

# Package ‘dChipIO’

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**Title** Methods for Reading dChip Files

**Depends** R (>= 2.6.0)

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**Description** Functions for reading DCP and CDF.bin files generated by the dChip software.

**License** LGPL (>= 2.1)

**URL** <https://github.com/HenrikBengtsson/dChipIO>

**BugReports** <https://github.com/HenrikBengtsson/dChipIO/issues>

**LazyLoad** TRUE

**biocViews** Infrastructure, DataImport

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dChipIO-package

*Package dChipIO*

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### Description

Functions for reading DCP and CDF.bin files generated by the dChip software.

The example data used in this package originates from the Affymetrix Fusion SDK library [3].

### To get started

To get started, see:

1. `readCdfBin()` - reads a dChip CDF.bin file.
2. `readDcp()` - reads a dChip DCP data file.

### License

The releases of this package is licensed under LGPL version 2.1 or newer.

### Author(s)

Henrik Bengtsson.

### References

- [1] The dChip software, <http://www.dchip.org/>
- [2] Thread 'DCP File Format', 'dChip Software', Google Groups, December 2008. <https://groups.google.com/forum/#!topic/dchip-software/Q7mTJPPpZ5U>
- [3] Affymetrix Inc, Fusion Software Developers Kit (SDK), 2008. [http://www.affymetrix.com/estore/partners\\_programs/programs/developer/fusion/index.affx?terms=no](http://www.affymetrix.com/estore/partners_programs/programs/developer/fusion/index.affx?terms=no)

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readCdfBin

*Reads a dChip CDF.bin file*

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### Description

Reads a dChip CDF.bin file.

Please note that this method is incomplete as it currently doesn't read all fields. It is only made available so that someone else can continue the development.

### Usage

```
readCdfBin(con, units=NULL, ...)
```

**Arguments**

con            A [connection](#) or a [character](#) filename.  
units         An [integer vector](#) specifying the units to be read. If [NULL](#), all units are read.  
...            Not used.

**Value**

Returns a [list](#) structure containing the file header and the unit data.

**Author(s)**

Henrik Bengtsson

**See Also**

To read only the CDF.bin file header, see [readCdfBinHeader\(\)](#).

**Examples**

```
path <- system.file("exData", package="dChipIO")
chipType <- "Test3"
filename <- sprintf("%s.CDF.bin", chipType)
pathname <- file.path(path, filename)

hdr <- readCdfBinHeader(pathname)
print(hdr)

data <- readCdfBin(pathname)
str(data)

# Read a subset of the units
units <- c(10:11, 15:20, 150:105, 2,2,2)
dataT <- readCdfBin(pathname, units=units)
str(dataT)

# Assert correctness
for (ff in c("unitNames", "numProbes", "CellPos")) {
  stopifnot(length(dataT[[ff]]) == length(units))
  stopifnot(identical(dataT[[ff]], data[[ff]][units]))
}
```

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readCdfBinHeader         *Reads the file header of a dChip CDF.bin file*

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**Description**

Reads the file header of a dChip CDF.bin file.

**Usage**

```
readCdfBinHeader(con, ...)
```

**Arguments**

con	A <a href="#">connection</a> or a <a href="#">character</a> filename.
...	Not used.

**Value**

Returns a [list](#) structure containing the file header.

**Author(s)**

Henrik Bengtsson

**See Also**

To read the CDF.bin file data, see [readCdfBin\(\)](#).

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readDcp	<i>Reads a dChip DCP file</i>
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**Description**

Reads a dChip DCP file.

**Usage**

```
readDcp(con, fields=c("rawIntensities", "normalizedIntensities", "calls", "thetas",
  "thetaStds", "excludes"), cells=NULL, units=NULL, .nbrOfUnits=NULL, ...)
```

**Arguments**

con	A <a href="#">connection</a> or a <a href="#">character</a> filename.
fields	A <a href="#">character vector</a> specifying the fields to be read.
cells	An <a href="#">integer vector</a> specifying the indices of the cell data to be read.
units	An <a href="#">integer vector</a> specifying the indices of the unit data to be read.
.nbrOfUnits	A <a href="#">integer</a> specifying the number of units available in the file. If <a href="#">NULL</a> , this is inferred from the file size and the file header. The dChip software itself instead uses the corresponding value in the CDF.bin file, but that file is specified by the user leaving room for errors.
...	Not used.

**Value**

Returns a [list](#) structure containing the file header and the requested data fields.

**Author(s)**

Henrik Bengtsson

**See Also**

To read only the DCP file header, see [readDcpHeader\(\)](#).

**Examples**

```
path <- system.file("exData", package="dChipIO")

filename <- "Test3-1-121502.dcp"
pathname <- file.path(path, filename)

hdr <- readDcpHeader(pathname)
print(hdr)

data <- readDcp(pathname)
str(data)

# Read a subset of the units
units <- c(10:11, 15:20, 150:105, 2,2,2)
dataT <- readDcp(pathname, units=units)
str(dataT)

# Assert correctness
for (ff in c("calls", "thetas", "thetaStds", "excludes")) {
  stopifnot(length(dataT[[ff]]) == length(units))
  stopifnot(identical(dataT[[ff]], data[[ff]][units]))
}
```

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readDcpHeader

*Reads the file header of a dChip DCP file*

---

**Description**

Reads the file header of a dChip DCP file.

**Usage**

```
readDcpHeader(con, ...)
```

**Arguments**

con            A [connection](#) or a [character](#) filename.  
...            Not used.

**Value**

Returns a [list](#) structure containing the file header.

**Author(s)**

Henrik Bengtsson

**See Also**

To read also the DCP file data, see [readDcp\(\)](#).

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readDcpRectangle	<i>Reads a spatial subset of probe-level data from a dChip DCP file</i>
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**Description**

Reads a spatial subset of probe-level data from a dChip DCP file.

**Usage**

```
readDcpRectangle(filename, fields=c("rawIntensities", "normalizedIntensities"),
  xrange=c(0, Inf), yrange=c(0, Inf), ..., asMatrix=TRUE)
```

**Arguments**

filename	The pathname of the DCP file.
fields	The cell fields to be read.
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.
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]).
...	Additional arguments passed to <a href="#">readDcp()</a> .

**Value**

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

**Author(s)**

Henrik Bengtsson

**See Also**

The [readDcp\(\)](#) method is used internally. This method was inspired by `readCelRectangle()` of the **affxparser** package.

**Examples**

```
path <- system.file("exData", package="dChipIO")

filename <- "Test3-1-121502.dcp"
pathname <- file.path(path, filename)

data <- readDcpRectangle(pathname)

layout(matrix(1:4, nrow=2, byrow=TRUE))
image(data$rawIntensities, main="Raw probe signals")
image(data$normalizedIntensities, main="Normalized probe signals")
```

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