL structure similar to what [readCel\(\)](#). In addition, if `asMatrix` is [TRUE](#), the CEL data fields are returned as matrices, otherwise not.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### See Also

The [readCel\(\)](#) method is used internally.

### Examples

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

rotate270 <- function(x, ...) {
  x <- t(x)
  nc <- ncol(x)
  if (nc < 2) return(x)
  x[,nc:1,drop=FALSE]
}

# Search for some available CEL files
path <- system.file("rawData", package="AffymetrixDataTestFiles")
file <- findFiles(pattern="[(.]|cel|CEL)$", path=path, recursive=TRUE)
```

```

# Read CEL intensities in the upper left corner
cel <- readCelRectangle(file, xrange=c(0,250), yrange=c(0,250))
z <- rotate270(cel$intensities)
sub <- paste("Chip type:", cel$header$chiptype)
image(z, col=gray.colors(256), axes=FALSE, main=basename(file), sub=sub)
text(x=0, y=1, labels="(0,0)", adj=c(0,-0.7), cex=0.8, xpd=TRUE)
text(x=1, y=0, labels="(250,250)", adj=c(1,1.2), cex=0.8, xpd=TRUE)

# Clean up
rm(rotate270, files, file, cel, z, sub)

#####
} # STOP #
#####

```

---

readCelUnits	<i>Reads probe-level data ordered as units (probesets) from one or several Affymetrix CEL files</i>
--------------	---

---

## Description

Reads probe-level data ordered as units (probesets) from one or several Affymetrix CEL files by using the unit and group definitions in the corresponding Affymetrix CDF file.

## Usage

```
readCelUnits(filenamees, units=NULL, stratifyBy=c("nothing", "pmmm", "pm", "mm"),
```

## Arguments

filenamees	The filenamees of the CEL files.
units	An <a href="#">integer vector</a> of unit indices specifying which units to be read. If <a href="#">NULL</a> , all units are read.
stratifyBy	Argument passed to low-level method <a href="#">readCdfUnits</a> .
cdf	A <a href="#">character</a> filename of a CDF file, or a CDF <a href="#">list</a> structure. If <a href="#">NULL</a> , the CDF file is searched for by <a href="#">findCdf()</a> first starting from the current directory and then from the directory where the first CEL file is.
...	Arguments passed to low-level method <a href="#">readCel</a> , e.g. <a href="#">readXY</a> and <a href="#">readStdvs</a> .
addDimnames	If <a href="#">TRUE</a> , dimension names are added to arrays, otherwise not. The size of the returned CEL structure in bytes increases by 30-40% with dimension names.
dropArrayDim	If <a href="#">TRUE</a> and only one array is read, the elements of the group field do <i>not</i> have an array dimension.
transforms	A <a href="#">list</a> of exactly <code>length(filenamees)</code> <a href="#">functions</a> . If <a href="#">NULL</a> , no transformation is performed. Intensities read are passed through the corresponding transform function before being returned.
readMap	A <a href="#">vector</a> remapping cell indices to file indices. If <a href="#">NULL</a> , no mapping is used.

`verbose` Either a `logical`, a `numeric`, or a `Verbose` object specifying how much verbose/debug information is written to standard output. If a `Verbose` object, how detailed the information is specified by the threshold level of the object. If a `numeric`, the value is used to set the threshold of a new `Verbose` object. If `TRUE`, the threshold is set to -1 (minimal). If `FALSE`, no output is written (and neither is the `R.utils` package required).

### Value

A named `list` with one element for each unit read. The names corresponds to the names of the units read. Each unit element is in turn a `list` structure with groups (aka blocks). Each group contains requested fields, e.g. `intensities`, `stdvs`, and `pixels`. If more than one CEL file is read, an extra dimension is added to each of the fields corresponding, which can be used to subset by CEL file.

Note that neither CEL headers nor information about outliers and masked cells are returned. To access these, use `readCelHeader()` and `readCel()`.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### References

[1] Affymetrix Inc, Affymetrix GCOS 1.x compatible file formats, June 14, 2005. <http://www.affymetrix.com/support/developer/>

### See Also

Internally, `readCelHeader()`, `readCdfUnits()` and `readCel()` are used.

### Examples

```
#####
if (require("AffymetrixDataTestFiles")) {           # START #
#####

# Search for some available CEL files
path <- system.file("rawData", package="AffymetrixDataTestFiles")
files <- findFiles(pattern=".(cel|CEL)$", path=path, recursive=TRUE, firstOnly=FALSE)
files <- grep("FusionSDK_Test3", files, value=TRUE)
files <- grep("Calvin", files, value=TRUE)

# Fake more CEL files if not enough
files <- rep(files, length.out=5)
print(files);
rm(files);

#####
}           # STOP #
#####
```



---

readChp	<i>A function to read Affymetrix CHP files</i>
---------	--

---

### Description

This function will parse any type of CHP file and return the results in a list. The contents of the list will depend on the type of CHP file that is parsed and readers are referred to Affymetrix documentation of what should be there, and how to interpret it.

### Usage

```
readChp(filename, withQuant = TRUE)
```

### Arguments

filename	The name of the CHP file to read.
withQuant	A boolean value, currently largely unused.

### Details

This is an interface to the Affymetrix Fusion SDK. The Affymetrix documentation should be consulted for explicit details.

### Value

A list is returned. The contents of the list depend on the type of CHP file that was read. Users may want to translate the different outputs into specific containers.

### Troubleshooting

It is considered a bug if the file contains information not accessible by this function, please report it.

### Author(s)

R. Gentleman

### See Also

[readCel](#)

### Examples

```
if (require("AffymetrixDataTestFiles")) {
  path <- system.file("rawData", package="AffymetrixDataTestFiles")
  files <- findFiles(pattern=".(chp|CHP)$", path=path,
                    recursive=TRUE, firstOnly=FALSE)

  s1 = readChp(files[1])
  length(s1)
  names(s1)
  names(s1[[7]])
}
```

---

`readClfEnv`*Parsing a CLF file using Affymetrix Fusion SDK*

---

### Description

This function parses a CLF file using the Affymetrix Fusion SDK. CLF (chip layout) files contain information associating probe ids with chip x- and y- coordinates.

### Usage

```
readClfEnv(file, readBody = TRUE)
```

### Arguments

<code>file</code>	character(1) providing a path to the CLF file to be input.
<code>readBody</code>	logical(1) indicating whether the entire file should be parsed (TRUE) or only the file header information describing the chips to which the file is relevant.

### Value

An environment. The header element is always present; the remainder are present when `readBody=TRUE`.

<code>header</code>	A list with information about the CLF file. The list contains elements described in the CLF file format document referenced below.
<code>dims</code>	A length-two integer vector of chip x- and y-coordinates.
<code>id</code>	An integer vector of length <code>prod(dims)</code> containing probe identifiers.
<code>x</code>	An integer vector of length <code>prod(dims)</code> containing x-coordinates corresponding to the entries in <code>id</code> .
<code>y</code>	An integer vector of length <code>prod(dims)</code> containing y-coordinates corresponding to the entries in <code>id</code> .

### Author(s)

Martin Morgan [mtmorgan@fhcrc.org](mailto:mtmorgan@fhcrc.org)

### See Also

[https://www.affymetrix.com/support/developer/fusion/File\\_Format\\_CLF\\_aptv161.pdf](https://www.affymetrix.com/support/developer/fusion/File_Format_CLF_aptv161.pdf) describes CLF file content.

---

readClfHeader	<i>Read the header of a CLF file.</i>
---------------	---------------------------------------

---

**Description**

Reads the header of a CLF file. The exact information stored in this file can be viewed in the readClfEnv documentation which reads the header in addition to the body.

**Usage**

```
readClfHeader(file)
```

**Arguments**

file	file a CLF file
------	-----------------

**Value**

A list of header elements.

---

readClf	<i>Parsing a CLF file using Affymetrix Fusion SDK</i>
---------	---

---

**Description**

This function parses a CLF file using the Affymetrix Fusion SDK. CLF (chip layout) files contain information associating probe ids with chip x- and y- coordinates.

**Usage**

```
readClf(file)
```

**Arguments**

file	character(1) providing a path to the CLF file to be input.
------	--

**Value**

An list. The header element is always present.

header	A list with information about the CLF file. The list contains elements described in the CLF file format document referenced below.
dims	A length-two integer vector of chip x- and y-coordinates.
id	An integer vector of length <code>prod(dims)</code> containing probe identifiers.
x	An integer vector of length <code>prod(dims)</code> containing x-coordinates corresponding to the entries in <code>id</code> .
y	An integer vector of length <code>prod(dims)</code> containing y-coordinates corresponding to the entries in <code>id</code> .

**Author(s)**

Martin Morgan [mtmorgan@fhcrc.org](mailto:mtmorgan@fhcrc.org)

**See Also**

[https://www.affymetrix.com/support/developer/fusion/File\\_Format\\_CLF\\_aptv161.pdf](https://www.affymetrix.com/support/developer/fusion/File_Format_CLF_aptv161.pdf) describes CLF file content.

---

readPgfEnv

*Parsing a PGF file using Affymetrix Fusion SDK*

---

**Description**

This function parses a PGF file using the Affymetrix Fusion SDK. PGF (probe group) files describe probes present within probe sets, including the type (e.g., pm, mm) of the probe and probeset.

**Usage**

```
readPgfEnv(file, readBody = TRUE, indices = NULL)
```

**Arguments**

<code>file</code>	character(1) providing a path to the PGF file to be input.
<code>readBody</code>	logical(1) indicating whether the entire file should be parsed (TRUE) or only the file header information describing the chips to which the file is relevant.
<code>indices</code>	integer(n) vector of positive integers indicating which probesets to read. These integers must be sorted (increasing) and unique.

**Value**

An environment. The `header` element is always present; the remainder are present when `readBody=TRUE`.

The elements present when `readBody=TRUE` describe probe sets, atoms, and probes. Elements within probe sets, for instance, are coordinated such that the `i`th index of one vector (e.g., `probesetId`) corresponds to the `i`th index of a second vector (e.g., `probesetType`). The atoms contained within probeset `i` are in positions `probesetStartAtom[i] : (probesetStartAtom[i+1] - 1)` of the atom vectors. A similar map applies to probes within atoms, using `atomStartProbe` as the index.

The PGF file format includes optional elements; these elements are always present in the environment, but with appropriate default values.

<code>header</code>	A list with information about the PGF file. The list contains elements described in the PGF file format document referenced below.
<code>probesetId</code>	integer vector of probeset identifiers.
<code>probesetType</code>	character vector of probeset types. Types are described in the PGF file format document.
<code>probesetName</code>	character vector of probeset names.

probesetStartAtom	integer vector of the start index (e.g., in the element <code>atomId</code> of atoms belonging to this probeset).
atomId	integer vector of atom identifiers.
atomExonPosition	integer vector of probe interrogation position relative to the target sequence.
atomStartProbe	integer vector of the start index (e.g., in the element <code>probeId</code> of probes belonging to this atom).
probeId	integer vector of probe identifiers.
probeType	character vector of probe types. Types are described in the PGF file format document.
probeGcCount	integer vector of probe GC content.
probeLength	integer vector of probe lengths.
probeInterrogationPosition	integer vector of the position, within the probe, at which interrogation occurs.
probeSequence	character vector of the probe sequence.

**Author(s)**

Martin Morgan [mtmorgan@fhcrc.org](mailto:mtmorgan@fhcrc.org)

**See Also**

[https://www.affymetrix.com/support/developer/fusion/File\\_Format\\_PGF\\_aptv161.pdf](https://www.affymetrix.com/support/developer/fusion/File_Format_PGF_aptv161.pdf) describes PGF file content.

The internal function `.pgfProbeIndexFromProbesetIndex` provides a map between the indices of probe set entries and the indices of the probes contained in the probe set.

---

readPgfHeader	<i>Read the header of a PGF file into a list.</i>
---------------	---

---

**Description**

This function reads the header of a PGF file into a list more details on what the exact fields are can be found in the details section.

**Usage**

```
readPgfHeader(file)
```

**Arguments**

file            file:A file in PGF format

**Details**

[https://www.affymetrix.com/support/developer/fusion/File\\_Format\\_PGF\\_aptv161.pdf](https://www.affymetrix.com/support/developer/fusion/File_Format_PGF_aptv161.pdf)

**Value**

A list corresponding to the elements in the header.

---

 readPgf

*Parsing a PGF file using Affymetrix Fusion SDK*


---

**Description**

This function parses a PGF file using the Affymetrix Fusion SDK. PGF (probe group) files describe probes present within probe sets, including the type (e.g., pm, mm) of the probe and probeset.

**Usage**

```
readPgf(file, indices = NULL)
```

**Arguments**

`file` character (1) providing a path to the PGF file to be input.  
`indices` integer (n) a vector of indices of the probesets to be read.

**Value**

An list. The `header` element is always present; the remainder are present when `readBody=TRUE`.

The elements present when `readBody=TRUE` describe probe sets, atoms, and probes. Elements within probe sets, for instance, are coordinated such that the `i`th index of one vector (e.g., `probesetId`) corresponds to the `i`th index of a second vector (e.g., `probesetType`). The atoms contained within probeset `i` are in positions `probesetStartAtom[i] : (probesetStartAtom[i+1] - 1)` of the atom vectors. A similar map applies to probes within atoms, using `atomStartProbe` as the index.

The PGF file format includes optional elements; these elements are always present in the list, but with appropriate default values.

`header` A list with information about the PGF file. The list contains elements described in the PGF file format document referenced below.

`probesetId` integer vector of probeset identifiers.

`probesetType` character vector of probeset types. Types are described in the PGF file format document.

`probesetName` character vector of probeset names.

`probesetStartAtom` integer vector of the start index (e.g., in the element `atomId` of atoms belonging to this probeset).

`atomId` integer vector of atom identifiers.

`atomExonPosition` integer vector of probe interrogation position relative to the target sequence.

`atomStartProbe` integer vector of the start index (e.g., in the element `probeId` of probes belonging to this atom).

`probeId` integer vector of probe identifiers.

probeType	character vector of probe types. Types are described in the PGF file format document.
probeGcCount	integer vector of probe GC content.
probeLength	integer vector of probe lengths.
probeInterrogationPosition	integer vector of the position, within the probe, at which interrogation occurs.
probeSequence	character vector of the probe sequence.

**Author(s)**

Martin Morgan [mtmorgan@fhcrc.org](mailto:mtmorgan@fhcrc.org)

**See Also**

[https://www.affymetrix.com/support/developer/fusion/File\\_Format\\_PGF\\_aptv161.pdf](https://www.affymetrix.com/support/developer/fusion/File_Format_PGF_aptv161.pdf) describes PGF file content.

The internal function `.pgfProbeIndexFromProbesetIndex` provides a map between the indices of probe set entries and the indices of the probes contained in the probe set.

---

updateCel	<i>Updates a CEL file</i>
-----------	---------------------------

---

**Description**

Updates a CEL file.

**Usage**

```
updateCel(filename, indices=NULL, intensities=NULL, stdvs=NULL, pixels=NULL, writeMap=NULL, verbose=0)
```

**Arguments**

filename	The filename of the CEL file.
indices	A <a href="#">numeric vector</a> of cell (probe) indices specifying which cells to updated. If <code>NULL</code> , all indices are considered.
intensities	A <a href="#">numeric vector</a> of intensity values to be stored. Alternatively, it can also be a named <a href="#">data.frame</a> or <a href="#">matrix</a> (or <a href="#">list</a> ) where the named columns (elements) are the fields to be updated.
stdvs	A optional <a href="#">numeric vector</a> .
pixels	A optional <a href="#">numeric vector</a> .
writeMap	An optional write map.
...	Not used.
verbose	An <a href="#">integer</a> specifying how much verbose details are outputted.

**Details**

Currently only binary (v4) CEL files are supported. The current version of the method does not make use of the Fusion SDK, but its own code to navigate and update the CEL file.

**Value**

Returns (invisibly) the pathname of the file updated.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

# Search for some available Calvin CEL files
path <- system.file("rawData", package="AffymetrixDataTestFiles")
files <- findFiles(pattern=".(cel|CEL)$", path=path, recursive=TRUE, firstOnly=FALSE)
files <- grep("FusionSDK_HG-U133A", files, value=TRUE)
files <- grep("Calvin", files, value=TRUE)
file <- files[1]

# Convert to an XDA CEL file
filename <- file.path(tempdir(), basename(file))
if (file.exists(filename))
  file.remove(filename)
convertCel(file, filename)

fields <- c("intensities", "stdvs", "pixels")

# Cells to be updated
idxs <- 1:2

# Get CEL header
hdr <- readCelHeader(filename)

# Get the original data
cel <- readCel(filename, indices=idxs, readStdvs=TRUE, readPixels=TRUE)
print(cel[fields])
cel0 <- cel

# - - - - -
# Square-root the intensities
# - - - - -
updateCel(filename, indices=idxs, intensities=sqrt(cel$intensities))
cel <- readCel(filename, indices=idxs, readStdvs=TRUE, readPixels=TRUE)
print(cel[fields])

# - - - - -
# Update a few cell values by a data frame
# - - - - -
data <- data.frame(
  intensities=cel0$intensities,
  stdvs=c(201.1, 3086.1)+0.5,
  pixels=c(9,9+1)
)
updateCel(filename, indices=idxs, data)
```



```

# Assert correctness of update
cel <- readCel(filename, indices=idxs, readStdvts=TRUE, readPixels=TRUE)
print(cel[fields])
for (ff in fields) {
# stopifnot(all.equal(cel[[ff]], data[[ff]], .Machine$double.eps^0.25))
}

# -----
# Update a region of the CEL file
# -----
# Load pre-defined data
side <- 306
pathname <- system.file("extras/easternEgg.gz", package="affxparser")
con <- gzfile(pathname, open="rb")
z <- readBin(con=con, what="integer", size=1, signed=FALSE, n=side^2)
close(con)
z <- matrix(z, nrow=side)
side <- min(hdr$cols - 2*22, side)
z <- as.double(z[1:side,1:side])
x <- matrix(22+0:(side-1), nrow=side, ncol=side, byrow=TRUE)
idxs <- as.vector((1 + x) + hdr$cols*t(x))
# Load current data in the same region
z0 <- readCel(filename, indices=idxs)$intensities
# Mix the two data sets
z <- (0.3*z^2 + 0.7*z0)
# Update the CEL file
updateCel(filename, indices=idxs, intensities=z)

# Make some spatial changes
rotate270 <- function(x, ...) {
  x <- t(x)
  nc <- ncol(x)
  if (nc < 2) return(x)
  x[,nc:1,drop=FALSE]
}

# Display a spatial image of the updated CEL file
cel <- readCelRectangle(filename, xrange=c(0,350), yrange=c(0,350))
z <- rotate270(cel$intensities)
sub <- paste("Chip type:", cel$header$chiptype)
image(z, col=gray.colors(256), axes=FALSE, main=basename(filename), sub=sub)
text(x=0, y=1, labels="(0,0)", adj=c(0,-0.7), cex=0.8, xpd=TRUE)
text(x=1, y=0, labels="(350,350)", adj=c(1,1.2), cex=0.8, xpd=TRUE)

# Clean up
file.remove(filename)
rm(files, cel, cel0, idxs, data, ff, fields, rotate270)

#####
# STOP #
#####

```

**Description**

Updates a CEL file unit by unit.

*Please note that, contrary to `readCelUnits()`, this method can only update a single CEL file at the time.*

**Usage**

```
updateCelUnits(filename, cdf=NULL, data, ..., verbose=0)
```

**Arguments**

filename	The filename of the CEL file.
cdf	A (optional) CDF <code>list</code> structure either with field <code>indices</code> or fields <code>x</code> and <code>y</code> . If <code>NULL</code> , the unit names (and from there the cell indices) are inferred from the names of the elements in <code>data</code> .
data	A <code>list</code> structure in a format similar to what is returned by <code>readCelUnits()</code> for a single CEL file only.
...	Optional arguments passed to <code>readCdfCellIndices()</code> , which is called if <code>cdf</code> is not given.
verbose	An <code>integer</code> specifying how much verbose details are outputted.

**Value**

Returns what `updateCel()` returns.

**Working with re-arranged CDF structures**

Note that if the `cdf` structure is specified the CDF file is *not* queried, but all information about cell `x` and `y` locations, that is, cell indices is expected to be in this structure. This can be very useful when one work with a `cdf` structure that originates from the underlying CDF file, but has been restructured for instance through the `applyCdfGroups()` method, and `data` correspondingly. This update method knows how to update such structures too.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

Internally, `updateCel()` is used.

**Examples**

```
#####
if (require("AffymetrixDataTestFiles")) { # START #
#####

# Search for some available Calvin CEL files
path <- system.file("rawData", package="AffymetrixDataTestFiles")
files <- findFiles(pattern=".(cel|CEL)$", path=path, recursive=TRUE, firstOnly=FALSE)
files <- grep("FusionSDK_Test3", files, value=TRUE)
files <- grep("Calvin", files, value=TRUE)
```

```

file <- files[1]

# Convert to an XDA CEL file
pathname <- file.path(tempdir(), basename(file))
if (file.exists(pathname))
  file.remove(pathname)
convertCel(file, pathname)

# Check for the CDF file
hdr <- readCelHeader(pathname)
cdfFile <- findCdf(hdr$chiptype)

hdr <- readCdfHeader(cdfFile)
nbrOfUnits <- hdr$nunits
print(nbrOfUnits);

# -----
# Example: Read and re-write the same data
# -----
units <- c(101, 51)
data1 <- readCelUnits(pathname, units=units, readStdvs=TRUE)
cat("Original data:\n")
str(data1)
updateCelUnits(pathname, data=data1)
data2 <- readCelUnits(pathname, units=units, readStdvs=TRUE)
cat("Updated data:\n")
str(data2)
stopifnot(identical(data1, data2))

# -----
# Example: Random read and re-write "stress test"
# -----
for (kk in 1:10) {
  nunits <- sample(min(1000,nbrOfUnits), size=1)
  units <- sample(nbrOfUnits, size=nunits)
  cat(sprintf("%02d. Selected %d random units: reading", kk, nunits));
  t <- system.time({
    data1 <- readCelUnits(pathname, units=units, readStdvs=TRUE)
  }, gcFirst=TRUE)[3]
  cat(sprintf(" [%.2fs=%.2fs/unit], updating", t, t/nunits))
  t <- system.time({
    updateCelUnits(pathname, data=data1)
  }, gcFirst=TRUE)[3]
  cat(sprintf(" [%.2fs=%.2fs/unit], validating", t, t/nunits))
  data2 <- readCelUnits(pathname, units=units, readStdvs=TRUE)
  stopifnot(identical(data1, data2))
  cat(". done\n")
}

#####
} # STOP #
#####

```

---

`writeCdfHeader`      *Writes a CDF header*

---

### Description

Writes a CDF header. *This method is not intended to be used explicitly. To write a CDF, use `writeCdf()` instead.*

### Usage

```
writeCdfHeader(con, cdfHeader, unitNames, qcUnitLengths, unitLengths, verbose=0)
```

### Arguments

`con`                    An open [connection](#) to which nothing has been written.

`cdfHeader`            A CDF header [list](#) structure.

`unitNames`            A [character vector](#) of all unit names.

`qcUnitLengths`        An [integer vector](#) of all the number of bytes in each of the QC units.

`unitLengths`          An [integer vector](#) of all the number of bytes in each of the (ordinary) units.

`verbose`              An [integer](#) specifying how much verbose details are outputted.

### Value

Returns nothing.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

### See Also

This method is called by `writeCdf()`. See also `writeCdfQcUnits()` and `writeCdfUnits()`.

---

`writeCdfQcUnits`      *Writes CDF QC units*

---

### Description

Writes CDF QC units. *This method is not intended to be used explicitly. To write a CDF, use `writeCdf()` instead.*

### Usage

```
writeCdfQcUnits(con, cdfQcUnits, verbose=0)
```

**Arguments**

con	An open <a href="#">connection</a> to which a CDF header already has been written by <a href="#">writeCdfHeader()</a> .
cdfQcUnits	A <a href="#">list</a> structure of CDF QC units as returned by <a href="#">readCdf()</a> ( <i>not</i> <a href="#">readCdfUnits()</a> ).
verbose	An <a href="#">integer</a> specifying how much verbose details are outputted.

**Value**

Returns nothing.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

This method is called by [writeCdf\(\)](#). See also [writeCdfHeader\(\)](#) and [writeCdfUnits\(\)](#).

---

writeCdf	<i>Creates a binary CDF file</i>
----------	----------------------------------

---

**Description**

This function creates a binary CDF file given a valid CDF structure containing all necessary elements.

*Warning: The API for this function is likely to be changed in future versions.*

**Usage**

```
writeCdf(fname, cdfheader, cdf, cdfqc, overwrite=FALSE, verbose=0)
```

**Arguments**

fname	name of the CDF file.
cdfheader	A list with a structure equal to the output of <a href="#">readCdfHeader</a> .
cdf	A list with a structure equal to the output of <a href="#">readCdf</a> .
cdfqc	A list with a structure equal to the output of <a href="#">readCdfQc</a> .
overwrite	Overwrite existing file?
verbose	how verbose should the output be. 0 means no output, with higher numbers being more verbose.

**Details**

This function has been validated mainly by reading in various ASCII or binary CDF files which are written back as new CDF files, and compared element by element with the original files.

**Value**

This function is used for its byproduct: creating a CDF file.

**Author(s)**

Kasper Daniel Hansen, (khansen@stat.berkeley.edu)

**See Also**

To read the CDF "regular" and QC units with all necessary fields and values for writing a CDF file, see [readCdf](#), [readCdfQc\(\)](#) and [readCdfHeader](#). To compare two CDF files, see [compareCdfs](#).

---

writeCdfUnits	<i>Writes CDF units</i>
---------------	-------------------------

---

**Description**

Writes CDF units. *This method is not intended to be used explicitly. To write a CDF, use [writeCdf\(\)](#) instead.*

**Usage**

```
writeCdfUnits(con, cdfUnits, verbose=0)
```

**Arguments**

con	An open <a href="#">connection</a> to which a CDF header and QC units already have been written by <a href="#">writeCdfHeader()</a> and <a href="#">writeCdfQcUnits()</a> , respectively.
cdfUnits	A <a href="#">list</a> structure of CDF units as returned by <a href="#">readCdf()</a> ( <i>not</i> <a href="#">readCdfUnits()</a> ).
verbose	An <a href="#">integer</a> specifying how much verbose details are outputted.

**Value**

Returns nothing.

**Author(s)**

Henrik Bengtsson (<http://www.braju.com/R/>)

**See Also**

This method is called by [writeCdf\(\)](#). See also [writeCdfHeader\(\)](#) and [writeCdfQcUnits\(\)](#).

---

writeCelHeader	<i>Writes a CEL header to a connection</i>
----------------	--

---

### Description

Writes a CEL header to a connection.

### Usage

```
writeCelHeader(con, header, outputVersion=c("4"), ...)
```

### Arguments

con	A <a href="#">connection</a> .
header	A <a href="#">list</a> structure describing the CEL header, similar to the structure returned by <a href="#">readCelHeader()</a> .
outputFormat	A <a href="#">character</a> string specifying the output format. Currently only CEL version 4 (binary;XDA) are supported.
...	Not used.

### Details

Currently only CEL version 4 (binary;XDA) headers can be written.

### Value

Returns (invisibly) the pathname of the file created.

### Redundant fields

The CEL v4 header contains redundant information. To avoid inconsistency this method generates such redundant values from the original values. This is consistent to how the CEL reader in Fusion SDK does it, cf. [readCelHeader\(\)](#). The redundant information is in the (CEL v3) header field, which contains the CEL header information as it would appear in the CEL v3 format. This in turn contains a DAT header field reproducing the DAT header from the image analysis. It is from this DAT header that the chip type is extracted.

### Author(s)

Henrik Bengtsson (<http://www.braju.com/R/>)

writeTpmmap

*Writes BPPMAP and TPMPAP files.*

---

**Description**

Writes BPPMAP and TPMPAP files.

**Usage**

```
writeTpmmap(filename, bppmaplist, verbose = 0)
```

```
tpmap2bppmap(tpmapname, bppmapname, verbose = 0)
```

**Arguments**

filename	The filename.
bppmaplist	A list structure similar to the result of readBppmap.
tpmapname	Filename of the TPMPAP file.
bppmapname	Filename of the BPPMAP file.
verbose	How verbose do we want to be.

**Details**

writeTpmmap writes a text probe map file, while tpmap2bppmap converts such a file to a binary probe mapping file. Somehow Affymetrix has different names for the same structure, depending on whether the file is binary or text. I have seen many TPMPAP files referred to as BPPMAP files.

**Value**

These functions are called for their side effects (creating files).

**Author(s)**

Kasper Daniel Hansen <khansen@stat.berkeley.edu>

**See Also**

[readBppmap](#)



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