



3. Data manipulation

Thomas Lumley
Ken Rice

UW Biostatistics

Liège, September 2009

Merging: order

The data might need to be sorted first

```
index1 <- order(baseline$IDNO)
baseline <- baseline[index1,]
index2 <- order(events$IDNO)
events <- events[index2,]
if (!all(baseline$IDNO==events$IDNO)) {
  stop("PANIC: They still don't match!")
} else {
  alldata <- cbind(baseline, events[,c("TTODTH", "DEATH",
    "TTOMI", "INCMI")])
}
```

Note that `order(baseline$IDNO)` gives a subset of row numbers containing all the rows but in a different (increasing) order.

Merging: merge

Or there might be different rows in the two data sets

- Some people are missing from one or other data set (eg baseline and year 5 visits)
- Some people have multiple records in one data set (eg baseline data and all hospitalisations)

The `merge` function can do an `database outer join`, giving a data set that has all the possible matches between a row in one and a row in the other

Merging: merge

```
combined <- merge(baseline, hospvisits, by="IDNO", all=TRUE)
```

- `by=IDNO` says that the `IDNO` variable indicates individuals who should be matched.
- `all=TRUE` says that even people with no records in the `hospvisits` data set should be kept in the merged version.

How does it work: match

You could imagine a dumb algorithm for merging

```
for(row in firstdataset){
  for(otherrow in seconddataset){
    if (row$IDNO==otherrow$IDNO)
      ##add the row to the result
  }
}
```

More efficiently, the `match` function gives indices to match one variable to another

```
> match(c("B","I","O","S","T","A","T"),LETTERS)
[1]  2  9 15 19 20  1 20
> letters[match(c("B","I","O","S","T","A","T"),LETTERS)]
[1] "b" "i" "o" "s" "t" "a" "t"
```

Reshaping

Sometimes data sets are the wrong shape. Data with multiple observations of similar quantities can be in **long** form (multiple records per person) or **wide** form (multiple variables per person).

Example: The SeattleSNPs genetic variation discovery resource supplies data in a format

```
SNP    sample a11 a12
000095 D001  C  T
000095 D002  T  T
000095 D003  T  T
```

so that data for a single person is broken across many lines. To convert this to one line per person

```
> data<-read.table("http://pga.gs.washington.edu/data/il6
                    /ilkn6.prettybase.txt",
                    col.names=c("SNP","sample","allele1","allele2"))
> dim(data)
[1] 2303    4
> wideData<-reshape(data, direction="wide", idvar="sample",
                    timevar="SNP")
> dim(wideData)
[1] 47 99
> names(wideData)
[1] "sample"          "allele1.95"      "allele2.95"      "allele1.205"
[5] "allele2.205"     "allele1.276"     "allele2.276"     "allele1.321"
[9] "allele2.321"     "allele1.657"     "allele2.657"     "allele1.1086"
...
```


-
- `direction="wide"` says we are going from long to wide format
 - `idvar="sample"` says that `sample` identifies the rows in wide format
 - `timevar="SNP"` says that `SNP` identifies which rows go into the same column in wide form (for repeated measurements over time it would be the time variable)

Broken down by age and sex

A common request for Table 1 or Table 2 in a medical paper is to compute means and standard deviations, percentages, or frequency tables of many variables broken down by groups (eg case/control status, age and sex, exposure,...).

That is, we need to apply a simple computation to subsets of the data, and apply it to many variables. One useful function is `by()`, another is `tapply()`, which is very similar (but harder to remember).

```
> by(airquality$Ozone, list(month=airquality$Month),  
      mean, na.rm=TRUE)
```

```
month: 5
```

```
[1] 23.61538
```

```
-----
```

```
month: 6
```

```
[1] 29.44444
```

```
-----
```

```
month: 7
```

```
[1] 59.11538
```

```
-----
```

```
month: 8
```

```
[1] 59.96154
```

```
-----
```

```
month: 9
```

```
[1] 31.44828
```

Notes

- The first argument is the variable to be analyzed.
- The second argument is a list of variable defining subsets. In this case, a single variable, but we could do `list(month=airquality$Month, toohot=airquality$Temp>85)` to get a breakdown by month and temperature
- The third argument is the analysis function to use on each subset
- Any other arguments (`na.rm=TRUE`) are also given to the analysis function
- The result is really a vector (with a single grouping variable) or array (with multiple grouping variables). It prints differently.

Confusing digression: str()

How do I know it is an array? Because `str()` summarises the internal structure of a variable.

```
> a<- by(airquality$Ozone, list(month=airquality$Month,
                               toohot=airquality$Temp>85),
        mean, na.rm=TRUE)
```

```
> str(a)
by [1:5, 1:2] 23.6 22.1 49.3 40.9 22.0 ...
- attr(*, "dimnames")=List of 2
  ..$ month : chr [1:5] "5" "6" "7" "8" ...
  ..$ toohot: chr [1:2] "FALSE" "TRUE"
- attr(*, "call")= language by.data.frame(data =
  as.data.frame(data), INDICES = INDICES,
  FUN = FUN, na.rm = TRUE)
- attr(*, "class")= chr "by"
```

One function, many variables

There is a general function, `apply()` for doing something to rows or columns of a matrix (or slices of a higher-dimensional array).

```
> apply(psa[,1:8],2,mean,na.rm=TRUE)
```

id	nadir	pretx	ps	bss	grade
25.500000	16.360000	670.751163	80.833333	2.520833	2.146341
grade	age	obstime			
2.146341	67.440000	28.460000			

In this case there is a special, faster, function `colMeans`, but `apply()` can be used with other functions such as `sd()`, `IQR()`, `min()`,...

apply

- the first argument is an array or matrix or dataframe
- the second argument says which margins to keep (1=rows, 2=columns, ...), so 2 means that the result should keep the columns: apply the function to each column.
- the third argument is the analysis function
- any other arguments are given to the analysis function

There is a widespread belief that `apply()` is faster than a `for()` loop over the columns. This is a useful belief, since it encourages people to use `apply()`, but it is not true. (We'll see `for()` loops later)

New functions

Suppose you want the mean and standard deviation for each variable. One solution is to apply a new function. Watch carefully,...

```
> apply(psa[,1:8], 2,
  function(x) {c(mean=mean(x,na.rm=TRUE), stddev=sd(x,na.rm=TRUE))}
  )
```

	id	nadir	pretx	ps	bss	grade
mean	25.50000	16.3600	670.7512	80.83333	2.5208333	2.1463415
stddev	14.57738	39.2462	1287.6384	11.07678	0.6838434	0.7924953

	age	obstime
mean	67.440000	28.46000
stddev	5.771711	18.39056

New function

```
function(x) { c(mean=mean(x,na.rm=TRUE), stddev=sd(x,na.rm=TRUE)) }
```

translates as: “If you give me a vector, which I will call `x`, I will mean it and sd it and give you the results”

We could give this function a name and then refer to it by name

```
mean.and.sd <- function(x) { c(mean=mean(x,na.rm=TRUE),  
                                stddev=sd(x,na.rm=TRUE))  
                                }
```

```
apply(psa[,1:8], 2, mean.and.sd)
```

which would save typing if we used the function many times. The {curly brackets} are optional for a function with just one expression, but necessary for longer functions

by() revisited

Now we know how to write simple functions we can use `by()` more generally

```
> by(psa[,1:8], list(remission=psa$inrem),  
     function(subset) round(apply(subset, 2, mean.and.sd), 2))
```

```
remission: no
```

	id	nadir	pretx	ps	bss	grade	age	obstime
mean	31.03	22.52	725.99	79.71	2.71	2.11	67.17	21.75
stddev	11.34	44.91	1362.34	10.29	0.52	0.83	5.62	15.45

```
-----  
remission: yes
```

	id	nadir	pretx	ps	bss	grade	age	obstime
mean	11.29	0.53	488.45	83.57	2.07	2.23	68.14	45.71
stddev	12.36	0.74	1044.14	12.77	0.83	0.73	6.30	13.67

Notes

```
function(subset) {round(apply(subset, 2, mean.and.sd), 2)}
```

translates as “If you give me a data frame, which I will call subset, I will apply the `mean.and.sd` function to each variable, round to 2 decimal places, and give you the results”