

Package ‘data.table’

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Imports methods

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Description Fast aggregation of large data (e.g. 100GB in RAM), fast ordered joins, fast add/modify/delete of columns by group using no copies at all, list columns, a fast friendly file reader and parallel file writer. Offers a natural and flexible syntax, for faster development.

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URL <http://r-datatable.com>

BugReports <https://github.com/Rdatatable/data.table/issues>

MailingList datatable-help@lists.r-forge.r-project.org

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data.table-package *Enhanced data.frame*

Description

`data.table` *inherits* from `data.frame`. It offers fast and memory efficient: file reader and writer, aggregations, updates, equi, non-equi, rolling, range and interval joins, in a short and flexible syntax, for faster development.

It is inspired by `A[B]` syntax in `R` where `A` is a matrix and `B` is a 2-column matrix. Since a `data.table` *is* a `data.frame`, it is compatible with `R` functions and packages that accept *only* `data.frames`.

Type `vignette(package="data.table")` to get started. The [Introduction to data.table](#) vignette introduces `data.table`'s `x[i, j, by]` syntax and is a good place to start. If you have read the vignettes and the help page below, please feel free to ask questions on Stack Overflow [data.table tag](#) or on [datatable-help](#) mailing list. To report a bug please type: `bug.report(package = "data.table")`.

Please check the [homepage](#) for up to the minute live NEWS.

Tip: one of the *quickest* ways to learn the features is to type `example(data.table)` and study the output at the prompt.

Usage

```
data.table(..., keep.rownames=FALSE, check.names=FALSE, key=NULL, stringsAsFactors=FALSE)
```

```
## S3 method for class 'data.table'
x[i, j, by, keyby, with = TRUE,
  nomatch = getOption("datatable.nomatch"),           # default: NA_integer_
  mult = "all",
  roll = FALSE,
  rollends = if (roll=="nearest") c(TRUE,TRUE)
              else if (roll>=0) c(FALSE,TRUE)
              else c(TRUE,FALSE),
  which = FALSE,
  .SDcols,
  verbose = getOption("datatable.verbose"),           # default: FALSE
  allow.cartesian = getOption("datatable.allow.cartesian"), # default: FALSE
  drop = NULL, on = NULL]
```

Arguments

`...` Just as `...` in `data.frame`. Usual recycling rules are applied to vectors of different lengths to create a list of equal length vectors.

`keep.rownames` If `...` is a matrix or `data.frame`, TRUE will retain the rownames of that object in a column named `rn`.

`check.names` Just as `check.names` in `data.frame`.

`key` Character vector of one or more column names which is passed to `setkey`. It may be a single comma separated string such as `key="x,y,z"`, or a vector of names such as `key=c("x","y","z")`.

`stringsAsFactors`

Logical (default is FALSE). Convert all character columns to factors?

`x` A `data.table`.

`i` Integer, logical or character vector, single column numeric matrix, expression of column names, list, `data.frame` or `data.table`.

integer and logical vectors work the same way they do in `[.data.frame]` except logical NAs are treated as FALSE.

expression is evaluated within the frame of the `data.table` (i.e. it sees column names as if they are variables) and can evaluate to any of the other types.

character, list and `data.frame` input to `i` is converted into a `data.table` internally using `as.data.table`.

If `i` is a `data.table`, the columns in `i` to be matched against `x` can be specified using one of these ways:

- on argument (see below). It allows for both equi- and the newly implemented non-equi joins.
- If not, `x` *must be keyed*. Key can be set using `setkey`. If `i` is also keyed, then first *key* column of `i` is matched against first *key* column of `x`, second against second, etc..

If `i` is not keyed, then first column of `i` is matched against first *key* column of `x`, second column of `i` against second *key* column of `x`, etc...

This is summarised in code as `min(length(key(x)), if (haskey(i)) length(key(i)) else ncol(x))`

Using `on=` is recommended (even during keyed joins) as it helps understand the code better and also allows for *non-equi* joins.

When the binary operator `==` alone is used, an *equi* join is performed. In SQL terms, `x[i]` then performs a *right join* by default. `i` prefixed with `!` signals a *not-join* or *not-select*.

Support for *non-equi* join was recently implemented, which allows for other binary operators `>=`, `>`, `<=` and `<`.

See [Keys and fast binary search based subset](#) and [Secondary indices and auto indexing](#).

Advanced: When `i` is a single variable name, it is not considered an expression of column names and is instead evaluated in calling scope.

`j` When `with=TRUE` (default), `j` is evaluated within the frame of the `data.table`; i.e., it sees column names as if they are variables. This allows to not just *select* columns in `j`, but also compute on them e.g., `x[, a]` and `x[, sum(a)]` returns

`x$a` and `sum(x$a)` as a vector respectively. `x[, .(a, b)]` and `x[, .(sa=sum(a), sb=sum(b))]` returns a two column `data.table` each, the first simply *selecting* columns `a`, `b` and the second *computing* their sums.

The expression `.()` is a *shorthand* alias to `list()`; they both mean the same. As long as `j` returns a `list`, each element of the list becomes a column in the resulting `data.table`. This is the default *enhanced* mode.

When `with=FALSE`, `j` can only be a vector of column names or positions to select (as in `data.frame`).

Advanced: `j` also allows the use of special *read-only* symbols: `.SD`, `.N`, `.I`, `.GRP`, `.BY`.

Advanced: When `i` is a `data.table`, the columns of `i` can be referred to in `j` by using the prefix `i.`, e.g., `X[Y, .(val, i.val)]`. Here `val` refers to `X`'s column and `i.val` `Y`'s.

Advanced: Columns of `x` can now be referred to using the prefix `x.` and is particularly useful during joining to refer to `x`'s *join* columns as they are otherwise masked by `i`'s. For example, `X[Y, .(x.a-i.a, b), on="a"]`.

See [Introduction to data.table](#) vignette and examples.

by

Column names are seen as if they are variables (as in `j` when `with=TRUE`). The `data.table` is then grouped by the `by` and `j` is evaluated within each group. The order of the rows within each group is preserved, as is the order of the groups. `by` accepts:

- A single unquoted column name: e.g., `DT[, .(sa=sum(a)), by=x]`
- a `list()` of expressions of column names: e.g., `DT[, .(sa=sum(a)), by=(x>0, y)]`
- a single character string containing comma separated column names (where spaces are significant since column names may contain spaces even at the start or end): e.g., `DT[, sum(a), by="x,y,z"]`
- a character vector of column names: e.g., `DT[, sum(a), by=c("x", "y")]`
- or of the form `startcol:endcol`: e.g., `DT[, sum(a), by=x:z]`

Advanced: When `i` is a `list` (or `data.frame` or `data.table`), `DT[i, j, by=.EACHI]` evaluates `j` for the groups in `'DT'` that each row in `i` joins to. That is, you can join (in `i`) and aggregate (in `j`) simultaneously. We call this *grouping by each i*. See [this StackOverflow answer](#) for a more detailed explanation until we [roll out vignettes](#).

Advanced: In the `X[Y, j]` form of grouping, the `j` expression sees variables in `X` first, then `Y`. We call this *join inherited scope*. If the variable is not in `X` or `Y` then the calling frame is searched, its calling frame, and so on in the usual way up to and including the global environment.

keyby

Same as `by`, but with an additional `setkey()` run on the `by` columns of the result, for convenience. It is common practice to use `'keyby='` routinely when you wish the result to be sorted.

with

By default `with=TRUE` and `j` is evaluated within the frame of `x`; column names can be used as variables.

When `with=FALSE` `j` is a character vector of column names, a numeric vector of column positions to select or of the form `startcol:endcol`, and the value returned is always a `data.table`. `with=FALSE` is often useful in `data.table` to

	select columns dynamically. Note that <code>x[, cols, with=FALSE]</code> is equivalent to <code>x[, .SD, .SDcols=cols]</code> .
<code>nomatch</code>	Same as <code>nomatch</code> in <code>match</code> . When a row in <code>i</code> has no match to <code>x</code> , <code>nomatch=NA</code> (default) means NA is returned. <code>0</code> means no rows will be returned for that row of <code>i</code> . Use <code>options(datatable.nomatch=0)</code> to change the default value (used when <code>nomatch</code> is not supplied).
<code>mult</code>	When <code>i</code> is a list (or <code>data.frame</code> or <code>data.table</code>) and <i>multiple</i> rows in <code>x</code> match to the row in <code>i</code> , <code>mult</code> controls which are returned: "all" (default), "first" or "last".
<code>roll</code>	When <code>i</code> is a <code>data.table</code> and its row matches to all but the last <code>x</code> join column, and its value in the last <code>i</code> join column falls in a gap (including after the last observation in <code>x</code> for that group), then: <ul style="list-style-type: none"> • <code>+Inf</code> (or <code>TRUE</code>) rolls the <i>prevailing</i> value in <code>x</code> forward. It is also known as last observation carried forward (LOCF). • <code>-Inf</code> rolls backwards instead; i.e., next observation carried backward (NOCB). • finite positive or negative number limits how far values are carried forward or backward. • "nearest" rolls the nearest value instead. Rolling joins apply to the last join column, generally a date but can be any variable. It is particularly fast using a modified binary search. A common idiom is to select a contemporaneous regular time series (<code>dts</code>) across a set of identifiers (<code>ids</code>): <code>DT[CJ(ids,dts),roll=TRUE]</code> where <code>DT</code> has a 2-column key (<code>id,date</code>) and <code>CJ</code> stands for <i>cross join</i> .
<code>rollends</code>	A logical vector length 2 (a single logical is recycled) indicating whether values falling before the first value or after the last value for a group should be rolled as well. <ul style="list-style-type: none"> • If <code>rollends[2]=TRUE</code>, it will roll the last value forward. <code>TRUE</code> by default for LOCF and <code>FALSE</code> for NOCB rolls. • If <code>rollends[1]=TRUE</code>, it will roll the first value backward. <code>TRUE</code> by default for NOCB and <code>FALSE</code> for LOCF rolls. When <code>roll</code> is a finite number, that limit is also applied when rolling the ends.
<code>which</code>	<code>TRUE</code> returns the row numbers of <code>x</code> that <code>i</code> matches to. If <code>NA</code> , returns the row numbers of <code>i</code> that have no match in <code>x</code> . By default <code>FALSE</code> and the rows in <code>x</code> that match are returned.
<code>.SDcols</code>	Specifies the columns of <code>x</code> to be included in the special symbol <code>.SD</code> which stands for Subset of <code>data.table</code> . May be character column names or numeric positions. This is useful for speed when applying a function through a subset of (possible very many) columns; e.g., <code>DT[, lapply(.SD, sum), by="x,y", .SDcols=301:350]</code> . For convenient interactive use, the form <code>startcol:endcol</code> is also allowed (as in <code>by</code>), e.g., <code>DT[, lapply(.SD, sum), by=x:y, .SDcols=a:f]</code>
<code>verbose</code>	<code>TRUE</code> turns on status and information messages to the console. Turn this on by default using <code>options(datatable.verbose=TRUE)</code> . The quantity and types of verbosity may be expanded in future.

allow.cartesian	FALSE prevents joins that would result in more than $nrow(x)+nrow(i)$ rows. This is usually caused by duplicate values in i 's join columns, each of which join to the same group in x over and over again: a <i>misspecified</i> join. Usually this was not intended and the join needs to be changed. The word 'cartesian' is used loosely in this context. The traditional cartesian join is (deliberately) difficult to achieve in <code>data.table</code> : where every row in i joins to every row in x (a $nrow(x)*nrow(i)$ row result). 'cartesian' is just meant in a 'large multiplicative' sense.
drop	Never used by <code>data.table</code> . Do not use. It needs to be here because <code>data.table</code> inherits from <code>data.frame</code> . See datatable-faq .
on	Indicate which columns in i should be joined with columns in x along with the type of binary operator to join with. When specified, this overrides the keys set on x and i . There are multiple ways of specifying <code>on</code> argument: <ul style="list-style-type: none"> • As a character vector, e.g., <code>X[Y, on=c("a", "b")]</code>. This assumes both these columns are present in X and Y. • As a <i>named</i> character vector, e.g., <code>X[Y, on=c(x="a", y="b")]</code>. This is useful when column names to join by are different between the two tables. NB: <code>X[Y, on=c("a", y="b")]</code> is also possible if column "a" is common between the two tables. • For convenience during interactive scenarios, it is also possible to use <code>.()</code> syntax as <code>X[Y, on=.(a, b)]</code>. • From v1.9.8, (non-equi) joins using binary operators <code>>=</code>, <code>></code>, <code><=</code>, <code><</code> are also possible, e.g., <code>X[Y, on=c("x>=a", "y<=b")]</code>, or for interactive use as <code>X[Y, on=.(x>=a, y<=b)]</code>. See examples as well as Secondary indices and auto indexing .

Details

`data.table` builds on base R functionality to reduce 2 types of time:

1. programming time (easier to write, read, debug and maintain), and
2. compute time (fast and memory efficient).

The general form of `data.table` syntax is:

```
DT[ i, j, by ] # + extra arguments
|   |   |
|   |   -----> grouped by what?
|   -----> what to do?
---> on which rows?
```

The way to read this out loud is: "Take DT, subset rows by i , *then* compute j grouped by by . Here are some basic usage examples expanding on this definition. See the vignette (and examples) for working examples.

```

X[, a]                # return col 'a' from X as vector. If not found, search in parent frame.
X[, .(a)]             # same as above, but return as a data.table.
X[, sum(a)]           # return sum(a) as a vector (with same scoping rules as above)
X[, .(sum(a)), by=c]  # get sum(a) grouped by 'c'.
X[, sum(a), by=c]     # same as above, .() can be omitted in by on single expression for convenience
X[, sum(a), by=c:f]   # get sum(a) grouped by all columns in between 'c' and 'f' (both inclusive)

X[, sum(a), keyby=b]  # get sum(a) grouped by 'b', and sort that result by the grouping column
X[, sum(a), by=b][order(b)] # same order as above, but by chaining compound expressions
X[c>1, sum(a), by=c]  # get rows where c>1 is TRUE, and on those rows, get sum(a) grouped by 'c'
X[Y, .(a, b), on="c"] # get rows where Y$c == X$c, and select columns 'X$a' and 'X$b' for those rows
X[Y, .(a, i.a), on="c"] # get rows where Y$c == X$c, and then select 'X$a' and 'Y$a' (=i.a)
X[Y, sum(a*i.a), on="c" by=.EACHI] # for *each* 'Y$c', get sum(a*i.a) on matching rows in 'X$c'

X[, plot(a, b), by=c] # j accepts any expression, generates plot for each group and returns no data
# see ?assign to add/update/delete columns by reference using the same consistent interface

```

A `data.table` is a list of vectors, just like a `data.frame`. However :

1. it never has or uses rownames. Rownames based indexing can be done by setting a *key* of one or more columns or done *ad-hoc* using the `on` argument (now preferred).
2. it has enhanced functionality in `[.data.table]` for fast joins of keyed tables, fast aggregation, fast last observation carried forward (LOCF) and fast add/modify/delete of columns by reference with no copy at all.

See the `see also` section for the several other *methods* that are available for operating on `data.tables` efficiently.

Note

If `keep.rownames` or `check.names` are supplied they must be written in full because **R** does not allow partial argument names after `'...'`. For example, `data.table(DF, keep=TRUE)` will create a column called "keep" containing TRUE and this is correct behaviour; `data.table(DF, keep.rownames=TRUE)` was intended.

POSIXlt is not supported as a column type because it uses 40 bytes to store a single datetime. They are implicitly converted to POSIXct type with *warning*. You may also be interested in `IDateTime` instead; it has methods to convert to and from POSIXlt.

References

<https://github.com/Rdatatable/data.table/wiki> (data.table homepage)
<http://crantastic.org/packages/data-table> (User reviews)
http://en.wikipedia.org/wiki/Binary_search

See Also

[special-symbols](#), [data.frame](#), [\[.data.frame\]](#), [as.data.table](#), [setkey](#), [setorder](#), [setDT](#), [setDF](#), [J](#), [SJ](#), [CJ](#), [merge.data.table](#), [tables](#), [test.data.table](#), [IDateTime](#), [unique.data.table](#), [copy](#), [:=](#), [alloc.col](#), [truelength](#), [rbindlist](#), [setNumericRounding](#), [datatable-optimize](#), [fsetdiff](#), [funion](#), [fintersect](#), [fsetequal](#), [anyDuplicated](#), [uniqueN](#), [rowid](#), [rleid](#), [na.omit](#), [frank](#)

Examples

```

## Not run:
example(data.table) # to run these examples at the prompt
## End(Not run)

DF = data.frame(x=rep(c("b","a","c"),each=3), y=c(1,3,6), v=1:9)
DT = data.table(x=rep(c("b","a","c"),each=3), y=c(1,3,6), v=1:9)
DT
identical(dim(DT), dim(DF)) # TRUE
identical(DT$a, DF$a) # TRUE
is.list(DF) # TRUE
is.list(DT) # TRUE

is.data.frame(DT) # TRUE

tables()

# basic row subset operations
DT[2] # 2nd row
DT[3:2] # 3rd and 2nd row
DT[order(x)] # no need for order(DT$x)
DT[order(x), ] # same as above. The ',' is optional
DT[y>2] # all rows where DT$y > 2
DT[y>2 & v>5] # compound logical expressions
DT[!2:4] # all rows other than 2:4
DT[-(2:4)] # same

# select|compute columns data.table way
DT[, v] # v column (as vector)
DT[, list(v)] # v column (as data.table)
DT[, .(v)] # same as above, .() is a shorthand alias to list()
DT[, sum(v)] # sum of column v, returned as vector
DT[, .(sum(v))] # same, but return data.table (column autonamed V1)
DT[, .(sv=sum(v))] # same, but column named "sv"
DT[, .(v, v*2)] # return two column data.table, v and v*2

# subset rows and select|compute data.table way
DT[2:3, sum(v)] # sum(v) over rows 2 and 3, return vector
DT[2:3, .(sum(v))] # same, but return data.table with column V1
DT[2:3, .(sv=sum(v))] # same, but return data.table with column sv
DT[2:5, cat(v, "\n")] # just for j's side effect

# select columns the data.frame way
DT[, 2, with=FALSE] # 2nd column, returns a data.table always
colNum = 2
DT[, colNum, with=FALSE] # same, equivalent to DT[, .SD, .SDcols=colNum]
DT[["v"]] # same as DT[, v] but much faster

# grouping operations - j and by
DT[, sum(v), by=x] # ad hoc by, order of groups preserved in result
DT[, sum(v), keyby=x] # same, but order the result on by cols

```

```

DT[, sum(v), by=x][order(x)] # same but by chaining expressions together

# fast ad hoc row subsets (subsets as joins)
DT["a", on="x"] # same as x == "a" but uses binary search (fast)
DT["a", on=(x)] # same, for convenience, no need to quote every column
DT[."a"), on="x"] # same
DT[x=="a"] # same, single "=" internally optimised to use binary search (fast)
DT[x!="b" | y!=3] # not yet optimized, currently vector scan subset
DT[.("b", 3), on=c("x", "y")] # join on columns x,y of DT; uses binary search (fast)
DT[.("b", 3), on=(x, y)] # same, but using on=(.)
DT[.("b", 1:2), on=c("x", "y")] # no match returns NA
DT[.("b", 1:2), on=(x, y), nomatch=0] # no match row is not returned
DT[.("b", 1:2), on=c("x", "y"), roll=Inf] # locf, nomatch row gets rolled by previous row
DT[.("b", 1:2), on=(x, y), roll=-Inf] # nocb, nomatch row gets rolled by next row
DT["b", sum(v*y), on="x"] # on rows where DT$x=="b", calculate sum(v*y)

# all together now
DT[x!="a", sum(v), by=x] # get sum(v) by "x" for each i != "a"
DT[!"a", sum(v), by=.EACHI, on="x"] # same, but using subsets-as-joins
DT[c("b","c"), sum(v), by=.EACHI, on="x"] # same
DT[c("b","c"), sum(v), by=.EACHI, on=(x)] # same, using on=(.)

# joins as subsets
X = data.table(x=c("c","b"), v=8:7, foo=c(4,2))
X

DT[X, on="x"] # right join
X[DT, on="x"] # left join
DT[X, on="x", nomatch=0] # inner join
DT[!X, on="x"] # not join
DT[X, on=(y<=foo)] # NEW non-equi join (v1.9.8+)
DT[X, on="y<=foo"] # same as above
DT[X, on=c("y<=foo")] # same as above
DT[X, on=(y>=foo)] # NEW non-equi join (v1.9.8+)
DT[X, on=(x, y<=foo)] # NEW non-equi join (v1.9.8+)
DT[X, .(x,y,x.y,v), on=(x, y>=foo)] # Select x's join columns as well

DT[X, on="x", mult="first"] # first row of each group
DT[X, on="x", mult="last"] # last row of each group
DT[X, sum(v), by=.EACHI, on="x"] # join and eval j for each row in i
DT[X, sum(v)*foo, by=.EACHI, on="x"] # join inherited scope
DT[X, sum(v)*i.v, by=.EACHI, on="x"] # 'i,v' refers to X's v column
DT[X, on=(x, v>v), sum(y)*foo, by=.EACHI] # NEW non-equi join with by=.EACHI (v1.9.8+)

# setting keys
kDT = copy(DT) # (deep) copy DT to kDT to work with it.
setkey(kDT,x) # set a 1-column key. No quotes, for convenience.
setkeyv(kDT,"x") # same (v in setkeyv stands for vector)
v="x"
setkeyv(kDT,v) # same
# key(kDT)<-"x" # copies whole table, please use set* functions instead
haskey(kDT) # TRUE
key(kDT) # "x"

```

```

# fast *keyed* subsets
kDT["a"] # subset-as-join on *key* column 'x'
kDT["a", on="x"] # same, being explicit using 'on=' (preferred)

# all together
kDT[!"a", sum(v), by=.EACHI] # get sum(v) for each i != "a"

# multi-column key
setkey(kDT,x,y) # 2-column key
setkeyv(kDT,c("x","y")) # same

# fast *keyed* subsets on multi-column key
kDT["a"] # join to 1st column of key
kDT["a", on="x"] # on= is optional, but is preferred
kDT[.("a")] # same, .() is an alias for list()
kDT[list("a")] # same
kDT[.("a", 3)] # join to 2 columns
kDT[.("a", 3:6)] # join 4 rows (2 missing)
kDT[.("a", 3:6), nomatch=0] # remove missing
kDT[.("a", 3:6), roll=TRUE] # locf rolling join
kDT[.("a", 3:6), roll=Inf] # same as above
kDT[.("a", 3:6), roll=-Inf] # nocb rolling join
kDT[!.(("a"))] # not join
kDT[!"a"] # same

# more on special symbols, see also ?"special-symbols"
DT[.N] # last row
DT[, .N] # total number of rows in DT
DT[, .N, by=x] # number of rows in each group
DT[, .SD, .SDcols=x:y] # select columns 'x' and 'y'
DT[, .SD[1]] # first row of all columns
DT[, .SD[1], by=x] # first row of 'y' and 'v' for each group in 'x'
DT[, c(.N, lapply(.SD, sum)), by=x] # get rows *and* sum columns 'v' and 'y' by group
DT[, .I[1], by=x] # row number in DT corresponding to each group
DT[, grp := .GRP, by=x] # add a group counter column
X[, DT[.BY, y, on="x"], by=x] # join within each group

# add/update/delete by reference (see ?assign)
print(DT[, z:=42L]) # add new column by reference
print(DT[, z:=NULL]) # remove column by reference
print(DT["a", v:=42L, on="x"]) # subassign to existing v column by reference
print(DT["b", v2:=84L, on="x"]) # subassign to new column by reference (NA padded)

DT[, m:=mean(v), by=x][[]] # add new column by reference by group
# NB: postfix [] is shortcut to print()

# advanced usage
DT = data.table(x=rep(c("b","a","c"),each=3), v=c(1,1,1,2,2,1,1,2,2), y=c(1,3,6), a=1:9, b=9:1)

DT[, sum(v), by=(y%2)] # expressions in by
DT[, sum(v), by=(bool = y%2)] # same, using a named list to change by column name
DT[, .SD[2], by=x] # get 2nd row of each group
DT[, tail(.SD,2), by=x] # last 2 rows of each group

```

```

DT[, lapply(.SD, sum), by=x]           # sum of all (other) columns for each group
DT[, .SD[which.min(v)], by=x]        # nested query by group

DT[, list(MySum=sum(v),
          MyMin=min(v),
          MyMax=max(v)),
      by=.(x, y%2)]                  # by 2 expressions

DT[, .(a = .(a), b = .(b)), by=x]    # list columns
DT[, .(seq = min(a):max(b)), by=x]   # j is not limited to just aggregations
DT[, sum(v), by=x][V1<20]           # compound query
DT[, sum(v), by=x][order(-V1)]       # ordering results
DT[, c(.N, lapply(.SD,sum)), by=x]   # get number of observations and sum per group
DT[, {tmp <- mean(y);
      .(a = a-tmp, b = b-tmp)
    }, by=x]                         # anonymous lambda in 'j', j accepts any valid
                                     # expression. TO REMEMBER: every element of
                                     # the list becomes a column in result.

pdf("new.pdf")
DT[, plot(a,b), by=x]                # can also plot in 'j'
dev.off()

# using rleid, get max(y) and min of all cols in .SDcols for each consecutive run of 'v'
DT[, c(.(y=max(y)), lapply(.SD, min)), by=rleid(v), .SDcols=v:b]

# Follow r-help posting guide, SUPPORT is here (*not* r-help) :
# http://stackoverflow.com/questions/tagged/data.table
# or
# datatable-help@lists.r-forge.r-project.org

## Not run:
vignette("datatable-intro")
vignette("datatable-reference-semantics")
vignette("datatable-keys-fast-subset")
vignette("datatable-secondary-indices-and-auto-indexing")
vignette("datatable-reshape")
vignette("datatable-faq")

test.data.table()                    # over 5700 low level tests

# keep up to date with latest stable version on CRAN
update.packages()
# get the latest devel (needs Rtools for windows, xcode for mac)
install.packages("data.table", repos = "https://Rdatatable.github.io/data.table", type = "source")

## End(Not run)

```

Description

Fast add, remove and update subsets of columns, by reference. := operator can be used in two ways: LHS := RHS form, and Functional form. See Usage.

set is a low overhead loopable version of :=. It is particularly useful for repetitively updating rows of certain columns by reference (using a for-loop). See Examples. It can not perform grouping operations.

Usage

```
# 1. LHS := RHS form
# DT[i, LHS := RHS, by = ...]
# DT[i, c("LHS1", "LHS2") := list(RHS1, RHS2), by = ...]

# 2. Functional form
# DT[i, `:=`(LHS1 = RHS1,
#           LHS2 = RHS2,
#           ...), by = ...]

set(x, i = NULL, j, value)
```

Arguments

LHS	A character vector of column names (or numeric positions) or a variable that evaluates as such. If the column doesn't exist, it is added, <i>by reference</i> .
RHS	A list of replacement values. It is recycled in the usual way to fill the number of rows satisfying i, if any. To remove a column use NULL.
x	A data.table. Or, set() accepts data.frame, too.
i	Optional. Indicates the rows on which the values must be updated with. If not provided, implies <i>all rows</i> . The := form is more powerful as it allows <i>subsets</i> and <i>joins</i> based add/update columns by reference. See Details. In set, only integer type is allowed in i indicating which rows value should be assigned to. NULL represents all rows more efficiently than creating a vector such as 1:nrow(x).
j	Column name(s) (character) or number(s) (integer) to be assigned value when column(s) already exist, and only column name(s) if they are to be added newly.
value	A list of replacement values to assign by reference to x[i, j].

Details

:= is defined for use in j only. It *adds* or *updates* or *removes* column(s) by reference. It makes no copies of any part of memory at all. Read the [Reference Semantics HTML vignette](#) to follow with examples. Some typical usages are:

```
DT[, col := val]           # update (or add at the end if doesn't exist) a column call
DT[i, col := val]        # same as above, but only for those rows specified in i and
DT[i, "col a" := val]    # same. column is called "col a"
DT[i, (3:6) := val]      # update existing columns 3:6 with value. Aside: parens ar
```

```

DT[i, colvector := val, with = FALSE]      # OLD syntax. The contents of "colvector" in calling so
DT[i, (colvector) := val]                  # same (NOW PREFERRED) shorthand syntax. The parens are e
DT[i, colC := mean(colB), by = colA]       # update (or add) column called "colC" by reference by
DT[, `:=`(new1 = sum(colB), new2 = sum(colC))] # Functional form

```

All of the following result in a friendly error (by design) :

```

x := 1L
DT[i, col] := val
DT[i]$col := val
DT[, {col1 := 1L; col2 := 2L}]             # Use the functional form, `:=`() , instead (see above).

```

For additional resources, check the [FAQs vignette](#). Also have a look at StackOverflow's [data.table](#) tag.

`:=` in `j` can be combined with all types of `i` (such as binary search), and all types of `by`. This is one reason why `:=` has been implemented in `j`. See the [Reference Semantics HTML vignette](#) and also FAQ 2.16 for analogies to SQL.

When LHS is a factor column and RHS is a character vector with items missing from the factor levels, the new level(s) are automatically added (by reference, efficiently), unlike base methods.

Unlike `<-` for `data.frame`, the (potentially large) LHS is not coerced to match the type of the (often small) RHS. Instead the RHS is coerced to match the type of the LHS, if necessary. Where this involves double precision values being coerced to an integer column, a warning is given (whether or not fractional data is truncated). The motivation for this is efficiency. It is best to get the column types correct up front and stick to them. Changing a column type is possible but deliberately harder: provide a whole column as the RHS. This RHS is then *plonked* into that column slot and we call this *plonk syntax*, or *replace column syntax* if you prefer. By needing to construct a full length vector of a new type, you as the user are more aware of what is happening, and it's clearer to readers of your code that you really do intend to change the column type.

`data.tables` are *not* copied-on-change by `:=`, `setkey` or any of the other `set*` functions. See [copy](#).

Value

DT is modified by reference and returned invisibly. If you require a copy, take a [copy](#) first (using `DT2 = copy(DT)`).

Advanced (internals):

It is easy to see how *sub-assigning* to existing columns is done internally. Removing columns by reference is also straightforward by modifying the vector of column pointers only (using `memmove` in C). However adding (new) columns is more tricky as to how the `data.table` can be grown *by reference*: the list vector of column pointers is *over-allocated*, see [truelength](#). By defining `:=` in `j` we believe update syntax is natural, and scales, but it also bypasses `[<-` dispatch and allows `:=` to update by reference with no copies of any part of memory at all.

Since `[.data.table` incurs overhead to check the existence and type of arguments (for example), `set()` provides direct (but less flexible) assignment by reference with low overhead, appropriate for use inside a for loop. See examples. `:=` is more powerful and flexible than `set()` because `:=` is intended to be combined with `i` and `by` in single queries on large datasets.

Note:

`DT[a > 4, b := c]` is different from `DT[a > 4][, b := c]`. The first expression updates (or adds) column `b` with the value `c` on those rows where `a > 4` evaluates to `TRUE`. `X` is updated *by reference*, therefore no assignment needed.

The second expression on the other hand updates a *new* `data.table` that's returned by the subset operation. Since the subsetted `data.table` is ephemeral (it is not assigned to a symbol), the result would be lost; unless the result is assigned, for example, as follows: `ans <- DT[a > 4][, b := c]`.

See Also

[data.table](#), [copy](#), [alloc.col](#), [truelength](#), [set](#)

Examples

```
DT = data.table(a = LETTERS[c(3L,1:3)], b = 4:7)
DT[, c := 8]           # add a numeric column, 8 for all rows
DT[, d := 9L]         # add an integer column, 9L for all rows
DT[, c := NULL]       # remove column c
DT[2, d := -8L]       # subassign by reference to d; 2nd row is -8L now
DT                    # DT changed by reference
DT[2, d := 10L][]     # shorthand for update and print

DT[b > 4, b := d * 2L] # subassign to b with d*2L on those rows where b > 4 is TRUE
DT[b > 4][, b := d * 2L] # different from above. [, := ] is performed on the subset
                        # which is an new (ephemeral) data.table. Result needs to be
                        # assigned to a variable (using `<-`).

DT[, e := mean(d), by = a] # add new column by group by reference
DT["A", b := 0L, on = "a"] # ad-hoc update of column b for group "A" using
  # joins-as-subsets with binary search and 'on='
# same as above but using keys
setkey(DT, a)
DT["A", b := 0L]       # binary search for group "A" and set column b using keys
DT["B", f := mean(d)] # subassign to new column, NA initialized

## Not run:
# Speed example ...

m = matrix(1, nrow = 2e6L, ncol = 100L)
DF = as.data.frame(m)
DT = as.data.table(m)

system.time(for (i in 1:1000) DF[i, 1] = i)
# 15.856 seconds
system.time(for (i in 1:1000) DT[i, V1 := i])
# 0.279 seconds (57 times faster)
system.time(for (i in 1:1000) set(DT, i, 1L, i))
# 0.002 seconds (7930 times faster, overhead of [.data.table is avoided)

# However, normally, we call [.data.table *once* on *large* data, not many times on small data.
# The above is to demonstrate overhead, not to recommend looping in this way. But the option
```

```
# of set() is there if you need it.
## End(Not run)
```

address	<i>Address in RAM of a variable</i>
---------	-------------------------------------

Description

Returns the pointer address of its argument.

Usage

```
address(x)
```

Arguments

x Anything.

Details

Sometimes useful in determining whether a value has been copied or not, programatically.

Value

A character vector length 1.

References

<http://stackoverflow.com/a/10913296/403310> (but implemented in C without using `.Internal(inspect())`)

all.equal	<i>Equality Test Between Two Data Tables</i>
-----------	--

Description

Convenient test of data equality between `data.table` objects. Performs some factor level *stripping*.

Usage

```
## S3 method for class 'data.table'
all.equal(target, current, trim.levels=TRUE, check.attributes=TRUE,
  ignore.col.order=FALSE, ignore.row.order=FALSE, tolerance=sqrt(.Machine$double.eps),
  ...)
```


Arguments

target, current	data.tables to compare
trim.levels	A logical indicating whether or not to remove all unused levels in columns that are factors before running equality check. It effect only when check.attributes is TRUE and ignore.row.order is FALSE.
check.attributes	A logical indicating whether or not to check attributes, will apply not only to data.table but also attributes of the columns. It will skip c("row.names", ".internal.selfref") data.table attributes.
ignore.col.order	A logical indicating whether or not to ignore columns order in data.table.
ignore.row.order	A logical indicating whether or not to ignore rows order in data.table. This option requires datasets to use data types on which join can be made, so no support for <i>list</i> , <i>complex</i> , <i>raw</i> , but still supports integer64 .
tolerance	A numeric value used when comparing numeric columns, by default <code>sqrt(.Machine\$double.eps)</code> . Unless non-default value provided it will be forced to 0 if used together with <code>ignore.row.order</code> and duplicate rows detected or factor columns present.
...	Passed down to internal call of all.equal .

Details

For efficiency data.table method will exit on detected non-equality issues, unlike most [all.equal](#) methods which process equality checks further. Besides that fact it also handles the most time consuming case of `ignore.row.order = TRUE` very efficiently.

Value

Either TRUE or a vector of mode "character" describing the differences between target and current.

See Also

[all.equal](#)

Examples

```
dt1 <- data.table(A = letters[1:10], X = 1:10, key = "A")
dt2 <- data.table(A = letters[5:14], Y = 1:10, key = "A")
isTRUE(all.equal(dt1, dt1))
is.character(all.equal(dt1, dt2))

# ignore.col.order
x <- copy(dt1)
y <- dt1[, .(X, A)]
all.equal(x, y)
all.equal(x, y, ignore.col.order = TRUE)
```

```

# ignore.row.order
x <- setkeyv(copy(dt1), NULL)
y <- dt1[sample(nrow(dt1))]
all.equal(x, y)
all.equal(x, y, ignore.row.order = TRUE)

# check.attributes
x = copy(dt1)
y = setkeyv(copy(dt1), NULL)
all.equal(x, y)
all.equal(x, y, check.attributes = FALSE)

# trim.levels
x <- data.table(A = factor(letters[1:10])[1:4]) # 10 levels
y <- data.table(A = factor(letters[1:5])[1:4]) # 5 levels
all.equal(x, y, trim.levels = FALSE)
all.equal(x, y, trim.levels = FALSE, check.attributes = FALSE)
all.equal(x, y)

```

as.data.table

Coerce to data.table

Description

Functions to check if an object is `data.table`, or coerce it if possible.

Usage

```
as.data.table(x, keep.rownames=FALSE, ...)
```

```
## S3 method for class 'data.table'
as.data.table(x, ...)
```

```
is.data.table(x)
```

Arguments

<code>x</code>	An R object.
<code>keep.rownames</code>	Default is <code>FALSE</code> . If <code>TRUE</code> , adds the input object's names as a separate column named <code>"rn"</code> . <code>keep.rownames = "id"</code> names the column <code>"id"</code> instead.
<code>...</code>	Additional arguments to be passed to or from other methods.

Details

`as.data.table` is a generic function with many methods, and other packages can supply further methods.

If a list is supplied, each element is converted to a column in the `data.table` with shorter elements recycled automatically. Similarly, each column of a matrix is converted separately.

character objects are *not* converted to factor types unlike `as.data.frame`.

If a `data.frame` is supplied, all classes preceding "data.frame" are stripped. Similarly, for `data.table` as input, all classes preceding "data.table" are stripped. `as.data.table` methods returns a *copy* of original data. To modify by reference see [setDT](#) and [setDF](#).

`keep.rownames` argument can be used to preserve the (row)names attribute in the resulting `data.table`.

See Also

[data.table](#), [setDT](#), [setDF](#), [copy](#), [setkey](#), [J](#), [SJ](#), [CJ](#), [merge.data.table](#), [:=](#), [alloc.col](#), [truelength](#), [rbindlist](#), [setNumericRounding](#), [datatable-optimize](#)

Examples

```
nn = c(a=0.1, b=0.2, c=0.3, d=0.4)
as.data.table(nn)
as.data.table(nn, keep.rownames=TRUE)
as.data.table(nn, keep.rownames="rownames")

# char object not converted to factor
cc = c(X="a", Y="b", Z="c")
as.data.table(cc)
as.data.table(cc, keep.rownames=TRUE)
as.data.table(cc, keep.rownames="rownames")

mm = matrix(1:4, ncol=2, dimnames=list(c("r1", "r2"), c("c1", "c2")))
as.data.table(mm)
as.data.table(mm, keep.rownames=TRUE)
as.data.table(mm, keep.rownames="rownames")

ll = list(a=1:2, b=3:4)
as.data.table(ll)
as.data.table(ll, keep.rownames=TRUE)
as.data.table(ll, keep.rownames="rownames")

df = data.frame(x=rep(c("x","y","z"),each=2), y=c(1,3,6), row.names=LETTERS[1:6])
as.data.table(df)
as.data.table(df, keep.rownames=TRUE)
as.data.table(df, keep.rownames="rownames")

dt = data.table(x=rep(c("x","y","z"),each=2), y=c(1:6))
as.data.table(dt)
```

Description

Efficient conversion xts to data.table.

Usage

```
## S3 method for class 'xts'
as.data.table(x, keep.rownames = TRUE, ...)
```

Arguments

```
x                xts to convert to data.table
keep.rownames    keep xts index as index column in result data.table
...              ignored, just for consistency with as.data.table
```

See Also

[as.xts.data.table](#)

Examples

```
## Not run:
data(sample_matrix, package = "xts")
sample.xts <- xts::as.xts(sample_matrix) # xts might not be attached on search path
# print head of xts
print(head(sample.xts))
# print dt
print(as.data.table(sample.xts))

## End(Not run)
```

as.xts.data.table	<i>Efficient data.table to xts conversion</i>
-------------------	---

Description

Efficient conversion of data.table to xts, data.table must have *POSIXct* or *Date* type in first column.

Usage

```
as.xts.data.table(x, ...)
```

Arguments

```
x                data.table to convert to xts, must have POSIXct or Date in the first column. All
                  others non-numeric columns will be omitted with warning.
...              ignored, just for consistency with generic method.
```

See Also[as.data.table.xts](#)**Examples**

```
## Not run:
sample.dt <- data.table(date = as.Date((Sys.Date()-999):Sys.Date(),origin="1970-01-01"),
  quantity = sample(10:50,1000,TRUE),
  value = sample(100:1000,1000,TRUE))

# print dt
print(sample.dt)
# print head of xts
print(head(as.xts.data.table(sample.dt))) # xts might not be attached on search path

## End(Not run)
```

between

*Convenience functions for range subsets.***Description**

Intended for use in `i` in `[.data.table]`.

`between` is equivalent to `x >= lower & x <= upper` when `incbounds=TRUE`, or `x > lower & y < upper` when `FALSE`.

`inrange` checks whether each value in `x` is in between any of the intervals provided in `lower`, `upper`.

Usage

```
between(x, lower, upper, incbounds=TRUE)
```

```
x %between% y
```

```
inrange(x, lower, upper, incbounds=TRUE)
```

```
x %inrange% y
```

Arguments

<code>x</code>	Any orderable vector, i.e., those with relevant methods for <code>`<=`</code> , such as <code>numeric</code> , <code>character</code> , <code>Date</code> , etc. in case of <code>between</code> and a numeric vector in case of <code>inrange</code> .
<code>lower</code>	Lower range bound.
<code>upper</code>	Upper range bound.
<code>y</code>	A length-2 vector or list, with <code>y[[1]]</code> interpreted as <code>lower</code> and <code>y[[2]]</code> as <code>upper</code> .
<code>incbounds</code>	<code>TRUE</code> means inclusive bounds, i.e., <code>[lower,upper]</code> . <code>FALSE</code> means exclusive bounds, i.e., <code>(lower,upper)</code> . It is set to <code>TRUE</code> by default for infix notations.

Details

From v1.9.8+, `between` is vectorised. `lower` and `upper` are recycled to `length(x)` if necessary.

non-equi joins were recently implemented in v1.9.8. It extends binary search based joins in `data.table` to other binary operators including `>=`, `<=`, `>`, `<`. `inrange` makes use of this new functionality and performs a range join.

Value

Logical vector as the same length as `x` with value `TRUE` for those that lie within the specified range.

Note

Current implementation does not make use of ordered keys for `%between%`.

See Also

[data.table](#), [like](#), [%chin%](#)

Examples

```
X = data.table(a=1:5, b=6:10, c=c(5:1))
X[b %between% c(7,9)]
X[between(b, 7, 9)] # same as above
# NEW feature in v1.9.8, vectorised between
X[c %between% list(a,b)]
X[between(c, a, b)] # same as above
X[between(c, a, b, incbounds=FALSE)] # open interval

# inrange()
Y = data.table(a=c(8,3,10,7,-10), val=runif(5))
range = data.table(start = 1:5, end = 6:10)
Y[a %inrange% range]
Y[inrange(a, range$start, range$end)] # same as above
Y[inrange(a, range$start, range$end, incbounds=FALSE)] # open interval
```

chmatch

Faster match of character vectors

Description

`chmatch` returns a vector of the positions of (first) matches of its first argument in its second. Both arguments must be character vectors.

`%chin%` is like `%in%`, but for character vectors.

Usage

```
chmatch(x, table, nomatch=NA_integer_)
x %chin% table
chorder(x)
chgroup(x)
```

Arguments

x	character vector: the values to be matched, or the values to be ordered or grouped
table	character vector: the values to be matched against.
nomatch	the value to be returned in the case when no match is found. Note that it is coerced to integer.

Details

Fast versions of `match`, `%in%` and `order`, optimised for character vectors. `chgroup` groups together duplicated values but retains the group order (according the first appearance order of each group), efficiently. They have been primarily developed for internal use by `data.table`, but have been exposed since that seemed appropriate.

Strings are already cached internally by R (CHARSXP) and that is utilised by these functions. No hash table is built or cached, so the first call is the same speed as subsequent calls. Essentially, a counting sort (similar to `base::sort.list(x, method="radix")`, see [setkey](#)) is implemented using the (almost) unused `truelength` of CHARSXP as the counter. *Where R has used `truelength` of CHARSXP (where a character value is shared by a variable name), the non zero `truelengths` are stored first and reinstated afterwards.* Each of the `ch*` functions implements a variation on this theme. Remember that internally in R, `length` of a CHARSXP is the `nchar` of the string and `DATAPTR` is the string itself.

Methods that do build and cache a hash table (such as the [fastmatch package](#)) are *much* faster on subsequent calls (almost instant) but a little slower on the first. Therefore `chmatch` may be particularly suitable for ephemeral vectors (such as local variables in functions) or tasks that are only done once. Much depends on the length of `x` and `table`, how many unique strings each contains, and whether the position of the first match is all that is required.

It may be possible to speed up `fastmatch`'s hash table build time by using the technique in `data.table`, and we have suggested this to its author. If successful, `fastmatch` would then be fastest in all cases.

Value

As `match` and `%in%`. `chorder` and `chgroup` return an integer index vector.

Note

The name `chmatch` was taken by [charmatch](#), hence `chmatch`.

See Also

[match](#), [%in%](#), [fmatch](#)

Examples

```

# Please type 'example(chmatch)' to run this and see timings on your machine

# N is set small here (1e5) because CRAN runs all examples and tests every night, to catch
# any problems early as R itself changes and other packages run.
# The comments here apply when N has been changed to 1e7.
N = 1e5

u = as.character(as.hexmode(1:10000))
y = sample(u,N,replace=TRUE)
x = sample(u)

# With N=1e7 ...
system.time(a <- match(x,y))      # 4.8s
system.time(b <- chmatch(x,y))    # 0.9s  Faster than 1st fmatch
identical(a,b)
if (fastmatchloaded<-suppressWarnings(require(fastmatch))) {
  print(system.time(c <- fmatch(x,y))) # 2.1s  Builds and caches hash
  print(system.time(c <- fmatch(x,y))) # 0.00s  Uses hash
  identical(a,c)
}

system.time(a <- x %in% y)        # 4.8s
system.time(b <- x %chin% y)     # 0.9s
identical(a,b)
if (fastmatchloaded) {
  match <- fmatch                # fmatch is drop in replacement
  print(system.time(c <- match(x,y))) # 0.00s
  print(system.time(c <- x %in% y))  # 4.8s  %in% still prefers base::match
  # Anyone know how to get %in% to use fmatch (without masking %in% too)?
  rm(match)
  identical(a,c)
}

# Different example with more unique strings ...
u = as.character(as.hexmode(1:(N/10)))
y = sample(u,N,replace=TRUE)
x = sample(u,N,replace=TRUE)
system.time(a <- match(x,y))      # 34.0s
system.time(b <- chmatch(x,y))    # 6.4s
identical(a,b)
if (fastmatchloaded) {
  print(system.time(c <- fmatch(x,y))) # 7.9s
  print(system.time(c <- fmatch(x,y))) # 4.0s
  identical(a,c)
}

```


Description

In `data.table` parlance, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory, which is as large as one column.. The only other `data.table` operator that modifies input by reference is `:=`. Check out the See Also section below for other `set*` function `data.table` provides.

`copy()` copies an entire object.

Usage

```
copy(x)
```

Arguments

x A `data.table`.

Details

`data.table` provides functions that operate on objects *by reference* and minimise full object copies as much as possible. Still, it might be necessary in some situations to work on an object's copy which can be done using `DT.copy <- copy(DT)`. It may also be sometimes useful before `:=` (or `set`) is used to subassign to a column by reference.

A `copy()` may be required when doing `dt_names = names(DT)`. Due to R's *copy-on-modify*, `dt_names` still points to the same location in memory as `names(DT)`. Therefore modifying `DT` *by reference* now, say by adding a new column, `dt_names` will also get updated. To avoid this, one has to *explicitly* copy: `dt_names <- copy(names(DT))`.

Value

Returns a copy of the object.

See Also

[data.table](#), [setkey](#), [setDT](#), [setDF](#), [set :=](#), [setorder](#), [setattr](#), [setnames](#)

Examples

```
# Type 'example(copy)' to run these at prompt and browse output

DT = data.table(A=5:1,B=letters[5:1])
DT2 = copy(DT)           # explicit copy() needed to copy a data.table
setkey(DT2,B)           # now just changes DT2
identical(DT,DT2)       # FALSE. DT and DT2 are now different tables

DT = data.table(A=5:1, B=letters[5:1])
nm1 = names(DT)
nm2 = copy(names(DT))
DT[, C := 1L]
identical(nm1, names(DT)) # TRUE, nm1 is also changed by reference
identical(nm2, names(DT)) # FALSE, nm2 is a copy, different from names(DT)
```

data.table-class *S4 Definition for data.table*

Description

A data.table can be used in S4 class definitions as either a parent class (inside a contains argument of setClass), or as an element of an S4 slot.

Author(s)

Steve Lianoglou

See Also

[data.table](#)

Examples

```
## Used in inheritance.
setClass('SuperDataTable', contains='data.table')

## Used in a slot
setClass('Something', representation(x='character', dt='data.table'))
x <- new("Something", x='check', dt=data.table(a=1:10, b=11:20))
```

datatable.optimize *Optimisations in data.table*

Description

data.table internally optimises certain expressions in order to improve performance. This section briefly summarises those optimisations.

Note that there's no additional input needed from the user to take advantage of these optimisations. They happen automatically.

Run the code under the *example* section to get a feel for the performance benefits from these optimisations.

Details

data.table reads the global option datatable.optimize to figure out what level of optimisation is required. The default value Inf activates *all* available optimisations.

At optimisation level ≥ 1 , i.e., `getOption("datatable.optimize") ≥ 1` , these are the optimisations:

- The base function `order` is internally replaced with data.table's *fast ordering*. That is, `dt[order(...)]` gets internally optimised to `dt[forder(...)]`.

- The expression `dt[, lapply(.SD, fun), by=.]` gets optimised to `dt[, list(fun(a), fun(b), ...), by=.]` where `a, b, ...` are columns in `.SD`. This improves performance tremendously.
- Similarly, the expression `dt[, c(.N, lapply(.SD, fun)), by=.]` gets optimised to `dt[, list(.N, fun(a), fun(b), ...)]`. `.N` is just for example here.
- `base::mean` function is internally optimised to use `data.table`'s `fastmean` function. `mean()` from `base` is an S3 generic and gets slow with many groups.

At optimisation level `>= 2`, i.e., `getOption("datatable.optimize") >= 2`, additional optimisations are implemented on top of the optimisations already shown above.

- When expressions in `j` which contains only these functions `min`, `max`, `mean`, `median`, `var`, `sd`, `prod`, for example, `dt[, list(mean(x), median(x), min(y), max(y)), by=z]`, they are very effectively optimised using, what we call, *GForce*. These functions are replaced with `gmean`, `gmedian`, `gmin`, `gmax` instead.
Normally, once the rows belonging to each groups are identified, the values corresponding to the group is gathered and the `j`-expression is evaluated. This can be improved by computing the result directly without having to gather the values or evaluating the expression for each group (which can get costly with large number of groups) by implementing it specifically for a particular function. As a result, it is extremely fast.
- In addition to all the functions above, `'N'` is also optimised to use *GForce*. It when used separately or combined with the functions mentioned above still uses *GForce*.
- Expressions of the form `DT[i, j, by]` are also optimised when `i` is a *subset* operation and `j` is any/all of the functions discussed above.

Auto indexing: `data.table` also allows for blazing fast subsets by creating an *index* on the first run. Any successive subsets on the same column then reuses this index to *binary search* (instead of *vector scan*) and is therefore fast.

At the moment, expressions of the form `dt[col == val]` and `dt[col %in% val]` are both optimised. We plan to expand this to more operators and conditions in the future.

Auto indexing can be switched off with the global option `options(datatable.auto.index = FALSE)`. To switch off using existing indices set global option `options(datatable.use.index = FALSE)`.

See Also

[setNumericRounding](#), [getNumericRounding](#)

Examples

```
## Not run:
# Generate a big data.table with a relatively many columns
set.seed(1L)
dt = lapply(1:20, function(x) sample(c(-100:100), 5e6L, TRUE))
setDT(dt)[, id := sample(1e5, 5e6, TRUE)]
print(object.size(dt), units="Mb") # 400MB, not huge, but will do

# 'order' optimisation
options(datatable.optimize = 1L) # optimisation 'on'
system.time(ans1 <- dt[order(id)])
```

```

options(datatable.optimize = 0L) # optimisation 'off'
system.time(ans2 <- dt[order(id)])
identical(ans1, ans2)

# optimisation of 'lapply(.SD, fun)'
options(datatable.optimize = 1L) # optimisation 'on'
system.time(ans1 <- dt[, lapply(.SD, min), by=id])
options(datatable.optimize = 0L) # optimisation 'off'
system.time(ans2 <- dt[, lapply(.SD, min), by=id])
identical(ans1, ans2)

# optimisation of 'mean'
options(datatable.optimize = 1L) # optimisation 'on'
system.time(ans1 <- dt[, lapply(.SD, mean), by=id])
system.time(ans2 <- dt[, lapply(.SD, base::mean), by=id])
identical(ans1, ans2)

# optimisation of 'c(.N, lapply(.SD, ))'
options(datatable.optimize = 1L) # optimisation 'on'
system.time(ans1 <- dt[, c(.N, lapply(.SD, min)), by=id])
options(datatable.optimize = 0L) # optimisation 'off'
system.time(ans2 <- dt[, c(N=.N, lapply(.SD, min)), by=id])
identical(ans1, ans2)

# GForce
options(datatable.optimize = 2L) # optimisation 'on'
system.time(ans1 <- dt[, lapply(.SD, median), by=id])
system.time(ans2 <- dt[, lapply(.SD, function(x) as.numeric(stats::median(x))), by=id])
identical(ans1, ans2)

# restore optimization
options(datatable.optimize = Inf)

# auto indexing
options(datatable.auto.index = FALSE)
system.time(ans1 <- dt[id == 100L]) # vector scan
system.time(ans2 <- dt[id == 100L]) # vector scan
system.time(dt[id

options(datatable.auto.index = TRUE)
system.time(ans1 <- dt[id == 100L]) # index + binary search subset
system.time(ans2 <- dt[id == 100L]) # only binary search subset
system.time(dt[id

## End(Not run)

```

Description

`dcast.data.table` is a much faster version of `reshape2::dcast`, but for `data.tables`. More importantly, it's capable of handling very large data quite efficiently in terms of memory usage in comparison to `reshape2::dcast`.

From 1.9.6, `dcast` is implemented as an S3 generic in `data.table`. To melt or cast `data.tables`, it is not necessary to load `reshape2` anymore. If you have load `reshape2`, do so before loading `data.table` to prevent unwanted masking.

NEW: `dcast.data.table` can now cast multiple `value.var` columns and also accepts multiple functions to `fun.aggregate`. See Examples for more.

Usage

```
## S3 method for class 'data.table'
dcast(data, formula, fun.aggregate = NULL, sep = "_",
      ..., margins = NULL, subset = NULL, fill = NULL,
      drop = TRUE, value.var = guess(data),
      verbose = getOption("datatable.verbose"))
```

Arguments

<code>data</code>	A <code>data.table</code> .
<code>formula</code>	A formula of the form LHS ~ RHS to cast, see Details.
<code>fun.aggregate</code>	Should the data be aggregated before casting? If the formula doesn't identify a single observation for each cell, then aggregation defaults to length with a message. NEW: it is possible to provide a list of functions to <code>fun.aggregate</code> . See Examples.
<code>sep</code>	Character vector of length 1, indicating the separating character in variable names generated during casting. Default is <code>_</code> for backwards compatibility.
<code>...</code>	Any other arguments that may be passed to the aggregating function.
<code>margins</code>	Not implemented yet. Should take variable names to compute margins on. A value of <code>TRUE</code> would compute all margins.
<code>subset</code>	Specified if casting should be done on a subset of the data. Ex: <code>subset = .(col1 <= 5)</code> or <code>subset = .(variable != "January")</code> .
<code>fill</code>	Value with which to fill missing cells. If <code>fun.aggregate</code> is present, takes the value by applying the function on a 0-length vector.
<code>drop</code>	<code>FALSE</code> will cast by including all missing combinations. NEW: Following #1512 , <code>c(FALSE, TRUE)</code> will only include all missing combinations of formula LHS. And <code>c(TRUE, FALSE)</code> will only include all missing combinations of formula RHS. See Examples.
<code>value.var</code>	Name of the column whose values will be filled to cast. Function <code>'guess()'</code> tries to, well, guess this column automatically, if none is provided. NEW: it is now possible to cast multiple <code>value.var</code> columns simultaneously. See Examples.
<code>verbose</code>	Not used yet. May be dropped in the future or used to provide informative messages through the console.

Details

The cast formula takes the form LHS ~ RHS, ex: `var1 + var2 ~ var3`. The order of entries in the formula is essential. There are two special variables: `.` and `...`. `.` represents no variable; `...` represents all variables not otherwise mentioned in formula; see Examples.

`dcast` also allows `value.var` columns of type `list`.

When variable combinations in formula doesn't identify a unique value in a cell, `fun.aggregate` will have to be specified, which defaults to `length` if unspecified. The aggregating function should take a vector as input and return a single value (or a list of length one) as output. In cases where `value.var` is a list, the function should be able to handle a list input and provide a single value or list of length one as output.

If the formula's LHS contains the same column more than once, ex: `dcast(DT, x+x~ y)`, then the answer will have duplicate names. In those cases, the duplicate names are renamed using `make.unique` so that key can be set without issues.

Names for columns that are being cast are generated in the same order (separated by an underscore, `_`) from the (unique) values in each column mentioned in the formula RHS.

From v1.9.4, `dcast` tries to preserve attributes wherever possible.

NEW: From v1.9.6, it is possible to cast multiple `value.var` columns and also cast by providing multiple `fun.aggregate` functions. Multiple `fun.aggregate` functions should be provided as a list, for e.g., `list(mean, sum, function(x) paste(x, collapse=""))`. `value.var` can be either a character vector or list of length=1, or a list of length equal to `length(fun.aggregate)`. When `value.var` is a character vector or a list of length 1, each function mentioned under `fun.aggregate` is applied to every column specified under `value.var` column. When `value.var` is a list of length equal to `length(fun.aggregate)` each element of `fun.aggregate` is applied to each element of `value.var` column.

Value

A keyed `data.table` that has been cast. The key columns are equal to the variables in the formula LHS in the same order.

See Also

[melt.data.table](#), [rowid](#), <https://cran.r-project.org/package=reshape>

Examples

```
require(data.table)
names(ChickWeight) <- tolower(names(ChickWeight))
DT <- melt(as.data.table(ChickWeight), id=2:4) # calls melt.data.table

# dcast is a S3 method in data.table from v1.9.6
dcast(DT, time ~ variable, fun=mean)
dcast(DT, diet ~ variable, fun=mean)
dcast(DT, diet+chick ~ time, drop=FALSE)
dcast(DT, diet+chick ~ time, drop=FALSE, fill=0)

# using subset
dcast(DT, chick ~ time, fun=mean, subset=.(time < 10 & chick < 20))
```

```

# drop argument, #1512
DT <- data.table(v1 = c(1.1, 1.1, 1.1, 2.2, 2.2, 2.2),
                 v2 = factor(c(1L, 1L, 1L, 3L, 3L, 3L), levels=1:3),
                 v3 = factor(c(2L, 3L, 5L, 1L, 2L, 6L), levels=1:6),
                 v4 = c(3L, 2L, 2L, 5L, 4L, 3L))

# drop=TRUE
dcast(DT, v1 + v2 ~ v3) # default is drop=TRUE
dcast(DT, v1 + v2 ~ v3, drop=FALSE) # all missing combinations of both LHS and RHS
dcast(DT, v1 + v2 ~ v3, drop=c(FALSE, TRUE)) # all missing combinations of only LHS
dcast(DT, v1 + v2 ~ v3, drop=c(TRUE, FALSE)) # all missing combinations of only RHS

# using . and ...
DT <- data.table(v1 = rep(1:2, each = 6),
                 v2 = rep(rep(1:3, 2), each = 2),
                 v3 = rep(1:2, 6),
                 v4 = rnorm(6))
dcast(DT, ... ~ v3, value.var = "v4") #same as v1 + v2 ~ v3, value.var = "v4"
dcast(DT, v1 + v2 + v3 ~ ., value.var = "v4")

## for each combination of (v1, v2), add up all values of v4
dcast(DT, v1 + v2 ~ ., value.var = "v4", fun.aggregate = sum)

## Not run:
# benchmark against reshape2's dcast, minimum of 3 runs
set.seed(45)
DT <- data.table(aa=sample(1e4, 1e6, TRUE),
                 bb=sample(1e3, 1e6, TRUE),
                 cc = sample(letters, 1e6, TRUE), dd=runif(1e6))
system.time(dcast(DT, aa ~ cc, fun=sum)) # 0.12 seconds
system.time(dcast(DT, bb ~ cc, fun=mean)) # 0.04 seconds
# reshape2::dcast takes 31 seconds
system.time(dcast(DT, aa + bb ~ cc, fun=sum)) # 1.2 seconds

## End(Not run)

# NEW FEATURE - multiple value.var and multiple fun.aggregate
dt = data.table(x=sample(5,20,TRUE), y=sample(2,20,TRUE),
               z=sample(letters[1:2], 20,TRUE), d1 = runif(20), d2=1L)
# multiple value.var
dcast(dt, x + y ~ z, fun=sum, value.var=c("d1","d2"))
# multiple fun.aggregate
dcast(dt, x + y ~ z, fun=list(sum, mean), value.var="d1")
# multiple fun.agg and value.var (all combinations)
dcast(dt, x + y ~ z, fun=list(sum, mean), value.var=c("d1", "d2"))
# multiple fun.agg and value.var (one-to-one)
dcast(dt, x + y ~ z, fun=list(sum, mean), value.var=list("d1", "d2"))

```

Description

`duplicated` returns a logical vector indicating which rows of a `data.table` are duplicates of a row with smaller subscripts.

`unique` returns a `data.table` with duplicated rows removed, by columns specified in `by` argument. When no `by` then duplicated rows by all columns are removed.

`anyDuplicated` returns the *index* `i` of the first duplicated entry if there is one, and 0 otherwise.

`uniqueN` is equivalent to `length(unique(x))` when `x` is an atomic vector, and `nrow(unique(x))` when `x` is a `data.frame` or `data.table`. The number of unique rows are computed directly without materialising the intermediate unique `data.table` and is therefore faster and memory efficient.

Usage

```
## S3 method for class 'data.table'
duplicated(x, incomparables=FALSE, fromLast=FALSE, by=seq_along(x), ...)

## S3 method for class 'data.table'
unique(x, incomparables=FALSE, fromLast=FALSE, by=seq_along(x), ...)

## S3 method for class 'data.table'
anyDuplicated(x, incomparables=FALSE, fromLast=FALSE, by=seq_along(x), ...)

uniqueN(x, by=if (is.list(x)) seq_along(x) else NULL, na.rm=FALSE)
```

Arguments

<code>x</code>	A <code>data.table</code> . <code>uniqueN</code> accepts atomic vectors and <code>data.frames</code> as well.
<code>...</code>	Not used at this time.
<code>incomparables</code>	Not used. Here for S3 method consistency.
<code>fromLast</code>	logical indicating if duplication should be considered from the reverse side, i.e., the last (or rightmost) of identical elements would correspond to <code>duplicated = FALSE</code> .
<code>by</code>	character or integer vector indicating which combinations of columns from <code>x</code> to use for uniqueness checks. By default all columns are being used. That was changed recently for consistency to <code>data.frame</code> methods. In version < 1.9.8 default was <code>key(x)</code> .
<code>na.rm</code>	Logical (default is <code>FALSE</code>). Should missing values (including <code>NaN</code>) be removed?

Details

Because `data.tables` are usually sorted by key, tests for duplication are especially quick when only the keyed columns are considered. Unlike `unique.data.frame`, `paste` is not used to ensure equality of floating point data. It is instead accomplished directly and is therefore quite fast. `data.table` provides `setNumericRounding` to handle cases where limitations in floating point representation is undesirable.

v1.9.4 introduces `anyDuplicated` method for `data.tables` and is similar to base in functionality. It also implements the logical argument `fromLast` for all three functions, with default value `FALSE`.

Value

duplicated returns a logical vector of length nrow(x) indicating which rows are duplicates.

unique returns a data table with duplicated rows removed.

anyDuplicated returns a integer value with the index of first duplicate. If none exists, 0L is returned.

uniqueN returns the number of unique elements in the vector, data.frame or data.table.

See Also

[setNumericRounding](#), [data.table](#), [duplicated](#), [unique](#), [all.equal](#), [fsetdiff](#), [funion](#), [fintersect](#), [fsetequal](#)

Examples

```
DT <- data.table(A = rep(1:3, each=4), B = rep(1:4, each=3),
                 C = rep(1:2, 6), key = "A,B")
duplicated(DT)
unique(DT)

duplicated(DT, by="B")
unique(DT, by="B")

duplicated(DT, by=c("A", "C"))
unique(DT, by=c("A", "C"))

DT = data.table(a=c(2L,1L,2L), b=c(1L,2L,1L)) # no key
unique(DT) # rows 1 and 2 (row 3 is a duplicate of row 1)

DT = data.table(a=c(3.142, 4.2, 4.2, 3.142, 1.223, 1.223), b=rep(1,6))
unique(DT) # rows 1,2 and 5

DT = data.table(a=tan(pi*(1/4 + 1:10)), b=rep(1,10)) # example from ?all.equal
length(unique(DT$a)) # 10 strictly unique floating point values
all.equal(DT$a,rep(1,10)) # TRUE, all within tolerance of 1.0
DT[,which.min(a)] # row 10, the strictly smallest floating point value
identical(unique(DT),DT[1]) # TRUE, stable within tolerance
identical(unique(DT),DT[10]) # FALSE

# fromLast=TRUE
DT <- data.table(A = rep(1:3, each=4), B = rep(1:4, each=3),
                 C = rep(1:2, 6), key = "A,B")
duplicated(DT, by="B", fromLast=TRUE)
unique(DT, by="B", fromLast=TRUE)

# anyDuplicated
anyDuplicated(DT, by=c("A", "B")) # 3L
any(duplicated(DT, by=c("A", "B"))) # TRUE

# uniqueN, unique rows on key columns
uniqueN(DT, by = key(DT))
```

```
# uniqueN, unique rows on all columns
uniqueN(DT)
# uniqueN while grouped by "A"
DT[, .(uN=uniqueN(.SD)), by=A]

# uniqueN's na.rm=TRUE
x = sample(c(NA, NaN, runif(3)), 10, TRUE)
uniqueN(x, na.rm = FALSE) # 5, default
uniqueN(x, na.rm=TRUE) # 3
```

first

First item of an object

Description

Returns the first item of a vector or list, or the first row of a `data.frame` or `data.table`.

Usage

```
first(x, ...)
```

Arguments

<code>x</code>	A vector, list, <code>data.frame</code> or <code>data.table</code> . Otherwise the S3 method of <code>xts::first</code> is deployed.
<code>...</code>	Not applicable for <code>data.table::first</code> . Any arguments here are passed through to <code>xts::first</code> .

Value

If no other arguments are supplied it depends on the type of `x`. The first item of a vector or list. The first row of a `data.frame` or `data.table`. Otherwise, whatever `xts::first` returns (if package `xts` has been loaded, otherwise a helpful error).

If any argument is supplied in addition to `x` (such as `n` or `keep` in `xts::first`), regardless of `x`'s type, then `xts::first` is called if `xts` has been loaded, otherwise a helpful error.

See Also

[NROW](#), [head](#), [tail](#), [last](#)

Examples

```
first(1:5) # [1] 1
x = data.table(x=1:5, y=6:10)
first(x) # same as x[1]
```

foverlaps

*Fast overlap joins***Description**

A *fast* binary-search based *overlap join* of two `data.tables`. This is very much inspired by `findOverlaps` function from the Bioconductor package `IRanges` (see link below under See Also).

Usually, `x` is a very large `data.table` with small interval ranges, and `y` is much smaller *keyed* `data.table` with relatively larger interval spans. For a usage in genomics, see the examples section.

NOTE: This is still under development, meaning it's stable, but some features are yet to be implemented. Also, some arguments and/or the function name itself could be changed.

Usage

```
foverlaps(x, y, by.x = if (!is.null(key(x))) key(x) else key(y),
  by.y = key(y), maxgap = 0L, minoverlap = 1L,
  type = c("any", "within", "start", "end", "equal"),
  mult = c("all", "first", "last"),
  nomatch = getOption("datatable.nomatch"),
  which = FALSE, verbose = getOption("datatable.verbose"))
```

Arguments

<code>x, y</code>	<code>data.tables</code> . <code>y</code> needs to be keyed, but not necessarily <code>x</code> . See examples.
<code>by.x, by.y</code>	A vector of column names (or numbers) to compute the overlap joins. The last two columns in both <code>by.x</code> and <code>by.y</code> should each correspond to the start and end interval columns in <code>x</code> and <code>y</code> respectively. And the start column should always be \leq end column. If <code>x</code> is keyed, <code>by.x</code> is equal to <code>key(x)</code> , else <code>key(y)</code> . <code>by.y</code> defaults to <code>key(y)</code> .
<code>maxgap</code>	It should be a non-negative integer value, ≥ 0 . Default is 0 (no gap). For intervals $[a, b]$ and $[c, d]$, where $a \leq b$ and $c \leq d$, when $c > b$ or $d < a$, the two intervals don't overlap. If the gap between these two intervals is \leq <code>maxgap</code> , these two intervals are considered as overlapping. Note: This is not yet implemented.
<code>minoverlap</code>	It should be a positive integer value, > 0 . Default is 1. For intervals $[a, b]$ and $[c, d]$, where $a \leq b$ and $c \leq d$, when $c \leq b$ and $d \geq a$, the two intervals overlap. If the length of overlap between these two intervals is \geq <code>minoverlap</code> , then these two intervals are considered to be overlapping. Note: This is not yet implemented.
<code>type</code>	Default value is <code>any</code> . Allowed values are <code>any</code> , <code>within</code> , <code>start</code> , <code>end</code> and <code>equal</code> . Note: <code>equal</code> is not yet implemented. But this is just a normal join of the type <code>y[x, ...]</code> , unless you require also using <code>maxgap</code> and <code>minoverlap</code> arguments. The types shown here are identical in functionality to the function <code>findOverlaps</code> in the bioconductor package <code>IRanges</code> . Let $[a, b]$ and $[c, d]$ be intervals in <code>x</code> and <code>y</code> with $a \leq b$ and $c \leq d$. For <code>type="start"</code> , the intervals overlap iff $a == c$.

For type="end", the intervals overlap iff $b == d$. For type="within", the intervals overlap iff $a >= c$ and $b <= d$. For type="equal", the intervals overlap iff $a == c$ and $b == d$. For type="any", as long as $c <= b$ and $d >= a$, they overlap. In addition to these requirements, they also have to satisfy the minoverlap argument as explained above.

NB: maxgap argument, when > 0 , is to be interpreted according to the type of the overlap. This will be updated once maxgap is implemented.

mult	When multiple rows in y match to the row in x, mult=. controls which values are returned - "all" (default), "first" or "last".
nomatch	Same as nomatch in <code>match</code> . When a row (with interval say, [a,b]) in x has no match in y, nomatch=NA (default) means NA is returned for y's non-by.y columns for that row of x. nomatch=0 means no rows will be returned for that row of x. The default value (used when nomatch is not supplied) can be changed from NA to 0 using options(datatable.nomatch=0).
which	When TRUE, if mult="all" returns a two column data.table with the first column corresponding to x's row number and the second corresponding to y's. when nomatch=NA, no matches return NA for y, and if nomatch=0, those rows where no match is found will be skipped; if mult="first" or "last", a vector of length equal to the number of rows in x is returned, with no-match entries filled with NA or 0 corresponding to the nomatch argument. Default is FALSE, which returns a join with the rows in y.
verbose	TRUE turns on status and information messages to the console. Turn this on by default using options(datatable.verbose=TRUE). The quantity and types of verbosity may be expanded in future.

Details

Very briefly, `foverlaps()` collapses the two-column interval in y to one-column of *unique* values to generate a lookup table, and then performs the join depending on the type of overlap, using the already available binary search feature of `data.table`. The time (and space) required to generate the lookup is therefore proportional to the number of unique values present in the interval columns of y when combined together.

Overlap joins takes advantage of the fact that y is sorted to speed-up finding overlaps. Therefore y has to be keyed (see `?setkey`) prior to running `foverlaps()`. A key on x is not necessary, although it *might* speed things further. The columns in `by.x` argument should correspond to the columns specified in `by.y`. The last two columns should be the *interval* columns in both `by.x` and `by.y`. The first interval column in `by.x` should always be \leq the second interval column in `by.x`, and likewise for `by.y`. The `storage.mode` of the interval columns must be either double or integer. It therefore works with `bit64::integer64` type as well.

The lookup generation step could be quite time consuming if the number of unique values in y are too large (ex: in the order of tens of millions). There might be improvements possible by constructing lookup using RLE, which is a pending feature request. However most scenarios will not have too many unique values for y.

Value

A new `data.table` by joining over the interval columns (along with other additional identifier columns) specified in `by.x` and `by.y`.

NB: When which=TRUE: a) mult="first" or "last" returns a vector of matching row numbers in y, and b) when mult="all" returns a data.table with two columns with the first containing row numbers of x and the second column with corresponding row numbers of y.

nomatch=NA or 0 also influences whether non-matching rows are returned or not, as explained above.

See Also

[data.table](http://www.bioconductor.org/packages/release/bioc/html/IRanges.html), <http://www.bioconductor.org/packages/release/bioc/html/IRanges.html>, [setNumericRounding](#)

Examples

```
require(data.table)
## simple example:
x = data.table(start=c(5,31,22,16), end=c(8,50,25,18), val2 = 7:10)
y = data.table(start=c(10, 20, 30), end=c(15, 35, 45), val1 = 1:3)
setkey(y, start, end)
foverlaps(x, y, type="any", which=TRUE) ## return overlap indices
foverlaps(x, y, type="any") ## return overlap join
foverlaps(x, y, type="any", mult="first") ## returns only first match
foverlaps(x, y, type="within") ## matches iff 'x' is within 'y'

## with extra identifiers (ex: in genomics)
x = data.table(chr=c("Chr1", "Chr1", "Chr2", "Chr2", "Chr2"),
               start=c(5,10, 1, 25, 50), end=c(11,20,4,52,60))
y = data.table(chr=c("Chr1", "Chr1", "Chr2"), start=c(1, 15,1),
               end=c(4, 18, 55), geneid=letters[1:3])
setkey(y, chr, start, end)
foverlaps(x, y, type="any", which=TRUE)
foverlaps(x, y, type="any")
foverlaps(x, y, type="any", nomatch=0L)
foverlaps(x, y, type="within", which=TRUE)
foverlaps(x, y, type="within")
foverlaps(x, y, type="start")

## x and y have different column names - specify by.x
x = data.table(seq=c("Chr1", "Chr1", "Chr2", "Chr2", "Chr2"),
               start=c(5,10, 1, 25, 50), end=c(11,20,4,52,60))
y = data.table(chr=c("Chr1", "Chr1", "Chr2"), start=c(1, 15,1),
               end=c(4, 18, 55), geneid=letters[1:3])
setkey(y, chr, start, end)
foverlaps(x, y, by.x=c("seq", "start", "end"),
           type="any", which=TRUE)
```

Description

Similar to `base::rank` but *much faster*. And it accepts vectors, lists, `data.frames` or `data.tables` as input. In addition to the `ties.method` possibilities provided by `base::rank`, it also provides `ties.method="dense"`.

`bit64::integer64` type is also supported.

Usage

```
frank(x, ..., na.last=TRUE, ties.method=c("average",
  "first", "random", "max", "min", "dense"))
```

```
frankv(x, cols=seq_along(x), order=1L, na.last=TRUE,
  ties.method=c("average", "first", "random",
  "max", "min", "dense"))
```

Arguments

<code>x</code>	A vector, or list with all it's elements identical in length or <code>data.frame</code> or <code>data.table</code> .
<code>...</code>	Only for lists, <code>data.frames</code> and <code>data.tables</code> . The columns to calculate ranks based on. Do not quote column names. If <code>...</code> is missing, all columns are considered by default. To sort by a column in descending order prefix a "-", e.g., <code>frank(x, a, -b, c)</code> . The <code>-b</code> works when <code>b</code> is of type character as well.
<code>cols</code>	A character vector of column names (or numbers) of <code>x</code> , to which obtain ranks for.
<code>order</code>	An integer vector with only possible values of 1 and -1, corresponding to ascending and descending order. The length of <code>order</code> must be either 1 or equal to that of <code>cols</code> . If <code>length(order) == 1</code> , it's recycled to <code>length(cols)</code> .
<code>na.last</code>	Control treatment of NAs. If <code>TRUE</code> , missing values in the data are put last; if <code>FALSE</code> , they are put first; if <code>NA</code> , they are removed; if <code>"keep"</code> they are kept with rank <code>NA</code> .
<code>ties.method</code>	A character string specifying how ties are treated, see <code>Details</code> .

Details

To be consistent with other `data.table` operations, NAs are considered identical to other NAs (and NaNs to other NaNs), unlike `base::rank`. Therefore, for `na.last=TRUE` and `na.last=FALSE`, NAs (and NaNs) are given identical ranks, unlike `rank`.

`frank` is not limited to vectors. It accepts `data.tables` (and lists and `data.frames`) as well. It accepts unquoted column names (with names preceded with a - sign for descending order, even on character vectors), for e.g., `frank(DT, a, -b, c, ties.method="first")` where `a, b, c` are columns in `DT`. The equivalent in `frankv` is the `order` argument.

In addition to the `ties.method` values possible using `base::rank`, it also provides another additional argument `"dense"` which returns the ranks without any gaps in the ranking. See examples.

Value

A numeric vector of length equal to `NROW(x)` (unless `na.last = NA`, when missing values are removed). The vector is of integer type unless `ties.method = "average"` when it is of double type (irrespective of ties).

See Also

[data.table](#), [setkey](#), [setorder](#)

Examples

```
# on vectors
x = c(4, 1, 4, NA, 1, NA, 4)
# NAs are considered identical (unlike base R)
# default is average
frankv(x) # na.last=TRUE
frankv(x, na.last=FALSE)

# ties.method = min
frankv(x, ties.method="min")
# ties.method = dense
frankv(x, ties.method="dense")

# on data.table
DT = data.table(x, y=c(1, 1, 1, 0, NA, 0, 2))
frankv(DT, cols="x") # same as frankv(x) from before
frankv(DT, cols="x", na.last="keep")
frankv(DT, cols="x", ties.method="dense", na.last=NA)
frank(DT, x, ties.method="dense", na.last=NA) # equivalent of above using frank
# on both columns
frankv(DT, ties.method="first", na.last="keep")
frank(DT, ties.method="first", na.last="keep") # equivalent of above using frank

# order argument
frank(DT, x, -y, ties.method="first")
# equivalent of above using frankv
frankv(DT, order=c(1L, -1L), ties.method="first")
```

fread

Fast and friendly file finagler

Description

Similar to `read.table` but faster and more convenient. All controls such as `sep`, `colClasses` and `nrows` are automatically detected. `bit64::integer64` types are also detected and read directly without needing to read as character before converting.

Dates are read as character currently. They can be converted afterwards using the excellent `fasttime` package or standard base functions.

'fread' is for *regular* delimited files; i.e., where every row has the same number of columns. In future, secondary separator (sep2) may be specified *within* each column. Such columns will be read as `list` where each cell is itself a vector.

Usage

```
fread(input, sep="auto", sep2="auto", nrows=-1L, header="auto", na.strings="NA", file,
stringsAsFactors=FALSE, verbose=getOption("datatable.verbose"), autostart=1L,
skip=0L, select=NULL, drop=NULL, colClasses=NULL,
integer64=getOption("datatable.integer64"),           # default: "integer64"
dec=if (sep!=".") "." else ",", col.names,
check.names=FALSE, encoding="unknown", quote="\\"",
strip.white=TRUE, fill=FALSE, blank.lines.skip=FALSE, key=NULL,
showProgress=getOption("datatable.showProgress"),    # default: TRUE
data.table=getOption("datatable.fread.datatable")    # default: TRUE
)
```

Arguments

input	Either the file name to read (containing no <code>\n</code> character), a shell command that preprocesses the file (e.g. <code>fread("grep blah filename")</code>) or the input itself as a string (containing at least one <code>\n</code>), see examples. In both cases, a length 1 character string. A filename input is passed through <code>path.expand</code> for convenience and may be a URL starting <code>http://</code> or <code>file://</code> .
sep	The separator between columns. Defaults to the first character in the set <code>[\, \t ; :]</code> that exists on line <code>autostart</code> outside quoted (<code>"</code>) regions, and separates the rows above <code>autostart</code> into a consistent number of fields, too.
sep2	The separator <i>within</i> columns. A <code>list</code> column will be returned where each cell is a vector of values. This is much faster using less working memory than <code>strsplit</code> afterwards or similar techniques. For each column <code>sep2</code> can be different and is the first character in the same set above <code>[\, \t ; :]</code> , other than <code>sep</code> , that exists inside each field outside quoted regions on line <code>autostart</code> . NB: <code>sep2</code> is not yet implemented.
nrows	The number of rows to read, by default <code>-1</code> means all. Unlike <code>read.table</code> , it doesn't help speed to set this to the number of rows in the file (or an estimate), since the number of rows is automatically determined and is already fast. Only set <code>nrows</code> if you require the first 10 rows, for example. ' <code>nrows=0</code> ' is a special case that just returns the column names and types; e.g., a dry run for a large file or to quickly check format consistency of a set of files before starting to read any.
header	Does the first data line contain column names? Defaults according to whether every non-empty field on the first data line is type character. If so, or <code>TRUE</code> is supplied, any empty column names are given a default name.
na.strings	A character vector of strings which are to be interpreted as NA values. By default <code>", , "</code> for columns read as type character is read as a blank string (<code>"</code>) and <code>", NA, "</code> is read as NA. Typical alternatives might be <code>na.strings=NULL</code> (no coercion to NA at all!) or perhaps <code>na.strings=c("NA", "N/A", "null")</code> .

file	File path, useful when we want to ensure that no shell commands will be executed. File path can also be provided to input argument.
stringsAsFactors	Convert all character columns to factors?
verbose	Be chatty and report timings?
autostart	Any line number within the region of machine readable delimited text, by default 30. If the file is shorter or this line is empty (e.g. short files with trailing blank lines) then the last non empty line (with a non empty line above that) is used. This line and the lines above it are used to auto detect sep, sep2 and the number of fields. It's extremely unlikely that autostart should ever need to be changed, we hope.
skip	If 0 (default) use the procedure described below starting on line autostart to find the first data row. skip>0 means ignore autostart and take line skip+1 as the first data row (or column names according to header="auto"!TRUE FALSE as usual). skip="string" searches for "string" in the file (e.g. a substring of the column names row) and starts on that line (inspired by read.xls in package gdata).
select	Vector of column names or numbers to keep, drop the rest.
drop	Vector of column names or numbers to drop, keep the rest.
colClasses	A character vector of classes (named or unnamed), as read.csv. Or a named list of vectors of column names or numbers, see examples. colClasses in fread is intended for rare overrides, not for routine use. fread will only promote a column to a higher type if colClasses requests it. It won't downgrade a column to a lower type since NAs would result. You have to coerce such columns afterwards yourself, if you really require data loss.
integer64	"integer64" (default) reads columns detected as containing integers larger than 2^{31} as type bit64::integer64. Alternatively, "double" "numeric" reads as base::read.csv does; i.e., possibly with loss of precision and if so silently. Or, "character".
dec	The decimal separator as in base::read.csv. If not "." (default) then usually ",",. See details.
col.names	A vector of optional names for the variables (columns). The default is to use the header column if present or detected, or if not "V" followed by the column number.
check.names	default is FALSE. If TRUE then the names of the variables in the data.table are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by make.names) so that they are, and also to ensure that there are no duplicates.
encoding	default is "unknown". Other possible options are "UTF-8" and "Latin-1". Note: it is not used to re-encode the input, rather enables handling of encoded strings in their native encoding.
quote	By default ("\""), if a field starts with a doublequote, fread handles embedded quotes robustly as explained under Details. If it fails, then another attempt is made to read the field as is, i.e., as if quotes are disabled. By setting quote="", the field is always read as if quotes are disabled.

<code>strip.white</code>	default is TRUE. Strips leading and trailing whitespaces of unquoted fields. If FALSE, only header trailing spaces are removed.
<code>fill</code>	logical (default is FALSE). If TRUE then in case the rows have unequal length, blank fields are implicitly filled.
<code>blank.lines.skip</code>	logical, default is FALSE. If TRUE blank lines in the input are ignored.
<code>key</code>	Character vector of one or more column names which is passed to <code>setkey</code> . It may be a single comma separated string such as <code>key="x,y,z"</code> , or a vector of names such as <code>key=c("x","y","z")</code> . Only valid when argument <code>data.table=TRUE</code> .
<code>showProgress</code>	TRUE displays progress on the console using <code>\r</code> . It is produced in <code>fread</code> 's C code where the very nice (but R level) <code>txtProgressBar</code> and <code>tkProgressBar</code> are not easily available.
<code>data.table</code>	TRUE returns a <code>data.table</code> . FALSE returns a <code>data.frame</code> .

Details

Once the separator is found on line `autostart`, the number of columns is determined. Then the file is searched backwards from `autostart` until a row is found that doesn't have that number of columns. Thus, the first data row is found and any human readable banners are automatically skipped. This feature can be particularly useful for loading a set of files which may not all have consistently sized banners. Setting `skip>0` overrides this feature by setting `autostart=skip+1` and turning off the search upwards step.

A sample of 1,000 rows is used to determine column types (100 rows from 10 points). The lowest type for each column is chosen from the ordered list: `logical`, `integer`, `integer64`, `double`, `character`. This enables `fread` to allocate exactly the right number of rows, with columns of the right type, up front once. The file may of course still contain data of a higher type in rows outside the sample. In that case, the column types are bumped mid read and the data read on previous rows is coerced. Setting `verbose=TRUE` reports the line and field number of each mid read type bump and how long this type bumping took (if any).

There is no line length limit, not even a very large one. Since we are encouraging `list` columns (i.e. `sep2`) this has the potential to encourage longer line lengths. So the approach of scanning each line into a buffer first and then rescanning that buffer is not used. There are no buffers used in `fread`'s C code at all. The field width limit is limited by R itself: the maximum width of a character string (currently $2^{31}-1$ bytes, 2GB).

The filename extension (such as `.csv`) is irrelevant for "auto" `sep` and `sep2`. Separator detection is entirely driven by the file contents. This can be useful when loading a set of different files which may not be named consistently, or may not have the extension `.csv` despite being `csv`. Some datasets have been collected over many years, one file per day for example. Sometimes the file name format has changed at some point in the past or even the format of the file itself. So the idea is that you can loop `fread` through a set of files and as long as each file is regular and delimited, `fread` can read them all. Whether they all stack is another matter but at least each one is read quickly without you needing to vary `colClasses` in `read.table` or `read.csv`.

If an empty line is encountered then reading stops there, with warning if any text exists after the empty line such as a footer. The first line of any text discarded is included in the warning message.

Line endings: All known line endings are detected automatically: `\n` (*NIX including Mac), `\r\n` (Windows CRLF), `\r` (old Mac) and `\n\r` (just in case). There is no need to convert input files first.

fread running on any architecture will read a file from any architecture. Both `\r` and `\n` may be embedded in character strings (including column names) provided the field is quoted.

Decimal separator and locale: `fread(...,dec=",")` should just work. `fread` uses C function `strtod` to read numeric data; e.g., `1.23` or `1,23`. `strtod` retrieves the decimal separator (`.` or `,` usually) from the locale of the R session rather than as an argument passed to the `strtod` function. So for `fread(...,dec=",")` to work, `fread` changes this (and only this) R session's locale temporarily to a locale which provides the desired decimal separator.

On Windows, "French_France.1252" is tried which should be available as standard (any locale with comma decimal separator would suffice) and on unix "fr_FR.utf8" (you may need to install this locale on unix). `fread()` is very careful to set the locale back again afterwards, even if the function fails with an error. The choice of locale is determined by `options()$datatable.fread.dec.locale`. This may be a *vector* of locale names and if so they will be tried in turn until the desired `dec` is obtained; thus allowing more than two different decimal separators to be selected. This is a new feature in v1.9.6 and is experimental. In case of problems, turn it off with `options(datatable.fread.dec.experiment=FALSE)`.

Quotes:

When `quote` is a single character,

- Spaces and other whitespace (other than `sep` and `\n`) may appear in unquoted character fields, e.g., `...,2,Joe Bloggs,3.14,...`
- When character columns are *quoted*, they must start and end with that quoting character immediately followed by `sep` or `\n`, e.g., `...,2,"Joe Bloggs",3.14,...`

In essence quoting character fields are *required* only if `sep` or `\n` appears in the string value. Quoting may be used to signify that numeric data should be read as text. Unescaped quotes may be present in a quoted field, e.g., `...,2,"Joe, "Bloggs""`, `3.14,...`, as well as escaped quotes, e.g., `...,2,"Joe \"",Bloggs\""`, `3.14,...`

If an embedded quote is followed by the separator inside a quoted field, the embedded quotes up to that point in that field must be balanced; e.g. `...,2,"www.blah?x="one",y="two""`, `3.14,...`

On those fields that do not satisfy these conditions, e.g., fields with unbalanced quotes, `fread` re-attempts that field as if it isn't quoted. This is quite useful in reading files that contains fields with unbalanced quotes as well, automatically.

To read fields *as is* instead, use `quote = ""`.

Value

A `data.table` by default. A `data.frame` when argument `data.table=FALSE`; e.g. `options(datatable.fread.datatable=FALSE)`

References

Background :

- <https://cran.r-project.org/doc/manuals/R-data.html>
- <http://stackoverflow.com/questions/1727772/quickly-reading-very-large-tables-as-dataframes-in-r>
- <http://www.biostat.jhsph.edu/~rpeng/docs/R-large-tables.html>
- <https://stat.ethz.ch/pipermail/r-help/2007-August/138315.html>
- <http://www.cerebralmastication.com/2009/11/loading-big-data-into-r/>
- <http://stackoverflow.com/questions/9061736/faster-than-scan-with-rcpp>
- <http://stackoverflow.com/questions/415515/how-can-i-read-and-manipulate-csv-file-data-in-c>

<http://stackoverflow.com/questions/9352887/strategies-for-reading-in-csv-files-in-pieces>
<http://stackoverflow.com/questions/11782084/reading-in-large-text-files-in-r>
<http://stackoverflow.com/questions/45972/mmap-vs-reading-blocks>
<http://stackoverflow.com/questions/258091/when-should-i-use-mmap-for-file-access>
<http://stackoverflow.com/a/9818473/403310>
<http://stackoverflow.com/questions/9608950/reading-huge-files-using-memory-mapped-files>
 finagler = "to get or achieve by guile or manipulation" <http://dictionary.reference.com/browse/finagler>

See Also

[read.csv](#), [url](#), [Sys.setlocale](#)

Examples

```
## Not run:

# Demo speedup
n=1e6
DT = data.table( a=sample(1:1000,n,replace=TRUE),
                 b=sample(1:1000,n,replace=TRUE),
                 c=rnorm(n),
                 d=sample(c("foo", "bar", "baz", "qux", "quux"),n,replace=TRUE),
                 e=rnorm(n),
                 f=sample(1:1000,n,replace=TRUE) )
DT[2,b:=NA_integer_]
DT[4,c:=NA_real_]
DT[3,d:=NA_character_]
DT[5,d:=""]
DT[2,e:=+Inf]
DT[3,e:= -Inf]

write.table(DT,"test.csv",sep=",",row.names=FALSE,quote=FALSE)
cat("File size (MB):", round(file.info("test.csv")$size/1024^2), "\n")
# 50 MB (1e6 rows x 6 columns)

system.time(DF1 <- read.csv("test.csv",stringsAsFactors=FALSE))
# 60 sec (first time in fresh R session)

system.time(DF1 <- read.csv("test.csv",stringsAsFactors=FALSE))
# 30 sec (immediate repeat is faster, varies)

system.time(DF2 <- read.table("test.csv",header=TRUE,sep=",",quote="",
                             stringsAsFactors=FALSE,comment.char="",nrows=n,
                             colClasses=c("integer","integer","numeric",
                                           "character","numeric","integer")))
# 10 sec (consistently). All known tricks and known nrows, see references.

require(data.table)
system.time(DT <- fread("test.csv"))
# 3 sec (faster and friendlier)
```

```

require(sqldf)
system.time(SQLDF <- read.csv.sql("test.csv",dbname=NULL))
# 20 sec (friendly too, good defaults)

require(ff)
system.time(FFDF <- read.csv.ffdf(file="test.csv",nrows=n))
# 20 sec (friendly too, good defaults)

identical(DF1,DF2)
all.equal(as.data.table(DF1), DT)
identical(DF1,within(SQLDF,{b<-as.integer(b);c<-as.numeric(c)}))
identical(DF1,within(as.data.frame(FFDF),d<-as.character(d)))

# Scaling up ...
l = vector("list",10)
for (i in 1:10) l[[i]] = DT
DTbig = rbindlist(l)
tables()
write.table(DTbig,"testbig.csv",sep="," ,row.names=FALSE,quote=FALSE)
# 500MB (10 million rows x 6 columns)

system.time(DF <- read.table("testbig.csv",header=TRUE,sep="," ,
  quote="",stringsAsFactors=FALSE,comment.char="",nrows=1e7,
  colClasses=c("integer","integer","numeric",
               "character","numeric","integer")))
# 100-200 sec (varies)

system.time(DT <- fread("testbig.csv"))
# 30-40 sec

all(mapply(all.equal, DF, DT))

# Real data example (Airline data)
# http://stat-computing.org/dataexpo/2009/the-data.html

download.file("http://stat-computing.org/dataexpo/2009/2008.csv.bz2",
  destfile="2008.csv.bz2")
# 109MB (compressed)

system("bunzip2 2008.csv.bz2")
# 658MB (7,009,728 rows x 29 columns)

colClasses = sapply(read.csv("2008.csv",nrows=100),class)
# 4 character, 24 integer, 1 logical. Incorrect.

colClasses = sapply(read.csv("2008.csv",nrows=200),class)
# 5 character, 24 integer. Correct. Might have missed data only using 100 rows
# since read.table assumes colClasses is correct.

system.time(DF <- read.table("2008.csv", header=TRUE, sep="," ,
  quote="",stringsAsFactors=FALSE,comment.char="",nrows=7009730,
  colClasses=colClasses))

```

```

# 360 secs

system.time(DT <- fread("2008.csv"))
# 40 secs

table(sapply(DT,class))
# 5 character and 24 integer columns. Correct without needing to worry about colClasses
# issue above.

# Reads URLs directly :
fread("http://www.stats.ox.ac.uk/pub/datasets/csb/ch11b.dat")

## End(Not run)

# Reads text input directly :
fread("A,B\n1,2\n3,4")

# Reads pasted input directly :
fread("A,B
1,2
3,4
")

# Finds the first data line automatically :
fread("
This is perhaps a banner line or two or ten.
A,B
1,2
3,4
")

# Detects whether column names are present automatically :
fread("
1,2
3,4
")

# Numerical precision :

DT = fread("A\n1.010203040506070809010203040506\n") # silent loss of precision
DT[,sprintf("%.15E",A)] # stored accurately as far as double precision allows

DT = fread("A\n1.46761e-313\n") # detailed warning about ERANGE; read as 'numeric'
DT[,sprintf("%.15E",A)] # beyond what double precision can store accurately to 15 digits

# For greater accuracy use colClasses to read as character, then package Rmpfr.

# colClasses
data = "A,B,C,D\n1,3,5,7\n2,4,6,8\n"
fread(data, colClasses=c(B="character",C="character",D="character")) # as read.csv
fread(data, colClasses=list(character=c("B","C","D"))) # saves typing

```

```

fread(data, colClasses=list(character=2:4)) # same using column numbers

# drop
fread(data, colClasses=c("B"="NULL", "C"="NULL")) # as read.csv
fread(data, colClasses=list(NULL=c("B", "C"))) #
fread(data, drop=c("B", "C")) # same but less typing, easier to read
fread(data, drop=2:3) # same using column numbers

# select
# (in read.csv you need to work out which to drop)
fread(data, select=c("A", "D")) # less typing, easier to read
fread(data, select=c(1,4)) # same using column numbers

# skip blank lines
fread("a,b\n1,a\n2,b\n\n3,c\n", blank.lines.skip=TRUE)
# fill
fread("a,b\n1,a\n2\n3,c\n", fill=TRUE)
fread("a,b\n\n1,a\n2\n\n3,c\n\n", fill=TRUE)

# fill with skip blank lines
fread("a,b\n\n1,a\n2\n\n3,c\n\n", fill=TRUE, blank.lines.skip=TRUE)

# check.names usage
fread("a b,a b\n1,2\n")
fread("a b,a b\n1,2\n", check.names=TRUE) # no duplicates + syntactically valid names

```

fsort

Fast parallel sort

Description

Similar to `base::sort` but parallel. Experimental.

Usage

```
fsort(x, decreasing = FALSE, na.last = FALSE, internal=FALSE, verbose=FALSE, ...)
```

Arguments

<code>x</code>	A vector. Type double, currently.
<code>decreasing</code>	Decreasing order?
<code>na.last</code>	Control treatment of NAs. If TRUE, missing values in the data are put last; if FALSE, they are put first; if NA, they are removed; if "keep" they are kept with rank NA.
<code>internal</code>	Internal use only. Temporary variable. Will be removed.
<code>verbose</code>	Print tracing information.
<code>...</code>	Not sure yet. Should be consistent with base R.

Details

Returns the input in sorted order. Fast using parallelism.

Value

The input in sorted order.

Examples

```
x = runif(1e6)
system.time(ans1 <- sort(x, method="quick"))
system.time(ans2 <- fsort(x))
identical(ans1, ans2)
```

 fwrite

Fast CSV writer

Description

As `write.csv` but much faster (e.g. 2 seconds versus 1 minute) and just as flexible. Modern machines almost surely have more than one CPU so `fwrite` uses them; on all operating systems including Linux, Mac and Windows.

This is new functionality as of Nov 2016. We may need to refine argument names and defaults.

Usage

```
fwrite(x, file = "", append = FALSE, quote = "auto",
  sep = ",", sep2 = c("","|",""),
  eol = if (.Platform$OS.type=="windows") "\r\n" else "\n",
  na = "", dec = ".", row.names = FALSE, col.names = TRUE,
  qmethod = c("double","escape"),
  logicalAsInt = FALSE, dateTimeAs = c("ISO","squash","epoch","write.csv"),
  buffMB = 8L, nThread = getDTthreads(),
  showProgress = getOption("datatable.showProgress"),
  verbose = getOption("datatable.verbose"))
```

Arguments

<code>x</code>	Any list of same length vectors; e.g. <code>data.frame</code> and <code>data.table</code> .
<code>file</code>	Output file name. <code>""</code> indicates output to the console.
<code>append</code>	If <code>TRUE</code> , the file is opened in append mode and column names (header row) are not written.
<code>quote</code>	When <code>"auto"</code> , character fields, factor fields and column names will only be surrounded by double quotes when they need to be; i.e., when the field contains the separator <code>sep</code> , a line ending <code>\n</code> , the double quote itself or (when <code>list</code> columns are present) <code>sep2[2]</code> (see <code>sep2</code> below). If <code>FALSE</code> the fields are not wrapped

with quotes even if this would break the CSV due to the contents of the field. If TRUE double quotes are always included other than around numeric fields, as `write.csv`.

<code>sep</code>	The separator between columns. Default is <code>","</code> .
<code>sep2</code>	For columns of type <code>list</code> where each item is an atomic vector, <code>sep2</code> controls how to separate items <i>within</i> the column. <code>sep2[1]</code> is written at the start of the output field, <code>sep2[2]</code> is placed between each item and <code>sep2[3]</code> is written at the end. <code>sep2[1]</code> and <code>sep2[3]</code> may be any length strings including empty <code>""</code> (default). <code>sep2[2]</code> must be a single character and (when <code>list</code> columns are present and therefore <code>sep2</code> is used) different from both <code>sep</code> and <code>dec</code> . The default <code>()</code> is chosen to visually distinguish from the default <code>sep</code> . In speaking, writing and in code comments we may refer to <code>sep2[2]</code> as simply <code>"sep2"</code> .
<code>eol</code>	Line separator. Default is <code>"\r\n"</code> for Windows and <code>"\n"</code> otherwise.
<code>na</code>	The string to use for missing values in the data. Default is a blank string <code>""</code> .
<code>dec</code>	The decimal separator, by default <code>."</code> . See link in references. Cannot be the same as <code>sep</code> .
<code>row.names</code>	Should row names be written? For compatibility with <code>data.frame</code> and <code>write.csv</code> since <code>data.table</code> never has row names. Hence default FALSE unlike <code>write.csv</code> .
<code>col.names</code>	Should the column names (header row) be written? If missing, <code>append=TRUE</code> and the file already exists, the default is set to FALSE for convenience to prevent column names appearing again mid file.
<code>qmethod</code>	A character string specifying how to deal with embedded double quote characters when quoting strings. <ul style="list-style-type: none"> • "escape" - the quote character (as well as the backslash character) is escaped in C style by a backslash, or • "double" (default, same as <code>write.csv</code>), in which case the double quote is doubled with another one.
<code>logicalAsInt</code>	Should logical values be written as 1 and 0 rather than "TRUE" and "FALSE"?
<code>dateTimeAs</code>	How <code>Date/IDate</code> , <code>ITime</code> and <code>POSIXct</code> items are written. <ul style="list-style-type: none"> • "ISO" (default) - 2016-09-12, 18:12:16 and 2016-09-12T18:12:16.999999Z. 0, 3 or 6 digits of fractional seconds are printed if and when present for convenience, regardless of any R options such as <code>digits.secs</code>. The idea being that if milli and microseconds are present then you most likely want to retain them. R's internal UTC representation is written faithfully to encourage ISO standards, stymie timezone ambiguity and for speed. An option to consider is to start R in the UTC timezone simply with <code>"\$ TZ='UTC' R"</code> at the shell (NB: it must be one or more spaces between <code>TZ='UTC'</code> and R, anything else will be silently ignored; this TZ setting applies just to that R process) or <code>Sys.setenv(TZ='UTC')</code> at the R prompt and then continue as if UTC were local time. • "squash" - 20160912, 181216 and 20160912181216999. This option allows fast and simple extraction of <code>yyyy</code>, <code>mm</code>, <code>dd</code> and (most commonly to group by) <code>yyyymm</code> parts using integer <code>div</code> and <code>mod</code> operations. In R for example, one line helper functions could use <code>%/%10000</code>, <code>%/%100%100</code>, <code>%100</code> and <code>%/%100</code> respectively. <code>POSIXct</code> UTC is squashed to 17 digits (including 3

digits of milliseconds always, even if 000) which may be read comfortably as integer64 (automatically by fread()).

- "epoch" - 17056, 65536 and 1473703936.999999. The underlying number of days or seconds since the relevant epoch (1970-01-01, 00:00:00 and 1970-01-01T00:00:00Z respectively), negative before that (see ?Date). 0, 3 or 6 digits of fractional seconds are printed if and when present.
- "write.csv" - this currently affects POSIXct only. It is written as write.csv does by using the as.character method which heeds digits.secs and converts from R's internal UTC representation back to local time (or the "tz" attribute) as of that historical date. Accordingly this can be slow. All other column types (including Date, IDate and ITime which are independent of timezone) are written as the "ISO" option using fast C code which is already consistent with write.csv.

The first three options are fast due to new specialized C code. The epoch to date-part conversion uses a fast approach by Howard Hinnant (see references) using a day-of-year starting on 1 March. You should not be able to notice any difference in write speed between those three options. The date range supported for Date and IDate is [0000-03-01, 9999-12-31]. Every one of these 3,652,365 dates have been tested and compared to base R including all 2,790 leap days in this range.

This option applies to vectors of date/time in list column cells, too.

A fully flexible format string (such as "%m/%d/%Y") is not supported. This is to encourage use of ISO standards and because that flexibility is not known how to make fast at C level. We may be able to support one or two more specific options if required.

buffMB	The buffer size (MB) per thread in the range 1 to 1024, default 8MB. Experiment to see what works best for your data on your hardware.
nThread	The number of threads to use. Experiment to see what works best for your data on your hardware.
showProgress	Display a progress meter on the console? Ignored when file=="".
verbose	Be chatty and report timings?

Details

fwrite began as a community contribution with [pull request #1613](#) by Otto Seiskari. This gave Matt Dowle the impetus to specialize the numeric formatting and to parallelize: <http://blog.h2o.ai/2016/04/fast-csv-writing-for-r/>. Final items were tracked in [issue #1664](#) such as automatic quoting, bit64::integer64 support, decimal/scientific formatting exactly matching write.csv between 2.225074e-308 and 1.797693e+308 to 15 significant figures, row.names, dates (between 0000-03-01 and 9999-12-31), times and sep2 for list columns where each cell can itself be a vector.

References

http://howardhinnant.github.io/date_algorithms.html
https://en.wikipedia.org/wiki/Decimal_mark

See Also

[setDTthreads](#), [fread](#), [write.csv](#), [write.table](#), [bit64::integer64](#)

Examples

```

DF = data.frame(A=1:3, B=c("foo", "A,Name", "baz"))
fwrite(DF)
write.csv(DF, row.names=FALSE, quote=FALSE) # same

fwrite(DF, row.names=TRUE, quote=TRUE)
write.csv(DF) # same

DF = data.frame(A=c(2.1, -1.234e-307, pi), B=c("foo", "A,Name", "bar"))
fwrite(DF, quote='auto') # Just DF[2,2] is auto quoted
write.csv(DF, row.names=FALSE) # same numeric formatting

DT = data.table(A=c(2, 5.6, -3), B=list(1:3, c("foo", "A,Name", "bar"), round(pi*1:3, 2)))
fwrite(DT)
fwrite(DT, sep="|", sep2=c("{", ",", "}")

## Not run:

set.seed(1)
DT = as.data.table( lapply(1:10, sample,
                          x=as.numeric(1:5e7), size=5e6))
system.time(fwrite(DT, "/dev/shm/tmp1.csv")) # 382MB
system.time(write.csv(DT, "/dev/shm/tmp2.csv",
                      quote=FALSE, row.names=FALSE)) # 0.8s
system("diff /dev/shm/tmp1.csv /dev/shm/tmp2.csv") # 60.6s

set.seed(1)
N = 1e7
DT = data.table(
  str1=sample(sprintf("
  str2=sample(sprintf("
  str3=sample(sapply(sample(2:30, 100, TRUE), function(n)
    paste0(sample(LETTERS, n, TRUE), collapse="")), N, TRUE),
  str4=sprintf("
  num1=sample(round(rnorm(1e6, mean=6.5, sd=15), 2), N, replace=TRUE),
  num2=sample(round(rnorm(1e6, mean=6.5, sd=15), 10), N, replace=TRUE),
  str5=sample(c("Y", "N"), N, TRUE),
  str6=sample(c("M", "F"), N, TRUE),
  int1=sample(ceiling(rexp(1e6)), N, replace=TRUE),
  int2=sample(N, N, replace=TRUE)-N/2
)
system.time(fwrite(DT, "/dev/shm/tmp1.csv")) # 774MB
system.time(write.csv(DT, "/dev/shm/tmp2.csv", row.names=F, quote=F)) # 1.1s
system("diff /dev/shm/tmp1.csv /dev/shm/tmp2.csv") # 63.2s

unlink("/dev/shm/tmp1.csv")
unlink("/dev/shm/tmp2.csv")

```

```
## End(Not run)
```

IDateTime	<i>Integer based date class</i>
-----------	---------------------------------

Description

Date and time classes with integer storage for fast sorting and grouping. Still experimental!

Usage

```
as.IDate(x, ...)
## Default S3 method:
as.IDate(x, ...)
## S3 method for class 'Date'
as.IDate(x, ...)
## S3 method for class 'IDate'
as.Date(x, ...)
## S3 method for class 'IDate'
as.POSIXct(x, tz = "UTC", time = 0, ...)
## S3 method for class 'IDate'
as.chron(x, time = NULL, ...)
## S3 method for class 'IDate'
round(x, digits = c("weeks", "months", "quarters", "years"), ...)

as.ITime(x, ...)
## Default S3 method:
as.ITime(x, ...)
## S3 method for class 'ITime'
as.POSIXct(x, tz = "UTC", date = as.Date(Sys.time()), ...)
## S3 method for class 'ITime'
as.chron(x, date = NULL, ...)
## S3 method for class 'ITime'
as.character(x, ...)
## S3 method for class 'ITime'
format(x, ...)

IDateTime(x, ...)
## Default S3 method:
IDateTime(x, ...)

second(x)
minute(x)
hour(x)
yday(x)
```

```
wday(x)
mday(x)
week(x)
isoweek(x)
month(x)
quarter(x)
year(x)
```

Arguments

<code>x</code>	an object
<code>...</code>	arguments to be passed to or from other methods. For <code>as.IDate.default</code> , arguments are passed to <code>as.Date</code> . For <code>as.ITime.default</code> , arguments are passed to <code>as.POSIXlt</code> .
<code>tz</code>	time zone (see <code>strptime</code>).
<code>date</code>	date object convertible with <code>as.IDate</code> .
<code>time</code>	time-of-day object convertible with <code>as.ITime</code> .
<code>digits</code>	really units; one of the units listed for rounding. May be abbreviated.

Details

`IDate` is a date class derived from `Date`. It has the same internal representation as the `Date` class, except the storage mode is integer. `IDate` is a relatively simple wrapper, and it should work in almost all situations as a replacement for `Date`.

Functions that use `Date` objects generally work for `IDate` objects. This package provides specific methods for `IDate` objects for `mean`, `cut`, `seq`, `c`, `rep`, and `split` to return an `IDate` object.

`ITime` is a time-of-day class stored as the integer number of seconds in the day. `as.ITime` does not allow days longer than 24 hours. Because `ITime` is stored in seconds, you can add it to a `POSIXct` object, but you should not add it to a `Date` object.

Conversions to and from `Date`, `POSIXct`, and `chron` formats are provided.

`ITime` does not account for time zones. When converting `ITime` and `IDate` to `POSIXct` with `as.POSIXct`, a time zone may be specified.

In `as.POSIXct` methods for `ITime` and `IDate`, the second argument is required to be `tz` based on the generic template, but to make converting easier, the second argument is interpreted as a date instead of a time zone if it is of type `IDate` or `ITime`. Therefore, you can use either of the following: `as.POSIXct(time, date)` or `as.POSIXct(date, time)`.

`IDateTime` takes a date-time input and returns a data table with columns `date` and `time`.

Using integer storage allows dates and/or times to be used as data table keys. With positive integers with a range less than 100,000, grouping and sorting is fast because radix sorting can be used (see `sort.list`).

Several convenience functions like `hour` and `quarter` are provided to group or extract by hour, month, and other date-time intervals. `as.POSIXlt` is also useful. For example, `as.POSIXlt(x)$mon` is the integer month. The R base convenience functions `weekdays`, `months`, and `quarters` can

also be used, but these return character values, so they must be converted to factors for use with `data.table`. `isoweek` is ISO 8601-consistent.

The `round` method for `IDate`'s is useful for grouping and plotting. It can round to weeks, months, quarters, and years.

Value

For `as.IDate`, a class of `IDate` and `Date` with the date stored as the number of days since some origin.

For `as.ITime`, a class of `ITime` stored as the number of seconds in the day.

For `IDateTime`, a data table with columns `idate` and `itime` in `IDate` and `ITime` format.

`second`, `minute`, `hour`, `yday`, `wday`, `mday`, `week`, `month`, `quarter`, and `year` return integer values for second, minute, hour, day of year, day of week, day of month, week, month, quarter, and year, respectively.

These values are all taken directly from the POSIX1t representation of `x`, with the notable difference that while `yday`, `wday`, and `mon` are all 0-based, here they are 1-based.

Author(s)

Tom Short, t.short@ieee.org

References

G. Grothendieck and T. Petzoldt, "Date and Time Classes in R," R News, vol. 4, no. 1, June 2004.

H. Wickham, <http://gist.github.com/10238>.

ISO 8601, <http://www.iso.org/iso/home/standards/iso8601.htm>

See Also

[as.Date](#), [as.POSIXct](#), [strptime](#), [DateTimeClasses](#)

Examples

```
# create IDate:
(d <- as.IDate("2001-01-01"))

# S4 coercion also works
identical(as.IDate("2001-01-01"), as("2001-01-01", "IDate"))

# create ITime:
(t <- as.ITime("10:45"))

# S4 coercion also works
identical(as.ITime("10:45"), as("10:45", "ITime"))

(t <- as.ITime("10:45:04"))

(t <- as.ITime("10:45:04", format = "%H:%M:%S"))
```

```

as.POSIXct("2001-01-01") + as.ITime("10:45")

datetime <- seq(as.POSIXct("2001-01-01"), as.POSIXct("2001-01-03"), by = "5 hour")
(af <- data.table(IDateTime(datetime), a = rep(1:2, 5), key = "a, idate, itime"))

af[, mean(a), by = "itime"]
af[, mean(a), by = list(hour = hour(itime))]
af[, mean(a), by = list(wday = factor(weekdays(idate)))]
af[, mean(a), by = list(wday = wday(idate))]

as.POSIXct(af$idate)
as.POSIXct(af$idate, time = af$itime)
as.POSIXct(af$idate, af$itime)
as.POSIXct(af$idate, time = af$itime, tz = "GMT")

as.POSIXct(af$itime, af$idate)
as.POSIXct(af$itime) # uses today's date

(seqdates <- seq(as.IDate("2001-01-01"), as.IDate("2001-08-03"), by = "3 weeks"))
round(seqdates, "months")

if (require(chron)) {
  as.chron(as.IDate("2000-01-01"))
  as.chron(as.ITime("10:45"))
  as.chron(as.IDate("2000-01-01"), as.ITime("10:45"))
  as.chron(as.ITime("10:45"), as.IDate("2000-01-01"))
  as.ITime(chron(times = "11:01:01"))
  IDateTime(chron("12/31/98", "10:45:00"))
}

```

J

*Creates a Join data table***Description**

Creates a `data.table` to be passed in as the `i` to a `[.data.table]` join.

Usage

```

# DT[J(...)] # J() only for use inside DT[...].
SJ(...) # DT[SJ(...)]
CJ(..., sorted = TRUE, unique = FALSE) # DT[CJ(...)]

```

Arguments

`...` Each argument is a vector. Generally each vector is the same length but if they are not then the usual silent repetition is applied.

`sorted` logical. Should the input order be retained?

`unique` logical. When TRUE, only unique values of each vectors are used (automatically).

Details

SJ and CJ are convenience functions for creating a `data.table` in the context of a `data.table` 'query' on `x`.

`x[data.table(id)]` is the same as `x[J(id)]` but the latter is more readable. Identical alternatives are `x[list(id)]` and `x[.(id)]`.

`x` must have a key when passing in a join table as the `i`. See [\[.data.table\]](#)

Value

`J` : the same result as calling `list`. `J` is a direct alias for `list` but results in clearer more readable code.

`SJ` : (S)orted (J)oin. The same value as `J()` but additionally `setkey()` is called on all the columns in the order they were passed in to `SJ`. For efficiency, to invoke a binary merge rather than a repeated binary full search for each row of `i`.

`CJ` : (C)ross (J)oin. A `data.table` is formed from the cross product of the vectors. For example, 10 ids, and 100 dates, `CJ` returns a 1000 row table containing all the dates for all the ids. It gains sorted, which by default is `TRUE` for backwards compatibility. `FALSE` retains input order.

See Also

[data.table](#), [test.data.table](#)

Examples

```
DT = data.table(A=5:1,B=letters[5:1])
setkey(DT,B) # re-orders table and marks it sorted.
DT[J("b")] # returns the 2nd row
DT[.( "b")] # same. Style of package plyr.
DT[list("b")] # same

# CJ usage examples
CJ(c(5,NA,1), c(1,3,2)) # sorted and keyed data.table
do.call(CJ, list(c(5,NA,1), c(1,3,2))) # same as above
CJ(c(5,NA,1), c(1,3,2), sorted=FALSE) # same order as input, unkeyed
# use for 'unique=' argument
x = c(1,1,2)
y = c(4,6,4)
CJ(x, y, unique=TRUE) # unique(x) and unique(y) are computed automatically
```

last

Last item of an object

Description

Returns the last item of a vector or list, or the last row of a `data.frame` or `data.table`.

Usage

```
last(x, ...)
```

Arguments

<code>x</code>	A vector, list, <code>data.frame</code> or <code>data.table</code> . Otherwise the S3 method of <code>xts::last</code> is deployed.
<code>...</code>	Not applicable for <code>data.table::last</code> . Any arguments here are passed through to <code>xts::last</code> .

Value

If no other arguments are supplied it depends on the type of `x`. The last item of a vector or list. The last row of a `data.frame` or `data.table`. Otherwise, whatever `xts::last` returns (if package `xts` has been loaded, otherwise a helpful error).

If any argument is supplied in addition to `x` (such as `n` or `keep` in `xts::last`), regardless of `x`'s type, then `xts::last` is called if `xts` has been loaded, otherwise a helpful error.

See Also

[NROW](#), [head](#), [tail](#), [first](#)

Examples

```
last(1:5) # [1] 5
x = data.table(x=1:5, y=6:10)
last(x) # same as x[5]
```

like

Convenience function for calling [regexpr](#).

Description

Intended for use in `i` in `[.data.table]`.

Usage

```
like(vector, pattern)
vector %like% pattern
```

Arguments

<code>vector</code>	Either a character vector or a factor. A factor is faster.
<code>pattern</code>	Passed on to grepl .

Value

Logical vector, TRUE for items that match pattern.

Note

Current implementation does not make use of sorted keys.

See Also

[data.table](#), [grepl](#)

Examples

```
DT = data.table(Name=c("Mary", "George", "Martha"), Salary=c(2,3,4))
DT[Name %like% "^Mar"]
```

melt.data.table

Fast melt for data.table

Description

An S3 method for melting data.tables written in C for speed and memory efficiency. Since v1.9.6, melt.data.table allows melting into multiple columns simultaneously.

It is not necessary to load reshape2 anymore. But if you have to, then load reshape2 package *before* loading data.table.

Usage

```
## fast melt a data.table
## S3 method for class 'data.table'
melt(data, id.vars, measure.vars,
      variable.name = "variable", value.name = "value",
      ..., na.rm = FALSE, variable.factor = TRUE,
      value.factor = FALSE,
      verbose = getOption("datatable.verbose"))
```

Arguments

data	A data.table object to melt.
id.vars	vector of id variables. Can be integer (corresponding id column numbers) or character (id column names) vector. If missing, all non-measure columns will be assigned to it.
measure.vars	vector of measure variables. Can be integer (corresponding measure column numbers) or character (measure column names) vector. If missing, all non-id columns will be assigned to it. measure.vars also now accepts a list of character/integer vectors to melt into multiple columns - i.e., melt into more than one value columns simultaneously. Use patterns to provide multiple patterns conveniently. See also Examples .

<code>variable.name</code>	name for the measured variable names column. The default name is 'variable'.
<code>value.name</code>	name for the molten data values column. The default name is 'value'.
<code>na.rm</code>	If TRUE, NA values will be removed from the molten data.
<code>variable.factor</code>	If TRUE, the variable column will be converted to factor, else it will be a character column.
<code>value.factor</code>	If TRUE, the value column will be converted to factor, else the molten value type is left unchanged.
<code>verbose</code>	TRUE turns on status and information messages to the console. Turn this on by default using <code>options(datatable.verbose=TRUE)</code> . The quantity and types of verbosity may be expanded in future.
<code>...</code>	any other arguments to be passed to/from other methods.

Details

If `id.vars` and `measure.vars` are both missing, all non-numeric/integer/logical columns are assigned as id variables and the rest as measure variables. If only one of `id.vars` or `measure.vars` is supplied, the rest of the columns will be assigned to the other. Both `id.vars` and `measure.vars` can have the same column more than once and the same column can be both as id and measure variables.

`melt.data.table` also accepts list columns for both id and measure variables.

When all `measure.vars` are not of the same type, they'll be coerced according to the hierarchy `list > character > numeric > integer > logical`. For example, if any of the measure variables is a list, then entire value column will be coerced to a list. Note that, if the type of value column is a list, `na.rm = TRUE` will have no effect.

From version 1.9.6, `melt` gains a feature with `measure.vars` accepting a list of character or integer vectors as well to melt into multiple columns in a single function call efficiently. The function `patterns` can be used to provide regular expression patterns. When used along with `melt`, if `cols` argument is not provided, the patterns will be matched against `names(data)`, for convenience.

Attributes are preserved if all value columns are of the same type. By default, if any of the columns to be melted are of type factor, it'll be coerced to character type. This is to be compatible with `reshape2`'s `melt.data.frame`. To get a factor column, set `value.factor = TRUE`. `melt.data.table` also preserves ordered factors.

Value

An unkeyed `data.table` containing the molten data.

See Also

`dcast`, <http://had.co.nz/reshape/>

Examples

```

set.seed(45)
require(data.table)
DT <- data.table(
  i_1 = c(1:5, NA),
  i_2 = c(NA,6,7,8,9,10),
  f_1 = factor(sample(c(letters[1:3]), NA), 6, TRUE)),
  f_2 = factor(c("z", "a", "x", "c", "x", "x"), ordered=TRUE),
  c_1 = sample(c(letters[1:3]), NA), 6, TRUE),
  d_1 = as.Date(c(1:3,NA,4:5), origin="2013-09-01"),
  d_2 = as.Date(6:1, origin="2012-01-01"))
# add a couple of list cols
DT[, l_1 := DT[, list(c=list(rep(i_1, sample(5,1))))], by = i_1]$c]
DT[, l_2 := DT[, list(c=list(rep(c_1, sample(5,1))))], by = i_1]$c]

# id, measure as character/integer/numeric vectors
melt(DT, id=1:2, measure="f_1")
melt(DT, id=c("i_1", "i_2"), measure=3) # same as above
melt(DT, id=1:2, measure=3:L, value.factor=TRUE) # same, but 'value' is factor
melt(DT, id=1:2, measure=3:4, value.factor=TRUE) # 'value' is *ordered* factor

# preserves attribute when types are identical, ex: Date
melt(DT, id=3:4, measure=c("d_1", "d_2"))
melt(DT, id=3:4, measure=c("i_1", "d_1")) # attribute not preserved

# on list
melt(DT, id=1, measure=c("l_1", "l_2")) # value is a list
melt(DT, id=1, measure=c("c_1", "l_1")) # c1 coerced to list

# on character
melt(DT, id=1, measure=c("c_1", "f_1")) # value is char
melt(DT, id=1, measure=c("c_1", "i_2")) # i2 coerced to char

# on na.rm=TRUE. NAs are removed efficiently, from within C
melt(DT, id=1, measure=c("c_1", "i_2"), na.rm=TRUE) # remove NA

# measure.vars can be also a list
# melt "f_1,f_2" and "d_1,d_2" simultaneously, retain 'factor' attribute
# convenient way using internal function patterns()
melt(DT, id=1:2, measure=patterns("^f_", "^d_"), value.factor=TRUE)
# same as above, but provide list of columns directly by column names or indices
melt(DT, id=1:2, measure=list(3:4, c("d_1", "d_2")), value.factor=TRUE)

# na.rm=TRUE removes rows with NAs in any 'value' columns
melt(DT, id=1:2, measure=patterns("f_", "d_"), value.factor=TRUE, na.rm=TRUE)

# return 'NA' for missing columns, 'na.rm=TRUE' ignored due to list column
melt(DT, id=1:2, measure=patterns("l_", "c_"), na.rm=TRUE)

```

merge

Merge two data.tables

Description

Fast merge of two `data.tables`. The `data.table` method behaves very similarly to that of `data.frames` except that, by default, it attempts to merge

- at first based on the shared key columns, and if there are none,
- then based on key columns of the first argument `x`, and if there are none,
- then based on the common columns between the two `data.tables`.

Set the `by`, or `by.x` and `by.y` arguments explicitly to override this default.

Usage

```
## S3 method for class 'data.table'
merge(x, y, by = NULL, by.x = NULL, by.y = NULL,
      all = FALSE, all.x = all, all.y = all, sort = TRUE, suffixes = c(".x", ".y"),
      allow.cartesian=getOption("datatable.allow.cartesian"), # default FALSE
      ...)
```

Arguments

<code>x, y</code>	<code>data.tables</code> . <code>y</code> is coerced to a <code>data.table</code> if it isn't one already.
<code>by</code>	A vector of shared column names in <code>x</code> and <code>y</code> to merge on. This defaults to the shared key columns between the two tables. If <code>y</code> has no key columns, this defaults to the key of <code>x</code> .
<code>by.x, by.y</code>	Vectors of column names in <code>x</code> and <code>y</code> to merge on.
<code>all</code>	logical; <code>all = TRUE</code> is shorthand to save setting both <code>all.x = TRUE</code> and <code>all.y = TRUE</code> .
<code>all.x</code>	logical; if <code>TRUE</code> , then extra rows will be added to the output, one for each row in <code>x</code> that has no matching row in <code>y</code> . These rows will have 'NA's in those columns that are usually filled with values from <code>y</code> . The default is <code>FALSE</code> , so that only rows with data from both <code>x</code> and <code>y</code> are included in the output.
<code>all.y</code>	logical; analogous to <code>all.x</code> above.
<code>sort</code>	logical. If <code>TRUE</code> (default), the merged <code>data.table</code> is sorted by setting the key to the <code>by / by.x</code> columns. If <code>FALSE</code> , the result is not sorted.
<code>suffixes</code>	A character(2) specifying the suffixes to be used for making non-by column names unique. The suffix behavior works in a similar fashion as the merge.data.frame method does.
<code>allow.cartesian</code>	See <code>allow.cartesian</code> in [.data.table] .
<code>...</code>	Not used at this time.

Details

`merge` is a generic function in base R. It dispatches to either the `merge.data.frame` method or `merge.data.table` method depending on the class of its first argument. Note that, unlike SQL, NA is matched against NA (and NaN against NaN) while merging.

In versions \leq v1.9.4, if the specified columns in `by` was not the key (or head of the key) of `x` or `y`, then a `copy` is first rekeyed prior to performing the merge. This was less performant and memory inefficient. The concept of secondary keys (implemented in v1.9.4) was used to overcome this limitation from v1.9.6+. No deep copies are made anymore and therefore very performant and memory efficient. Also there is better control for providing the columns to merge on with the help of newly implemented `by.x` and `by.y` arguments.

For a more data.table-centric way of merging two data.tables, see [[.data.table](#); e.g., `x[y, ...]`]. See FAQ 1.12 for a detailed comparison of `merge` and `x[y, ...]`.

Value

A new data.table based on the merged data.tables, and sorted by the columns set (or inferred for) the `by` argument if argument `sort` is set to TRUE.

See Also

[data.table](#), [as.data.table](#), [[.data.table](#)], [merge.data.frame](#)

Examples

```
(dt1 <- data.table(A = letters[1:10], X = 1:10, key = "A"))
(dt2 <- data.table(A = letters[5:14], Y = 1:10, key = "A"))
merge(dt1, dt2)
merge(dt1, dt2, all = TRUE)

(dt1 <- data.table(A = letters[rep(1:3, 2)], X = 1:6, key = "A"))
(dt2 <- data.table(A = letters[rep(2:4, 2)], Y = 6:1, key = "A"))
merge(dt1, dt2, allow.cartesian=TRUE)

(dt1 <- data.table(A = c(rep(1L, 5), 2L), B = letters[rep(1:3, 2)], X = 1:6, key = "A,B"))
(dt2 <- data.table(A = c(rep(1L, 5), 2L), B = letters[rep(2:4, 2)], Y = 6:1, key = "A,B"))
merge(dt1, dt2)
merge(dt1, dt2, by="B", allow.cartesian=TRUE)

# test it more:
d1 <- data.table(a=rep(1:2,each=3), b=1:6, key="a,b")
d2 <- data.table(a=0:1, bb=10:11, key="a")
d3 <- data.table(a=0:1, key="a")
d4 <- data.table(a=0:1, b=0:1, key="a,b")

merge(d1, d2)
merge(d2, d1)
merge(d1, d2, all=TRUE)
merge(d2, d1, all=TRUE)

merge(d3, d1)
```

```

merge(d1, d3)
merge(d1, d3, all=TRUE)
merge(d3, d1, all=TRUE)

merge(d1, d4)
merge(d1, d4, by="a", suffixes=c(".d1", ".d4"))
merge(d4, d1)
merge(d1, d4, all=TRUE)
merge(d4, d1, all=TRUE)

# new feature, no need to set keys anymore
set.seed(1L)
d1 <- data.table(a=sample(rep(1:3,each=2)), z=1:6)
d2 <- data.table(a=2:0, z=10:12)
merge(d1, d2, by="a")
merge(d1, d2, by="a", all=TRUE)

# new feature, using by.x and by.y arguments
setnames(d2, "a", "b")
merge(d1, d2, by.x="a", by.y="b")
merge(d1, d2, by.x="a", by.y="b", all=TRUE)
merge(d2, d1, by.x="b", by.y="a")

```

na.omit.data.table	<i>Remove rows with missing values on columns specified</i>
--------------------	---

Description

This is a `data.table` method for the S3 generic `stats::na.omit`. The internals are written in C for speed. See examples for benchmark timings.

`bit64::integer64` type is also supported.

Usage

```

## S3 method for class 'data.table'
na.omit(object, cols=seq_along(object), invert=FALSE, ...)

```

Arguments

<code>object</code>	A <code>data.table</code> .
<code>cols</code>	A vector of column names (or numbers) on which to check for missing values. Default is all the columns.
<code>invert</code>	logical. If <code>FALSE</code> omits all rows with any missing values (default). <code>TRUE</code> returns just those rows with missing values instead.
<code>...</code>	Further arguments special methods could require.

Details

The `data.table` method consists of an additional argument `cols`, which when specified looks for missing values in just those columns specified. The default value for `cols` is all the columns, to be consistent with the default behaviour of `stats::na.omit`.

It does not add the attribute `na.action` as `stats::na.omit` does.

Value

A `data.table` with just the rows where the specified columns have no missing value in any of them.

See Also

[data.table](#)

Examples

```
DT = data.table(x=c(1,NaN,NA,3), y=c(NA_integer_, 1:3), z=c("a", NA_character_, "b", "c"))
# default behaviour
na.omit(DT)
# omit rows where 'x' has a missing value
na.omit(DT, cols="x")
# omit rows where either 'x' or 'y' have missing values
na.omit(DT, cols=c("x", "y"))

## Not run:
# Timings on relatively large data
set.seed(1L)
DT = data.table(x = sample(c(1:100, NA_integer_), 5e7L, TRUE),
               y = sample(c(rnorm(100), NA), 5e7L, TRUE))
system.time(ans1 <- na.omit(DT)) ## 2.6 seconds
system.time(ans2 <- stats::na.omit.data.frame(DT)) ## 29 seconds
# identical? check each column separately, as ans2 will have additional attribute
all(sapply(1:2, function(i) identical(ans1[[i]], ans2[[i]]))) ## TRUE

## End(Not run)
```

patterns

Obtain matching indices corresponding to patterns

Description

`patterns` returns the matching indices in the argument `cols` corresponding to the regular expression patterns provided. The patterns must be supported by [grep](#).

From v1.9.6, [melt.data.table](#) has an enhanced functionality in which `measure.vars` argument can accept a *list of column names* and melt them into separate columns. See the [Efficient reshaping using data.tables](#) vignette linked below to learn more.

Usage

```
patterns(..., cols=character(0))
```

Arguments

```
...      A set of regular expression patterns.
cols     A character vector of names to which each pattern is matched.
```

See Also

[melt](https://github.com/Rdatatable/data.table/wiki/Getting-started), <https://github.com/Rdatatable/data.table/wiki/Getting-started>

Examples

```
dt = data.table(x1 = 1:5, x2 = 6:10, y1 = letters[1:5], y2 = letters[6:10])
# melt all columns that begin with 'x' & 'y', respectively, into separate columns
melt(dt, measure.vars = patterns("^x", "^y", cols=names(dt)))
# when used with melt, 'cols' is implicitly assumed to be names of input
# data.table, if not provided.
melt(dt, measure.vars = patterns("^x", "^y"))
```

```
print.data.table      data.table Printing Options
```

Description

`print.data.table` extends the functionalities of `print.data.frame`.

Key enhancements include automatic output compression of many observations and concise column-wise class summary.

Usage

```
## S3 method for class 'data.table'
print(x,
      topn=getOption("datatable.print.topn"),      # default: 5
      nrows=getOption("datatable.print.nrows"),    # default: 100
      class=getOption("datatable.print.class"),   # default: FALSE
      row.names=getOption("datatable.print.row.names"), # default: TRUE
      quote=FALSE,...)
```

Arguments

```
x      A data.table.
topn   The number of rows to be printed from the beginning and end of tables with
       more than nrows rows.
nrows  The number of rows which will be printed before truncation is enforced.
```

<code>class</code>	If TRUE, the resulting output will include above each column its storage class (or a self-evident abbreviation thereof).
<code>row.names</code>	If TRUE, row indices will be printed alongside x.
<code>quote</code>	If TRUE, all output will appear in quotes, as in <code>print.default</code> .
<code>...</code>	Other arguments ultimately passed to <code>format</code> .

Details

By default, with an eye to the typically large number of observations in a `codetable`, only the beginning and end of the object are displayed (specifically, `head(x, topn)` and `tail(x, topn)` are displayed unless `nrow(x) < nrows`, in which case all rows will print).

See Also

[print.default](#)

Examples

```
#output compression
DT <- data.table(a = 1:1000)
print(DT, nrows = 100, topn = 4)

#`quote` can be used to identify whitespace
DT <- data.table(blanks = c(" 12", " 34"),
                noblanks = c("12", "34"))
print(DT, quote = TRUE)

#`class` provides handy column type summaries at a glance
DT <- data.table(a = vector("integer", 3),
                b = vector("complex", 3),
                c = as.IDate(paste0("2016-02-0", 1:3)))
print(DT, class = TRUE)

#`row.names` can be eliminated to save space
DT <- data.table(a = 1:3)
print(DT, row.names = FALSE)
```

rbindlist

Makes one data.table from a list of many

Description

Same as `do.call("rbind", l)` on `data.frames`, but much faster. See DETAILS for more.

Usage

```
rbindlist(l, use.names=fill, fill=FALSE, idcol=NULL)
# rbind(..., use.names=TRUE, fill=FALSE, idcol=NULL)
```

Arguments

<code>l</code>	A list containing <code>data.table</code> , <code>data.frame</code> or <code>list</code> objects. At least one of the inputs should have column names set. <code>...</code> is the same but you pass the objects by name separately.
<code>use.names</code>	If <code>TRUE</code> items will be bound by matching column names. By default <code>FALSE</code> for <code>rbindlist</code> (for backwards compatibility) and <code>TRUE</code> for <code>rbind</code> (consistency with base). Columns with duplicate names are bound in the order of occurrence, similar to base. When <code>TRUE</code> , at least one item of the input list has to have non-null column names.
<code>fill</code>	If <code>TRUE</code> fills missing columns with NAs. By default <code>FALSE</code> . When <code>TRUE</code> , <code>use.names</code> has to be <code>TRUE</code> , and all items of the input list has to have non-null column names.
<code>idcol</code>	Generates an index column. Default (<code>NULL</code>) is not to. If <code>idcol=TRUE</code> then the column is auto named <code>.id</code> . Alternatively the column name can be directly provided, e.g., <code>idcol = "id"</code> . If input is a named list, ids are generated using them, else using integer vector from 1 to length of input list. See examples.

Details

Each item of `l` can be a `data.table`, `data.frame` or `list`, including `NULL` (skipped) or an empty object (0 rows). `rbindlist` is most useful when there are a variable number of (potentially many) objects to stack, such as returned by `lapply(fileNames, fread)`. `rbind` however is most useful to stack two or three objects which you know in advance. `...` should contain at least one `data.table` for `rbind(...)` to call the fast method and return a `data.table`, whereas `rbindlist(l)` always returns a `data.table` even when stacking a plain list with a `data.frame`, for example.

In versions `<= v1.9.2`, each item for `rbindlist` should have the same number of columns as the first non empty item. `rbind.data.table` gained a `fill` argument to fill missing columns with `NA` in `v1.9.2`, which allowed for `rbind(...)` binding unequal number of columns.

In version `> v1.9.2`, these functionalities were extended to `rbindlist` (and written entirely in C for speed). `rbindlist` has `use.names` argument, which is set to `FALSE` by default for backwards compatibility. It also contains `fill` argument as well and can bind unequal columns when set to `TRUE`.

With these changes, the only difference between `rbind(...)` and `rbindlist(l)` is their *default argument* `use.names`.

If column `i` of input items do not all have the same type; e.g, a `data.table` may be bound with a list or a column is factor while others are character types, they are coerced to the highest type (`SEXPTYPE`).

Note that any additional attributes that might exist on individual items of the input list would not be preserved in the result.

Value

An unkeyed `data.table` containing a concatenation of all the items passed in.

See Also

[data.table](#), [split.data.table](#)

Examples

```

# default case
DT1 = data.table(A=1:3,B=letters[1:3])
DT2 = data.table(A=4:5,B=letters[4:5])
l = list(DT1,DT2)
rbindlist(l)

# bind correctly by names
DT1 = data.table(A=1:3,B=letters[1:3])
DT2 = data.table(B=letters[4:5],A=4:5)
l = list(DT1,DT2)
rbindlist(l, use.names=TRUE)

# fill missing columns, and match by col names
DT1 = data.table(A=1:3,B=letters[1:3])
DT2 = data.table(B=letters[4:5],C=factor(1:2))
l = list(DT1,DT2)
rbindlist(l, use.names=TRUE, fill=TRUE)

# generate index column, auto generates indices
rbindlist(l, use.names=TRUE, fill=TRUE, idcol=TRUE)
# let's name the list
setattr(l, 'names', c("a", "b"))
rbindlist(l, use.names=TRUE, fill=TRUE, idcol="ID")

```

rleid

Generate run-length type group id

Description

A convenience function for generating a *run-length* type *id* column to be used in grouping operations. It accepts atomic vectors, lists, data.frames or data.tables as input.

Usage

```

rleid(..., prefix=NULL)
rleidv(x, cols=seq_along(x), prefix=NULL)

```

Arguments

x	A vector, list, data.frame or data.table.
...	A sequence of numeric, integer64, character or logical vectors, all of same length. For interactive use.
cols	Only meaningful for lists, data.frames or data.tables. A character vector of column names (or numbers) of x.
prefix	Either NULL (default) or a character vector of length=1 which is prefixed to the row ids, returning a character vector (instead of an integer vector).

Details

At times aggregation (or grouping) operations need to be performed where consecutive runs of identical values should belong to the same group (See [rle](#)). The use for such a function has come up repeatedly on StackOverflow, see the [See Also](#) section. This function allows to generate "run-length" groups directly.

`rleid` is designed for interactive use and accepts a sequence of vectors as arguments. For programming, `rleidv` might be more useful.

Value

When `prefix = NULL`, an integer vector with same length as `NROW(x)`, else a character vector with the value in `prefix` prefixed to the ids obtained.

See Also

[data.table](#), [rowid](#), <http://stackoverflow.com/q/21421047/559784>

Examples

```
DT = data.table(grp=rep(c("A", "B", "C", "A", "B"), c(2,2,3,1,2)), value=1:10)
rleid(DT$grp) # get run-length ids
rleidv(DT, "grp") # same as above

rleid(DT$grp, prefix="grp") # prefix with 'grp'

# get sum of value over run-length groups
DT[, sum(value), by=.(grp, rleid(grp))]
DT[, sum(value), by=.(grp, rleid(grp, prefix="grp"))]
```

rowid

Generate unique row ids within each group

Description

Convenience functions for generating a unique row ids within each group. It accepts atomic vectors, lists, data.frames or data.tables as input.

`rowid` is intended for interactive use, particularly along with the function `dcast` to generate unique ids directly in the formula.

`rowidv(dt, cols=c("x", "y"))` is equivalent to column N in the code `dt[, N := seq_len(.N), by=c("x", "y")]`.

See examples for more.

Usage

```
rowid(..., prefix=NULL)
rowidv(x, cols=seq_along(x), prefix=NULL)
```

Arguments

<code>x</code>	A vector, list, data.frame or data.table.
<code>...</code>	A sequence of numeric, integer64, character or logical vectors, all of same length. For interactive use.
<code>cols</code>	Only meaningful for lists, data.frames or data.tables. A character vector of column names (or numbers) of <code>x</code> .
<code>prefix</code>	Either NULL (default) or a character vector of length=1 which is prefixed to the row ids, returning a character vector (instead of an integer vector).

Value

When `prefix = NULL`, an integer vector with same length as `NROW(x)`, else a character vector with the value in `prefix` prefixed to the ids obtained.

See Also

[dcast.data.table](#), [rleid](#)

Examples

```
DT = data.table(x=c(20,10,10,30,30,20), y=c("a", "a", "a", "b", "b", "b"), z=1:6)

rowid(DT$x) # 1,1,2,1,2,2
rowidv(DT, cols="x") # same as above

rowid(DT$x, prefix="group") # prefixed with 'group'

rowid(DT$x, DT$y) # 1,1,2,1,2,1
rowidv(DT, cols=c("x","y")) # same as above
DT[, .(N=seq_len(.N)), by=(x,y)]$N # same as above

# convenient usage with dcast
dcast(DT, x ~ rowid(x, prefix="group"), value.var="z")
#   x group1 group2
# 1: 10     2     3
# 2: 20     1     6
# 3: 30     4     5
```

 setattr

Set attributes of objects by reference

Description

In `data.table`, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory which is as large as one column. The only other `data.table` operator that modifies input by reference is `:=`. Check out the See Also section below for other `set*` function that `data.table` provides.

Usage

```
setattr(x, name, value)
setnames(x, old, new)
```

Arguments

x	setnames accepts <code>data.frame</code> and <code>data.table</code> . <code>setattr</code> accepts any input; e.g, list, columns of a <code>data.frame</code> or <code>data.table</code> .
name	The character attribute name.
value	The value to assign to the attribute or <code>NULL</code> removes the attribute, if present.
old	When <code>new</code> is provided, character names or numeric positions of column names to change. When <code>new</code> is not provided, the new column names, which must be the same length as the number of columns. See examples.
new	Optional. New column names, must be the same length as columns provided to <code>old</code> argument.

Details

`setnames` operates on `data.table` and `data.frame` not other types like `list` and `vector`. It can be used to change names *by name* with built-in checks and warnings (e.g., if any old names are missing or appear more than once).

`setattr` is a more general function that allows setting of any attribute to an object *by reference*.

A very welcome change in R 3.1+ was that `'names<-'` and `'colnames<-'` no longer copy the *entire* object as they used to (up to 4 times), see examples below. They now take a shallow copy. The `'set*'` functions in `data.table` are still useful because they don't even take a shallow copy. This allows changing names and attributes of a (usually very large) `data.table` in the global environment *from within functions*. Like a database.

Value

The input is modified by reference, and returned (invisibly) so it can be used in compound statements; e.g., `setnames(DT, "V1", "Y")[, .N, by=Y]`. If you require a copy, take a copy first (using `DT2=copy(DT)`). See `?copy`.

Note that `setattr` is also in package `bit`. Both packages merely expose R's internal `setAttrib` function at C level but differ in return value. `bit::setattr` returns `NULL` (invisibly) to remind you the function is used for its side effect. `data.table::setattr` returns the changed object (invisibly) for use in compound statements.

See Also

[data.table](#), [setkey](#), [setorder](#), [setcolorder](#), [set](#), [:=](#), [setDT](#), [setDF](#), [copy](#)

Examples

```
DF = data.frame(a=1:2,b=3:4)      # base data.frame to demo copies and syntax
try(tracemem(DF))                # try() for R sessions opted out of memory profiling
```

```

colnames(DF)[1] <- "A"           # 4 shallow copies (R >= 3.1, was 4 deep copies before)
names(DF)[1] <- "A"             # 3 shallow copies
names(DF) <- c("A", "b")       # 1 shallow copy
`names<-`(DF,c("A","b"))       # 1 shallow copy

DT = data.table(a=1:2,b=3:4,c=5:6) # compare to data.table
try(tracemem(DT))                 # by reference, no deep or shallow copies
setnames(DT,"b","B")             # by name, no match() needed (warning if "b" is missing)
setnames(DT,3,"C")              # by position with warning if 3 > ncol(DT)
setnames(DT,2:3,c("D","E"))      # multiple
setnames(DT,c("a","E"),c("A","F")) # multiple by name (warning if either "a" or "E" is missing)
setnames(DT,c("X","Y","Z"))      # replace all (length of names must be == ncol(DT))

DT <- data.table(x = 1:3, y = 4:6, z = 7:9)
setnames(DT, -2, c("a", "b"))    # NEW FR #1443, allows -ve indices in 'old' argument

DT = data.table(a=1:3, b=4:6)
f = function(...) {
  # ...
  setattr(DT,"myFlag",TRUE) # by reference
  # ...
  localDT = copy(DT)
  setattr(localDT,"myFlag2",TRUE)
  # ...
  invisible()
}
f()
attr(DT,"myFlag") # TRUE
attr(DT,"myFlag2") # NULL

```

setcolorder

Fast column reordering of a data.table by reference

Description

In `data.table` parlance, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory, which is as large as one column.. The only other `data.table` operator that modifies input by reference is `:=`. Check out the See Also section below for other `set*` function `data.table` provides.

`setcolorder` reorders the columns of `data.table`, *by reference*, to the new order provided.

Usage

```
setcolorder(x, neworder)
```


Arguments

x	A <code>data.table</code> .
neworder	Character vector of the new column name ordering. May also be column numbers.

Details

To reorder `data.table` columns, the idiomatic way is to use `setcolorder(x, neworder)`, instead of doing `x <- x[, neworder, with=FALSE]`. This is because the latter makes an entire copy of the `data.table`, which maybe unnecessary in most situations. `setcolorder` also allows column numbers instead of names for `neworder` argument, although we recommend using names as a good programming practice.

Value

The input is modified by reference, and returned (invisibly) so it can be used in compound statements. If you require a copy, take a copy first (using `DT2 = copy(DT)`). See `?copy`.

See Also

[setkey](#), [setorder](#), [setattr](#), [setnames](#), [set](#), [:=](#), [setDT](#), [setDF](#), [copy](#), [getNumericRounding](#), [setNumericRounding](#)

Examples

```
set.seed(45L)
DT = data.table(A=sample(3, 10, TRUE),
               B=sample(letters[1:3], 10, TRUE), C=sample(10))

setcolorder(DT, c("C", "A", "B"))
```

 setDF

Coerce a `data.table` to `data.frame` by reference

Description

In `data.table` parlance, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory, which is as large as one column. The only other `data.table` operator that modifies input by reference is `:=`. Check out the [See Also](#) section below for other `set*` function `data.table` provides.

A helper function to convert a `data.table` or list of equal length to `data.frame` by reference.

Usage

```
setDF(x, rownames=NULL)
```

Arguments

`x` A `data.table`, `data.frame` or `list` of equal length.
`rownames` A character vector to assign as the row names of `x`.

Details

This feature request came up on the [data.table mailing list](#). All `data.table` attributes including any keys of the input `data.table` are stripped off.

When using `rownames`, recall that the row names of a `data.frame` must be unique. By default, the assigned set of row names is simply the sequence `1, ..., nrow(x)` (or `length(x)` for lists).

Value

The input `data.table` is modified by reference to a `data.frame` and returned (invisibly). If you require a copy, take a copy first (using `DT2 = copy(DT)`). See `?copy`.

See Also

[data.table](#), [as.data.table](#), [setDT](#), [copy](#), [setkey](#), [setcolorder](#), [setattr](#), [setnames](#), [set](#), [:=](#), [setorder](#)

Examples

```
X = data.table(x=1:5, y=6:10)
## convert 'X' to data.frame, without any copy.
setDF(X)

X = data.table(x=1:5, y=6:10)
## idem, assigning row names
setDF(X, rownames = LETTERS[1:5])

X = list(x=1:5, y=6:10)
# X is converted to a data.frame without any copy.
setDF(X)
```

setDT

Coerce lists and data.frames to data.table by reference

Description

In `data.table` parlance, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory, which is as large as one column.. The only other `data.table` operator that modifies input by reference is `:=`. Check out the [See Also](#) section below for other `set*` function `data.table` provides.

`setDT` converts lists (both named and unnamed) and `data.frames` to `data.tables` *by reference*. This feature was requested on [Stackoverflow](#).

Usage

```
setDT(x, keep.rownames=FALSE, key=NULL, check.names=FALSE)
```

Arguments

x	A named or unnamed list, data.frame or data.table.
keep.rownames	For data.frames, TRUE retains the data.frame's row names under a new column rn.
key	Character vector of one or more column names which is passed to setkeyv . It may be a single comma separated string such as key="x,y,z", or a vector of names such as key=c("x","y","z").
check.names	Just as check.names in data.frame .

Details

When working on large lists or data.frames, it might be both time and memory consuming to convert them to a data.table using `as.data.table(.)`, as this will make a complete copy of the input object before to convert it to a data.table. The `setDT` function takes care of this issue by allowing to convert lists - both named and unnamed lists and data.frames *by reference* instead. That is, the input object is modified in place, no copy is being made.

Value

The input is modified by reference, and returned (invisibly) so it can be used in compound statements; e.g., `setDT(X)[, sum(B), by=A]`. If you require a copy, take a copy first (using `DT2 = copy(DT)`). See `?copy`.

See Also

[data.table](#), [as.data.table](#), [setDF](#), [copy](#), [setkey](#), [setcolorder](#), [setattr](#), [setnames](#), [set](#), [:=](#), [setorder](#)

Examples

```
set.seed(45L)
X = data.frame(A=sample(3, 10, TRUE),
              B=sample(letters[1:3], 10, TRUE),
              C=sample(10), stringsAsFactors=FALSE)

# Convert X to data.table by reference and
# get the frequency of each "A,B" combination
setDT(X)[, .N, by=.(A,B)]

# convert list to data.table
# autofill names
X = list(1:4, letters[1:4])
setDT(X)
# don't provide names
```

```

X = list(a=1:4, letters[1:4])
setDT(X, FALSE)

# setkey directly
X = list(a = 4:1, b=runif(4))
setDT(X, key="a")[]

# check.names argument
X = list(a=1:5, a=6:10)
setDT(X, check.names=TRUE)[]

```

setDTthreads

Set or get number of threads that data.table should use

Description

Set and get number of threads to be used in `data.table` functions that are parallelized with OpenMP. Default value 0 means to utilize all CPU available with an appropriate number of threads calculated by OpenMP. `getDTthreads()` returns the number of threads that will be used. This affects `data.table` only and does not change R itself or other packages using OpenMP. The most common usage expected is `setDTthreads(1)` to limit `data.table` to one thread for pre-existing explicitly parallel user code; e.g. via packages `parallel` and `foreach`. Otherwise, nested parallelism may bite. As `data.table` becomes more parallel automatically internally, we expect explicit user parallelism to be needed less often.

Usage

```

setDTthreads(threads)
getDTthreads()

```

Arguments

threads	An integer ≥ 0 . Default 0 means use all CPU available and leave the operating system to multi task.
---------	---

Value

A length 1 integer. The old value is returned by `setDTthreads` so you can store that value and pass it to `setDTthreads` again after the section of your code where you, probably, limited to one thread.

 setkey

Create key on a data table

Description

In `data.table` parlance, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory, which is as large as one column. The only other `data.table` operator that modifies input by reference is `:=`. Check out the See Also section below for other `set*` function `data.table` provides.

`setkey()` sorts a `data.table` and marks it as sorted (with an attribute `sorted`). The sorted columns are the key. The key can be any columns in any order. The columns are sorted in ascending order always. The table is changed *by reference* and is therefore very memory efficient.

`key()` returns the `data.table`'s key if it exists, and `NULL` if none exist.

`haskey()` returns a logical `TRUE/FALSE` depending on whether the `data.table` has a key (or not).

Usage

```
setkey(x, ..., verbose=getOption("datatable.verbose"), physical = TRUE)
setkeyv(x, cols, verbose=getOption("datatable.verbose"), physical = TRUE)
setindex(...)
setindexv(...)
key(x)
indices(x, vectors = FALSE)
haskey(x)
key(x) <- value # DEPRECATED, please use setkey or setkeyv instead.
```

Arguments

<code>x</code>	A <code>data.table</code> .
<code>...</code>	The columns to sort by. Do not quote the column names. If <code>...</code> is missing (i.e. <code>setkey(DT)</code>), all the columns are used. <code>NULL</code> removes the key.
<code>cols</code>	A character vector (only) of column names.
<code>value</code>	In (deprecated) <code>key<-</code> , a character vector (only) of column names.
<code>verbose</code>	Output status and information.
<code>physical</code>	<code>TRUE</code> changes the order of the data in RAM. <code>FALSE</code> adds a secondary key a.k.a. index.
<code>vectors</code>	logical scalar default <code>FALSE</code> , when set to <code>TRUE</code> then list of character vectors is returned, each vector refers to one index.

Details

`setkey` reorders (or sorts) the rows of a `data.table` by the columns provided. In versions 1.9+, for integer columns, a modified version of base's counting sort is implemented, which allows negative values as well. It is extremely fast, but is limited by the range of integer values being `<=`

1e5. If that fails, it falls back to a (fast) 4-pass radix sort for integers, implemented based on Pierre Terdiman's and Michael Herf's code (see links below). Similarly, a very fast 6-pass radix order for columns of type `double` is also implemented. This gives a speed-up of about 5-8x compared to 1.8.10 on `setkey` and all internal order/sort operations. Fast radix sorting is also implemented for character and `bit64::integer64` types.

The sort is *stable*; i.e., the order of ties (if any) is preserved, in both versions - $\leq 1.8.10$ and $\geq 1.9.0$.

In `data.table` versions $\leq 1.8.10$, for columns of type `integer`, the sort is attempted with the very fast "radix" method in `sort.list`. If that fails, the sort reverts to the default method in `order`. For character vectors, `data.table` takes advantage of R's internal global string cache and implements a very efficient order, also exported as `chorder`.

In v1.7.8, the `key<-` syntax was deprecated. The `<-` method copies the whole table and we know of no way to avoid that copy without a change in R itself. Please use the `set*` functions instead, which make no copy at all. `setkey` accepts unquoted column names for convenience, whilst `setkeyv` accepts one vector of column names.

The problem (for `data.table`) with the copy by `key<-` (other than being slower) is that R doesn't maintain the over allocated `truelength`, but it looks as though it has. Adding a column by reference using `:=` after a `key<-` was therefore a memory overwrite and eventually a segfault; the over allocated memory wasn't really there after `key<-`'s copy. `data.tables` now have an attribute `.internal.selfref` to catch and warn about such copies. This attribute has been implemented in a way that is friendly with `identical()` and `object.size()`.

For the same reason, please use the other `set*` functions which modify objects by reference, rather than using the `<-` operator which results in copying the entire object.

It isn't good programming practice, in general, to use column numbers rather than names. This is why `setkey` and `setkeyv` only accept column names. If you use column numbers then bugs (possibly silent) can more easily creep into your code as time progresses if changes are made elsewhere in your code; e.g., if you add, remove or reorder columns in a few months time, a `setkey` by column number will then refer to a different column, possibly returning incorrect results with no warning. (A similar concept exists in SQL, where "select * from ..." is considered poor programming style when a robust, maintainable system is required.) If you really wish to use column numbers, it's possible but deliberately a little harder; e.g., `setkeyv(DT, colnames(DT)[1:2])`.

Value

The input is modified by reference, and returned (invisibly) so it can be used in compound statements; e.g., `setkey(DT, a)[J("foo")]`. If you require a copy, take a copy first (using `DT2=copy(DT)`). `copy()` may also sometimes be useful before `:=` is used to subassign to a column by reference. See `?copy`.

Note

Despite its name, `base::sort.list(x, method="radix")` actually invokes a *counting sort* in R, not a radix sort. See `do_radixsort` in `src/main/sort.c`. A counting sort, however, is particularly suitable for sorting integers and factors, and we like it. In fact we like it so much that `data.table` contains a counting sort algorithm for character vectors using R's internal global string cache. This is particularly fast for character vectors containing many duplicates, such as grouped data in a key

column. This means that character is often preferred to factor. Factors are still fully supported, in particular ordered factors (where the levels are not in alphabetic order).

References

http://en.wikipedia.org/wiki/Radix_sort
http://en.wikipedia.org/wiki/Counting_sort
<http://cran.at.r-project.org/web/packages/bit/index.html>
<http://stereopsis.com/radix.html>

See Also

[data.table](#), [tables](#), [J](#), [sort.list](#), [copy](#), [setDT](#), [setDF](#), [set :=](#), [setorder](#), [setcolorder](#), [setattr](#), [setnames](#), [chorder](#), [setNumericRounding](#)

Examples

```
# Type 'example(setkey)' to run these at prompt and browse output

DT = data.table(A=5:1,B=letters[5:1])
DT # before
setkey(DT,B)          # re-orders table and marks it sorted.
DT # after
tables()              # KEY column reports the key'd columns
key(DT)
keycols = c("A","B")
setkeyv(DT,keycols)  # rather than key(DT)<-keycols (which copies entire table)

DT = data.table(A=5:1,B=letters[5:1])
DT2 = DT              # does not copy
setkey(DT2,B)        # does not copy-on-write to DT2
identical(DT,DT2)    # TRUE. DT and DT2 are two names for the same keyed table

DT = data.table(A=5:1,B=letters[5:1])
DT2 = copy(DT)       # explicit copy() needed to copy a data.table
setkey(DT2,B)        # now just changes DT2
identical(DT,DT2)    # FALSE. DT and DT2 are now different tables

DT = data.table(A=5:1,B=letters[5:1])
setindex(DT)         # set indices
setindex(DT, A)
setindex(DT, B)
indices(DT)          # get indices single vector
indices(DT, vectors = TRUE) # get indices list
```

Description

Change rounding to 0, 1 or 2 bytes when joining, grouping or ordering numeric (i.e. double, POSIXct) columns.

Usage

```
setNumericRounding(x)
getNumericRounding()
```

Arguments

x integer or numeric vector: 0 (default), 1 or 2 byte rounding

Details

Computers cannot represent some floating point numbers (such as 0.6) precisely, using base 2. This leads to unexpected behaviour when joining or grouping columns of type 'numeric'; i.e. 'double', see example below. In cases where this is undesirable, data.table allows rounding such data up to approximately 11 s.f. which is plenty of digits for many cases. This is achieved by rounding the last 2 bytes off the significand. Other possible values are 1 byte rounding, or no rounding (full precision, default).

It's bytes rather than bits because it's tied in with the radix sort algorithm for sorting numerics which sorts byte by byte. With the default rounding of 0 bytes, at most 8 passes are needed. With rounding of 2 bytes, at most 6 passes are needed (and therefore might be a tad faster).

For large numbers (integers $> 2^{31}$), we recommend using `bit64::integer64`, even though the default is to round off 0 bytes (full precision).

Value

setNumericRounding returns no value; the new value is applied. getNumericRounding returns the current value: 0, 1 or 2.

See Also

[datatable-optimize](#)
http://en.wikipedia.org/wiki/Double-precision_floating-point_format
http://en.wikipedia.org/wiki/Floating_point
http://docs.oracle.com/cd/E19957-01/806-3568/ncg_goldberg.html

Examples

```
DT = data.table(a=seq(0,1,by=0.2),b=1:2, key="a")
DT
setNumericRounding(0) # By default, rounding is turned off
DT[.(0.4)] # works
DT[.(0.6)] # no match, can be confusing since 0.6 is clearly there in DT
           # happens due to floating point representation limitations

setNumericRounding(2) # round off last 2 bytes
```



```
DT[.(0.6)] # works

# using type 'numeric' for integers > 2^31 (typically ids)
DT = data.table(id = c(1234567890123, 1234567890124, 1234567890125), val=1:3)
print(DT, digits=15)
DT[,.N,by=id] # 1 row, (last 2 bytes rounded)
setNumericRounding(0)
DT[,.N,by=id] # 3 rows, (no rounding, default)
# better to use bit64::integer64 for such ids
```

setops

Set operations for data tables

Description

Similar to base's set functions, `union`, `intersect`, `setdiff` and `setequal` but for `data.tables`. Additional `all` argument controls if/how duplicate rows are returned. `bit64::integer64` is also supported.

Unlike SQL, `data.table` functions will retain order of rows in result.

Usage

```
fintersect(x, y, all = FALSE)
fsetdiff(x, y, all = FALSE)
funion(x, y, all = FALSE)
fsetequal(x, y)
```

Arguments

<code>x,y</code>	<code>data.tables</code> .
<code>all</code>	Logical. Default is <code>FALSE</code> and removes duplicate rows on the result. When <code>TRUE</code> , if there are <code>xn</code> copies of a particular row in <code>x</code> and <code>yn</code> copies of the same row in <code>y</code> , then: <ul style="list-style-type: none"> • <code>fintersect</code> will return <code>min(xn, yn)</code> copies of that row. • <code>fsetdiff</code> will return <code>max(0, xn-yn)</code> copies of that row. • <code>funion</code> will return <code>xn+yn</code> copies of that row.

Details

Columns of type `complex` and `list` are not supported except for `funion`.

Value

A `data.table` in case of `fintersect`, `funion` and `fsetdiff`. Logical `TRUE` or `FALSE` for `fsetequal`.

References

<https://db.apache.org/derby/papers/Intersect-design.html>

See Also

[data.table](#), [rbindlist](#), [all.equal.data.table](#), [unique](#), [duplicated](#), [uniqueN](#), [anyDuplicated](#)

Examples

```
x = data.table(c(1,2,2,2,3,4,4))
y = data.table(c(2,3,4,4,4,5))
fintersect(x, y)           # intersect
fintersect(x, y, all=TRUE) # intersect all
fsetdiff(x, y)            # except
fsetdiff(x, y, all=TRUE)  # except all
funion(x, y)              # union
funion(x, y, all=TRUE)    # union all
fsetequal(x, y)           # setequal
```

setorder

Fast row reordering of a data.table by reference

Description

In `data.table` parlance, all `set*` functions change their input *by reference*. That is, no copy is made at all, other than temporary working memory, which is as large as one column. The only other `data.table` operator that modifies input by reference is `:=`. Check out the [See Also](#) section below for other `set*` function `data.table` provides.

`setorder` (and `setorderv`) reorders the rows of a `data.table` based on the columns (and column order) provided. It reorders the table *by reference* and is therefore very memory efficient.

Also `x[order(.)]` is now optimised internally to use `data.table`'s fast order by default. `data.table` always reorders in C-locale. To sort by session locale, use `x[base::order(.)]` instead.

`bit64::integer64` type is also supported for reordering rows of a `data.table`.

Usage

```
setorder(x, ..., na.last=FALSE)
setorderv(x, cols, order=1L, na.last=FALSE)
# optimised to use data.table's internal fast order
# x[order(., na.last=TRUE)]
```

Arguments

<code>x</code>	A <code>data.table</code> .
<code>...</code>	The columns to sort by. Do not quote column names. If <code>...</code> is missing (ex: <code>setorder(x)</code>), <code>x</code> is rearranged based on all columns in ascending order by default. To sort by a column in descending order prefix a <code>"-"</code> , i.e., <code>setorder(x, a, -b, c)</code> . The <code>-b</code> works when <code>b</code> is of type character as well.
<code>cols</code>	A character vector of column names of <code>x</code> , to which to order by. Do not add <code>"-"</code> here. Use <code>order</code> argument instead.

order	An integer vector with only possible values of 1 and -1, corresponding to ascending and descending order. The length of order must be either 1 or equal to that of cols. If length(order) == 1, it's recycled to length(cols).
na.last	logical. If TRUE, missing values in the data are placed last; if FALSE, they are placed first; if NA they are removed. na.last=NA is valid only for x[order(., na.last)] and it's default is TRUE. setorder and setorderv only accept TRUE/FALSE with default FALSE.

Details

data.table implements fast radix based ordering. In versions <= 1.9.2, it was only capable of increasing order (ascending). From 1.9.4 on, the functionality has been extended to decreasing order (descending) as well.

setorder accepts unquoted column names (with names preceded with a - sign for descending order) and reorders data.table rows *by reference*, for e.g., setorder(x, a, -b, c). Note that -b also works with columns of type character unlike base::order, which requires -xfrm(y) instead (which is slow). setorderv in turn accepts a character vector of column names and an integer vector of column order separately.

Note that [setkey](#) still requires and will always sort only in ascending order, and is different from setorder in that it additionally sets the sorted attribute.

na.last argument, by default, is FALSE for setorder and setorderv to be consistent with data.table's setkey and is TRUE for x[order(.)] to be consistent with base::order. Only x[order(.)] can have na.last = NA as it's a subset operation as opposed to setorder or setorderv which reorders the data.table by reference.

If setorder results in reordering of the rows of a keyed data.table, then it's key will be set to NULL.

Value

The input is modified by reference, and returned (invisibly) so it can be used in compound statements; e.g., setorder(DT,a,-b)[, cumsum(c), by=list(a,b)]. If you require a copy, take a copy first (using DT2 = copy(DT)). See ?copy.

See Also

[setkey](#), [setcolorder](#), [setattr](#), [setnames](#), [set](#), [:=](#), [setDT](#), [setDF](#), [copy](#), [setNumericRounding](#)

Examples

```
set.seed(45L)
DT = data.table(A=sample(3, 10, TRUE),
               B=sample(letters[1:3], 10, TRUE), C=sample(10))

# setorder
setorder(DT, A, -B)

# same as above, but using setorderv
setorderv(DT, c("A", "B"), c(1, -1))
```

shift *Fast lead/lag for vectors and lists*

Description

lead or lag vectors, lists, data.frames or data.tables implemented in C for speed. bit64::integer64 is also supported.

Usage

```
shift(x, n=1L, fill=NA, type=c("lag", "lead"), give.names=FALSE)
```

Arguments

x	A vector, list, data.frame or data.table.
n	Non-negative integer vector denoting the offset to lead or lag the input by. To create multiple lead/lag vectors, provide multiple values to n.
fill	Value to pad by.
type	default is "lag". The other possible value is "lead".
give.names	default is FALSE which returns an unnamed list. When TRUE, names are automatically generated corresponding to type and n.

Details

shift accepts vectors, lists, data.frames or data.tables. It always returns a list except when the input is a vector and `length(n) == 1` in which case a vector is returned, for convenience. This is so that it can be used conveniently within data.table's syntax. For example, `DT[, (cols) := shift(.SD, 1L), by=id]` would lag every column of .SD by 1 for each group and `DT[, newcol := colA + shift(colB)]` would assign the sum of two *vectors* to newcol.

Argument n allows multiple values. For example, `DT[, (cols) := shift(.SD, 1:2), by=id]` would lag every column of .SD by 1 and 2 for each group. If .SD contained four columns, the first two elements of the list would correspond to lag=1 and lag=2 for the first column of .SD, the next two for second column of .SD and so on. Please see examples for more.

shift is designed mainly for use in data.tables along with := or set. Therefore, it returns an unnamed list by default as assigning names for each group over and over can be quite time consuming with many groups. It may be useful to set names automatically in other cases, which can be done by setting give.names to TRUE.

Value

A list containing the lead/lag of input x.

See Also

[data.table](#)

Examples

```

# on vectors, returns a vector as long as length(n) == 1, #1127
x = 1:5
# lag with n=1 and pad with NA (returns vector)
shift(x, n=1, fill=NA, type="lag")
# lag with n=1 and 2, and pad with 0 (returns list)
shift(x, n=1:2, fill=0, type="lag")

# on data.tables
DT = data.table(year=2010:2014, v1=runif(5), v2=1:5, v3=letters[1:5])
# lag columns 'v1,v2,v3' DT by 1 and fill with 0
cols = c("v1","v2","v3")
anscols = paste("lead", cols, sep="_")
DT[, (anscols) := shift(.SD, 1, 0, "lead"), .SDcols=cols]

# return a new data.table instead of updating
# with names automatically set
DT = data.table(year=2010:2014, v1=runif(5), v2=1:5, v3=letters[1:5])
DT[, shift(.SD, 1:2, NA, "lead", TRUE), .SDcols=2:4]

# lag/lead in the right order
DT = data.table(year=2010:2014, v1=runif(5), v2=1:5, v3=letters[1:5])
DT = DT[sample(nrow(DT))]
# add lag=1 for columns 'v1,v2,v3' in increasing order of 'year'
cols = c("v1","v2","v3")
anscols = paste("lag", cols, sep="_")
DT[order(year), (cols) := shift(.SD, 1, type="lag"), .SDcols=cols]
DT[order(year)]

# while grouping
DT = data.table(year=rep(2010:2011, each=3), v1=1:6)
DT[, c("lag1", "lag2") := shift(.SD, 1:2), by=year]

# on lists
ll = list(1:3, letters[4:1], runif(2))
shift(ll, 1, type="lead")
shift(ll, 1, type="lead", give.names=TRUE)
shift(ll, 1:2, type="lead")

```

shouldPrint

For use by packages that mimic/divert auto printing e.g. IRkernel and knitr

Description

Not for use by users. Exported only for use by IRkernel (Jupyter) and knitr.

Usage

```
shouldPrint(x)
```

Arguments

x A `data.table`.

Details

Should IRkernel/Jupyter print a `data.table` returned invisibly by `DT[:,:=]` ? This is a read-once function since it resets an internal flag. If you need the value more than once in your logic, store the value from the first call.

Value

TRUE or FALSE.

References

<https://github.com/IRkernel/IRkernel/issues/127>

<https://github.com/Rdatatable/data.table/issues/933>

special-symbols

Special symbols

Description

`.SD`, `.BY`, `.N`, `.I` and `.GRP` are *read only* symbols for use in `j`. `.N` can be used in `i` as well. See the vignettes and examples here and in [data.table](#).

Details

The bindings of these variables are locked and attempting to assign to them will generate an error. If you wish to manipulate `.SD` before returning it, take a `copy(.SD)` first (see FAQ 4.5). Using `:=` in the `j` of `.SD` is reserved for future use as a (tortuously) flexible way to update `DT` by reference by group (even when groups are not contiguous in an ad hoc by).

These symbols are used in `j` and defined as follows.

- `.SD` is a `data.table` containing the **S**ubset of `x`'s **D**ata for each group, excluding any columns used in `by` (or `keyby`).
- `.BY` is a `list` containing a length 1 vector for each item in `by`. This can be useful when `by` is not known in advance. The `by` variables are also available to `j` directly by name; useful for example for titles of graphs if `j` is a plot command, or to branch with `if()` depending on the value of a group variable.
- `.N` is an integer, length 1, containing the number of rows in the group. This may be useful when the column names are not known in advance and for convenience generally. When grouping by `i`, `.N` is the number of rows in `x` matched to, for each row of `i`, regardless of whether `nomatch` is `NA` or `0`. It is renamed to `N` (no dot) in the result (otherwise a column called `".N"` could conflict with the `.N` variable, see FAQ 4.6 for more details and example), unless it is explicitly named; e.g., `DT[, list(total=.N), by=a]`.

- `.I` is an integer vector equal to `seq_len(nrow(x))`. While grouping, it holds for each item in the group, it's row location in `x`. This is useful to subset in `j`; e.g. `DT[, .I[which.max(somecol)], by=grp]`.
- `.GRP` is an integer, length 1, containing a simple group counter. 1 for the 1st group, 2 for the 2nd, etc.

See Also

[data.table](#), [:=](#), [set](#), [datatable-optimize](#)

Examples

```
## Not run:
DT = data.table(x=rep(c("b", "a", "c"), each=3), v=c(1,1,1,2,2,1,1,2,2), y=c(1,3,6), a=1:9, b=9:1)
DT
X = data.table(x=c("c", "b"), v=8:7, foo=c(4,2))
X

DT[.N]                # last row, only special symbol allowed in 'i'
DT[, .N]              # total number of rows in DT
DT[, .N, by=x]        # number of rows in each group
DT[, .SD, .SDcols=x:y] # select columns 'x' and 'y'
DT[, .SD[1]]          # first row of all columns
DT[, .SD[1], by=x]    # first row of 'y' and 'v' for each group in 'x'
DT[, c(.N, lapply(.SD, sum)), by=x] # get rows *and* sum columns 'v' and 'y' by group
DT[, .I[1], by=x]     # row number in DT corresponding to each group
DT[, .N, by=rleid(v)] # get count of consecutive runs of 'v'
DT[, c(.(y=max(y)), lapply(.SD, min)),
      by=rleid(v), .SDcols=v:b] # compute 'j' for each consecutive runs of 'v'
DT[, grp := .GRP, by=x] # add a group counter
X[, DT[.BY, y, on="x"], by=x] # join within each group

## End(Not run)
```

split

Split data.table into chunks in a list

Description

Split method for `data.table`. Faster and more flexible. Be aware that processing list of `data.tables` will be generally much slower than manipulation in single `data.table` by group using `by` argument, read more on [data.table](#).

Usage

```
## S3 method for class 'data.table'
split(x, f, drop = FALSE,
      by, sorted = FALSE, keep.by = TRUE, flatten = TRUE,
      ..., verbose = getOption("datatable.verbose"))
```

Arguments

<code>x</code>	data.table
<code>f</code>	factor or list of factors. Same as <code>split.data.frame</code> . Use by argument instead, this is just for consistency with data.frame method.
<code>drop</code>	logical. Default FALSE will not drop empty list elements caused by factor levels not referred by that factors. Works also with new arguments of split data.table method.
<code>by</code>	character vector. Column names on which split should be made. For <code>length(by) > 1L</code> and <code>flatten FALSE</code> it will result nested lists with data.tables on leafs.
<code>sorted</code>	When default FALSE it will retain the order of groups we are splitting on. When TRUE then sorted list(s) are returned. Does not have effect for <code>f</code> argument.
<code>keep.by</code>	logical default TRUE. Keep column provided to by argument.
<code>flatten</code>	logical default TRUE will unlist nested lists of data.tables. When using <code>f</code> results are always flattened to list of data.tables.
<code>...</code>	passed to data.frame way of processing when using <code>f</code> argument.
<code>verbose</code>	logical default FALSE. When TRUE it will print to console data.table split query used to split data.

Details

Argument `f` is just for consistency in usage to data.frame method. Recommended is to use by argument instead, it will be faster, more flexible, and by default will preserve order according to order in data.

Value

List of data.tables. If using `flatten FALSE` and `length(by) > 1L` then recursively nested lists having data.tables as leafs of grouping according to by argument.

See Also

[data.table](#), [rbindlist](#)

Examples

```
set.seed(123)
dt = data.table(x1 = rep(letters[1:2], 6),
               x2 = rep(letters[3:5], 4),
               x3 = rep(letters[5:8], 3),
               y = rnorm(12))
dt = dt[sample(.N)]
df = as.data.frame(dt)

# split consistency with data.frame: `x, f, drop`
all.equal(
  split(dt, list(dt$x1, dt$x2)),
  lapply(split(df, list(df$x1, df$x2)), setDT)
```



```

)

# nested list using `flatten` arguments
split(dt, by=c("x1", "x2"))
split(dt, by=c("x1", "x2"), flatten=FALSE)

# dealing with factors
fdt = dt[, c(lapply(.SD, as.factor), list(y=y)), .SDcols=x1:x3]
fdf = as.data.frame(fdt)
sdf = split(fdf, list(fdf$x1, fdf$x2))
all.equal(
  split(fdt, by=c("x1", "x2"), sorted=TRUE),
  lapply(sdf[sort(names(sdf))], setDT)
)

# factors having unused levels, drop FALSE, TRUE
fdt = dt[, .(x1 = as.factor(c(as.character(x1), "c"))[-13L],
  x2 = as.factor(c("a", as.character(x2)))[-1L],
  x3 = as.factor(c("a", as.character(x3), "z"))[c(-1L,-14L)],
  y = y)]
fdf = as.data.frame(fdt)
sdf = split(fdf, list(fdf$x1, fdf$x2))
all.equal(
  split(fdt, by=c("x1", "x2"), sorted=TRUE),
  lapply(sdf[sort(names(sdf))], setDT)
)
)
sdf = split(fdf, list(fdf$x1, fdf$x2), drop=TRUE)
all.equal(
  split(fdt, by=c("x1", "x2"), sorted=TRUE, drop=TRUE),
  lapply(sdf[sort(names(sdf))], setDT)
)
)

```

subset.data.table *Subsetting data.tables*

Description

Returns subsets of a `data.table`.

Usage

```
## S3 method for class 'data.table'
subset(x, subset, select, ...)
```

Arguments

<code>x</code>	<code>data.table</code> to subset.
<code>subset</code>	logical expression indicating elements or rows to keep
<code>select</code>	expression indicating columns to select from <code>data.table</code>
<code>...</code>	further arguments to be passed to or from other methods

Details

The subset argument works on the rows and will be evaluated in the data.table so columns can be referred to (by name) as variables in the expression.

The data.table that is returned will maintain the original keys as long as they are not selected out.

Value

A data.table containing the subset of rows and columns that are selected.

See Also

[subset](#)

Examples

```
dt <- data.table(a=sample(c('a', 'b', 'c'), 20, replace=TRUE),
                b=sample(c('a', 'b', 'c'), 20, replace=TRUE),
                c=sample(20, key=c('a', 'b')))

sub <- subset(dt, a == 'a')
all.equal(key(sub), key(dt))
```

tables

Display all objects of class 'data.table'

Description

Lists all data.table's in memory, including number of rows, column names and any keys.

Usage

```
tables(mb = TRUE, order.col = "NAME", width = 80, env=parent.frame(), silent=FALSE)
```

Arguments

mb	TRUE adds size of the data.table in MB to the output (slow in older versions of R).
order.col	Quoted column name to sort the output by
width	Number of characters to truncate the COLS output
env	Usually tables() is executed at the prompt where parent.frame() returns .GlobalEnv. tables() may also be useful inside functions where parent.frame() is the local scope of the function, or set it to .GlobalEnv
silent	By default tables() is expected to be called at the prompt for its compact print output. silent=TRUE prints nothing. The data statistics are returned as a data.table, silently, whether silent is TRUE or FALSE

Value

A data.table containing the information printed.

See Also

[data.table](#), [setkey](#), [ls](#), [objects](#), [object.size](#)

Examples

```
DT = data.table(A=1:10,B=letters[1:10])
DT2 = data.table(A=1:10000,ColB=10000:1)
setkey(DT,B)
tables()
```

test.data.table	<i>Runs a set of tests.</i>
-----------------	-----------------------------

Description

Runs a set of tests to check data.table is working correctly.

Usage

```
test.data.table(verbose=FALSE, pkg="pkg", silent=FALSE)
```

Arguments

verbose	If TRUE sets datatable.verbose to TRUE for the duration of the tests.
pkg	Root directory name under which all package content (ex: DESCRIPTION, src/, R/, inst/ etc..) resides.
silent	Logical, default FALSE, when TRUE it will not raise error on in case of test fails.

Details

Runs a series of tests. These can be used to see features and examples of usage, too. Running test.data.table will tell you the full location of the test file(s) to open.

Value

When silent equals to TRUE it will return TRUE if all tests were successful. FALSE otherwise. If silent equals to FALSE it will return TRUE if all tests were successful. Error otherwise.

See Also

[data.table](#)

Examples

```
## Not run:
test.data.table()

## End(Not run)
```

timetaken	<i>Pretty print of time taken</i>
-----------	-----------------------------------

Description

Pretty print of time taken since last started.at.

Usage

```
timetaken(started.at)
```

Arguments

started.at The result of proc.time() taken some time earlier.

Value

A character vector of the form hh:mm:ss, or ss.mmm if under 60 seconds.

Examples

```
started.at=proc.time()
Sys.sleep(1)
cat("Finished in",timetaken(started.at),"\n")
```

transform.data.table	<i>Data table utilities</i>
----------------------	-----------------------------

Description

Utilities for data.table transformation.

transform **by group is particularly slow. Please use := by group instead.**

within, transform and other similar functions in data.table are not just provided for users who expect them to work, but for non-data.table-aware packages to retain keys, for example. Hopefully the (much) faster and more convenient data.table syntax will be used in time. See examples.

Usage

```
## S3 method for class 'data.table'
transform(`_data`, ...)
## S3 method for class 'data.table'
within(data, expr, ...)
```

Arguments

```
data, _data    data.table to be transformed.
...           for transform, Further arguments of the form tag=value. Ignored for within.
expr         expression to be evaluated within the data.table.
```

Details

within is like with, but modifications (columns changed, added, or removed) are updated in the returned data.table.

Note that transform will keep the key of the data.table provided the *targets* of the transform (i.e. the columns that appear in ...) are not in the key of the data.table. within also retains the key provided the key columns are not *touched*.

Value

The modified value of a copy of data.

See Also

[transform](#), [within](#) and [:=](#)

Examples

```
DT <- data.table(a=rep(1:3, each=2), b=1:6)

DT2 <- transform(DT, c = a^2)
DT[, c:=a^2]
identical(DT,DT2)

DT2 <- within(DT, {
  b <- rev(b)
  c <- a*2
  rm(a)
})
DT[, `:=`(b = rev(b),
        c = a*2,
        a = NULL)]
identical(DT,DT2)

DT$d = ave(DT$b, DT$c, FUN=max)           # copies entire DT, even if it is 10GB in RAM
DT = DT[, transform(.SD, d=max(b)), by="c"] # same, but even worse as .SD is copied for each group
DT[, d:=max(b), by="c"]                 # same result, but much faster, shorter and scales
```

```
# Multiple update by group. Convenient, fast, scales and easy to read.
DT[, `:=`(minb = min(b),
          meanb = mean(b),
          bplused = sum(b+d)), by=c%/5]
DT
```

 transpose

Efficient transpose of list

Description

transpose is an efficient way to transpose lists, data frames or data tables.

Usage

```
transpose(l, fill=NA, ignore.empty=FALSE)
```

Arguments

l	A list, data.frame or data.table.
fill	Default is NA. It is used to fill shorter list elements so as to return each element of the transposed result of equal lengths.
ignore.empty	Default is FALSE. TRUE will ignore length-0 list elements.

Details

The list elements (or columns of data.frame/data.table) should be all atomic. If list elements are of unequal lengths, the value provided in fill will be used so that the resulting list always has all elements of identical lengths. The class of input object is also preserved in the transposed result.

The ignore.empty argument can be used to skip or include length-0 elements.

This is particularly useful in tasks that require splitting a character column and assigning each part to a separate column. This operation is quite common enough that a function `tstrsplit` is exported.

factor columns are converted to character type. Attributes are not preserved at the moment. This may change in the future.

Value

A transposed list, data.frame or data.table.

See Also

[data.table](#), [tstrsplit](#)

Examples

```
ll = list(1:5, 6:8)
transpose(ll)
setDT(transpose(ll, fill=0))[]

dt = data.table(x=1:5, y=6:10)
transpose(dt)
```

truelength	<i>Over-allocation access</i>
------------	-------------------------------

Description

These functions are experimental and somewhat advanced. By *experimental* we mean their names might change and perhaps the syntax, argument names and types. So if you write a lot of code using them, you have been warned! They should work and be stable, though, so please report problems with them.

Usage

```
truelength(x)
alloc.col(DT,
  n = getOption("datatable.alloccol"),      # default: 1024L
  verbose = getOption("datatable.verbose")) # default: FALSE
```

Arguments

x	Any type of vector, including <code>data.table</code> which is a list vector of column pointers.
DT	A <code>data.table</code> .
n	The number of spare column pointer slots to ensure are available. If DT is a 1,000 column <code>data.table</code> with 24 spare slots remaining, <code>n=1024L</code> means grow the 24 spare slots to be 1024. <code>truelength(DT)</code> will then be 2024 in this example.
verbose	Output status and information.

Details

When adding columns by reference using `:=`, we *could* simply create a new column list vector (one longer) and memcopy over the old vector, with no copy of the column vectors themselves. That requires negligible use of space and time, and is what v1.7.2 did. However, that copy of the list vector of column pointers only (but not the columns themselves), a *shallow copy*, resulted in inconsistent behaviour in some circumstances. So, as from v1.7.3 `data.table` over allocates the list vector of column pointers so that columns can be added fully by reference, consistently.

When the allocated column pointer slots are used up, to add a new column `data.table` must reallocate that vector. If two or more variables are bound to the same `data.table` this shallow copy may or may not be desirable, but we don't think this will be a problem very often (more discussion may

be required on `datatable-help`). Setting `options(datatable.verbose=TRUE)` includes messages if and when a shallow copy is taken. To avoid shallow copies there are several options: use `copy` to make a deep copy first, use `alloc.col` to reallocate in advance, or, change the default allocation rule (perhaps in your `.Rprofile`); e.g., `options(datatable.alloccol=10000L)`.

Please note : over allocation of the column pointer vector is not for efficiency per se. It's so that `:=` can add columns by reference without a shallow copy.

Value

`truelength(x)` returns the length of the vector allocated in memory. `length(x)` of those items are in use. Currently, it's just the list vector of column pointers that is over-allocated (i.e. `truelength(DT)`), not the column vectors themselves, which would in future allow fast row `insert()`. For tables loaded from disk however, `truelength` is 0 in R 2.14.0+ (and random in R \leq 2.13.2), which is perhaps unexpected. `data.table` detects this state and over-allocates the loaded `data.table` when the next column addition occurs. All other operations on `data.table` (such as fast grouping and joins) do not need `truelength`.

`alloc.col` *reallocates* DT by reference. This may be useful for efficiency if you know you are about to going to add a lot of columns in a loop. It also returns the new DT, for convenience in compound queries.

See Also

[copy](#)

Examples

```
DT = data.table(a=1:3,b=4:6)
length(DT)           # 2 column pointer slots used
truelength(DT)       # 1026 column pointer slots allocated
alloc.col(DT,2048)
length(DT)           # 2 used
truelength(DT)       # 2050 allocated, 2048 free
DT[,c:=7L]           # add new column by assigning to spare slot
truelength(DT)-length(DT) # 2047 slots spare
```

tstrsplit

strsplit and transpose the resulting list efficiently

Description

This is equivalent to `transpose(strsplit(...))`. This is a convenient wrapper function to split a column using `strsplit` and assign the transposed result to individual columns. See examples.

Usage

```
tstrsplit(x, ..., fill=NA, type.convert=FALSE, keep, names=FALSE)
```


Arguments

x	The vector to split (and transpose).
...	All the arguments to be passed to <code>strsplit</code> .
fill	Default is NA. It is used to fill shorter list elements so as to return each element of the transposed result of equal lengths.
type.convert	TRUE calls <code>type.convert</code> with <code>as.is=TRUE</code> on the columns.
keep	Specify indices corresponding to just those list elements to retain in the transposed result. Default is to return all.
names	TRUE auto names the list with V1, V2 etc. Default (FALSE) is to return an unnamed list.

Details

It internally calls `strsplit` first, and then `transpose` on the result.

`names` argument can be used to return an auto named list, although this argument does not have any effect when used with `:=`, which requires names to be provided explicitly. It might be useful in other scenarios.

Value

A transposed list after splitting by the pattern provided.

See Also

[data.table](#), [transpose](#)

Examples

```
x = c("abcde", "ghij", "klmnopq")
strsplit(x, "", fixed=TRUE)
tstrsplit(x, "", fixed=TRUE)
tstrsplit(x, "", fixed=TRUE, fill="<NA>")

# using keep to return just 1,3,5
tstrsplit(x, "", fixed=TRUE, keep=c(1,3,5))

# names argument
tstrsplit(x, "", fixed=TRUE, keep=c(1,3,5), names=LETTERS[1:3])

DT = data.table(x=c("A/B", "A", "B"), y=1:3)
DT[, c("c1") := tstrsplit(x, "/", fixed=TRUE, keep=1L)][]
DT[, c("c1", "c2") := tstrsplit(x, "/", fixed=TRUE)][]
```

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