## data.table

News from 1.6, 1.7 & 1.8

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LondonR, June 2012

#### Overview

- Real example
- Review of last presentation 2 years ago
- Package statistics
- New features
- Q&A



I have a data frame that is some 35,000 rows, by 7 columns, it looks like inis:



```
head(nuc)
```









```
chr feature
                start
                           end
                                 gene id pctAT
                                                    pctGC length
         CDS 67000042 67000051 NM 032291 0.600000 0.400000
                                                              10
         CDS 67091530 67091593 NM 032291 0.609375 0.390625
                                                              64
         CDS 67098753 67098777 NM 032291 0.600000 0.400000
                                                              25
4 1 CDS 67101627 67101698 NM_032291 0.472222 0.527778
                                                              72
         CDS 67105460 67105516 NM 032291 0.631579 0.368421
                                                              57
         CDS 67108493 67108547 NM 032291 0.436364 0.563636
                                                              55
```

```
gene id is a factor, that has about 3,500 unique levels. I want to, for each level of gene id get the
min(start), max(end), mean(pctAT), mean(pctGC), and sum(length).
```

I tried using lapply and do.call for this, but it's taking forever +30 minutes to run, the code I'm using is:

```
nuc_prof = lapply(levels(nuc$gene_id), function(gene){
                 t = nuc[nuc$gene_id==gene, ]
                  return(list(gene id=gene, start=min(t$start), end=max(t$end), pctGC =
                                                                                                                            mean(t\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{t}\poline{
})
nuc prof = do.call(rbind, nuc prof)
```

I'm certain I'm doing something wrong to slow this down. I haven't waited for it to finish as I'm sure it can be faster. Any ideas?

#### First answer



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do.call can be extremely slow on large objects. I think this is due to how it constructs the call, but I'm not certain. A faster alternative would be the data.table package. Or, as @Andrie suggested in a comment, use tapply for each calculation and cbind the results.

A note on your current implementation: rather than doing the subsetting in your function, you could use the split function to break up your data.frame into a list of data.frames you can loop over.

```
g <- function(tnuc) {
    list(gene_id=tnuc$gene_id[1], start=min(tnuc$start), end=max(tnuc$end),
        pctGC=mean(tnuc$pctGC), pct=mean(tnuc$pctAT), cdslength=sum(tnuc$length))
}
nuc_prof <- lapply(split(nuc, nuc$gene_id), g)</pre>
```

link edit flag

answered Jun 15 at 16:05



add comment

## Follow up answer



Since I'm in an evangelizing mood ... here's what the fast data.table solution would look like:

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link edit flag



NB: It isn't just the speed, but the simplicity. It's easy to write and easy to read.

#### User's reaction

Holy fudge buckets!!! data.table is awesome! That took about 3 seconds for the whole thing!!!

I think that congratulations are well in order for the frankly amazingly well written quick start guide and FAQ. Seriously. Where is the button to make all R and bioconductor packages like this one?

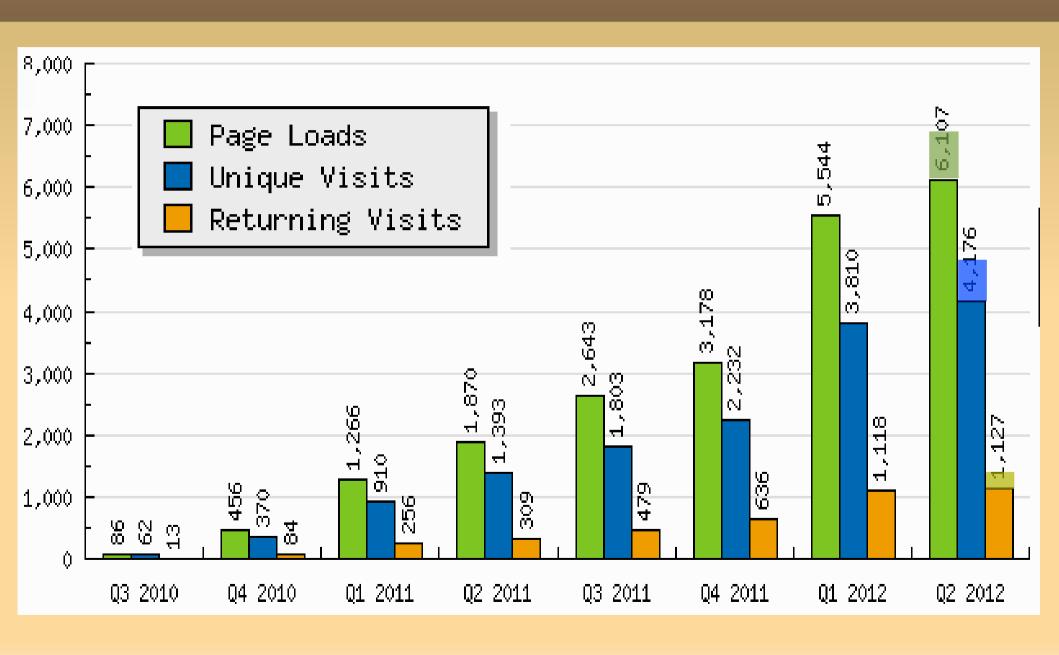
Davy Kavanagh, 15 Jun 2012

# Review of presentation 2 years ago

(Including why grouping is fast)

Link to pdf

### Since then





## Rank all packages by users

Rank	CRAN package	Users	AvgVote	NumVotes	Crantastic Rank	Inside-R Votes
1	ggplot2	77	4.0	50	7	<u>2018</u>
2	data.table	60	3.9	49	<u>12</u>	<u>1581</u>
3	<u>plyr</u>	55	3.7	32	<u>24</u>	<u>1338</u>
4	reshape	33	3.6	16	<u>31</u>	<u>772</u>
5	Sim.DiffProc	23	4.3	30	<u>9</u>	<u>825</u>
6	Sim.DiffProcGUI	23	4.3	30	<u>10</u>	<u>825</u>
7	lme4	23	3.6	7	<u>34</u>	<u>363</u>
8	<u>Hmisc</u>	21	3.9	11	<u>25</u>	<u>422</u>
9	lattice	19	4.7	4	4	<u>259</u>
10	RODBC	17	4.2	11	<u>19</u>	<u>520</u>

#### 15 reviews

- "It is much easier to subset, summarize, and investigate data.tables"
- "Improves programming and computing speed"
- "Great library for data.mining"
- "data.table is a perfect combination of useability and speed"
- "The more I use it, the better it gets"
- "A very useful package!"
- "The fast way to do SQL like operations in R"

#### Reviews continued

- "data.table is fast compared to ddply and ave"
- "data.table rocks!"
- "Efficient and simple"
- "I use it on a regular basis and I managed to cut computing time dramatically."
- "Amazing package!"
- "Fast"
- "I don't know where I would be w/o data.table"
- "Fast splitting/sorting operations in frames"

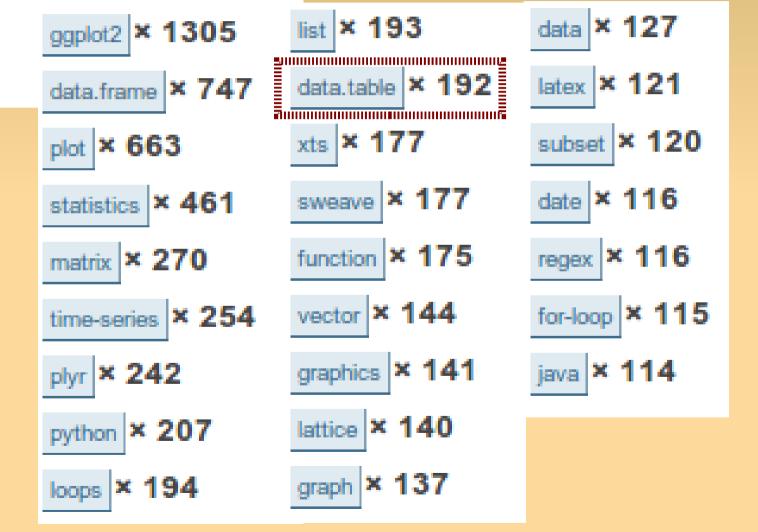
## Stack Overflow tag

13,629

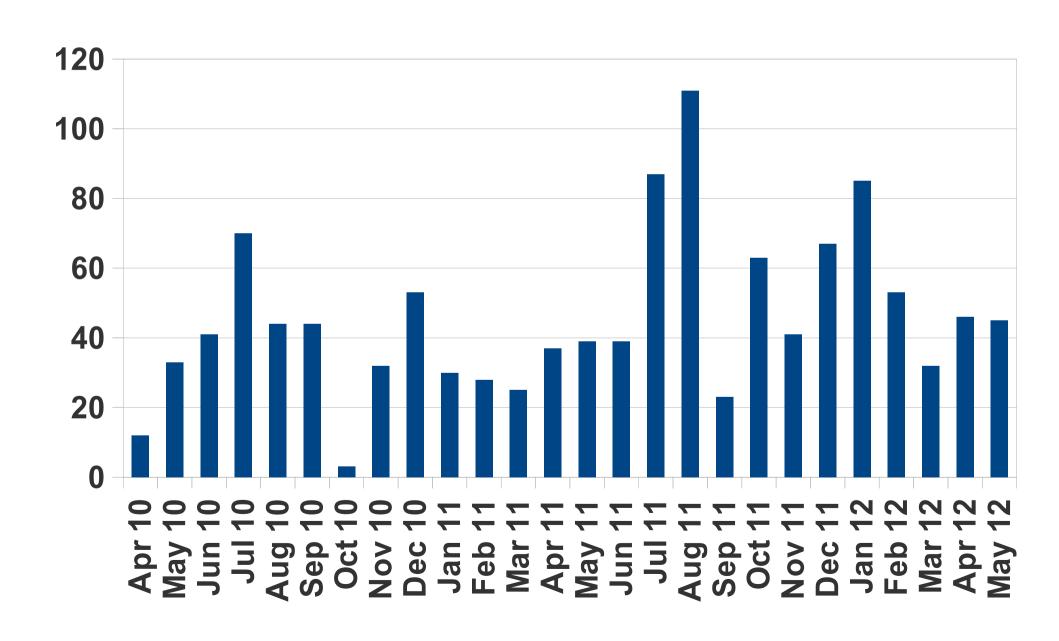
questions tagged

r about »

#### Related Tags



## datatable-help: posts per month



#### Other stats

- 24 articles "data.table" on R-bloggers
- 108 bugs fixed, 5 outstanding
- 66 feature requests implemented, 64 left
- 191 items in NEWS 1.6.0-1.8.1
- 2,600 lines of R
- 2,000 lines of C
- 653 unit tests

#### Thanked in NEWS

Chris Neff Prasad Chalasani Stavros Macrakis gkaupas Yike Lu Juliet Hannah Helge Liebert Branson Owen user1393348 Dieter Menne RYogi Iterator Leon Baum Yang Zhang **Prof Brian Ripley** Allan Engelhardt Sean Creighton Michael Weylandt Steven Bagley Ivo Welch **Christoph Jaeckel** Simon Urbanek Ivan Zhang ilprincipe Muhammad Waliji Joshua Ulrich Luke Tierney **Dennis Murphy** Josh O'Brien Eric Eugene Tyurin Vanja Malcolm Cook DM Nicolas Servant Alexander Peterhansl Joseph Voelkel Damian Betebenner Jean-Francois Rami user1165199 Jim Holtman Jelmer Ypma Karl Ove Hufthammer Thell Fowler Timothée Carayol Johann Hibschman Andreas Borg Ina

In appearance order in NEWS. Special thanks to Chris Neff for weeks of help to solve difficult crash bug Jan 2012.

#### Hierarchical indexes

- 4 years old (released Aug 2008)
- setkey(DT, id, date)
- setkey(DT, category, id, date)
- DT[X] or merge(DT,X)
- But, it was integer columns only
- NEW: character and double now ok fractional seconds in POSIXct ok

## Assign to a subset

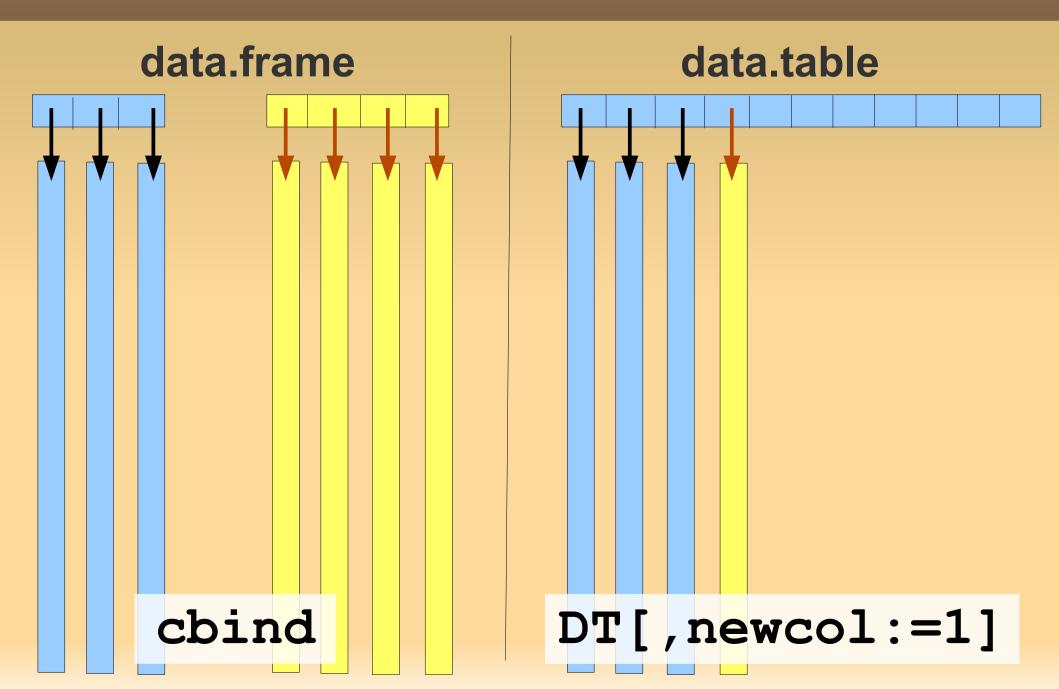
Link to question on S.O.

"In R I find myself doing something like this a lot:"

adataframe[adataframe\$col==something]<-aadataframe[adataframe\$col==something)]+1

- DT[col1==something, col2:=col3+1]
- Easy to write, easy to read

## Over allocation (add by reference)



## Delete in place

DT[,colname:=NULL]

Instant, regardless of size

By reference, memmove internally

Don't have to copy all but that column

## copy()

- data.table <u>IS</u> copied-on-change by <- as usual
- No copy by set\* functions (setkey, setnames, setattr)
- No copy by :=
- When you need a copy, call copy (DT)
- Why copy a 20GB data.table, even once.

#### Other

- Print method now prints head and tail
- Automatic optimization (sum -vs- mean)
- rbenchmark() replications default of 100 times overhead. Set to 1 and increase size of data, instead.
- Notice variable name repetition
- := by group now in v1.8.1

## Analogous to SQL

Link to data.table FAQ

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

Compound [] is key reason it's all inside [.data.table

## Not (that) much to learn

One manual page: ?data.table

Run example (data.table) at the prompt

 No methods, no functions, just use what you're used to in R

#### list columns

- Each <u>cell</u> can be a different type
- Each <u>cell</u> can be vector
- Each <u>cell</u> can itself be a data.table

Combining list columns with i and by

## list column example

```
data.table(x=letters[1:3],
y=list(1:10,
        letters[1:4],
        data.table(a=1:3,b=4:6))
   X
1: a 1,2,3,4,5,6,
2: b
       a,b,c,d
3: c <data.table>
```

Questions?
Suggestions?
Feedback?

Thank you!
Homepage