FAQs about the ${\bf data.table}$ package in R

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The first section, Beginner FAQs, is intended to be read in order, from start to finish.

Contents

1	\mathbf{Beg}	inner FAQs			
	1.1	Why does DT[,5] return 5?			
	1.2	Why does DT[,"region"] return "region"?			
	1.3	Why does DT[,region] return a vector? I'd like a 1-column data.table. There is			
		no drop argument like I'm used to in data.frame.			
	1.4	Why does DT[,x,y,z] not work? I wanted the 3 columns x,y and z			
	1.5	I assigned a variable mycol="x" but then DT[,mycol] returns "x". How do I get it			
		to look up the column name contained in the mycol variable?			
	1.6	Ok but I don't know the expressions in advance. How do I programatically pass			
		them in?			
	1.7	What are the benefits of being able to use column names as if they are variables			
		inside DT[]?			
	1.8	OK, I'm starting to see what data.table is about, but why didn't you enhance			
		data.frame in R? Why does it have to be a new package?			
	1.9	Why are the defaults the way they are? Why does it work the way it does?			
		Isn't this already done by with() and subset() in base?			
		Why does X [Y] return all the columns from Y too? Shouldn't it return a subset of X?			
		What is the difference between X[Y] and merge(X,Y)?			
		Anything else about X[Y,sum(foo*bar)]?			
	1.14	That's nice. How did you manage to change it?			
2	General syntax				
	2.1	How can I avoid writing a really long j expression? You've said I should use the			
		column <i>names</i> , but I've got a lot of columns			
	2.2	Why is the default for mult now "all"?			
	2.3	I'm using c() in the j and getting strange results			
	2.4	I have built up a complex table with many columns. I want to use it as a template			
		for a new table; i.e., create a new table with no rows, but with the column names			
		and types copied from my table. Can I do that easily?			
	2.5	Is a null data.table the same as DT[0]?			
	2.6	Why has the DT() alias been removed?			
	2.7	But my code uses j=DT() and it works. The previous FAQ says that DT() has			
		been removed			
	2.8	What are the scoping rules for j expressions?			
	2.9	Can I trace the j expression as it runs through the groups?			
		Inside each group, why are the group variables length 1?			
		Only the first 10 rows are printed, how do I print more?			
		With an X[Y] join, what if X contains a column called "Y"?			
	2.13	X[Z[Y]] is failing because X contains a column "Y". I'd like it to use the table Y in			
		calling scope.			

	2.14	Can you explain further why data.table is inspired by A[B] syntax in base?	11
	2.15	Can base be changed to do this then, rather than a new package?	13
	2.16	I've heard that data.table syntax is analogous to SQL	13
	2.17	What are the smaller syntax differences between data.frame and data.table?	14
	2.18	I'm using j for its side effect only, but I'm still getting data returned. How do I stop	
		that?	15
	2.19	Why does [.data.table now have a drop argument from v1.5?	15
	2.20	Rolling joins are cool and very fast! Was that hard to program?	15
	2.21	Why does DT[i,col:=value] return the whole of DT? I expected either no visible	
		value (consistent with <-), or a message or return value containing how many rows	
		were updated. It isn't obvious that the data has indeed been updated by reference.	15
	2.22	Ok, thanks. What was so difficult about the result of DT[i,col:=value] being	
		returned invisibly?	15
	2.23	I've noticed that base::cbind.data.frame (and base::rbind.data.frame) appear	
		to be changed by data.table. How is this possible? Why?	15
	2.24	I've read about method dispatch (e.g. merge may or may not dispatch to merge.data.t	able)
		but how does R know how to dispatch? Are dots significant or special? How on	
		earth does R know which function to dispatch and when?	16
		•	
3	Que	estions relating to compute time	17
	3.1	I have 20 columns and a large number of rows. Why is an expression of one column	
		so quick?	17
	3.2	I don't have a key on a large table, but grouping is still really quick. Why is that?	17
	3.3	Why is grouping by columns in the key faster than an ad hoc by?	17
4	T2		17
4		or messages	17
	4.1	Could not find function "DT"	17
	4.2 4.3	unused argument(s) (MySum = sum(v))	17
		'translateCharUTF8' must be called on a CHARSXP	18
	4.4	cbind(DT,DF) returns a strange format e.g. 'Integer,5'	18
	4.5	cannot change value of locked binding for '.SD'	18
	4.6	cannot change value of locked binding for '.N'	18
5	War	ning messages	19
5		rning messages The following object(s) are masked from 'package:base': cbind. rbind	19 19
5	5.1	The following object(s) are masked from 'package:base': cbind, rbind	19
5			
	5.1 5.2 Gen	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type	19
	5.1 5.2 Gen	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type	19 19
	5.1 5.2 Gen	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type	19 19 20
	5.1 5.2 Gen 6.1	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type neral questions about the package v1.3 appears to be missing from the CRAN archive?	19 19 20 20
	5.1 5.2 Gen 6.1 6.2	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type neral questions about the package v1.3 appears to be missing from the CRAN archive?	19 19 20 20 20
	5.1 5.2 Gen 6.1 6.2 6.3	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type teral questions about the package v1.3 appears to be missing from the CRAN archive? Is data.table compatible with S-plus? Is it available for Linux, Mac and Windows?	19 19 20 20 20 20
	5.1 5.2 Gen 6.1 6.2 6.3 6.4	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type neral questions about the package v1.3 appears to be missing from the CRAN archive? Is data.table compatible with S-plus? Is it available for Linux, Mac and Windows? I think it's great. What can I do?	19 19 20 20 20 20 20 20
	5.1 5.2 Gen 6.1 6.2 6.3 6.4 6.5	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type	19 19 20 20 20 20 20 20
	5.1 5.2 Gen 6.1 6.2 6.3 6.4 6.5	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type	19 19 20 20 20 20 20 21
	5.1 5.2 Gen 6.1 6.2 6.3 6.4 6.5 6.6	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type neral questions about the package v1.3 appears to be missing from the CRAN archive? Is data.table compatible with S-plus? Is it available for Linux, Mac and Windows? I think it's great. What can I do? I think it's not great. How do I warn others about my experience? I have a question. I know the r-help posting guide tells me to contact the maintainer (not r-help), but is there a larger group of people I can ask?	19 19 20 20 20 20 20 21 21
	5.1 5.2 Gen 6.1 6.2 6.3 6.4 6.5 6.6	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type neral questions about the package v1.3 appears to be missing from the CRAN archive? Is data.table compatible with S-plus? Is it available for Linux, Mac and Windows? I think it's great. What can I do? I think it's not great. How do I warn others about my experience? I have a question. I know the r-help posting guide tells me to contact the maintainer (not r-help), but is there a larger group of people I can ask? Where are the datatable-help archives?	19 19 20 20 20 20 20 21 21
	5.1 5.2 Gen 6.1 6.2 6.3 6.4 6.5 6.6	The following object(s) are masked from 'package:base': cbind, rbind Coerced numeric RHS to integer to match the column's type neral questions about the package v1.3 appears to be missing from the CRAN archive? Is data.table compatible with S-plus? Is it available for Linux, Mac and Windows? I think it's great. What can I do? I think it's not great. How do I warn others about my experience? I have a question. I know the r-help posting guide tells me to contact the maintainer (not r-help), but is there a larger group of people I can ask? Where are the datatable-help archives? I'd prefer not to contact datatable-help, can I mail just one or two people privately?	19 19 20 20 20 20 20 21 21

1 Beginner FAQs

1.1 Why does DT[,5] return 5?

Because by default, unlike a data.frame, the 2nd argument is an *expression* which is evaluated within the scope of DT. 5 evaluates to 5. It is generally bad practice to refer to columns by number rather than name. If someone else comes along and reads your code later, they may have to hunt around to find out which column is number 5. Furthermore, if you or someone else changes the column ordering of DT higher up in your R program, you might get bugs if you forget to change all the places in your code which refer to column number 5.

Say column 5 is called "region", just do DT[,region] instead. Notice there are no quotes around the column name. This is what we mean by j being evaluated within the scope of the data.table. That scope consists of an environment where the column names are variables.

You can place any R expression in j; e.g., DT[,colA*colB/2]. Further, j may be a set of R expressions (including calls to any R package) wrapped with list(), .() or an anonymous code block wrapped with braces . A simple example is DT[,fitdistr(d1-d1,"normal")].

Having said this, there are some circumstances where referring to a column by number is ok, such as a sequence of columns. In these situations just do DT[,5:10,with=FALSE] or DT[,c(1,4,10),with=FALSE]. See ?data.table for an explanation of the with argument. It lets you use data.table the same way as data.frame, when you need to.

Note that with() has been a base function for a long time. That's one reason we say data.table builds upon base functionality. There is little new here really, data.table is just making use of with() and building it into the syntax.

1.2 Why does DT[, "region"] return "region"?

See answer to 1.1 above. Try DT[,region] instead. Or DT[,"region",with=FALSE].

1.3 Why does DT[,region] return a vector? I'd like a 1-column data.table. There is no drop argument like I'm used to in data.frame.

Try DT[,.(region)] instead. .() is an alias for list() and ensures a data.table is returned.

1.4 Why does DT[,x,y,z] not work? I wanted the 3 columns x,y and z.

The j expression is the 2nd argument. The correct way to do this is DT[, (x,y,z)].

1.5 I assigned a variable mycol="x" but then DT[,mycol] returns "x". How do I get it to look up the column name contained in the mycol variable?

This is what we mean when we say the j expression 'sees' objects in the calling scope. The variable mycol does not exist as a column name of DT so R then looked in the calling scope and found mycol there and returned its value "x". This is correct behaviour. Had mycol been a column name, then that column's data would have been returned. What you probably meant was DT[,mycol,with=FALSE], which will return the x column's data as you wanted. Alternatively, since a data.table is a list, too, you can write DT[["x"]] or DT[[mycol]].

1.6 Ok but I don't know the expressions in advance. How do I programatically pass them in?

To create expressions use the quote() function. We refer to these as quote()-ed expressions to save confusion with the double quotes used to create a character vector such as c("x"). The simplest quote()-ed expression is just one column name :

```
q = quote(x)
DT[,eval(q)] # returns the column x as a vector
```

```
q = quote(list(x))
DT[,eval(q)] # returns the column x as a 1-column data.table
Since these are expressions, we are not restricted to column names only:
    q = quote(mean(x))
DT[,eval(q)] # identical to DT[,mean(x)]
q = quote(list(x,sd(y),mean(y*z)))
DT[,eval(q)] # identical to DT[,list(x,sd(y),mean(y*z))]
However, if it's just simply a vector of column names you need, it may be simpler to pass a character vector to j and use with=FALSE.
```

To pass an expression into your own function, one idiom is as follows:

quote() and eval() are like macros in other languages. Instead of j=myfunction() (which won't work without laboriously passing in all the arguments) it's j=eval(mymacro). This can be more efficient than a function call, and convenient. When data.table sees j=eval(mymacro) it knows to find mymacro in calling scope so as not to be tripped up if a column name happens to be called mymacro, too.

For example, let's make sure that exactly the same j is run for a set of different grouping criteria :

```
> DT = as.data.table(iris)
> whatToRun = quote( .(AvgWidth = mean(Sepal.Width),
                       MaxLength = max(Sepal.Length)) )
> DT[, eval(whatToRun), by=Species]
      Species AvgWidth MaxLength
                 3.428
                              5.8
1:
       setosa
2: versicolor
                 2.770
                              7.0
   virginica
                 2.974
                              7.9
> DT[, eval(whatToRun), by=.(FirstLetter=substring(Species,1,1))]
   FirstLetter AvgWidth MaxLength
1:
                  3.428
                               5.8
             s
                  2.872
                               7.9
> DT[, eval(whatToRun), by=.(Petal.Width=round(Petal.Width,0))]
   Petal.Width AvgWidth MaxLength
1:
             0 3.426531
             1 2.708108
                               7.0
2:
             2 2.976562
                               7.9
3:
```

1.7 What are the benefits of being able to use column names as if they are variables inside DT[...]?

j doesn't have to be just column names. You can write any R expression of column names directly as the j; e.g., DT[x=1000, sum(y*z)]. The same applies to i; e.g., DT[x>1000, sum(y*z)]. This runs the j expression on the set of rows where the i expression is true. You don't even need to return data; e.g., DT[x>1000, plot(y,z)]. Finally, you can do j by group by adding by=; e.g., DT[x>1000, sum(y*z), by=w]. This runs j for each group in column w but just over the rows where x>1000. By placing the 3 parts of the query (where, select and group by) inside the square brackets, data.table sees this query as a whole before any part of it is evaluated. Thus it can optimize the query for performance.

1.8 OK, I'm starting to see what data.table is about, but why didn't you enhance data.frame in R? Why does it have to be a new package?

As FAQ 1.1 highlights, j in [.data.table is fundamentally different from j in [.data.frame. Even something as simple as DF[,1] would break existing code in many packages and user code. This is by design. We want it to work this way for more complicated syntax to work. There are other differences, too (see FAQ 2.17).

Furthermore, data.table *inherits* from data.frame. It is a data.frame, too. A data.table can be passed to any package that only accepts data.frame and that package can use [.data.frame syntax on the data.table.

We have proposed enhancements to R wherever possible, too. One of these was accepted as a new feature in R 2.12.0 :

unique() and match() are now faster on character vectors where all elements are in the global CHARSXP cache and have unmarked encoding (ASCII). Thanks to Matt Dowle for suggesting improvements to the way the hash code is generated in unique.c.

A second proposal was to use memcpy in duplicate.c, which is much faster than a for loop in C. This would improve the *way* that R copies data internally (on some measures by 13 times). The thread on r-devel is here: http://tolstoy.newcastle.edu.au/R/e10/devel/10/04/0148.html.

1.9 Why are the defaults the way they are? Why does it work the way it does?

The simple answer is because the main author originally designed it for his own use. He wanted it that way. He finds it a more natural, faster way to write code, which also executes more quickly.

1.10 Isn't this already done by with() and subset() in base?

Some of the features discussed so far are, yes. The package builds upon base functionality. It does the same sorts of things but with less code required and executes many times faster if used correctly.

1.11 Why does X[Y] return all the columns from Y too? Shouldn't it return a subset of X?

This was changed in v1.5.3. X[Y] now includes Y's non-join columns. We refer to this feature as join inherited scope because not only are X columns available to the j expression, so are Y columns. The downside is that X[Y] is less efficient since every item of Y's non-join columns are duplicated to match the (likely large) number of rows in X that match. We therefore strongly encourage X[Y,j] instead of X[Y]. See next FAQ.

1.12 What is the difference between X[Y] and merge(X,Y)?

X[Y] is a join, looking up X's rows using Y (or Y's key if it has one) as an index. Y[X] is a join, looking up Y's rows using X (or X's key if it has one) as an index. x[X] merge(X,Y) does both ways at the same time. The number of rows of X[Y] and Y[X] usually differ; whereas the number of rows returned by x[X] and x[X] is the same.

BUT that misses the main point. Most tasks require something to be done on the data after a join or merge. Why merge all the columns of data, only to use a small subset of them afterwards? You may suggest merge(X[,ColsNeeded1],Y[,ColsNeeded2]), but that takes copies of the subsets of data and it requires the programmer to work out which columns are needed. X[Y,j] in data.table does all that in one step for you. When you write X[Y,sum(foo*bar)], data.table automatically inspects the j expression to see which columns it uses. It will only subset those columns only; the others are ignored. Memory is only created for the columns the j uses and Y columns enjoy standard R recycling rules within the context of each group. Let's say foo is in X and bar is in Y (along with 20 other columns in Y). Isn't X[Y,sum(foo*bar)] quicker to program and quicker to run than a merge followed by a subset?

1.13 Anything else about X[Y,sum(foo*bar)]?

This behaviour changed in v1.9.4 (Sep 2014). It now does the X[Y] join and then runs sum(foo*bar) over all the rows; i.e., X[Y][,sum(foo*bar)]. It used to run j for each group of X that each row of Y matches to. That can still be done as it's very useful but you now need to be explicit and specify by=.EACHI; i.e., X[Y,sum(foo*bar),by=.EACHI]. We call this grouping by each i. For example, and making it complicated by using join inherited scope, too:

```
> X = data.table(grp=c("a", "a", "b", "b", "b", "c", "c", "c"), foo=1:7)
> setkey(X,grp)
> Y = data.table(c("b", "c"), bar=c(4,2))
   grp foo
          1
1:
          2
2:
     а
3:
     b
          3
          4
4:
     b
5:
          5
     b
6:
          6
     С
          7
7:
     С
> Y
   V1 bar
1:
    b
2:
    С
> X[Y,sum(foo*bar)]
[1] 74
> X[Y,sum(foo*bar),by=.EACHI]
   grp V1
     b 48
1:
     c 26
2:
```

¹Here we mean either the merge *method* for data.table or the merge method for data.frame since both methods work in the same way in this respect. See ?merge.data.table and FAQ 2.24 for more information about method dispatch.

1.14 That's nice. How did you manage to change it?

The request to change came from users. The feeling was that if a query is doing grouping then an explicit 'by=' should be present for code readability reasons. An option is provided to return the old behaviour: options(datatable.old.bywithoutby), by default FALSE. This enables upgrading to test the other new features / bug fixes in v1.9.4, with later migration of any by-without-by queries when ready (by adding by=.EACHI to them). We retained 47 pre-change tests and added them back as new tests, tested under options(datatable.old.bywithoutby=TRUE). After a year we'll remove this option.

Of the 66 packages on CRAN or Bioconductor that depend or import data.table at the time of releasing v1.9.4, only one was affected by the change. That could be because many packages don't have comprehensive tests, or just that grouping by each row in i wasn't being used much by downstream packages. We always test the new version with all dependent packages before release and coordinate any changes with those maintainers. So this release was quite straightforward in that regard.

Another compelling reason to make the change was that previously, there was no efficient way to achieve what X[Y,sum(foo*bar)] does now. You had to write X[Y][,sum(foo*bar)]. That was suboptimal because X[Y] joined all the columns and passed them all to the second compound query without knowing that only foo and bar are needed. To solve that efficiency problem, extra programming effort was required: X[Y,list(foo,bar)][,sum(foo*bar)]. The change to by=.EACHI has simplified this by allowing both queries to be expressed inside a single DT[...] query for efficieny.

2 General syntax

2.1 How can I avoid writing a really long j expression? You've said I should use the column *names*, but I've got a lot of columns.

When grouping, the j expression can use column names as variables, as you know, but it can also use a reserved symbol .SD which refers to the Subset of the Data.table for each group (excluding the grouping columns). So to sum up all your columns it's just DT[,lapply(.SD,sum),by=grp]. It might seem tricky, but it's fast to write and fast to run. Notice you don't have to create an anonymous function. The .SD object is efficiently implemented internally and more efficient than passing an argument to a function. But if the .SD symbol appears in j then data.table has to populate .SD fully for each group even if j doesn't use all of it. So please don't do this, for example, DT[,sum(.SD[["sales"]]),by=grp]. That works but is inefficient and inelegant. This is what was intended: DT[,sum(sales),by=grp] and could be 100's of times faster. If you do use all the data in .SD for each group (such as in DT[,lapply(.SD,sum),by=grp]) then that's very good usage of .SD. Also see ?data.table for the .SDcols argument which allows you to specify a subset of columns for .SD.

2.2 Why is the default for mult now "all"?

In v1.5.3 the default was changed to "all". When i (or i's key if it has one) has fewer columns than x's key, mult was already set to "all" automatically. Changing the default makes this clearer and easier for users as it came up quite often.

In versions up to v1.3, "all" was slower. Internally, "all" was implemented by joining using "first", then again from scratch using "last", after which a diff between them was performed to work out the span of the matches in x for each row in i. Most often we join to single rows, though, where "first", "last" and "all" return the same result. We preferred maximum performance for the majority of situations so the default chosen was "first". When working with a non-unique key (generally a single column containing a grouping variable), DT["A"] returned the first row of that group so DT["A", mult="all"] was needed to return all the rows in that group.

In v1.4 the binary search in C was changed to branch at the deepest level to find first and last. That branch will likely occur within the same final pages of RAM so there should no longer be a speed disadvantage in defaulting mult to "all". We warned that the default might change and made the change in v1.5.3.

A future version of data.table may allow a distinction between a key and a unique key. Internally mult="all" would perform more like mult="first" when all x's key columns were joined to and x's key was a unique key. data.table would need checks on insert and update to make sure a unique key is maintained. An advantage of specifying a unique key would be that data.table would ensure no duplicates could be inserted, in addition to performance.

2.3 I'm using c() in the j and getting strange results.

This is a common source of confusion. In data.frame you are used to, for example:

```
> DF = data.frame(x=1:3,y=4:6,z=7:9)
> DF

    x y z
1 1 4 7
2 2 5 8
3 3 6 9
> DF[,c("y","z")]
    y z
1 4 7
2 5 8
3 6 9
```

which returns the two columns. In data.table you know you can use the column names directly and might try:

```
> DT = data.table(DF)
> DT[,c(y,z)]
[1] 4 5 6 7 8 9
```

but this returns one vector. Remember that the j expression is evaluated within the environment of DT and c() returns a vector. If 2 or more columns are required, use list() or .() instead:

```
> DT[,.(y,z)]
y z
1: 4 7
2: 5 8
3: 6 9
```

c() can be useful in a data.table too, but its behaviour is different from that in [.data.frame.

2.4 I have built up a complex table with many columns. I want to use it as a template for a new table; i.e., create a new table with no rows, but with the column names and types copied from my table. Can I do that easily?

Yes. If your complex table is called DT, try NEWDT = DT[0].

2.5 Is a null data.table the same as DT[0]?

```
No. By "null data.table" we mean the result of data.table(NULL) or as.data.table(NULL); i.e.,

> data.table(NULL)

Null data.table (0 rows and 0 cols)

> data.frame(NULL)

data frame with 0 columns and 0 rows

> as.data.table(NULL)

Null data.table (0 rows and 0 cols)

> as.data.frame(NULL)

data frame with 0 columns and 0 rows

> is.null(data.table(NULL))

[1] FALSE

> is.null(data.frame(NULL))

[1] FALSE
```

The null data.table|frame is NULL with some attributes attached, making it not NULL anymore. In R only pure NULL is NULL as tested by is.null(). When referring to the "null data.table" we use lower case null to help distinguish from upper case NULL. To test for the null data.table, use length(DT)==0 or ncol(DT)==0 (length is slightly faster as it's a primitive function). An empty data.table (DT[0]) has one or more columns, all of which are empty. Those empty columns still have names and types.

2.6 Why has the DT() alias been removed?

DT was introduced originally as a wrapper for a list of j expressions. Since DT was an alias for data.table, this was a convenient way to take care of silent recycling in cases where each item of the j list evaluated to different lengths. The alias was one reason grouping was slow, though. As of v1.3, list() or .() should be passed instead to the j argument. These are much faster, especially when there are many groups. Internally, this was a nontrivial change. Vector recycling is now done internally, along with several other speed enhancements for grouping.

2.7 But my code uses j=DT(...) and it works. The previous FAQ says that DT() has been removed.

Then you are using a version prior to 1.5.3. Prior to 1.5.3 [.data.table detected use of DT() in the j and automatically replaced it with a call to list(). This was to help the transition for existing users.

2.8 What are the scoping rules for j expressions?

Think of the subset as an environment where all the column names are variables. When a variable foo is used in the j of a query such as X[Y,sum(foo)], foo is looked for in the following order:

- 1. The scope of X's subset; i.e., X's column names.
- 2. The scope of each row of Y; i.e., Y's column names (join inherited scope)
- 3. The scope of the calling frame; e.g., the line that appears before the data.table query.
- 4. Exercise for reader: does it then ripple up the calling frames, or go straight to globalenv()?
- 5. The global environment

This is *lexical scoping* as explained in R FAQ 3.3.1. The environment in which the function was created is not relevant, though, because there is *no function*. No anonymous *function* is passed to the j. Instead, an anonymous *body* is passed to the j; for example,

```
> DT = data.table(x=rep(c("a","b"),c(2,3)),y=1:5)
> DT

    x y
1: a 1
2: a 2
3: b 3
4: b 4
5: b 5
> DT[,{z=sum(y);z+3},by=x]
    x V1
1: a 6
2: b 15
```

Some programming languages call this a lambda.

2.9 Can I trace the j expression as it runs through the groups?

Try something like this:

2.10 Inside each group, why are the group variables length 1?

In the previous FAQ, x is a grouping variable and (as from v1.6.1) has length 1 (if inspected or used in j). It's for efficiency and convenience. Therefore, there is no difference between the following two statements:

If you need the size of the current group, use .N rather than calling length() on any column.

2.11 Only the first 10 rows are printed, how do I print more?

There are two things happening here. First, if the number of rows in a data.table are large (> 100 by default), then a summary of the data.table is printed to the console by default. Second, the summary of a large data.table is printed by taking the top and bottom n rows of the data.table and only printing those. Both of these parameters (when to trigger a summary and how much of a table to use as a summary) are configurable by R's options mechanism, or by calling the print function directly.

For instance, to enforce the summary of a data.table to only happen when a data.table is greater than 50 rows, you could options(datatable.print.nrows=50). To disable the summary-by-default completely, you could options(datatable.print.nrows=Inf). You could also call print directly, as in print(your.data.table, nrows=Inf).

If you want to show more than just the top (and bottom) 10 rows of a data.table summary (say you like 20), set options(datatable.print.topn=20), for example. Again, you could also just call print directly, as in print(your.data.table, topn=20)

2.12 With an X[Y] join, what if X contains a column called "Y"?

When i is a single name such as Y it is evaluated in the calling frame. In all other cases such as calls to .() or other expressions, i is evaluated within the scope of X. This facilitates easy *self joins* such as X[J(unique(colA)),mult="first"].

2.13 X[Z[Y]] is failing because X contains a column "Y". I'd like it to use the table Y in calling scope.

The Z[Y] part is not a single name so that is evaluated within the frame of X and the problem occurs. Try tmp=Z[Y]; X[tmp]. This is robust to X containing a column "tmp" because tmp is a single name. If you often encounter conflics of this type, one simple solution may be to name all tables in uppercase and all column names in lowercase, or some similar scheme.

2.14 Can you explain further why data.table is inspired by A[B] syntax in base?

Consider A[B] syntax using an example matrix A:

```
> A = matrix(1:12,nrow=4)
> A
     [,1] [,2] [,3]
[1,]
              5
                    9
[2,]
                   10
              6
[3,]
        3
              7
                   11
[4,]
        4
              8
                   12
```

To obtain cells (1,2)=5 and (3,3)=11 many users (we believe) may try this first:

```
> A[c(1,3),c(2,3)]

[,1] [,2]

[1,] 5 9

[2,] 7 11
```

That returns the union of those rows and columns, though. To reference the cells, a 2-column matrix is required. ?Extract says :

When indexing arrays by [a single argument i can be a matrix with as many columns as there are dimensions of x; the result is then a vector with elements corresponding to the sets of indices in each row of i.

Let's try again.

> B

A matrix is a 2-dimension structure with row names and column names. Can we do the same with names?

```
> rownames(A) = letters[1:4]
> colnames(A) = LETTERS[1:3]
> A
  A B C
a 1 5
       9
b 2 6 10
c 3 7 11
d 4 8 12
> B = cbind(c("a", "c"), c("B", "C"))
> A[B]
[1] 5 11
So, yes we can. Can we do the same with data.frame?
> A = data.frame(A=1:4,B=letters[11:14],C=pi*1:4)
> rownames(A) = letters[1:4]
> A
  A B
a 1 k 3.141593
b 2 1 6.283185
c 3 m 9.424778
d 4 n 12.566371
```

```
[,1] [,2]
[1,] "a" "B"
[2,] "c" "C"

> A[B]
[1] "k" " 9.424778"
```

But, notice that the result was coerced to character. R coerced A to matrix first so that the syntax could work, but the result isn't ideal. Let's try making B a data.frame.

```
> B = data.frame(c("a","c"),c("B","C"))
> cat(try(A[B],silent=TRUE))

Error in `[.default`(A, B) : invalid subscript type 'list'
```

So we can't subset a data.frame by a data.frame in base R. What if we want row names and column names that aren't character but integer or float? What if we want more than 2 dimensions of mixed types? Enter data.table.

Furthermore, matrices, especially sparse matrices, are often stored in a 3 column tuple: (i,j,value). This can be thought of as a key-value pair where i and j form a 2-column key. If we have more than one value, perhaps of different types it might look like (i,j,val1,val2,val3,...). This looks very much like a data.frame. Hence data.table extends data.frame so that a data.frame X can be subset by a data.frame Y, leading to the X[Y] syntax.

2.15 Can base be changed to do this then, rather than a new package?

data.frame is used everywhere and so it is very difficult to make any changes to it. data.table inherits from data.frame. It is a data.frame, too. A data.table can be passed to any package that only accepts data.frame. When that package uses [.data.frame syntax on the data.table, it works. It works because [.data.table looks to see where it was called from. If it was called from such a package, [.data.table diverts to [.data.frame.

2.16 I've heard that data.table syntax is analogous to SQL.

Yes:

- i <==> where
- j <==> select
- := $\langle == \rangle$ update
- by $\langle == \rangle$ group by
- i <==> order by (in compound syntax)
- i <==> having (in compound syntax)
- nomatch=NA <==> outer join
- nomatch=0 <==> inner join
- mult="first"|"last" <==> N/A because SQL is inherently unordered
- roll=TRUE <==> N/A because SQL is inherently unordered

The general form is:

```
DT[where, select|update, group by][order by][...] ... [...]
```

A key advantage of column vectors in R is that they are *ordered*, unlike SQL². We can use ordered functions in data.table queries such as diff() and we can use *any* R function from any package, not just the functions that are defined in SQL. A disadvantage is that R objects must fit in memory, but with several R packages such as ff, bigmemory, mmap and indexing, this is changing.

2.17 What are the smaller syntax differences between data.frame and data.table?

- DT[3] refers to the 3rd row, but DF[3] refers to the 3rd column
- DT[3,] == DT[3], but DF[,3] == DF[3] (somewhat confusingly)
- For this reason we say the comma is optional in DT, but not optional in DF
- DT[[3]] == DF[3] == DF[[3]]
- DT[i,] where i is a single integer returns a single row, just like DF[i,], but unlike a matrix single row subset which returns a vector.
- DT[,j,with=FALSE] where j is a single integer returns a one column data.table, unlike DF[,j] which returns a vector by default
- DT[, "colA", with=FALSE][[1]] == DF[, "colA"].
- DT[,colA] == DF[,"colA"]
- DT[,list(colA)] == DF[,"colA",drop=FALSE]
- DT[NA] returns 1 row of NA, but DF[NA] returns a copy of DF containing NA throughout. The symbol NA is type logical in R and is therefore recycled by [.data.frame. Intention was probably DF[NA_integer_]. [.data.table does this automatically for convenience.
- DT[c(TRUE, NA, FALSE)] treats the NA as FALSE, but DF[c(TRUE, NA, FALSE)] returns NA rows for each NA
- DT[ColA==ColB] is simpler than DF[!is.na(ColA) & !is.na(ColB) & ColA==ColB,]
- data.frame(list(1:2,"k",1:4)) creates 3 columns, data.table creates one list column.
- check.names is by default TRUE in data.frame but FALSE in data.table, for convenience.
- stringsAsFactors is by default TRUE in data.frame but FALSE in data.table, for efficiency. Since a global string cache was added to R, characters items are a pointer to the single cached string and there is no longer a performance benefit of coverting to factor.
- Atomic vectors in list columns are collapsed when printed using ", " in data.frame, but "," in data.table with a trailing comma after the 6th item to avoid accidental printing of large embedded objects.

In [.data.frame we very often set drop=FALSE. When we forget, bugs can arise in edge cases where single columns are selected and all of a sudden a vector is returned rather than a single column data.frame. In [.data.table we took the opportunity to make it consistent and drop drop.

When a data.table is passed to a data.table-unaware package, that package it not concerned with any of these differences; it just works.

 $^{^2}$ It may be a surprise to learn that select top 10 * from ... does not reliably return the same rows over time in SQL. You do need to include an order by clause, or use a clustered index to guarantee row order; i.e., SQL is inherently unordered.

2.18 I'm using j for its side effect only, but I'm still getting data returned. How do I stop that?

In this case j can be wrapped with invisible(); e.g., DT[,invisible(hist(colB)),by=colA]³.

2.19 Why does [.data.table now have a drop argument from v1.5?

So that data.table can inherit from data.frame without using If we used ... then invalid argument names would not be caught.

The drop argument is never used by [.data.table. It is a placeholder for non data.table aware packages when they use the [.data.frame syntax directly on a data.table.

2.20 Rolling joins are cool and very fast! Was that hard to program?

The prevailing row on or before the i row is the final row the binary search tests anyway. So roll=TRUE is essentially just a switch in the binary search C code to return that row.

2.21 Why does DT[i,col:=value] return the whole of DT? I expected either no visible value (consistent with <-), or a message or return value containing how many rows were updated. It isn't obvious that the data has indeed been updated by reference.

This has changed in v1.8.3 to meet your expectations. Please upgrade. The whole of DT is returned (now invisibly) so that compound syntax can work; e.g., DT[i,done:=TRUE][,sum(done)]. The number of rows updated is returned when verbosity is on, either on a per query basis or globally using options(datatable.verbose=TRUE).

2.22 Ok, thanks. What was so difficult about the result of DT[i,col:=value] being returned invisibly?

R internally forces visibility on for [. The value of FunTab's eval column (see src/main/names.c) for [is 0 meaning force R_Visible on (see R-Internals section 1.6). Therefore, when we tried invisible() or setting R_Visible to 0 directly ourselves, eval in src/main/eval.c would force it on again.

To solve this problem, the key was to stop trying to stop the print method running after a :=. Instead, inside := we now (from v1.8.3) set a global flag which the print method uses to know whether to actually print or not.

2.23 I've noticed that base::cbind.data.frame (and base::rbind.data.frame) appear to be changed by data.table. How is this possible? Why?

It is a temporary, last resort solution until we discover a better way to solve the problems listed below. Essentially, the issue is that data.table inherits from data.frame, and, base::cbind and base::rbind (uniquely) do their own S3 dispatch internally as documented by ?cbind. The change is adding one for loop to the start of each function directly in base; e.g.,

```
> base::cbind.data.frame

function (..., deparse.level = 1)
{
    if (!identical(class(..1), "data.frame"))
        for (x in list(...)) {
        if (inherits(x, "data.table"))
            return(data.table::data.table(...))
    }
```

³hist() returns the breakpoints in addition to plotting to the graphics device

```
data.frame(..., check.names = FALSE)
}
<environment: namespace:base>
```

That modification is made dynamically; i.e., the base definition of cbind.data.frame is fetched, the for loop added to the beginning and then assigned back to base. This solution is intended to be robust to different definitions of base::cbind.data.frame in different versions of R, including unknown future changes. Again, it is a last resort until a better solution is known or made available. The competing requirements are:

- cbind(DT,DF) needs to work. Defining cbind.data.table doesn't work because base::cbind does its own S3 dispatch and requires that the *first* cbind method for each object it is passed is *identical*. This is not true in cbind(DT,DF) because the first method for DT is cbind.data.table but the first method for DF is cbind.data.frame. base::cbind then falls through to its internal bind code which appears to treat DT as a regular list and returns very odd looking and unusable matrix output. See FAQ 4.4. We cannot just advise users not to call cbind(DT,DF) because packages such as ggplot2 make such a call (test 168.5).
- This naturally leads to trying to mask cbind.data.frame instead. Since a data.table is a data.frame, cbind would find the same method for both DT and DF. However, this doesn't work either because base::cbind.appears to find methods in base first; i.e., base::cbind.data.frame isn't maskable. This is reproducible as follows:

```
> foo = data.frame(a=1:3)
> cbind.data.frame = function(...)cat("Not printed\n")
> cbind(foo)

a
1 1
2 2
3 3
```

• Finally, we tried masking cbind itself (v1.6.5 and v1.6.6). This allowed cbind(DT,DF) to work, but introduced compatibility issues with package IRanges, since IRanges also masks cbind. It worked if IRanges was lower on the search() path than data.table, but if IRanges was higher then data.table's cbind would never be called and the strange looking matrix output occurs again (FAQ 4.4).

If you know of a better solution, that still solves all the issues above, then please let us know and we'll gladly change it.

2.24 I've read about method dispatch (e.g. merge may or may not dispatch to merge.data.table) but *how* does R know how to dispatch? Are dots significant or special? How on earth does R know which function to dispatch and when?

This comes up quite a lot, but it's really earth shatteringly simple. A function such as merge is generic if it consists of a call to UseMethod. When you see people talking about whether or not functions are generic functions they are merely typing the function, without () afterwards, looking at the program code inside it and if they see a call to UseMethod then it is generic. What does UseMethod do? It literally slaps the function name together with the class of the first argument, separated by period (.) and then calls that function, passing along the same arguments. It's that simple. For example, merge(X,Y) contains a UseMethod call which means it then dispatches (i.e. calls) paste("merge",class(X),sep="."). Functions with dots in may or may not be methods. The dot is irrelevant really. Other than dot being the separator that UseMethod uses. Knowing this background should now highlight why, for example, it is obvious to R folk that as.data.table.data.frame is the data.frame method for the as.data.table generic function. Further, it may help to elucidate that, yes you are correct, it is not obvious from its name alone

that ls.fit is not the fit method of the ls generic function. You only know that by typing ls (not ls()) and observing it isn't a single call to UseMethod.

You might now ask: where is this documented in R? Answer: it's quite clear, but, you need to first know to look in ?UseMethod and *that* help file contains:

"When a function calling UseMethod('fun') is applied to an object with class attribute c('first', 'second'), the system searches for a function called fun.first and, if it finds it, applies it to the object. If no such function is found a function called fun.second is tried. If no class name produces a suitable function, the function fun.default is used, if it exists, or an error results."

Happily, an internet search for "How does R method dispatch work" (at the time of writing) returns the ?UseMethod help page as the top link. Admittedly, other links rapidly descend into the intracies of S3 vs S4, internal generics and so on.

However, features like basic S3 dispatch (pasting the function name together with the class name) is why some R folk love R. It's so simple. No complicated registration or signature is required. There isn't much needed to learn. To create the merge method for data.table all that was required, literally, was to merely create a function called merge.data.table.

3 Questions relating to compute time

3.1 I have 20 columns and a large number of rows. Why is an expression of one column so quick?

Several reasons:

- Only that column is grouped, the other 19 are ignored because data.table inspects the j expression and realises it doesn't use the other columns.
- One memory allocation is made for the largest group only, then that memory is re-used for the other groups. There is very little garbage to collect.
- R is an in-memory column store; i.e., the columns are contiguous in RAM. Page fetches from RAM into L2 cache are minimised.

3.2 I don't have a key on a large table, but grouping is still really quick. Why is that?

data.table uses radix sorting. This is significantly faster than other sort algorithms. See our presentations on our homepage for more information.

This is also one reason why setkey() is quick.

When no key is set, or we group in a different order from that of the key, we call it an *ad hoc* by.

3.3 Why is grouping by columns in the key faster than an ad hoc by?

Because each group is contiguous in RAM, thereby minimising page fetches and memory can be copied in bulk (memcpy in C) rather than looping in C.

4 Error messages

4.1 Could not find function "DT"

See FAQ 2.6 and FAQ 2.7.

4.2 unused argument(s) (MySum = sum(v))

This error is generated by DT[,MySum=sum(v)]. DT[,.(MySum=sum(v))] was intended, or DT[,j=.(MySum=sum(v))].

4.3 'translateCharUTF8' must be called on a CHARSXP

This error (and similar; e.g., 'getCharCE' must be called on a CHARSXP) may be nothing do with character data or locale. Instead, this can be a symptom of an earlier memory corruption. To date these have been reproducible and fixed (quickly). Please report it to datatable-help.

4.4 cbind(DT,DF) returns a strange format e.g. 'Integer,5'

This occurs prior to v1.6.5, for rbind(DT,DF) too. Please upgrade to v1.6.7 or later.

4.5 cannot change value of locked binding for '.SD'

.SD is locked by design. See ?data.table. If you'd like to manipulate .SD before using it, or returning it, and don't wish to modify DT using :=, then take a copy first (see ?copy); e.g.,

```
> DT = data.table(a=rep(1:3,1:3),b=1:6,c=7:12)
> DT
   a b
       C.
1:117
2: 2 2 8
3: 2 3 9
4: 3 4 10
5: 3 5 11
6: 3 6 12
> DT[, \{ mySD = copy(.SD) \}
       mySD[1,b:=99L]
       mySD },
      by=a]
   a b
        С
1: 1 99 7
2: 2 99 8
3: 2 3 9
4: 3 99 10
5: 3 5 11
6: 3 6 12
```

4.6 cannot change value of locked binding for '.N'

Please upgrade to v1.8.1 or later. From this version, if .N is returned by j it is renamed to N to avoid any abiguity in any subsequent grouping between the .N special variable and a column called ".N". The old behaviour can be reproduced by forcing .N to be called .N, like this:

```
> DT = data.table(a=c(1,1,2,2,2),b=c(1,2,2,2,1))
> DT

    a b
1: 1 1
2: 1 2
3: 2 2
4: 2 2
5: 2 1
> DT[,list(.N=.N),list(a,b)] # show intermediate result for exposition
```

```
a b .N
1:111
2: 1 2 1
3: 2 2 2
4: 2 1 1
> cat(try(
      DT[,list(.N=.N),by=list(a,b)][,unique(.N),by=a]
                                                          # compound query more typical
+ ,silent=TRUE))
Error in `[.data.table`(DT[, list(.N = .N), by = list(a, b)], , unique(.N), :
  The column '.N' can't be grouped because it conflicts with the special .N variable. Try setnames
If you are already running v1.8.1 or later then the error message is now more helpful than the
cannot change value of locked binding error. As you can see above, since this vignette was
produced using v1.8.1 or later. The more natural syntax now works:
> if (packageVersion("data.table") >= "1.8.1") {
      DT[,.N,by=list(a,b)][,unique(N),by=a]
+ }
  a V1
1:11
2: 2 2
3: 2 1
```

5 Warning messages

+ }

a V1 1: 1 1 2: 2 2 3: 2 1

5.1 The following object(s) are masked from 'package:base': cbind, rbind

This warning was present in v1.6.5 and v.1.6.6 only, when loading the package. The motivation was to allow cbind(DT,DF) to work, but as it transpired, broke (full) compatibility with package IRanges. Please upgrade to v1.6.7 or later.

5.2 Coerced numeric RHS to integer to match the column's type

Hopefully, this is self explanatory. The full message is:

> if (packageVersion("data.table") >= "1.9.3") {
+ DT[,.N,by=.(a,b)][,unique(N),by=a] # sam

Coerced numeric RHS to integer to match the column's type; may have truncated precision. Either change the column to numeric first by creating a new numeric vector length 5 (nrows of entire table) yourself and assigning that (i.e. 'replace' column), or coerce RHS to integer yourself (e.g. 1L or as.integer) to make your intent clear (and for speed). Or, set the column type correctly up front when you create the table and stick to it, please.

```
To generate it, try:

> DT = data.table(a=1:5,b=1:5)

> suppressWarnings(
+ DT[2,b:=6]  # works (slower) with warning
+ )
```

```
a b
1: 1 1
2: 2 6
3: 3 3
4: 4 4
5: 5 5
> class(6)
                    # numeric not integer
[1] "numeric"
> DT[2,b:=7L]
                     # works (faster) without warning
   a b
1: 1 1
2: 2 7
3: 3 3
4: 4 4
5: 5 5
> class(7L)
                     # L makes it an integer
[1] "integer"
> DT[,b:=rnorm(5)]
                    # 'replace' integer column with a numeric column
1: 1 -0.6789287
2: 2 0.7617814
3: 3 0.1430932
4: 4 -0.1027536
5: 5 -2.5685330
```

6 General questions about the package

6.1 v1.3 appears to be missing from the CRAN archive?

That is correct. v1.3 was available on R-Forge only. There were several large changes internally and these took some time to test in development.

6.2 Is data.table compatible with S-plus?

Not currently.

- A few core parts of the package are written in C and use internal R functions and R structures.
- The package uses lexical scoping which is one of the differences between R and S-plus explained by R FAQ 3.3.1.

6.3 Is it available for Linux, Mac and Windows?

Yes, for both 32-bit and 64-bit on all platforms. Thanks to CRAN. There are no special or OS-specific libraries used.

6.4 I think it's great. What can I do?

Please file suggestions, bug reports and enhancement requests on GitHub. This helps make the package better.

Please do vote for the package on Crantastic. This helps encourage the developers and helps other R users find the package. If you have time to write a comment too, that can help others in the community. Just simply clicking that you use the package, though, is much appreciated.

You can submit pull requests to change the code and/or documentation yourself.

6.5 I think it's not great. How do I warn others about my experience?

Please put your vote and comments on Crantastic. Please make it constructive so we have a chance to improve.

6.6 I have a question. I know the r-help posting guide tells me to contact the maintainer (not r-help), but is there a larger group of people I can ask?

Yes, there are two options. You can post to datatable-help. It's like r-help, but just for this package. Or the data.table tag on Stack Overflow. Feel free to answer questions in those places, too.

6.7 Where are the datatable-help archives?

The homepage contains links to the archives in several formats.

6.8 I'd prefer not to contact datatable-help, can I mail just one or two people privately?

Sure. You're more likely to get a faster answer from datatable-help or Stack Overflow, though. Asking publicly in those places helps build the knowledge base.

6.9 I have created a package that depends on data.table. How do I ensure my package is data.table-aware so that inheritance from data.frame works?

Either i) include data.table in the Depends: field of your DESCRIPTION file, or ii) include data.table in the Imports: field of your DESCRIPTION file AND import(data.table) in your NAMESPACE file.

6.10 Why is this FAQ in pdf format? Can it moved to HTML?

Yes we'd like to move it to a HTML vignette. Just haven't got to that yet. The benefits of vignettes (rather than a wiki) including the following:

- We include R code in the vignettes. This code is *actually run* when the file is created, not copy and pasted.
- This document is *reproducible*. Grab the .Rnw and you can run it yourself.
- CRAN checks the package (including running vignettes) every night on Linux, Mac and Windows, both 32bit and 64bit. Results are posted to http://cran.r-project.org/web/checks/check_results_data.table.html. Included there are results from r-devel; i.e., not yet released R. That serves as a very useful early warning system for any potential future issues as R itself develops.
- This file is bound into each version of the package. The package is not accepted on CRAN unless this file passes checks. Each version of the package will have its own FAQ file which will be relevant for that version. Contrast this to a single website, which can be ambiguous if the answer depends on the version.
- You can open it offline at your R prompt using vignette().
- You can extract the code from the document and play with it using edit(vignette("datatable-faq")).