

# Package ‘ncdfFlow’

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**Title** ncdfFlow: A package that provides HDF5 based storage for flow cytometry data.

**Version** 2.20.2

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**Description** Provides HDF5 storage based methods and functions for manipulation of flow cytometry data.

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**Depends** R (>= 2.14.0), flowCore(>= 1.37.15), RcppArmadillo, methods, BH

**Imports** Biobase,BiocGenerics,flowCore,flowViz,zlibbioc

**Suggests** testthat,parallel

**License** Artistic-2.0

**SystemRequirements** hdf5 (>= 1.8.0)

**biocViews** FlowCytometry

**LinkingTo** Rcpp,RcppArmadillo,BH

**RoxygenNote** 5.0.1

**NeedsCompilation** yes

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as.flowSet	<i>convert from a ncdfFlowSet to a flowSet</i>
------------	--

---

### Description

The main purpose of this API is to convert the archived data (stored in ncdfFlowSet) to flowSet when the speed is more concerned than memory efficiency. Although ncdfFlowSet is designed to minimize the disk-IO cost, so usually it is not necessary to do such coercion.

### Usage

```
as.flowSet(from, top)
```

### Arguments

from	a ncdfFlowSet
top	integer specifies a certain number of samples are evenly selected for the coercion. If this argument is missing, then coerce all the samples within the ncdfFlowSet. It is to be used with caution because it can incur the huge memory consumption given the flowSet is all-in-memory data structure.

### Examples

```
data(GvHD)
nc1 <- ncdfFlowSet(GvHD[1:4])
fs <- as.flowSet(nc1)
```

---

clone.ncdfFlowSet	<i>Clone a ncdfFlowSet</i>
-------------------	----------------------------

---

### Description

Create a new ncdfFlowSet object from an existing one

### Usage

```
clone.ncdfFlowSet(ncfs, ncdfFile = NULL, isEmpty = FALSE, isNew = TRUE,
  dim = 2, compress = 0)
```

**Arguments**

ncfs	A <a href="#">ncdfFlowSet</a> .
ncdfFile	A character scalar giving the output file name. By default, It is NULL and the function will generate a random file name, potentially adding the .cdf suffix unless a file extension is already present. It is only valid when isNewNcFile=TRUE
isEmpty	A logical scalar indicating whether the raw data should also be copied. If FALSE, an empty cdf file is created with the same dimensions (sample*events*channels) as the original one.
isNew	A logical scalar indicating whether the new cdf file should be created. If FALSE, the original cdf file is associated with the new ncdfFlowSet object.
dim	integer see details in <a href="#">read.ncdfFlowset</a> .
compress	integer see details in <a href="#">read.ncdfFlowset</a> .

**Value**

A ncdfFlowSet object

**See Also**

[read.ncdfFlowSet](#)

**Examples**

```
path<-system.file("extdata","compdata","data",package="flowCore")
files<-list.files(path,full.names=TRUE)[1:3]

#create ncdfFlowSet from fcs
nc1 <- read.ncdfFlowSet(files=files,ncdfFile="ncfsTest.nc",flowSetId="fs1",isWriteSlice= TRUE)

##clone the ncdfFlowSet object
nc2<-clone.ncdfFlowSet(nc1,"clone.nc")
nc2[[1]]

#optionally create the empty hdf file without writing the actual flow data into it
nc2 <- clone.ncdfFlowSet(nc1,"clone.nc", isEmpty = TRUE)

#add the actual raw data
fs1 <- read.flowSet(files=files)
nc2[[sampleNames(fs1)[1]]] <- fs1[[1]]
nc2[[1]]

#delete the cdf file associated with ncdfFlowSet before removing it from memory
unlink(nc2)
rm(nc2)

unlink(nc1)
rm(nc1)
```

---

densityplot, formula, ncdfFlowSet-method  
*flowViz plot methods.*

---

### Description

flowViz plot methods.

### Usage

```
## S4 method for signature 'formula,ncdfFlowSet'
densityplot(x, data, ...)

## S4 method for signature 'formula,ncdfFlowList'
densityplot(x, data, ...)

## S4 method for signature 'formula,ncdfFlowSet'
histogram(x, data, ...)

## S4 method for signature 'formula,ncdfFlowList'
histogram(x, data, ...)

## S4 method for signature 'formula,ncdfFlowSet'
xyplot(x, data, ...)

## S4 method for signature 'formula,ncdfFlowList'
xyplot(x, data, ...)
```

### Arguments

x	formula
data	ncdfFlowSet or ncdfFlowList
...	other arguments passed to flowViz

---

filter,ncdfFlowList,filter-method  
*Accessors compatible with those for flowSet*

---

### Description

Accessors compatible with those for flowSet

### Usage

```
## S4 method for signature 'ncdfFlowList,filter'
filter(x, filter, method = "missing",
       sides = "missing", circular = "missing", init = "missing")
```

```
## S4 method for signature 'ncdfFlowList,filterList'  
filter(x, filter, method = "missing",  
       sides = "missing", circular = "missing", init = "missing")  
  
## S4 method for signature 'ncdfFlowList,list'  
filter(x, filter, method = "missing",  
       sides = "missing", circular = "missing", init = "missing")  
  
## S4 method for signature 'ncdfFlowList'  
length(x)  
  
## S4 method for signature 'ncdfFlowList'  
sampleNames(object)  
  
## S4 method for signature 'ncdfFlowList'  
phenoData(object)  
  
## S4 method for signature 'ncdfFlowList'  
pData(object)  
  
## S4 replacement method for signature 'ncdfFlowList,data.frame'  
pData(object) <- value  
  
## S4 method for signature 'ncdfFlowList'  
colnames(x)  
  
## S4 replacement method for signature 'ncdfFlowList'  
colnames(x) <- value  
  
## S4 method for signature 'ncdfFlowList'  
markernames(object)  
  
## S4 replacement method for signature 'ncdfFlowList'  
markernames(object) <- value  
  
## S4 method for signature 'ncdfFlowSet,ANY'  
compensate(x, spillover)  
  
## S4 method for signature 'flowSet,data.frame'  
compensate(x, spillover)  
  
## S4 method for signature 'ncdfFlowSet,list'  
compensate(x, spillover)  
  
## S4 method for signature 'ncdfFlowSet'  
transform(`_data`, ...)  
  
## S4 replacement method for signature 'ncdfFlowSet,ANY'  
sampleNames(object) <- value  
  
## S4 replacement method for signature 'ncdfFlowSet'  
colnames(x) <- value
```

**Arguments**

x	ncdfFlowSet
filter	filter to be applied
method	missing not used
sides	missing not used
circular	missing not used
init	missing not used
object	ncdfFlowList
value	character vector
spillover	spillover matrix
_data	ncdfFlowSet
...	other arguments

---

getFileName	<i>get the cdf file name associated with ncdfFlowSet object</i>
-------------	---

---

**Description**

get the cdf file name associated with ncdfFlowSet object

**Usage**

```
getFileName(ncfs)
```

**Arguments**

ncfs	ncdfFlowSet
------	-------------

**Value**

character

---

getIndices,ncdfFlowSet,character-method	<i>getIndices extracts the event indices of one or multiple samples from ncdfFlowSet</i>
---	--

---

**Description**

These functions are mainly for internal usage and normally not to be used by users.

initIndices initializes the event indices for the entire ncdfFlowSet with NA

updateIndices updates the event indices of the target sample in ncdfFlowSet

**Usage**

```
## S4 method for signature 'ncdfFlowSet,character'
getIndices(obj, y)

## S4 method for signature 'ncdfFlowSet'
initIndices(obj)

## S4 method for signature 'ncdfFlowSet,character,logical'
updateIndices(obj, y, z)
```

**Arguments**

obj	ncdfFlowSet object
y	character sample name
z	logical vector to be assigned.

**Value**

a logical vector.

**Examples**

```
data(GvHD)
nc <- ncdfFlowSet(GvHD[1:2])
sn <- sampleNames(nc)[1]
nrow(nc[[sn]])
getIndices(nc, sn) #initial index is NA
#subset with filter
morphGate <- norm2Filter("FSC-H", "SSC-H", filterId = "MorphologyGate",scale = 2)
nc1 <- Subset(nc, morphGate)
ind <- getIndices(nc1, sn)
all.equal(sum(ind), nrow(nc1[[sn]]))
initIndices(nc1)
getIndices(nc1, sn) #reset indices
```

---

lapply,ncdfFlowList-method

*lapply method for ncdfFlowList*

---

**Description**

Depending on level parameter, loop either iterates through the list of ncdfFlowSet objects or everyflowFrame objects.

**Usage**

```
## S4 method for signature 'ncdfFlowList'
lapply(X, FUN, level = 2, ...)
```

**Arguments**

X	ncdfFlowList object
FUN	function to apply
level	numeric. It controls whether loop at 'ncdfFlowSet' level or 'sample' level. when level = 2 (default value),FUN is applied to each sample. When level = 1, FUN is applied to each object stored in data slot.
...	other arguments passed to FUN

---

ncdfFlow	<i>ncdfFlow: A package that provides CDF storage based flow cytometry data analysis.</i>
----------	--

---

**Description**

ncdfFlow: A package that provides CDF storage based flow cytometry data analysis.

**Details**

Define important flow cytometry data classes: `ncdfFlowSet` (a subclass of `flowSet`) and `ncdfFlowList` (a list of `ncdfFlowSet` object) and their accessors.

Provide important compensation,transformation,filter,gating,subsetting,splitting functions for data analysis of large volumns of flow cytometry data that is too big to be held in memory.

Package:	ncdfFlow
Version:	2.9.24
Date:	2014-04-16
Depends:	R (>= 2.8.1), flowCore
License:	Artistic-2.0

**Author(s)**

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Maintainer: Mike Jiang <wjiang2@fhcrc.org>

---

ncdfFlowList-class	<i>a class that stores multiple ncdfFlowSet objects</i>
--------------------	---

---

**Description**

It is a list of `ncdfFlowSet` objects

constuctor for `ncdfFlowList`

**Usage**

```
ncdfFlowList(x, samples = NULL)
```

```
## S4 method for signature 'ncdfFlowList'
show(object)
```



**Arguments**

x	list of ncdfFlowSet objects
samples	integer see samples slot of ncdfFlowList class. or character that specify the order to samples. If not given then reconstruct the index.
object	ncdfFlowList

**Value**

ncdfFlowList-class

**Objects from the Class**

Objects can be created by coercing a list of ncdfFlowSet objects as(`"ncdfFlowList", nclist = ... #a list of ncdfFlowSet objects`)

**Slots**

**data:** A list containing the [ncdfFlowSet](#) objects.

**samples:** A integer vector containing the index of the [ncdfFlowSet](#) object to which each sample belongs. The name of the vector is the sample names that determine the order of samples exposed to the user, which can be different from the physical storing order.

**See Also**

[ncdfFlowSet](#)

**Examples**

```
data(GvHD)
nc1 <- ncdfFlowSet(GvHD[1])
nc2 <- ncdfFlowSet(GvHD[2])
nc3 <- ncdfFlowSet(GvHD[3])
list1 <- list(nc1, nc2, nc3)
#coerce from list to ncdfFlowList
nclist <- ncdfFlowList(list1)
nclist
#coerce(collapse) from ncdfFlowList to a single flowFrame
collapsedData <- as(nclist, "flowFrame")
collapsedData
```

---

ncdfFlowSet, flowSet-method

*create ncdfFlowSet from flowSet*

---

**Description**

Normally the ncdfFlowSet is constructed by loading raw FCS files using `read.ncdfFlowSet`. In case there is a legacy flowSet object, we can convert it to ncdfFlowSet with this constructor.

**Usage**

```
## S4 method for signature 'flowSet'
ncdfFlowSet(x, ncdfFile, dim = 2, compress = 0)
```

**Arguments**

x	flowSet
ncdfFile	character specifies the file name of cdf file
dim	integer see details in <a href="#">read.ncdfFlowset</a> .
compress	integer see details in <a href="#">read.ncdfFlowset</a> .

**Examples**

```
data(GvHD)
fs <- GvHD[1:2]
ncfs <- ncdfFlowSet(fs)
```

---

ncdfFlowSet-class      *a class for storing flow cytometry raw data in HDF5 format*

---

**Description**

This class is a subclass of [flowSet](#). It stores the raw data in cdf file instead of memory so that the analysis tools provided by flowCore based packages can be used in the study that produces hundreds or thousands FCS files.

**Usage**

```
## S4 method for signature 'ncdfFlowSet'
show(object)
```

**Arguments**

object	ncdfFlowSet show,ncdfFlowSet-method
--------	-------------------------------------

**Slots**

**file:** A character containing the ncdf file name.

**maxEvents:** An integer containing the maximum number of events of all samples stored in this ncdfFlowSet object

**flowSetId:** A character for the id of ncdfFlowSet object

**indices:** Object of class "environment" containing events indices of each sample stored as "raw" vector. Each index value is either TRUE or FALSE and the entire indices vector is used to subset the raw data. the indices vector of each sample is NA by default when the ncdfFlowSet first created. It is assigned with actual value when ncdfFlowSet object is subsetted by [Subset](#) or other subsetting methods.

**origSampleVector:** A character vector containing the sample names, which indicates the original order of samples physically stored in cdf format

**origColNames:** A character vector containing the flow channel names, which indicates the original order of columns physically stored in cdf format

**frames:** Object of class "environment", which replicates the "frame" slot in `flowSet`, except that `exprs` matrix is empty and the actual data is stored in cdf file.

**phenoData:** see `phenoData`

**colnames:** see `colnames`. Here it serves as the current data view which does not reflect the actual number and order of columns stored in cdf file.

## Extends

Class "`flowSet`", directly.

---

ncfsApply,ncdfFlowSet-method

*apply method for ncdfFlowSet (for internal use)*

---

## Description

It is equivalent to `fsApply`. But the latter could cause memory issue when FUN returns a `flowFrame`. `ncdfApply` writes to a new cdf file instead of memory. Thus it will return a `ncdfFlowSet` object.

## Usage

```
## S4 method for signature 'ncdfFlowSet'
ncfsApply(x, FUN, ..., use.exprs = FALSE,
          ncdfFile = NULL)
```

## Arguments

<code>x</code>	<code>ncdfFlowSet</code>
<code>FUN</code>	function to apply
<code>...</code>	other arguments to pass to FUN
<code>use.exprs</code>	logical see <code>fsApply</code>
<code>ncdfFile</code>	logical whether to create a new hdf file or simply overwrite the existing file.

## Details

When the function given by argument "FUN" does not return the entire `flowFrame` object with the same size of the original one (such as `compensate`,`transform`...), `fsApply` should be used instead.

## Examples

```
data(GvHD)
nc <- ncdfFlowSet(GvHD[1:2])

#use fsApply when FUN does not return a flowFrame
fsApply(nc, nrow)
fsApply(nc, range)

#use ncfsApply when FUN returns a flowFrame
```

```
lgcl <- logicleTransform( w = 0.5, t= 10000, m =4.5)
translist <- transformList(c("FL1-H", "FL2-H"), lgcl)
nc1 <- ncfsApply(nc, transform, translist)
```

---

```
rbind2,ncdfFlowList,ANY-method
```

*combine multiple ncdfFlowSet objects into one*

---

## Description

Similar to [flowCore:rbind2](#). But one needs to first construct a `ncdfFlowList` and then apply `rbind2` to it instead of merging them pairwise

## Usage

```
## S4 method for signature 'ncdfFlowList,ANY'
rbind2(x, ncdfFile = tempfile(pattern = "ncfs"),
       dim = 2, compress = 0, samples = NULL)
```

## Arguments

<code>x</code>	<code>ncdfFlowList</code>
<code>ncdfFile</code>	character see details in <a href="#">read.ncdfFlowset</a> when all the <code>ncdfFlowSet</code> s shared the same cdf file, by supplying this argument, it will use the existing cdf and avoid writing to it unnecessarily.
<code>dim</code>	integer see details in <a href="#">read.ncdfFlowset</a> .
<code>compress</code>	integer see details in <a href="#">read.ncdfFlowset</a> .
<code>samples</code>	character the vector of sample names which determine the physical sample storage order in original cdf file. Default is <code>NULL</code> , which derives from the given <code>ncdfFlowSet</code> objects.

## Value

a new `ncdfFlowSet` with a new cdf file that combines multiple raw datasets.

## Examples

```
library(ncdfFlow)
data(GvHD)

nc1 <- ncdfFlowSet(GvHD[1:2])
nc2 <- ncdfFlowSet(GvHD[3:4])
nc3 <- ncdfFlowSet(GvHD[5:6])
ncslist <- ncdfFlowList(list(nc1,nc2,nc3))
nc4 <- rbind2(ncslist)
nc4
```

---

read.ncdfFlowSet	<i>create ncdfFlowSet from FCS files</i>
------------------	--

---

### Description

read FCS files from the disk and load them into a ncdfFlowSet object

### Usage

```
read.ncdfFlowSet(files = NULL, ncdfFile, flowSetId = flowCore:::guid(),
  isWriteSlice = TRUE, phenoData, channels = NULL, dim = 2,
  compress = 0, mc.cores = NULL, ...)
```

### Arguments

files	A character vector giving the source FCS raw file paths.
ncdfFile	A character scalar giving the output file name. Default is NULL and the function will generate a random file in the temporary folder, potentially adding the .cdf suffix unless a file extension is already present. It is sometimes useful to specify this file path to avoid the failure of writing large flow data set to cdf file due to the the shortage of disk space in system temporary folder. It is only valid when isNewNcFile=TRUE
flowSetId	A character scalar giving the unique ncdfFlowSet ID.
isWriteSlice	A logical scalar indicating whether the raw data should also be copied.if FALSE, an empty cdf file is created with the dimensions (sample*events*channels) supplied by raw FCS files.
phenoData	An object of AnnotatedDataFrame providing a way to manually set the phenotypic data for the whole data set in ncdfFlowSet.
channels	A character vector specifying which channels to extract from FCS files. It can be useful when FCS files do not share exactly the same channel names. Thus this argument is used to select those common channels that are of interests. Default value is NULL and the function will try to scan the FCS headers of all files and determine the common channels.
dim	integer the number of dimensions that specifies the physical storage format of hdf5 dataset. Default is 2, which stores each FCS data as a seperate 2d dataset. Normally, user shouldn't need to change this but dim can also be set to 3, which stores all FCS data as one single 3d dataset.
compress	integer the HDF5 compression ratio (from 0 to 9). Default is 0, which does not compress the data and is recommended (especially for 2d format) because the speed loss usually outweighs the disk saving.
mc.cores	numeric passed to parallel::mclapply. Default is NULL, which read FCS files in serial mode.
...	extra arguments to be passed to <a href="#">read.FCS</a> .

### Value

A ncdfFlowSet object

**See Also**[clone.ncdfFlowSet](#)**Examples**

```
library(ncdfFlow)

path<-system.file("extdata","compdata","data",package="flowCore")
files<-list.files(path,full.names=TRUE)[1:3]

#create ncdfFlowSet from fcs with the actual raw data written in cdf
nc1 <- read.ncdfFlowSet(files=files,ncdfFile="ncfsTest.nc",flowSetId="fs1",isWriteSlice= TRUE)
nc1
nc1[[1]]
unlink(nc1)
rm(nc1)

#create empty ncdfFlowSet from fcs and add data slices afterwards
nc1 <- read.ncdfFlowSet(files=files,ncdfFile="ncfsTest.nc",flowSetId="fs1",isWriteSlice= FALSE)
fs1<-read.flowSet(files)
nc1[[1]] <- fs1[[1]]
nc1[[1]]
nc1[[2]]
```

---

replacement method for `ncdfFlowSet`

*write the flow data from a flowFrame to ncdfFlowSet, flowFrame can have less channels than ncdfFlowSet, which is used for partial updating (useful for normalization)*

---

**Description**

write the flow data from a `flowFrame` to `ncdfFlowSet`

`flowFrame` can have less channels than `ncdfFlowSet`, which is used for partial updating (useful for normalization)

**Usage**

```
## S4 replacement method for signature 'ncdfFlowSet,ANY,ANY,flowFrame'
x[[i, j = "missing",
  only.exprs = FALSE, compress = 0, ...]] <- value
```

**Arguments**

<code>x</code>	a <code>ncdfFlowSet</code>
<code>i</code>	a numeric or character used as sample index of <code>ncdfFlowSet</code>
<code>j</code>	not used
<code>only.exprs</code>	a logical Default is <code>FALSE</code> . which will update the parameters and descriptions slot as well as the raw data. Sometime it is more efficient to set it to <code>TRUE</code> skip the overhead of colnames matching and updating when user is only concerned about raw data instead of the entire <code>flowFrame</code> .

compress	integer	It is only relevant to writing slice to '2d' format because the compression is set during the creation of hdf5 file for '3d' format. see details in <a href="#">read.ncdfFlowset</a> .
...		not used
value		flowFrame

## Examples

```

data(GvHD)
nc <- ncdFlowSet(GvHD[1:2])
samples <- sampleNames(nc)
sn <- samples[1]
#return the entire flowFrame
fr <- nc[[sn]]

apply(exprs(nc[[sn]]), 2, range)

#transform the data
lgcl <- logicleTransform( w = 0.5, t= 10000, m =4.5)
fr_trans <- transform(fr, `FL1-H` = lgcl(`FL1-H`), `FL2-H` = lgcl(`FL2-H`))

#update the data
nc[[sn]] <- fr_trans
apply(exprs(nc[[sn]]), 2, range)

#subset on channels
nc1 <- nc[,2:3]
#only write the channels of interest (reduce disk IO)
nc1[[sn]] <- fr_trans[,2:3]

#channel colnames
colnames(fr_trans)[3:4] <- c("<FL1-H>", "<FL2-H>")

#write data without matching up the colnames
nc[[sn, only.exprs = TRUE]] <- fr_trans

```

---

save\_ncfs

*save/load a ncdFlowSet object to/from disk.*

---

## Description

The ncdFlowSet object contains two parts: R object and cdf file. Save/load a ncdFlowSet mainly involves the R part using saveRDS/readRDS.

## Usage

```

save_ncfs(ncfs, path, overwrite = FALSE, cdf = c("copy", "move", "link",
  "skip", "symlink"))

load_ncfs(path)

```

**Arguments**

ncfs	A ncdfFlowSet
path	A character scalar giving the path to save/load the ncdfFlowSet to/from.
overwrite	A logical scalar specifying whether to overwrite the existing folder.
cdf	a character scalar. The valid options are : "copy", "move", "skip", "symlink", "link" specifying what to do with the cdf data file. Sometime it is more efficient to move or create a link of the existing cdf file to the archived folder.

**Value**

load\_ncfs returns a ncdfFlowSet object

**See Also**

[ncdfFlowSet-class](#)

**Examples**

```
## Not run:
#ncfs is a ncdfFlowSet
save_ncfs(fs, path = "tempFolder")
fs1 <- load_ncfs(path = "tempFolder")

## End(Not run)
```

---

split,ncdfFlowList,factor-method  
*split a ncdfFlowSet object.*

---

**Description**

Equivalent to split method for flowSet object.

**Usage**

```
## S4 method for signature 'ncdfFlowList,factor'
split(x, f, drop = FALSE, ...)

## S4 method for signature 'ncdfFlowList,character'
split(x, f, drop = FALSE, ...)

## S4 method for signature 'ncdfFlowSet,filter'
split(x, f, drop = FALSE, population = NULL,
      prefix = NULL, ...)

## S4 method for signature 'ncdfFlowSet,filterResultList'
split(x, f, drop = FALSE,
      population = NULL, prefix = NULL, ...)

## S4 method for signature 'ncdfFlowSet,list'
```



```

split(x, f, isNew = FALSE, drop = FALSE,
      population = NULL, prefix = NULL, ...)

## S4 method for signature 'ncdfFlowSet,factor'
split(x, f, isNew = FALSE, drop = FALSE, ...)

## S4 method for signature 'ncdfFlowSet,character'
split(x, f, drop = FALSE, ...)

```

### Arguments

```

x                ncdfFlowSet
f, drop, population, prefix, ...
                see split-methods
isNew           logical whether to create a new hdf file or using existing hdf file.

```

### Value

a list of ncdfFlowSet objects that may not may not share the same hdf file depending on isNew argument.

---

Subset,ncdfFlowSet,filterResultList-method  
*subset a ncdfFlowSet by filter*

---

### Description

Equivalent to Subset method for flowSet.

### Usage

```

## S4 method for signature 'ncdfFlowSet,filterResultList'
Subset(x, subset, select, ...)

## S4 method for signature 'ncdfFlowList,filterResultList'
Subset(x, subset, select, ...)

## S4 method for signature 'ncdfFlowSet,filter'
Subset(x, subset, ...)

## S4 method for signature 'ncdfFlowList,filter'
Subset(x, subset, ...)

## S4 method for signature 'ncdfFlowSet,list'
Subset(x, subset, select, validityCheck = TRUE,
      ...)

```

### Arguments

```

x                ncdfFlowSet or ncdfFlowList
subset, select, ...
                see Subset-methods
validityCheck   logical whether to skip validity check for speed.

```

**Value**

one or more ncdfFlowSet objects which share the same hdf5 file with the original one.

---

subset.ncdfFlowSet     *subset the ncdfFlowSet/ncdfFlowList based on 'pData'*

---

**Description**

subset the ncdfFlowSet/ncdfFlowList based on 'pData'

**Usage**

```
## S3 method for class 'ncdfFlowSet'
subset(x, subset, ...)

## S3 method for class 'ncdfFlowList'
subset(x, subset, ...)
```

**Arguments**

x	ncdfFlowSet or ncdfFlowList
subset	logical expression(within the context of pData) indicating samples to keep. see <a href="#">subset</a>
...	other arguments. (not used)

**Value**

a subset of codencdfFlowSet or ncdfFlowList object

---

unlink,ncdfFlowSet-method  
*delete the cdf file associated with the ncdfFlowSet object ncdfFlowSet object is unrecoverable after cdf is deleted. So this method is usually called when ncdfFlowSet object is no longer in need.*

---

**Description**

delete the cdf file associated with the ncdfFlowSet object  
ncdfFlowSet object is unrecoverable after cdf is deleted. So this method is usually called when ncdfFlowSet object is no longer in need.

**Usage**

```
## S4 method for signature 'ncdfFlowSet'
unlink(x, recursive = FALSE, force = FALSE)
```

**Arguments**

x	ncdfFlowSet
recursive	see <a href="#">unlink</a>
force	see <a href="#">unlink</a>

**Examples**

```
data(GvHD)
nc <- ncdfFlowSet(GvHD[1:2])
nc[[1]] # data is loaded from cdf file
unlink(nc)
```

---

[,ncdfFlowSet,ANY,ANY,ANY-method

*subsetting by sampleNames,channels(not for events) methods*


---

**Description**

similar to [\[.\]](#).

**Usage**

```
## S4 method for signature 'ncdfFlowSet,ANY,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 method for signature 'ncdfFlowList,ANY,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

**Arguments**

x	ncdfFlowSet
i	sample index(or name)
j	column(or channel) index (or name)
...	other arguments not used
drop	logical not used.

**Examples**

```
data(GvHD)
nc <- ncdfFlowSet(GvHD[1:2])
samples <- sampleNames(nc)
nc[1]
nc1 <- nc[samples[1]]
#nc1 and nc share the cdf file
all.equal(getFileName(nc1), getFileName(nc))
```

---

```
[[,ncdfFlowSet,ANY-method
      extract a flowFrame object from ncdfFlowSet
```

---

### Description

Similiar to `[[`, and there are cerntain ways to reduce the disk IO and optimize the speed.

### Usage

```
## S4 method for signature 'ncdfFlowSet,ANY'
x[[i, j, use.exprs = TRUE, ...]]

## S4 method for signature 'ncdfFlowList,numeric'
x[[i, j, ...]]

## S4 method for signature 'ncdfFlowList,logical'
x[[i, j, ...]]

## S4 method for signature 'ncdfFlowList,character'
x[[i, j, ...]]
```

### Arguments

<code>x</code>	a <code>ncdfFlowSet</code> or <code>ncdfFlowList</code>
<code>i</code>	a numeric or character used as sample index
<code>j</code>	a numeric or character used as channel index
<code>use.exprs</code>	a logical scalar indicating whether to read the actual data from cdf
<code>...</code>	other arguments. not used.

### Examples

```
data(GvHD)
nc <- ncdfFlowSet(GvHD[1:2])
samples <- sampleNames(nc)
sn <- samples[1]
#return the entire flowFrame
fr <- nc[[sn]]

#access the flowFrame meta data without loading the raw event data from disk
nc[[sn, use.exprs = FALSE]]

#only read a subset of channels (more efficient than reading entire data set)
nc[[sn, 1:2]]
```

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