

Basic use of dfunctions for data-frames in mets

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Simple data manipulation for data-frames

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Here are some key data-manipulation moves on a data-frame which is how we typically organize our data in R. After having read the data into R it will typically be a data-frame, if not we can force it to be a data-frame. The basic idea of the utility functions is to get a simple and easy to type way of making simple data-manipulation on a data-frame much like what is possible in SAS or STATA.

The functions, say, `dcut`, `dfactor` and so on are all functions that basically does what the base R `cut`, `factor` do, but are easier to use in the context of data-frames and have additional functionality.

```
1 library(mets)
2 data(melanoma)
```

```
1 is.data.frame(melanoma)
2 melanoma=as.data.frame(melanoma)
```

```
[1] TRUE
```

Here we work on the melanoma data that is already read into R and is a data-frame.

dUtility functions

The structure for all functions is

- `dfunction(dataframe,y~x | ifcond,...)`

to use the function on `y` in a dataframe grouped by `x` if condition `ifcond` is valid. The basic functions are

...

A generic function `daggregate`, `daggr`, can be called with a function as the argument

- `daggregate(dataframe,y~x | ifcond,fun=function,...)`

Renaming, deleting, keeping, dropping variables

```

1 melanoma=drename(melanoma,tykkelse~thick)
2 names(melanoma)

```

```
[1] "no"      "status"  "days"   "ulc"     "tykkelse" "sex"
```

Deleting variables

```

1 data(melanoma)
2 melanoma=drm(melanoma,~thick+sex)
3 names(melanoma)

```

```
[1] "no"      "status"  "days"   "ulc"
```

or sas style

```

1 data(melanoma)
2 melanoma=ddrop(melanoma,~thick+sex)
3 names(melanoma)

```

```
[1] "no"      "status"  "days"   "ulc"
```

alternatively we can also keep certain variables

```

1 data(melanoma)
2 melanoma=dkeep(melanoma,~thick+sex+status+days)
3 names(melanoma)

```

```
[1] "thick"   "sex"     "status"  "days"
```

Looking at the data

```

1 data(melanoma)
2 dstr(melanoma)

```

```

'data.frame':      205 obs. of  6 variables:
 $ no      : int  789 13 97 16 21 469 685 7 932 944 ...
 $ status: int   3 3 2 3 1 1 1 1 3 1 ...
 $ days   : int  10 30 35 99 185 204 210 232 232 279 ...
 $ ulc    : int   1 0 0 0 1 1 1 1 1 1 ...
 $ thick  : int  676 65 134 290 1208 484 516 1288 322 741 ...
 $ sex    : int   1 1 1 0 1 1 1 1 0 0 ...

```

The data can in Rstudio be seen as a data-table but to list certain parts of the data in output window

```

1 dlist(melanoma)

```

```

      no status days ulc thick sex
1    789 3      10  1   676  1
2     13 3       30  0    65  1
3     97 2       35  0   134  1
4     16 3       99  0   290  0
5     21 1      185  1  1208  1
---
201 317 2     4492  1   706  1
202 798 2     4668  0   612  0
203 806 2     4688  0    48  0
204 606 2     4926  0   226  0
205 328 2     5565  0   290  0

```

```
1 dlist(melanoma, ~.|sex==1)
```

```

      no  status days ulc  thick
1   789  3      10  1    676
2    13  3      30  0     65
3    97  2      35  0    134
5    21  1     185  1   1208
6   469  1     204  1    484
---
191 445  2     3909  1    806
195 415  2     4119  0     65
197 175  2     4207  0     65
198 493  2     4310  0    210
201 317  2     4492  1    706
```

```
1 dlist(melanoma, ~ulc+days+thick+sex|sex==1)
```

```

      ulc days thick sex
1     1   10   676  1
2     0   30    65  1
3     0   35   134  1
5     1  185  1208  1
6     1  204   484  1
---
191 1   3909  806  1
195 0   4119   65  1
197 0   4207   65  1
198 0   4310  210  1
201 1   4492  706  1
```

Getting summaries

```
1 dsummary(melanoma)
```

```

      no          status      days      ulc      thick
Min.   : 2.0      Min.   :1.00   Min.   : 10   Min.   :0.000   Min.   : 10
1st Qu.:222.0    1st Qu.:1.00   1st Qu.:1525 1st Qu.:0.000   1st Qu.: 97
Median :469.0    Median :2.00   Median :2005 Median :0.000   Median : 194
Mean   :463.9    Mean   :1.79   Mean   :2153 Mean   :0.439   Mean   : 292
3rd Qu.:731.0    3rd Qu.:2.00   3rd Qu.:3042 3rd Qu.:1.000   3rd Qu.: 356
Max.   :992.0    Max.   :3.00   Max.   :5565 Max.   :1.000   Max.   :1742

      sex
Min.   :0.0000
1st Qu.:0.0000
Median :0.0000
Mean   :0.3854
3rd Qu.:1.0000
Max.   :1.0000
```

or for specific variables

```
1 dsummary(melanoma, ~thick+status+sex)
```

```

      thick      status      sex
Min.   : 10   Min.   :1.00   Min.   :0.0000
1st Qu.: 97   1st Qu.:1.00   1st Qu.:0.0000
Median :194   Median :2.00   Median :0.0000
Mean   :292   Mean   :1.79   Mean   :0.3854
3rd Qu.:356   3rd Qu.:2.00   3rd Qu.:1.0000
Max.   :1742  Max.   :3.00   Max.   :1.0000
```

Summaries in different groups (sex)

```
1 dsummary(melanoma,thick+days+status~sex)
```

```
sex: 0
      thick      days      status
Min.   : 10.0   Min.   : 99   Min.   :1.000
1st Qu.: 97.0   1st Qu.:1636   1st Qu.:2.000
Median : 162.0   Median :2059   Median :2.000
Mean   : 248.6   Mean   :2283   Mean   :1.833
3rd Qu.: 306.0   3rd Qu.:3131   3rd Qu.:2.000
Max.   :1742.0   Max.   :5565   Max.   :3.000
```

```
-----
sex: 1
      thick      days      status
Min.   : 16.0   Min.   : 10   Min.   :1.000
1st Qu.: 105.0   1st Qu.:1052   1st Qu.:1.000
Median : 258.0   Median :1860   Median :2.000
Mean   : 361.1   Mean   :1946   Mean   :1.722
3rd Qu.: 484.0   3rd Qu.:2784   3rd Qu.:2.000
Max.   :1466.0   Max.   :4492   Max.   :3.000
```

and only among those with thin-tumours or only females (sex==1)

```
1 dsummary(melanoma,thick+days+status~sex|thick<97)
```

```
sex: 0
      thick      days      status
Min.   :10.00   Min.   : 355   Min.   :1.000
1st Qu.:32.00   1st Qu.:1762   1st Qu.:2.000
Median :64.00   Median :2227   Median :2.000
Mean   :51.48   Mean   :2425   Mean   :2.034
3rd Qu.:65.00   3rd Qu.:3185   3rd Qu.:2.000
Max.   :81.00   Max.   :4688   Max.   :3.000
```

```
-----
sex: 1
      thick      days      status
Min.   :16.00   Min.   : 30   Min.   :1.000
1st Qu.:30.00   1st Qu.:1820   1st Qu.:2.000
Median :65.00   Median :2886   Median :2.000
Mean   :55.75   Mean   :2632   Mean   :1.875
3rd Qu.:81.00   3rd Qu.:3328   3rd Qu.:2.000
Max.   :81.00   Max.   :4207   Max.   :3.000
```

```
1 dsummary(melanoma,thick+status~+1|sex==1)
```

```
      thick      status
Min.   : 16.0   Min.   :1.000
1st Qu.: 105.0   1st Qu.:1.000
Median : 258.0   Median :2.000
Mean   : 361.1   Mean   :1.722
3rd Qu.: 484.0   3rd Qu.:2.000
Max.   :1466.0   Max.   :3.000
```

Tables between variables

```
1 dtable(melanoma,~status+sex)
```

```
      sex  0  1
status
1         28 29
2         91 43
3          7  7
```

All bivariate tables

```
1 dtable(melanoma, ~status+sex+ulc, level=2)
```

```
      status
sex  1  2  3
0  28 91  7
1  29 43  7
```

```
      status
ulc  1  2  3
0  16 92  7
1  41 42  7
```

```
      sex
ulc  0  1
0  79 36
1  47 43
```

All univariate tables

```
1 dtable(melanoma, ~status+sex+ulc, level=1)
```

```
status
  1  2  3
57 134 14
```

```
sex
  0  1
126 79
```

```
ulc
  0  1
115 90
```

Making new variables for the analysis

To define a bunch of new covariates within a data-frame

```
1 melanoma= transform(melanoma,
2                     thick2=thick^2,
3                     lthick=log(thick) )
4 dhead(melanoma)
```

```
      no status days ulc thick sex  thick2  lthick
1  789      3   10   1   676   1  456976  6.516193
2   13      3   30   0    65   1   4225  4.174387
3   97      2   35   0   134   1  17956  4.897840
4   16      3   99   0   290   0  84100  5.669881
5   21      1  185   1  1208   1 1459264  7.096721
6  469      1  204   1   484   1  234256  6.182085
```

When the above definitions are done using a condition this can be achieved using the `dtransform` function that extends `transform` with a possible condition

```
1 melanoma=dtransform(melanoma, ll=thick*1.05^ulc, sex==1)
2 melanoma=dtransform(melanoma, ll=thick, sex!=1)
3 dmean(melanoma, ll~sex+ulc)
```

```

      sex ulc      ll
1    0    0 173.7342
2    1    0 197.3611
3    0    1 374.5532
4    1    1 523.1198

```

Making factors (groupings)

On the melanoma data the variable thick gives the thickness of the melanom tumour. For some analyses we would like to make a factor depending on the thickness. This can be done in several different ways

```
1 melanoma=dcut(melanoma,~thick,breaks=c(0,200,500,800,2000))
```

New variable is named thickcat.o by default.

To see levels of factors in data-frame

```
1 dlevels(melanoma)
```

```

thickcat.0 #levels=:4
[1] "[0,200]"      "(200,500]"    "(500,800]"    "(800,2e+03]"
-----

```

Checking group sizes

```
1 dtable(melanoma,~thickcat.0)
```

```

thickcat.0
  [0,200]  (200,500]  (500,800] (800,2e+03]
        109         64         20         12

```

With adding to the data-frame directly

```
1 dcut(melanoma,breaks=c(0,200,500,800,2000)) <- gr.thick1~thick
2 dlevels(melanoma)
```

```

thickcat.0 #levels=:4
[1] "[0,200]"      "(200,500]"    "(500,800]"    "(800,2e+03]"
-----

gr.thick1 #levels=:4
[1] "[0,200]"      "(200,500]"    "(500,800]"    "(800,2e+03]"
-----

```

new variable is named thickcat.o (after first cut-point), or to get quartiles with default names thick.cat.4

```
1 dcut(melanoma) <- ~ thick ### new variable is thickcat.4
2 dlevels(melanoma)
```

```

thickcat.0 #levels=:4
[1] "[0,200]"      "(200,500]"    "(500,800]"    "(800,2e+03]"
-----

gr.thick1 #levels=:4
[1] "[0,200]"      "(200,500]"    "(500,800]"    "(800,2e+03]"
-----

thickcat.4 #levels=:4
[1] "[10,97]"      "(97,194]"     "(194,356]"    "(356,1.74e+03]"
-----

```

or median groups, here starting again with the original data,

```
1 data(melanoma)
2 dcut(melanoma,breaks=2) <- ~ thick ### new variable is thick.2
3 dlevels(melanoma)
```

```
thickcat.2 #levels=:2
[1] "[10,194]" "(194,1.74e+03]"
-----
```

to control new names

```
1 data(melanoma)
2 mela= dcut(melanoma,thickcat4+dayscat4~thick+days,breaks=4)
3 dlevels(mela)
```

```
thickcat4 #levels=:4
[1] "[10,97]" "(97,194]" "(194,356]" "(356,1.74e+03]"
-----
dayscat4 #levels=:4
[1] "[10,1.52e+03]" "(1.52e+03,2e+03]" "(2e+03,3.04e+03]"
[4] "[3.04e+03,5.56e+03]"
-----
```

OR

```
1 data(melanoma)
2 dcut(melanoma,breaks=4) <- thickcat4+dayscat4~thick+days
3 dlevels(melanoma)
```

```
thickcat4 #levels=:4
[1] "[10,97]" "(97,194]" "(194,356]" "(356,1.74e+03]"
-----
dayscat4 #levels=:4
[1] "[10,1.52e+03]" "(1.52e+03,2e+03]" "(2e+03,3.04e+03]"
[4] "[3.04e+03,5.56e+03]"
-----
```

This can also be typed out more specifically

```
1 melanoma$gthick = cut(melanoma$thick,breaks=c(0,200,500,800,2000))
2 melanoma$gthick =
  ↪ cut(melanoma$thick,breaks=quantile(melanoma$thick),include.lowest=TRUE)
```

Working with factors

To see levels of covariates in data-frame

```
1 data(melanoma)
2 dcut(melanoma,breaks=4) <- thickcat4~thick
3 dlevels(melanoma)
```

```
thickcat4 #levels=:4
[1] "[10,97]" "(97,194]" "(194,356]" "(356,1.74e+03]"
-----
```

To releve the factor

```

1 dtable(melanoma,~thickcat4)
2 melanoma = drelevel(melanoma,~thickcat4,ref="(194,356]")
3 dlevels(melanoma)

```

```

thickcat4
      [10,97]      (97,194]      (194,356] (356,1.74e+03]
      56          53          45          51
thickcat4 #levels=:4
[1] "[10,97]"      "(97,194]"      "(194,356]"      "(356,1.74e+03]"
-----
thickcat4.(194,356] #levels=:4
[1] "(194,356]"      "[10,97]"      "(97,194]"      "(356,1.74e+03]"
-----

```

or to take the third level in the list of levels, same as above,

```

1 melanoma = drelevel(melanoma,~thickcat4,ref=2)
2 dlevels(melanoma)

```

```

thickcat4 #levels=:4
[1] "[10,97]"      "(97,194]"      "(194,356]"      "(356,1.74e+03]"
-----
thickcat4.(194,356] #levels=:4
[1] "(194,356]"      "[10,97]"      "(97,194]"      "(356,1.74e+03]"
-----
thickcat4.2 #levels=:4
[1] "(97,194]"      "[10,97]"      "(194,356]"      "(356,1.74e+03]"
-----

```

To combine levels of a factor (first combining first 3 groups into one)

```

1 melanoma = drelevel(melanoma,~thickcat4,newlevels=1:3)
2 dlevels(melanoma)

```

```

thickcat4 #levels=:4
[1] "[10,97]"      "(97,194]"      "(194,356]"      "(356,1.74e+03]"
-----
thickcat4.(194,356] #levels=:4
[1] "(194,356]"      "[10,97]"      "(97,194]"      "(356,1.74e+03]"
-----
thickcat4.2 #levels=:4
[1] "(97,194]"      "[10,97]"      "(194,356]"      "(356,1.74e+03]"
-----
thickcat4.1:3 #levels=:2
[1] "[10,97]-(194,356]" "(356,1.74e+03]"
-----

```

or to combine groups 1 and 2 into one group and 3 and 4 into another

```

1 dkeep(melanoma) <- ~thick+thickcat4
2 melanoma = drelevel(melanoma,gthick2~thickcat4,newlevels=list(1:2,3:4))
3 dlevels(melanoma)

```

```

thickcat4 #levels=:4
[1] "[10,97]"      "(97,194]"      "(194,356]"      "(356,1.74e+03]"
-----
gthick2 #levels=:2
[1] "[10,97]-(97,194]" "(194,356]-(356,1.74e+03]"
-----

```


Changing order of factor levels

```

1 dfactor(melanoma,levels=c(3,1,2,4)) <- thickcat4.2~thickcat4
2 dlevel(melanoma,~ "thickcat4*")
3 dtable(melanoma,~thickcat4+thickcat4.2)

```

```

thickcat4 #levels=:4
[1] "[10,97]"      "(97,194]"      "(194,356]"      "(356,1.74e+03]"
-----
thickcat4.2 #levels=:4
[1] "(194,356]"      "[10,97]"      "(97,194]"      "(356,1.74e+03]"
-----

      thickcat4.2 (194,356] [10,97] (97,194] (356,1.74e+03]
thickcat4
[10,97]                0      56      0      0
(97,194]               0      0     53      0
(194,356]             45      0      0      0
(356,1.74e+03]        0      0      0     51

```

Combine levels but now control factor-level names

```

1 melanoma=drelevel(melanoma,gthick3~thickcat4,newlevels=list(group1.2=1:2,group3.4=3:4))
2 dlevels(melanoma)

```

```

thickcat4 #levels=:4
[1] "[10,97]"      "(97,194]"      "(194,356]"      "(356,1.74e+03]"
-----
gthick2 #levels=:2
[1] "[10,97]-(97,194]"      "(194,356]-(356,1.74e+03]"
-----
thickcat4.2 #levels=:4
[1] "(194,356]"      "[10,97]"      "(97,194]"      "(356,1.74e+03]"
-----
gthick3 #levels=:2
[1] "group1.2" "group3.4"
-----

```

Making a factor from existing numeric variable and vice versa

A numeric variable "status" with values 1,2,3 into a factor by

```

1 data(melanoma)
2 melanoma = dfactor(melanoma,~status,
  ↪ labels=c("malignant-melanoma","censoring","dead-other"))
3 melanoma = dfactor(melanoma,sex1~sex,labels=c("females","males"))
4 dtable(melanoma,~sex1+status.f)

```

```

      status.f malignant-melanoma censoring dead-other
sex1
females                28      91      7
males                  29     43     7

```

A gender factor with values "M", "F" can be converted into numerics by

```

1 melanoma = dnumeric(melanoma,~sex1)
2 dstr(melanoma,"sex*")
3 dtable(melanoma,~'sex*',level=2)

```

```
'data.frame':      205 obs. of  3 variables:
 $ sex   : int  1 1 1 0 1 1 1 1 0 0 ...
 $ sexl  : Factor w/ 2 levels "females","males": 2 2 2 1 2 2 2 2 1 1 ...
 $ sexl.n: num  2 2 2 1 2 2 2 2 1 1 ...
```

```
      sex
sexl    0  1
females 126  0
males    0  79
```

```
      sex
sexl.n  0  1
1 126  0
2  0  79
```

```
      sexl
sexl.n females males
1      126      0
2       0      79
```