pic.plot by Example

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Contents

1 The first example

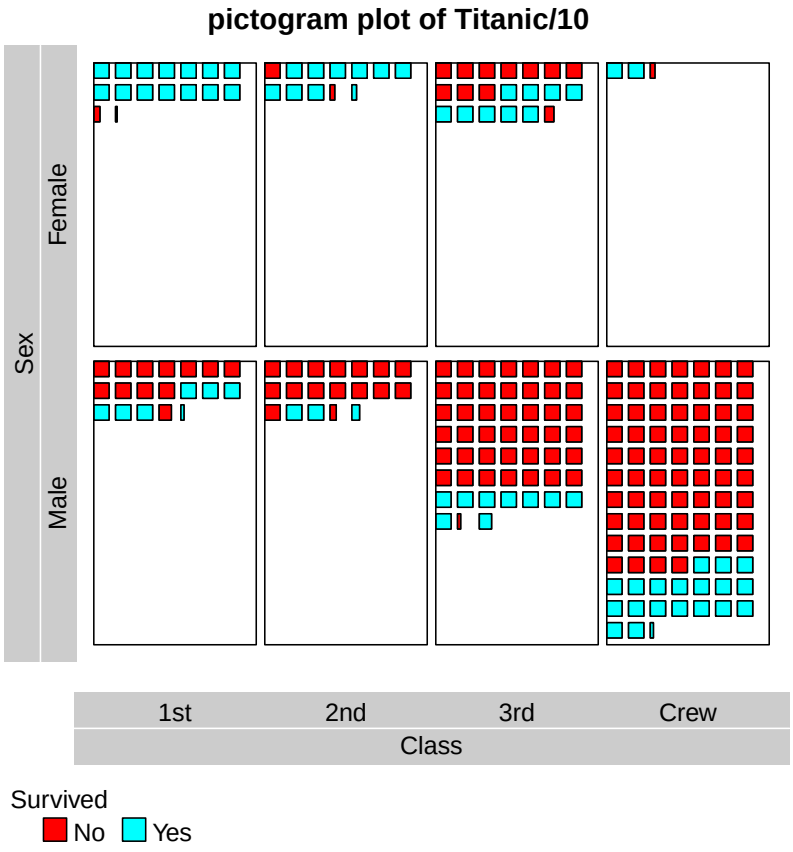
Here is the first example. 1

```
> margin.table(Titanic/10, 2:1)[2:1,]
```

```
        Class
Sex       1st  2nd  3rd Crew
  Female 14.5 10.6 19.6  2.3
  Male   18.0 17.9 51.0 86.2
```

This is a margin table of the data set `Titanic` divided by 10. Let's call `pic.plot()` and study the result. 2

```
> pic.plot(data = Titanic/10, grp.color = Survived)
```



Remarks: `pic.plot()` constructs graphical representations of contingency tables or data matrices. In this example the first two variables of the table `Titanic/10` are used to span the plotting area of the pictogram plot. Each of the eight resulting panels of the plot visualizes a cells of the table printed above. The small colored fields which we call pictogram elements represent units of data table. Since the frequencies of `Titanic` are divided by 10 we get decimal values and some picture elements which are smaller than the other. What's going on will be explained by the examples in the following sections.

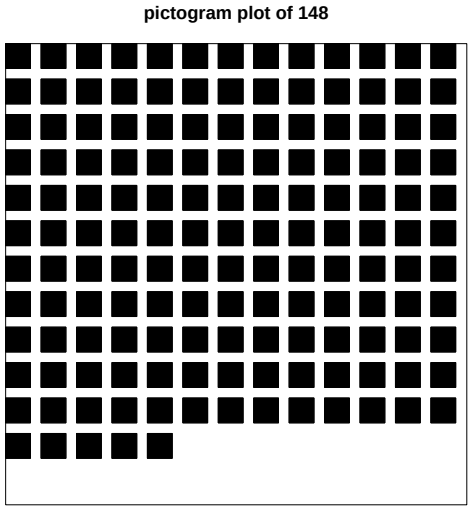
2 A single frequency as input

In this section we show different ways to represent a number or a frequency.

`data=148`

3

```
> pic.plot(data = 148)
```



Remarks: Using 148 as data argument `pic.plot()` creates 148 pictogram elements.

The size of the elements is maximized conditional to the expansion of plotting region. Therefore, the result depends on the height and the width of the graphical device. If you lower the width of your device the number of pictogram elements per row is decreased. To get pictogram plots exactly as shown in this paper you have to adjust height and width of your graphical device. E.g., for a postscript device setting `width=8, height=8` will work.

The `pic.aspect` argument changes the aspect ratio (width / height) of the picture elements. A value of 0.25 generates small bars whose height is four times as much as their width.

`pic.aspect=.25`

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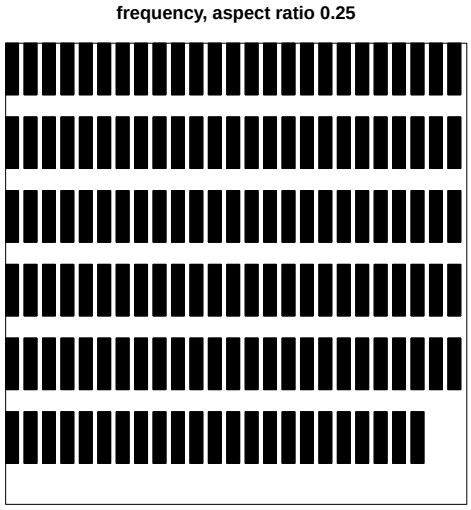
```
> pic.plot(data       = 148,
           pic.aspect = 0.25,
           main = "frequency, aspect ratio 0.25")
```



Remarks: The title of the plot is controlled by the argument `main`.

Consider the effect of setting `pic.aspect` to 1.

`pic.aspect=1`
`main`

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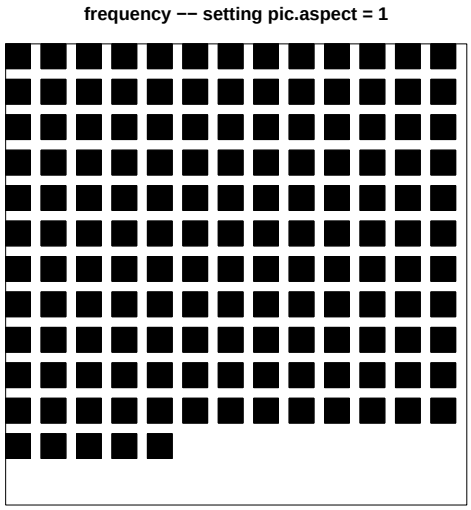
```
> pic.plot(data       = 148,
           pic.aspect = 1,
           main = "frequency -- setting pic.aspect = 1")
```



Remarks: Obviously the argument `pic.aspect = 1` (the default) has no effect. It sets the aspect ratio of the 148 pictogram elements to one. Apart from the title we reconstructs the first plot of this section.

If we assign a value greater than one to argument `pic.aspect` we get bars whose widths are greater than the heights. Here `pic.aspect` is set to four and the color of the pictogram elements to `orange`:

`colors="orange"`

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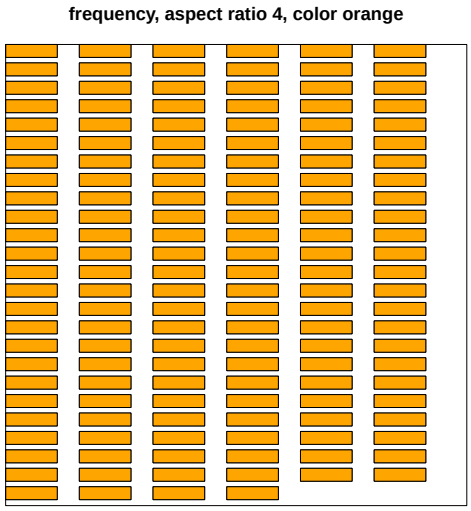
```
> pic.plot(data       = 148,
           pic.aspect = 4,
           colors     = "orange",
           main = "frequency, aspect ratio 4, color orange")
```



To remove spaces between the pictogram elements use `pic.space.factor = 0`.

`pic.space.factor=0`
`colors="lightblue"`

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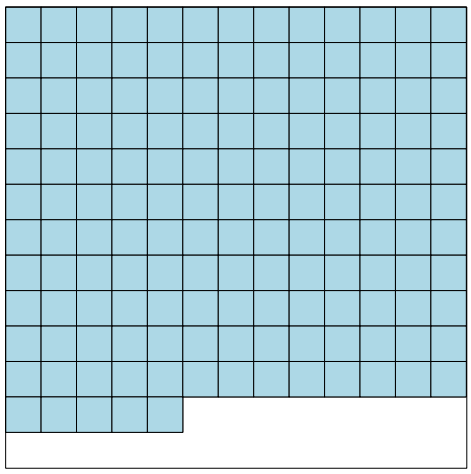
```
> pic.plot(data             = 148,
           pic.aspect       = 1,
           pic.space.factor = 0,
           colors           = "lightblue",
           main = "frequency, zero space between pics, red")
```



To control horizontal and vertical spaces differently assign two values to argument `pic.space.factor`, e.g. set `pic.space.factor = c(0, 0.4)`:

pic.space.factor

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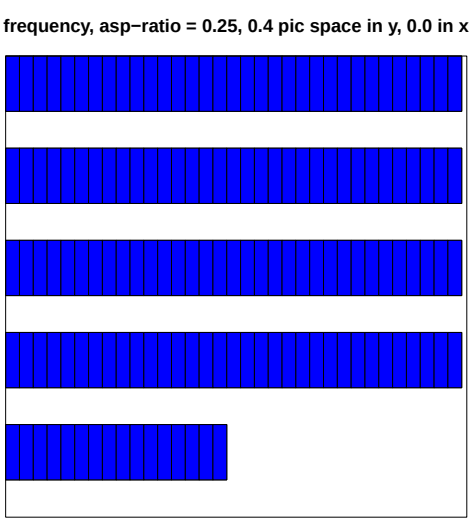
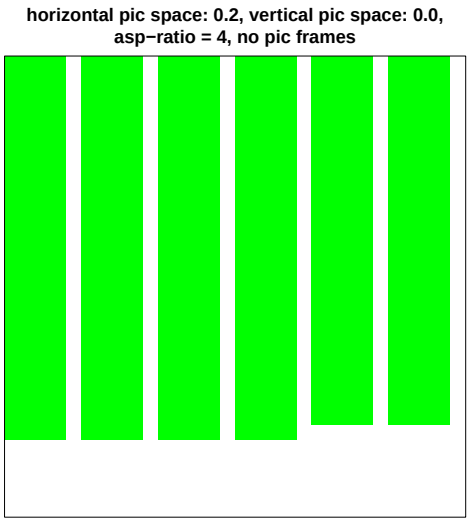
```
> pic.plot(data = 148,
           pic.aspect       = 0.25,
           pic.space.factor = c(0, 0.4),
           colors           = "blue",
           main = "frequency, asp-ratio = 0.25, 0.4 pic space in y, 0.0 in x")
```

Remarks: This statement constructs the left of the two following plots.





Border lines are controlled by argument `pic.frame`. To get vertical bars set `pic.frame = FALSE`, horizontal space 0.2 and vertical space 0.0, i.e. `pic.space.factor = c(0.2, 0.0)`.

pic.frame=FALSE

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```
> pic.plot(data = 148,
           pic.aspect       = 4,
           pic.space.factor = c(0.2, 0.0),
           colors           = "green",
           pic.frame        = FALSE,
           main = "horizontal pic space: 0.2, vertical pic space: 0.0,
                   asp-ratio = 4, no pic frames                  ")
```

Remarks: This call of `pic.plot()` results in the right plot above.

3 Grouping by coloring pictograms

R's `HairEyeColor` is a three-dimensional contingency table displaying the variables `Hair`, `Eye` and `Sex` of 592 persons. These data are used for a lot of examples of the following sections. 10

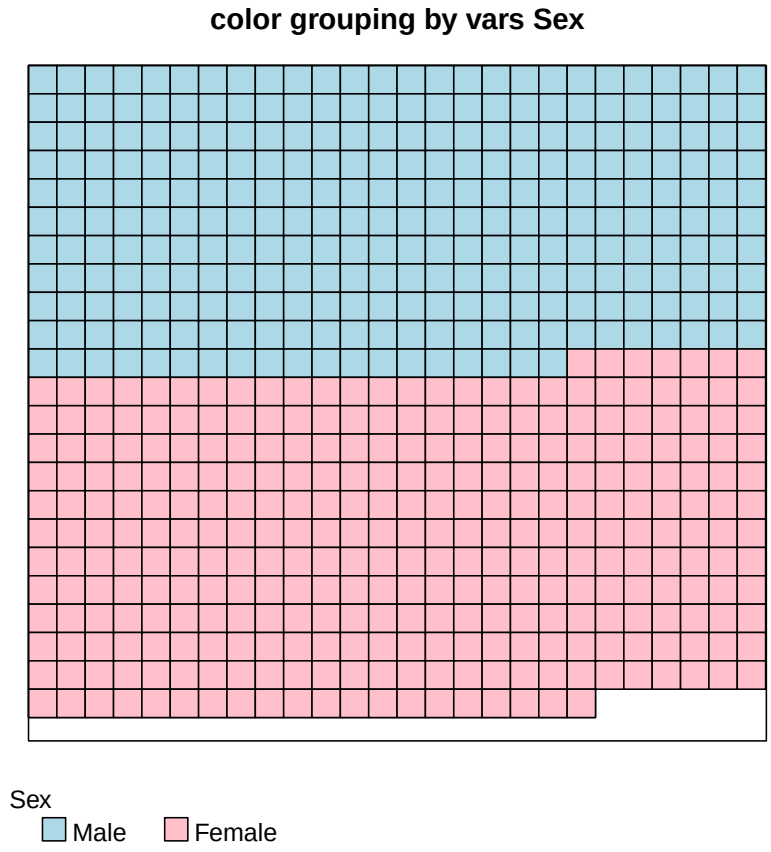
```
> HairEyeColor

, , Sex = Male

       Eye
Hair    Brown Blue Hazel Green
  Black    32   11    10     3
  Brown    53   50    25    15
  Red      10   10     7     7
  Blond     3   30     5     8

, , Sex = Female

       Eye
Hair    Brown Blue Hazel Green
  Black    36    9     5     2
  Brown    66   34    29    14
  Red      16    7     7     7
  Blond     4   64     5     8

> dimnames(HairEyeColor)

$Hair
[1] "Black" "Brown" "Red"   "Blond"

$Eye
[1] "Brown" "Blue"  "Hazel" "Green"

$Sex
[1] "Male"   "Female"
```

In this section we demonstrate how to control the colors of the pictogram elements. We show how the arguments `grp.color` and `colors` can be used to represent different levels of a variable by different colors. `grp.color` defines the variable to be evaluated for coloring the elements whereas `colors` fixes the set of colors.

In the first example the observations are split by the variable `Sex` into the two groups `Male` and `Female`.

grp.color=Sex
colors
11

```
> pic.plot(HairEyeColor, grp.xy = NULL,
           grp.color        = Sex,
           colors           = c("lightblue", "pink"),
           pic.space.factor = 0,
           main             = "color grouping by vars Sex")
```



Remarks: The grouping according to the gender is caused by `grp.color = Sex`. Each group is displayed by different colors (`colors=c("lightblue", "pink")`).

For there should not be any grouping concerning the axis the argument `grp.xy` is set to `NULL`; later on we explain the use of this argument in detail.

In the following example we define variable **1** of the data set to control the the colors of the pictogram elements. This setting is equivalent to `grp.color=Hair` because `Hair` is the first dimension of the contingency table.

For the argument `colors` is missing default colors are selected from the rainbow spectrum. To get an column-like alignment of the color legend we set `lab.legend="cols"`.

`grp.color=1`
`lab.legend`
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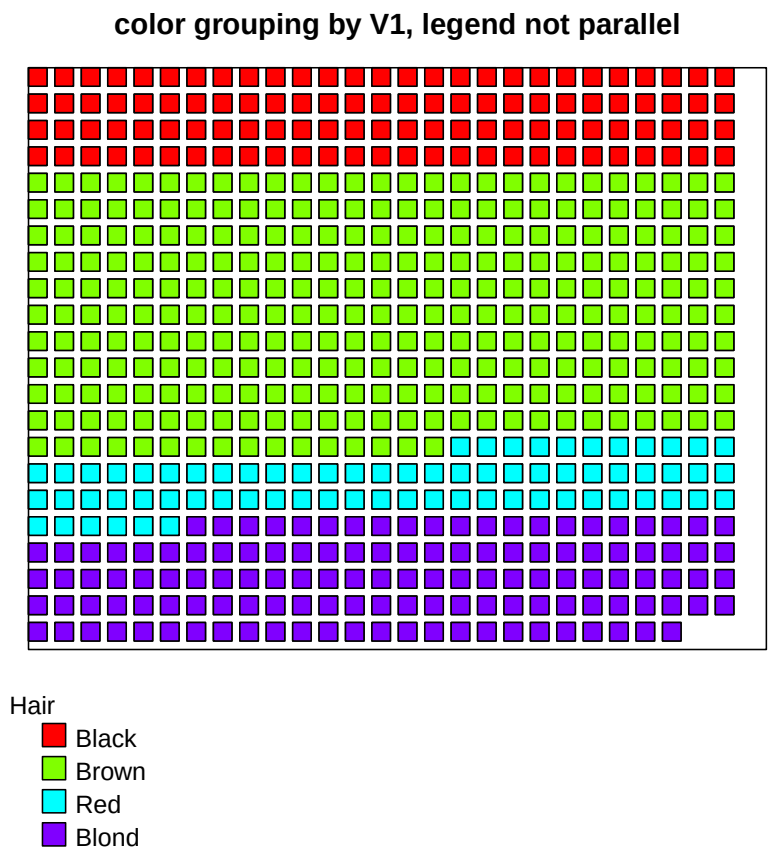
```
> pic.plot(HairEyeColor, grp.xy = NULL,
           grp.color        = 1,
           pic.space.factor = 0.3,
           lab.legend       = "cols",
           main = "color grouping by V1, legend not parallel")
```

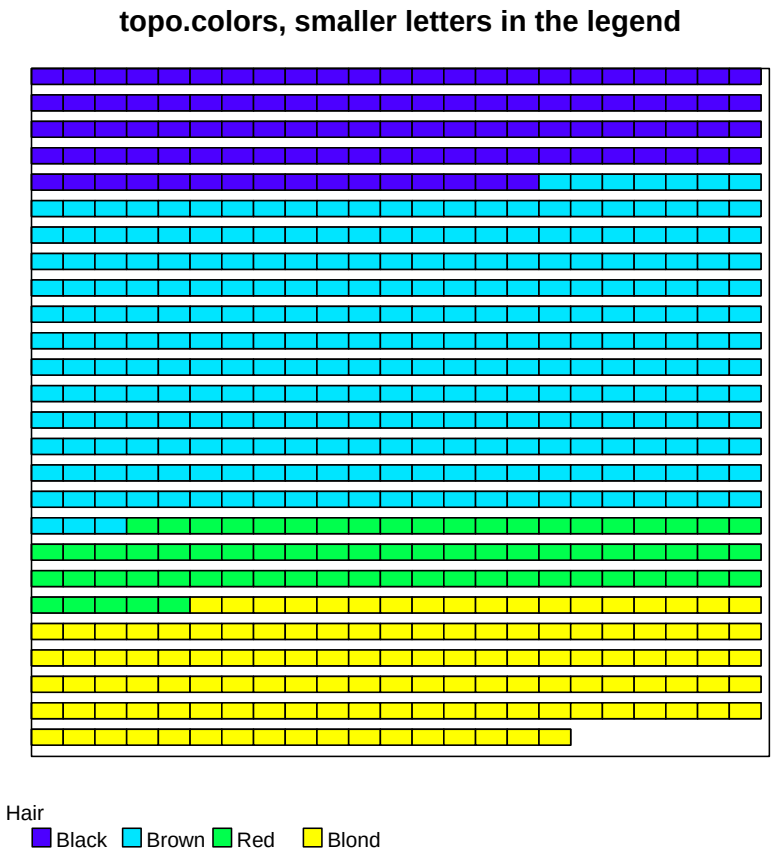


Remarks: Looking at the pictogram plot we see there are at first 36 red pictogram elements, then 53 green ones, etc. You can found these numbers in the first column of `HairEyeColor[,,"Female"]`. If you want to get a pictogram plot whose pictogram elements are *sorted* by color you have to rotate the contingency table by `aperm()`. We demonstrate an application of this function later in this section.

In this example we choose colors from the `topo.colors`, we request some space in the y direction and the pictogram elements should have a width-height-ratio of 2.

`colors=topo.colors(4)`
`lab.cex`
13

```
> pic.plot(HairEyeColor,
           grp.color        = 1,
           colors           = topo.colors(4),
           pic.space.factor = c(0, 0.4),
           pic.aspect       = 2,
           lab.legend       = "rows",
           lab.cex          = 0.8,
           main = "topo.colors, smaller letters in the legend", grp.xy = NULL)
```



Remarks: The color legend is parallel to the x direction (`lab.legend="rows"`) and the size of the legend is reduced a little bit due to the setting `lab.cex = 0.8`.

This example demonstrates the effect of a color grouping based on variable two (`Eye`). We suppress the frame of the pictogram elements, the legend should not be parallel to the x-axis and the size of the explanations is set to 0.8.

`colors=1:4`

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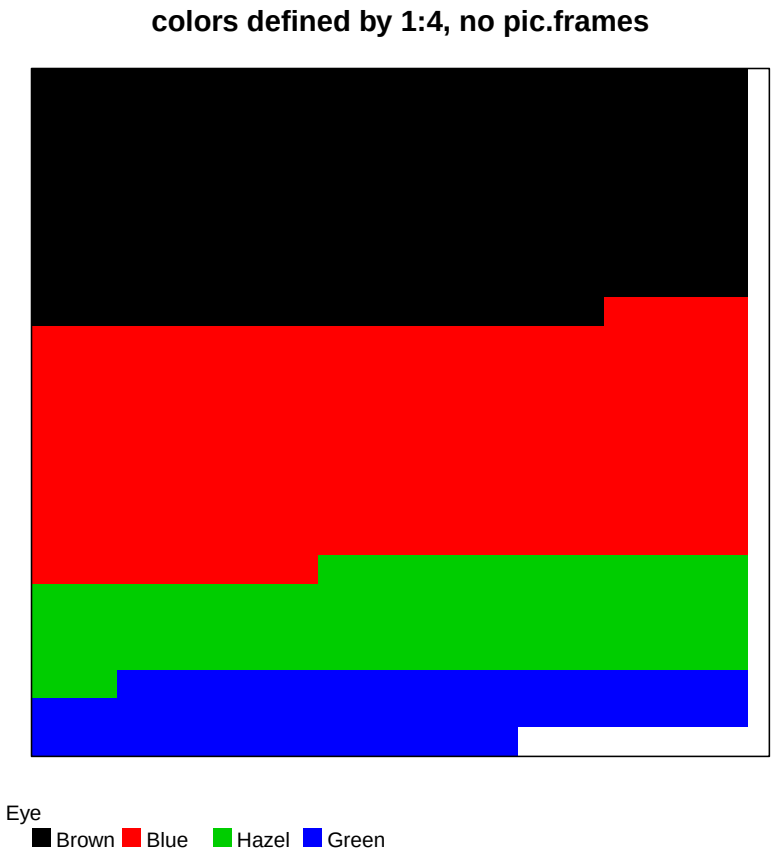
```
> pic.plot(HairEyeColor,
           grp.color        = 2,
           colors           = 1:4,
           pic.frame        = FALSE,
           pic.space.factor = 0,
           lab.cex          = 0.8,
           main = "colors defined by 1:4, no pic.frames", grp.xy = NULL)
```



Remarks: The colors are defined by the first four colors of R, see section *Color Specification* in the help of `par`.

4 Grouping by different pictogram elements

The examples of this section are based on the data set `HairEyeColor` again. Note that data set `HairEyeColor` consists of three variables: `Sex`, `Eye` and `Hair`. We would like to see differences between the levels of two variables. As before, the first one is linked to `grp.color` and its levels are displayed by different colors. The second variable is assigned to `grp.pic` and its levels are represented by different pictogram elements, such as symbols, raster graphics, etc. The set of pictogram elements (or icons) is controlled by the argument `pics` (`pics` is a short cut for *PIC*togram element*S*). Suppose we want to display variables `Hair` (with different colors) and `Eye` (with different symbols). We set `grp.color = 1` (or `grp.color = Hair`) and `grp.pic = 2` (or `grp.pic = Eye`).

grp.pic=2

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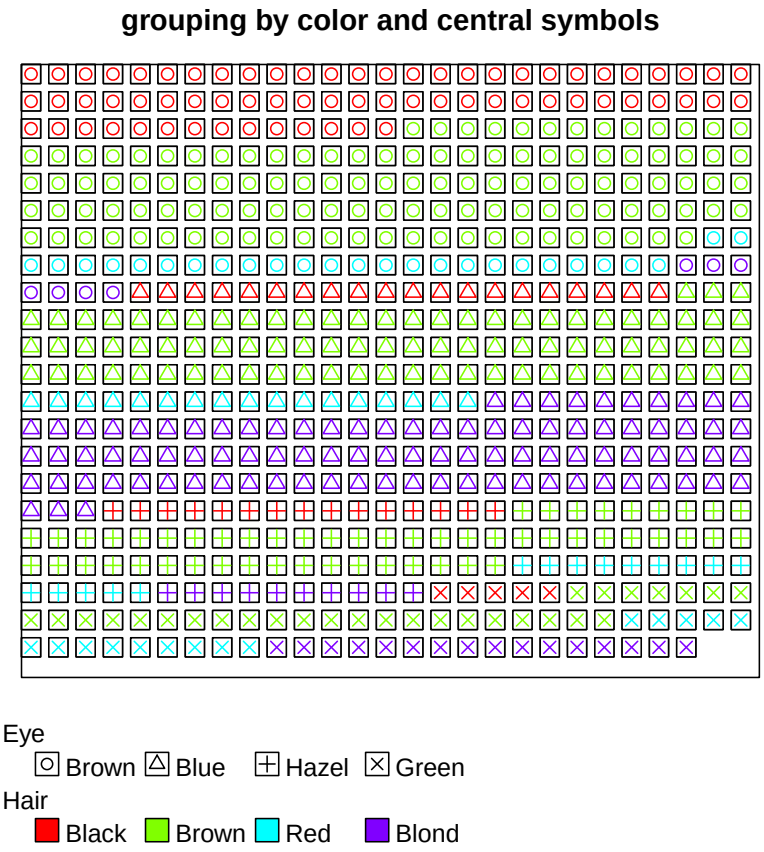
```
> pic.plot(HairEyeColor,
           grp.color = 1,
           grp.pic   = 2,
           main = "grouping by color and central symbols", grp.xy = NULL)
```



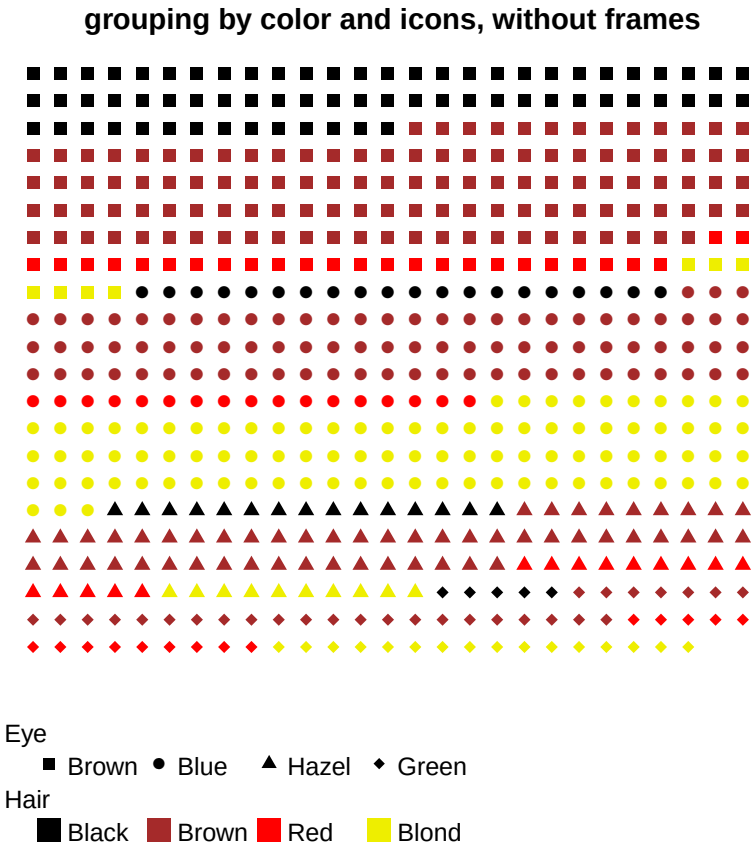
Remarks: As the set of icons has not been specified the icons are generated by `points` and the symbols are fixed by its argument `pch`. Level `i` of the variable results in setting `pch = i`. For further information see the description of `pch` in the help of `points`.

Now we get two legends. The first one shows what the symbols are used for and the second one explains the meaning of the colors.

Without changing the grouping variables we modify the call of the last example and change some of argument settings discussed above. The new argument `panel.frame` controls the border line of the field containing the pictogram elements.

`pics=15:18`
`panel.frame=FALSE`
16

```
> pic.plot(HairEyeColor,
           grp.color   = Hair,
           grp.pic     = Eye,
           colors      = c("black", "brown", "red", "yellow2"),
           pics        = 15:18,
           pic.frame   = FALSE,
           panel.frame = FALSE,
           main = "grouping by color and icons, without frames", grp.xy = NULL)
```

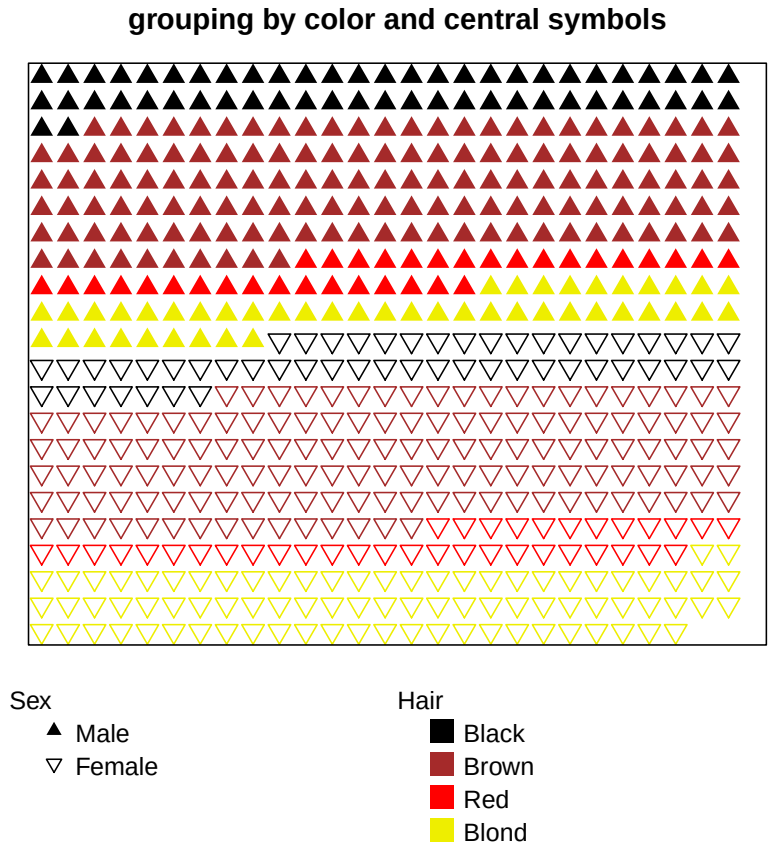


Remarks: The set of colors and symbols depends on the graphics system generating the plot and may vary.

If you want to study the distribution of hair colors within the groups of `Male` and `Female` you set `grp.pic = Sex` and `grp.color = Hair`.

`grp.pic="Sex"`
`grp.color="Hair"`
17

```
> pic.plot(HairEyeColor,
           grp.pic          = "Sex",
           grp.color        = "Hair",
           pics             = c(17, 6),
           colors           = c("black", "brown", "red", "yellow2"),
           pic.frame        = FALSE,
           pic.space.factor = 0,
           lab.legend       = "cols",
           main = "grouping by color and central symbols", grp.xy = NULL)
```



Remarks: In the example `grp.pic` and `grp.color` are set by character strings. When comparing the call of this page with other calls above you see that `"` can be used in the assignment of `grp.pic` and `grp.color`. But generally it is more comfortable to omit the quotation marks.

You may not be very happy with the last plot for the areas with the same color are splitted. This structure is induced by the order of the dimensions of the table: `Hair, Eye, Sex`. You can get a more suitable appearance after changing the order of the first two dimensions using the R function `aperm`.

`data=aperm(..)`

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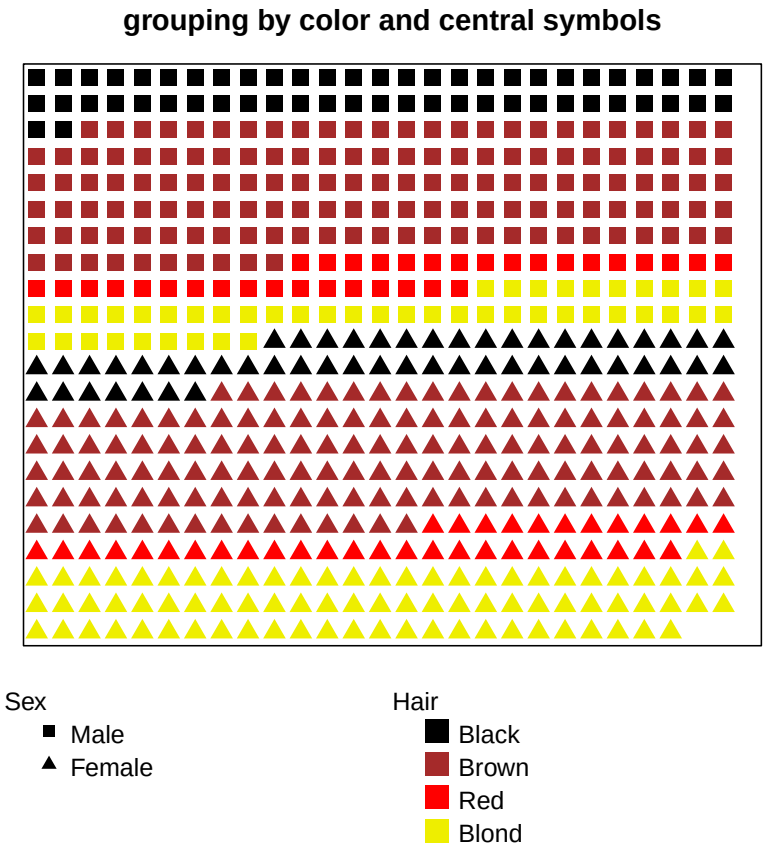
```
> pic.plot(aperm(HairEyeColor, c(2,1,3)), grp.xy = NULL,
           grp.pic          = Sex,
           grp.color        = Hair,
           pics             = c(15, 17),
           colors           = c("black", "brown", "red", "yellow2"),
           pic.frame        = FALSE,
           pic.space.factor = 0,
           lab.legend       = "cols",
           main = "grouping by color and central symbols")
```



Remarks: Now we see that there are some more blond Female entries than Male entries.

As a variation we now have a look at the two variables `Sex` and `Hair`, but the grouping definitions are exchanged.

`pics=c(1,3,6,8)`

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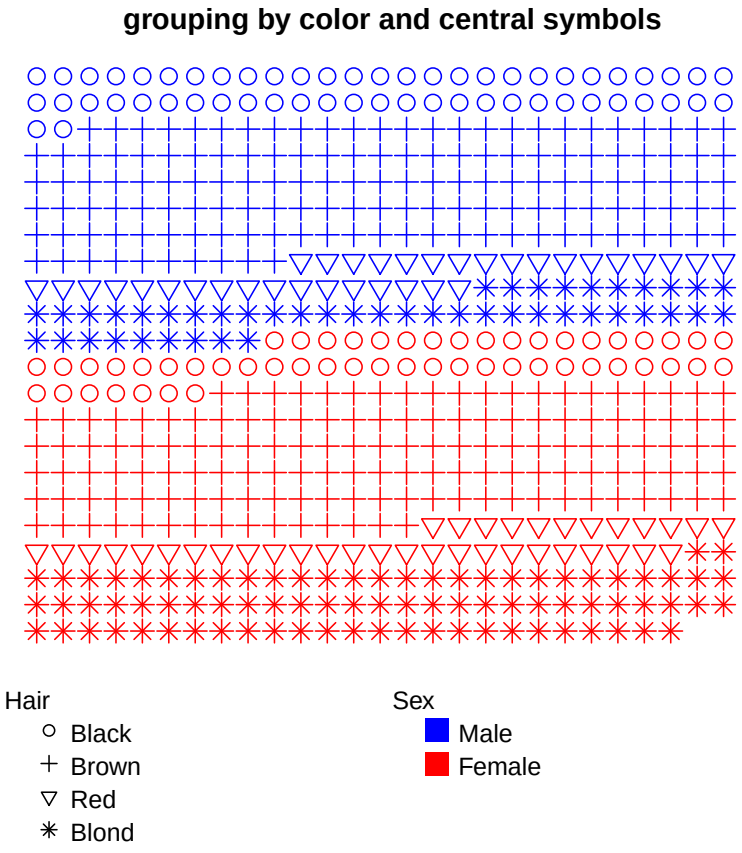
```
> pic.plot(aperm(HairEyeColor, c(2,1,3)),
           grp.pic          = Hair,
           grp.color        = Sex,
           colors           = c("blue", "red"),
           pics             = c(1, 3, 6, 8),
           pic.frame        = FALSE,
           pic.space.factor = 0,
           panel.frame      = FALSE,
           lab.legend       = "cols",
           main = "grouping by color and central symbols", grp.xy = NULL)
```



Remarks: You see the examples show a wide range of ways to construct simple pictogram plots. Each of them will focus special properties of a data set.

5 Layouts for placing pictogram elements

In this section we use the data set `HairEyeColor` once again. There are a lot of layouts to control the way how pictogram elements are displayed in the plotting area. The elements are arranged in lines or *stacks* of length `pic.stack.len`, their orientation being horizontal (`pic.horizontal = TRUE` or vertical (`pic.horizontal = FALSE`).

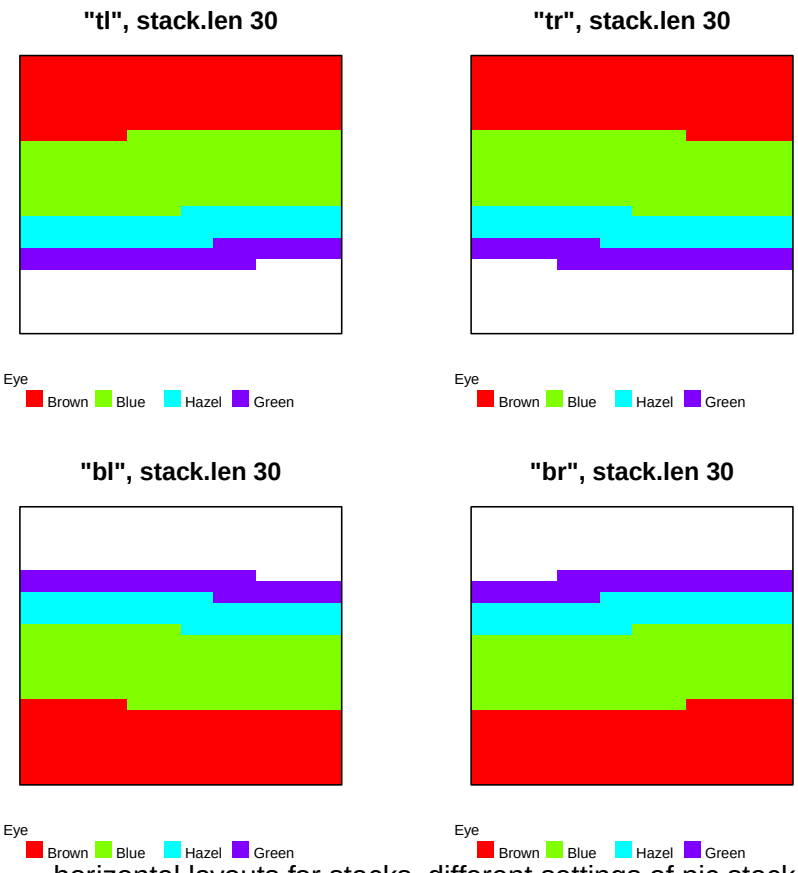
At first we consider *horizontal = TRUE*. In this case the first stack can be plotted at the bottom side (`"b"`) or at the top side of the plotting area (`"t"`). Usually the number of elements of the last stack is lower than `pic.stack.len`. Therefore, it makes a difference whether we start to draw the elements of the last stack beginning at left-hand side (`"l"`) or at the right-hand side (`"r"`). These decisions are controlled by the argument `pic.stack.type` and the letters `"b","t","l","r"`. The default value of this argument is `pic.stack.type = "lt"`.

The vertical case (`pic.horizontal = FALSE`) leads to the same discussion and the user has to encode the desired layout in the same way by magic letters out of the set of the four letters.

1 The following examples will clarify what's going on. Let us begin with the horizontal case.

pic.stack.type
pic.stack.len
20

```
> par(mfrow = c(2,2))
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = TRUE, pic.stack.type  = "tl",
           pic.stack.len   = 30,
           main = '"tl", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = TRUE, pic.stack.type  = "tr",
           pic.stack.len   = 30,
           main = '"tr", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = TRUE, pic.stack.type  = "bl",
           pic.stack.len   = 30,
           main = '"bl", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = TRUE, pic.stack.type  = "br",
           pic.stack.len   = 30,
           main = '"br", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> par(mfrow = c(1,1))
> mtext("horizontal layouts for stacks, different settings of pic.stack.type",
        cex = 1.2, side = 1, line = 4)
```



2 horizontal layouts for stacks, different settings of pic.stack.type

1 Vertical stacks result in strips running from top to bottom or vice versa. pic.horizontal=FALSE

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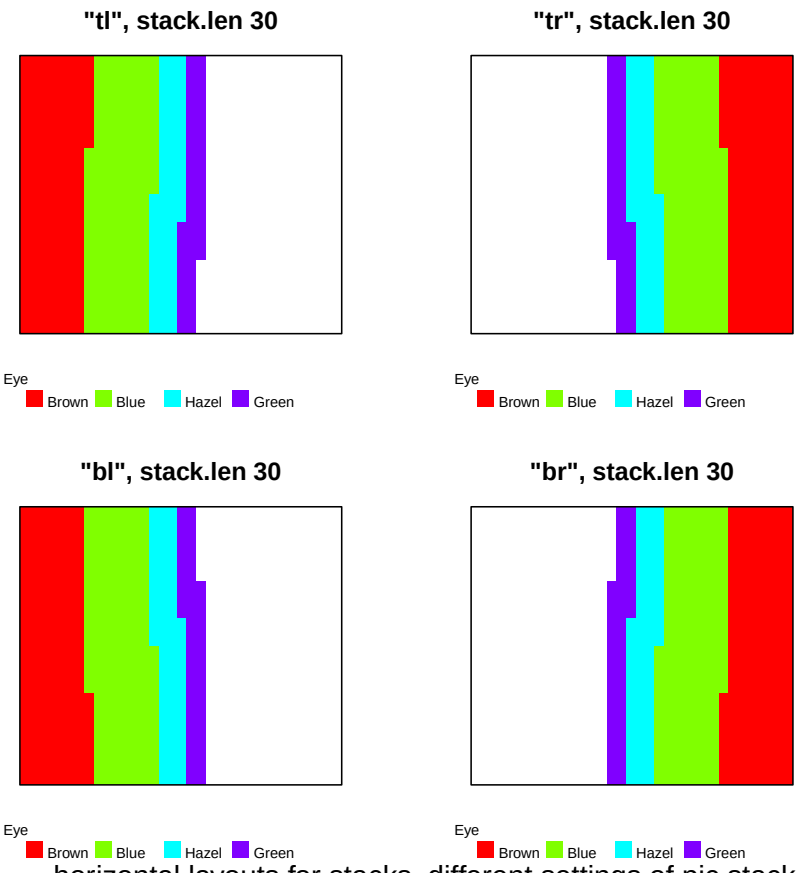
```
> par(mfrow = c(2,2))
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = FALSE,  pic.stack.type = "tl",
           pic.stack.len   = 30,
           main = '"tl", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = FALSE,  pic.stack.type = "tr",
           pic.stack.len   = 30,
           main = '"tr", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> pic.plot(HairEyeColor, grp.color = 2, lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = FALSE,  pic.stack.type = "bl",
           pic.stack.len   = 30,
           main = '"bl", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> pic.plot(HairEyeColor, grp.color = 2,  lab.cex = 0.7, pic.space.factor = 0,
           pic.horizontal  = FALSE, pic.stack.type = "br",
           pic.stack.len   = 30,
           main = '"br", stack.len 30', pic.frame = FALSE, grp.xy = NULL)
> par(mfrow = c(1,1))
> mtext("horizontal layouts for stacks, different settings of pic.stack.type",
        cex = 1.2, side = 1, line = 4)
```



2 horizontal layouts for stacks, different settings of pic.stack.type

6 Simple xy-groupings of the pictograms

Researchers often like to compare different subsets of a data set or *groups of elements*. They very often compute statistics or graphs of subsets of the observations and analyze the differences of the results. Within the framework of pictogram plots you are able to represent elements of different levels of one or more variables in different areas (called *panels*) of a pictogram plot. In this section we show how to define simple *xy-groupings* and how the results of the groupings look like.

By a simple *x-grouping* the horizontal range of the plot (or range of x) is split into several segments. In the rectangluar areas of the segments of vertical stripes the elements of the subsets are visualized. *y-groupings* lead to splittings along the vertical direction of the plot and you get *horizontally extending* panels. Using both of these elementary concepts the graphics area is fragmented like a chessboard and you get outputs that are similar to pairs plots. However, `pairs()` draws all of the data points in each of its chessboard squares whereas `pic.plot()` represents subsets of the data in the cells only. Beside these simple grouping approaches you can choose more than one variable for splitting the data in one or both of the direction(s). Examples are found in the next section *multiple xy-groupings*. These groupings induce recursive splittings of the ranges of x or y. Maybe you know this idea of structuring from lattice graphics or from the `ggplot2` package.

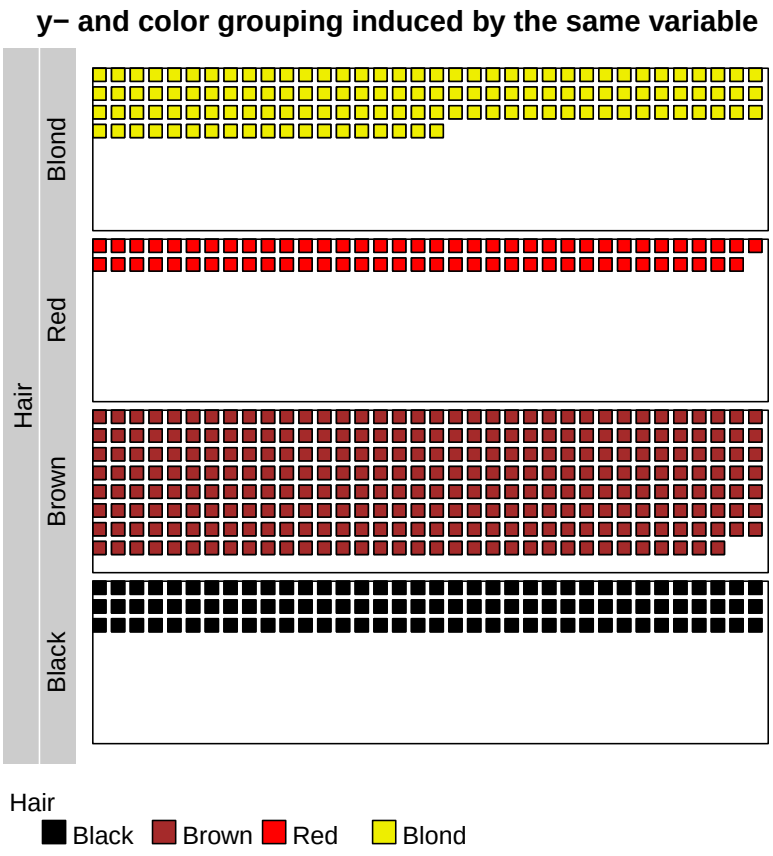
The user interface to define xy-groupings is based on R formulas. Especially in the context of regression R formulas are well known to describe models, e. g.: `y ~ x`. The variable on the left-hand side of a formula (`y`) has to be explained by the variable (`x`) on the right-hand side. Generally in scatter plots of these variables the dependent variable (`y`) spans the y-range, and in direction x you will find the values of the independent variable (`x`). Transferring this practice to pictogram plots `y ~ x` means that the vertical direction has to be split by the variable `y` and the other one by variable `x`.

`HairEyeColor` is the data set for the examples in this section.

In the first example of this section we split the vertical range according to the four levels of `Hair`. So four horizontally stripes or *panels* are displayed. Each panel consists of horizontal stacks of icons beginning at the top.

grp.xy=1~0
grp.color=1
22

```
> pic.plot(HairEyeColor,
           grp.xy         = Hair ~ 0,
           grp.color      = Hair,
           colors         = c("black", "brown", "red", "yellow2"),
           pic.stack.type = "tl",
           main = "y~ and color grouping induced by the same variable")
```

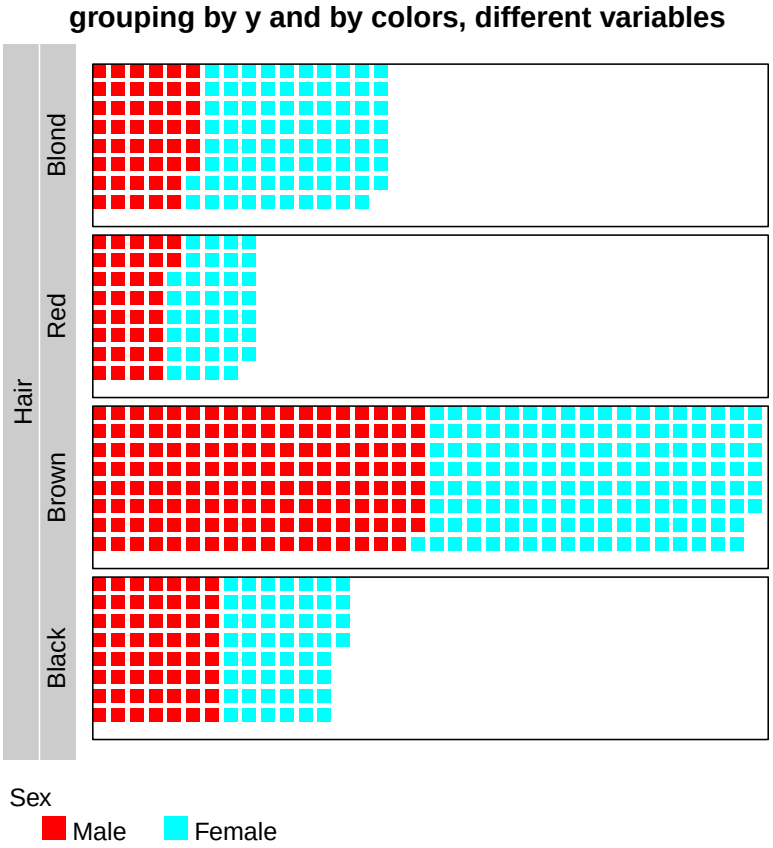


Remarks: The panels for displaying different subsets of the data are described by argument `grp.xy` using a formula notation: `Hair` has been written on the left-hand side of the `"~"` character and its levels define the vertical splitting of the plotting region into four rows. A `0` on the right-hand side of the formula indicates no horizontal splitting.

In the example of this page the formula is not set within quotation marks. Furthermore, it is allowed to call a variable by its name: `Hair`. The color grouping is defined by variable `Sex`. In the panels vertical stacks – beginning on the left – are filled in.

`grp.xy=Hair~.`
`grp.color=Sex`
23

```
> pic.plot(HairEyeColor,
           grp.xy         = Hair ~ 0,
           grp.color      = Sex,
           pic.stack.type = "lt",
           pic.horizontal = FALSE,
           pic.frame = FALSE,
           main = "grouping by y and by colors, different variables")
```



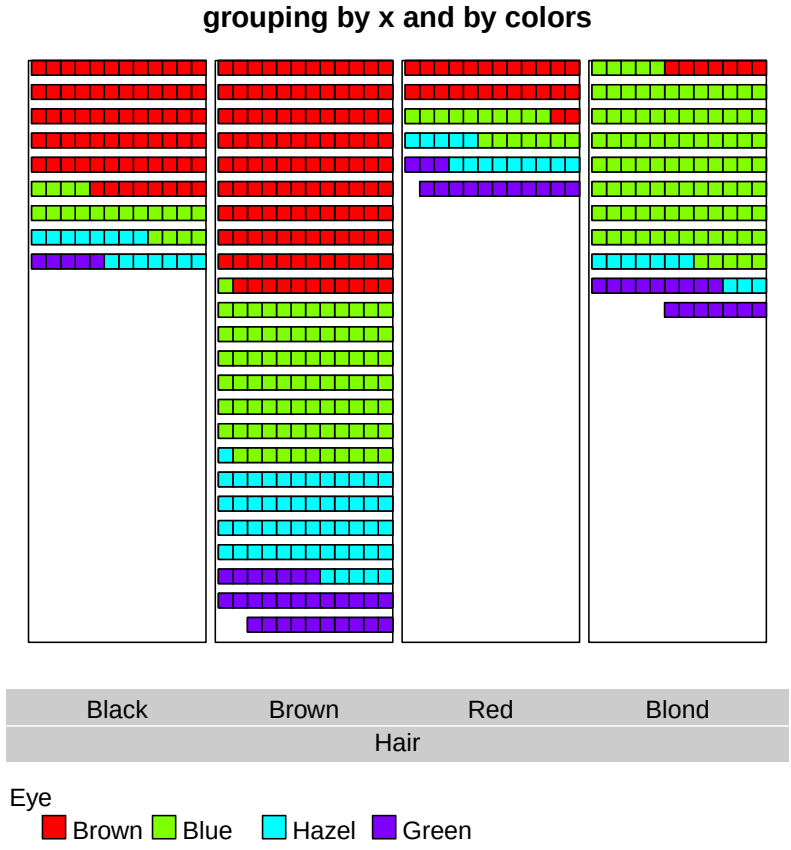
Remarks: `grp.color` is not defined by a *formula*. However, the "-characters are not necessary to bracket the variable names as described above.

Next we shows how to use variable 1 to split the horizontal range. Variable 2 (`Eye`) defines the colors. Furthermore, we see a different spacing in x (no space) and y (40 %).

`grp.xy=0~1`

24

```
> pic.plot(HairEyeColor,
           grp.xy           = 0 ~ 1,        # or:  grp.xy    = 0 ~ Hair
           grp.color        = 2,            # or:  grp.color = Sex
           pic.stack.type   = "tr",
           pic.space.factor = c(0, 0.4),
           main = "grouping by x and by colors")
```



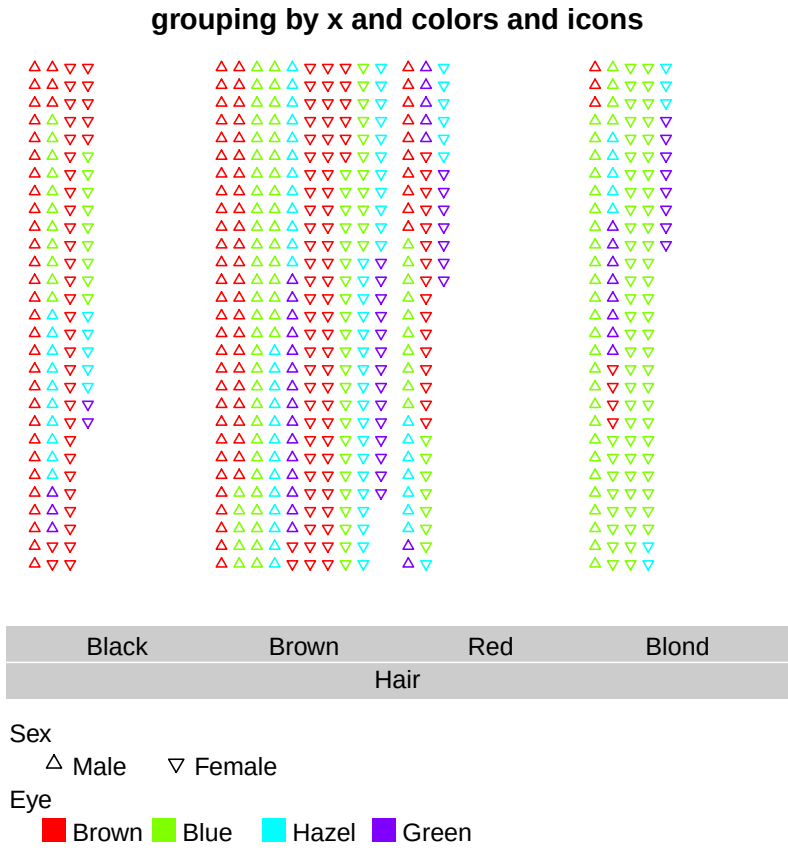
Remarks: Because of the order of the dimensions in the contingency table we get various ranges in the panels with color red or blue, for example. To get the symbols of a color in a joint area we have to rotate the input data, try
`pic.plot(aperm(HairEyeColor, c(1,3,2)), grp.xy = 0 ~ Hair, grp.color = Eye,..`
for example.

The following example of this series uses all of the three grouping concepts: color, pictogram and xy. No borderlines around the symbols and around the panels should be drawn.

grp.xy=~Hair

25

```
> pic.plot(HairEyeColor,
           grp.xy          = ~ Hair,
           grp.color       = Eye,
           grp.pic         = Sex,
           pics            = c(2, 6),
           pic.frame       = FALSE,
           pic.horizontal  = FALSE,
           panel.frame     = FALSE,
           main = "grouping by x and colors and icons")
```



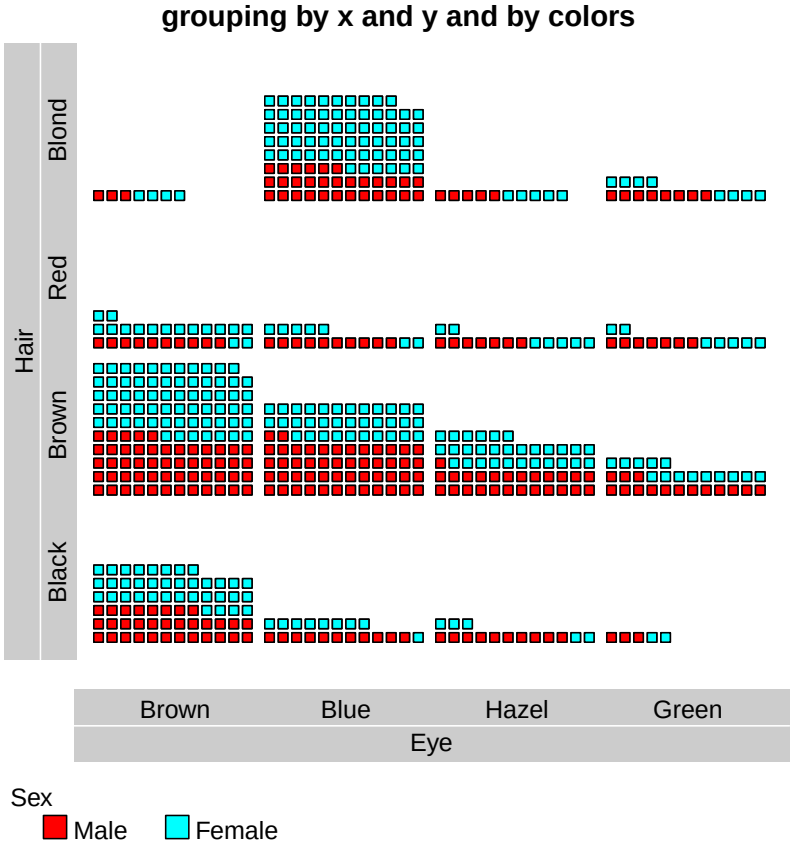
Remarks: The formula defining `grp.xy` consists of two symbols only: the tilde `~` and the variable name. Obviously the dot on the left-hand side can be omitted.

In the next call x- and y-groupings are combined. Setting `grp.xy = Hair ~ Eye`) we get a layout like a chessboard. The levels of variable `Eye` defines the groups along the x-axis and the levels of `Hair` split the vertical range. Males and Females are represented by colors.

grp.xy=1~2

26

```
> pic.plot(HairEyeColor,
           grp.xy         = Hair ~ Eye,
           grp.color      = Sex,
           pic.stack.type = "bl",
           panel.frame    = FALSE,
           main = "grouping by x and y and by colors")
```



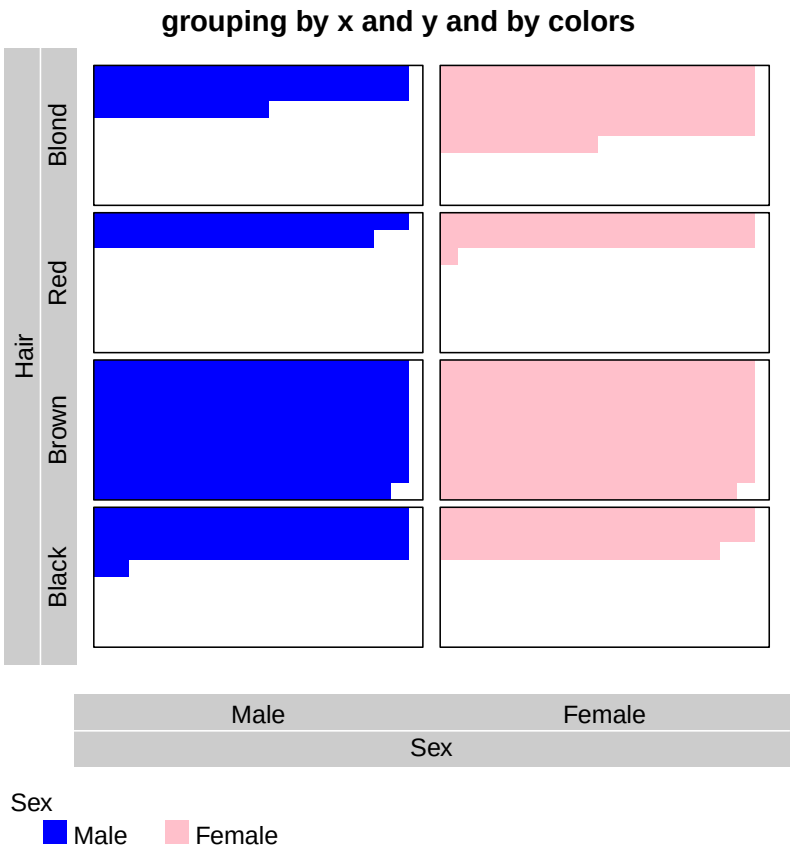
Remarks: It is peculiar that there are relatively more females with blue eyes in the group of blond-haired than in the group of brown-haired persons. Maybe a biologist can comment on this observation.

If we want to concentrate on differences between males and females regarding the color of `Hair` we can choose `Sex` for x-groupings and ignore the variable `Eye`.

grp.xy=Hair~Sex

27

```
> pic.plot(HairEyeColor,
           grp.xy    = Hair ~ Sex,
           grp.color = Sex,
           colors    = c("blue", "pink"),
           pic.frame = FALSE,
           pic.space = 0,
           main = "grouping by x and y and by colors")
```

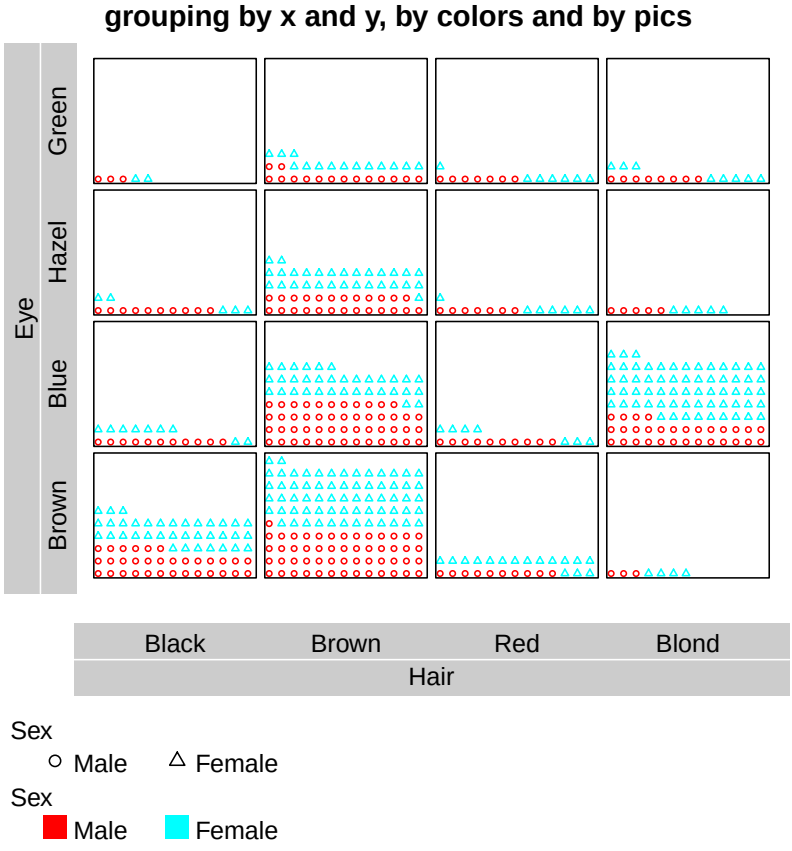


Remarks: Besides the definitions of groupings and the colors to be used for males and females the space between the rectangluar icons and the border lines of the elements have been removed.

The last example of this section shows the additional groupings by different pictogram elements (`pics`).

grp.xy="2~1"
pic.stack.type="b"
28

```
> pic.plot(HairEyeColor,
           grp.xy          = "Eye ~ Hair",
           grp.color       = Sex,
           grp.pic         = Sex,
           pic.stack.type = "b",
           pic.frame       = FALSE,
           main = "grouping by x and y, by colors and by pics")
```



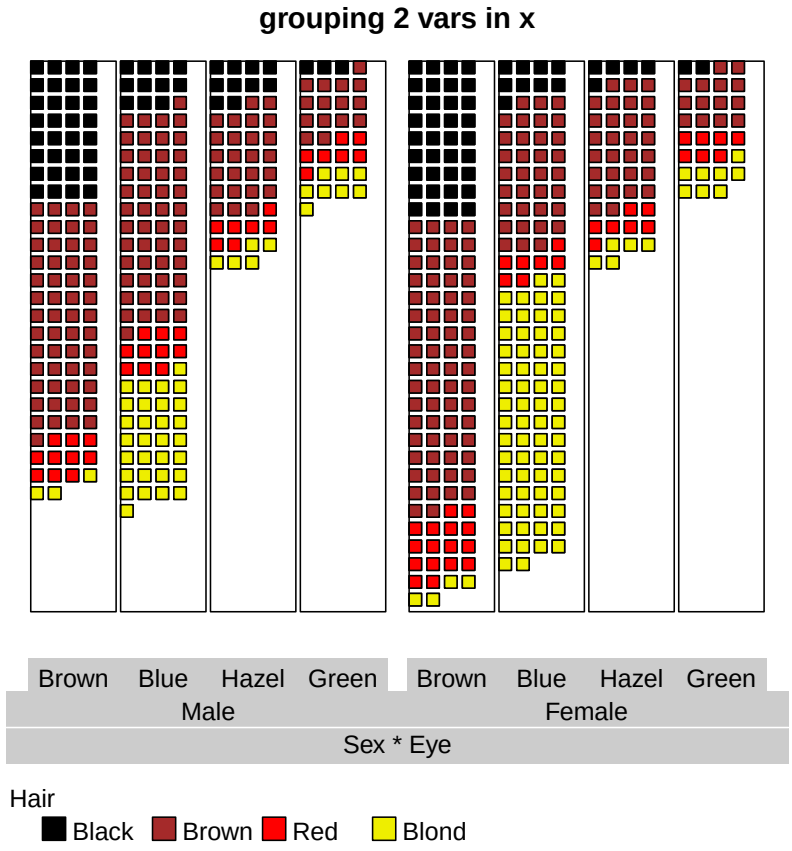
7 Multiple xy-groupings

In this section examples of multiple xy-groupings are presented based on the data set `HairEyeColor`. Let's start with a double splitting of the range of x. `Sex` and eye colors define the groupings concerning the x-axis. The third variable `Hair` is used to define the colors of the squares.

`grp.xy=~Sex+Eye`

29

```
> pic.plot(HairEyeColor,
           grp.xy          = ~ Sex + Eye,
           grp.color       = Hair,
           colors          = c("black", "brown", "red", "yellow2"),
           main = "grouping 2 vars in x")
```

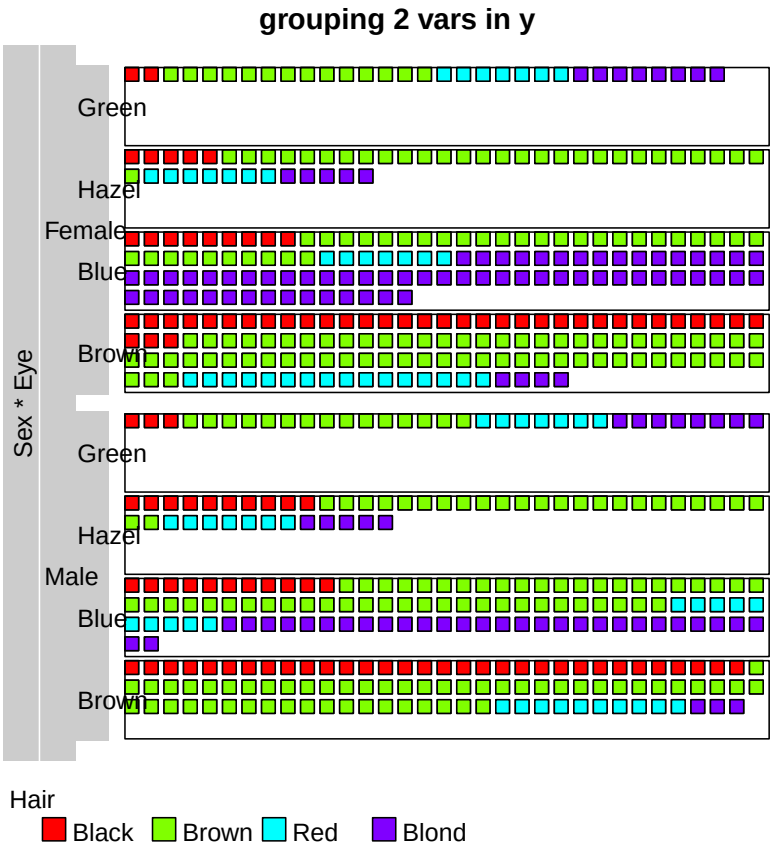


Remarks: In the call of `pic.plot()` two variables for xy-groupings have been separated by a `+` operator and it is clear that the order of the two names is important. At first the range is splitted due to the first variable on the right-hand side of the formula (`Sex`). Then each of the subranges is divided by the second variable (`Eye`).

The effect of two variables on the left-hand side of the formula is to guess easily. Here is a simple demonstration:

grp.xy=3+2~0
lab.parallel
30

```
> pic.plot(HairEyeColor,
           grp.xy         = 3 + 2 ~ 0,
           grp.color      = 1,
           lab.parallel   = c(NA, FALSE),
           main = "grouping 2 vars in y")
```

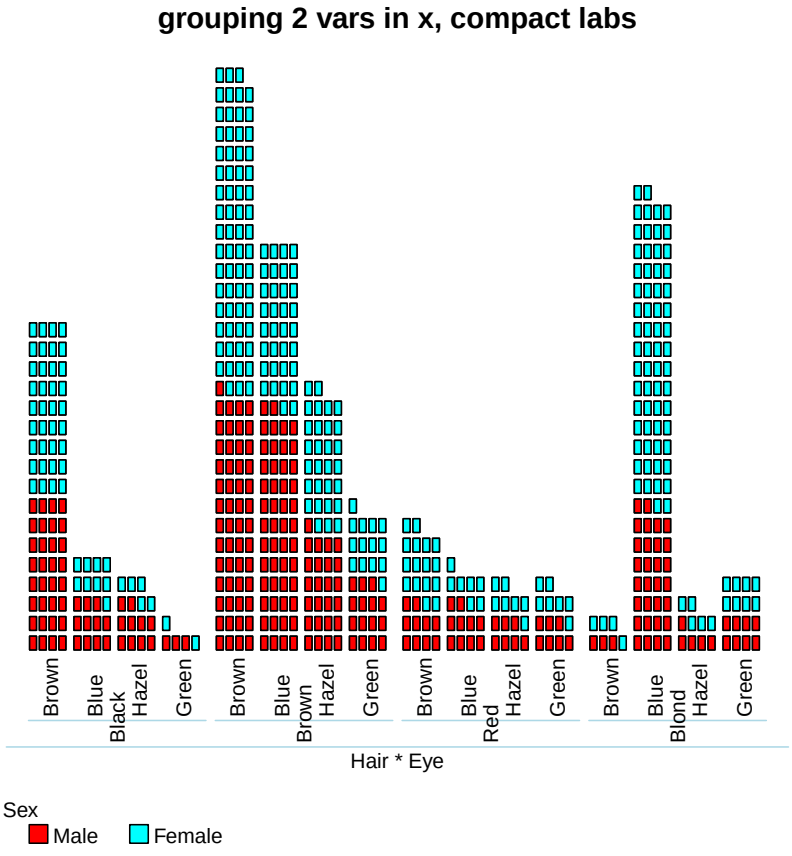


Remarks: In the grouping definitions the numbers of the variables are used. Furthermore, the second element of argument `lab.parallel` is set to `FALSE` to get margin entries of the levels that are not horizontal to the y-axis. The first argument characterizes the labeling of the x-axis and the third one controls the legend of the colors.

In the next example the output of `pic.plot()` looks like a skyline. This effect is achieved by parameters `pic.stack.type` (stacks of elements are put horizontally into the panels beginning at the bottom), `pic.aspect` (to get upright pictogram elements) and `panel.frame` (to suppress border lines).

`grp.xy=.~1+2`
`lab.boxes=0`
31

```
> pic.plot(HairEyeColor,
           grp.xy         = 0 ~ 1 + 2,
           grp.color      = 3,
           pic.stack.type = "bl",
           lab.parallel   = c(FALSE, NA),
           pic.aspect     = .5,
           panel.frame    = FALSE,
           lab.color      = "lightblue",
           lab.boxes      = 0,
           lab.cex        = 0.8,
           main = "grouping 2 vars in x, compact labs")
```

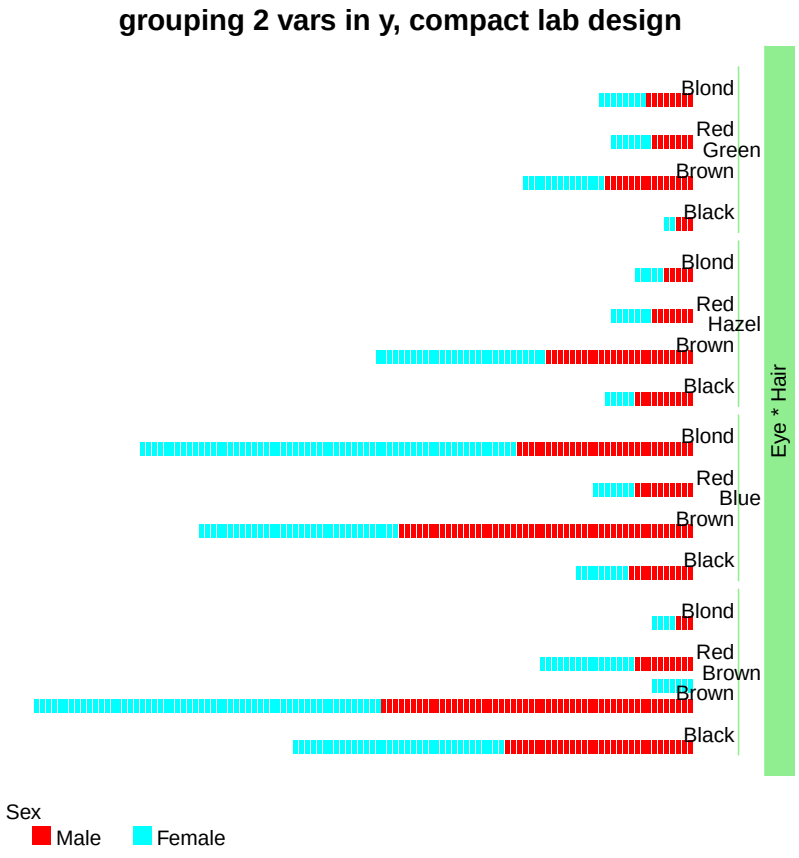


Remarks: `lab.cex` is set to 0.8 to get smaller characters in the margin texts. By `lab.boxes = 0` the boxes of the labels are reduced to thin lines. These thin lines are of color `"lightblue"` because of the argument `lab.color`.

Now the data are grouped by variables 2 and 1 and they split the y-range twice. Because of the aspect ratio of .3 the impression of a plot like a tally sheet appears.

grp.xy=2+1~.
lab.side="r"
lab.color="lightgreen"
lab.boxes=1
32

```
> pic.plot(HairEyeColor,
           grp.xy         = 2 + 1 ~ 0,
           grp.color      = 3,
           pic.aspect     = .3,
           pic.stack.type = "r",
           pic.frame      = FALSE,
           panel.frame    = FALSE,
           lab.cex        = 0.8,
           lab.boxes      = 1,
           lab.color      = "lightgreen",
           lab.side       = "r",
           lab.parallel   = c(TRUE, FALSE),
           main = "grouping 2 vars in y, compact lab design")
```



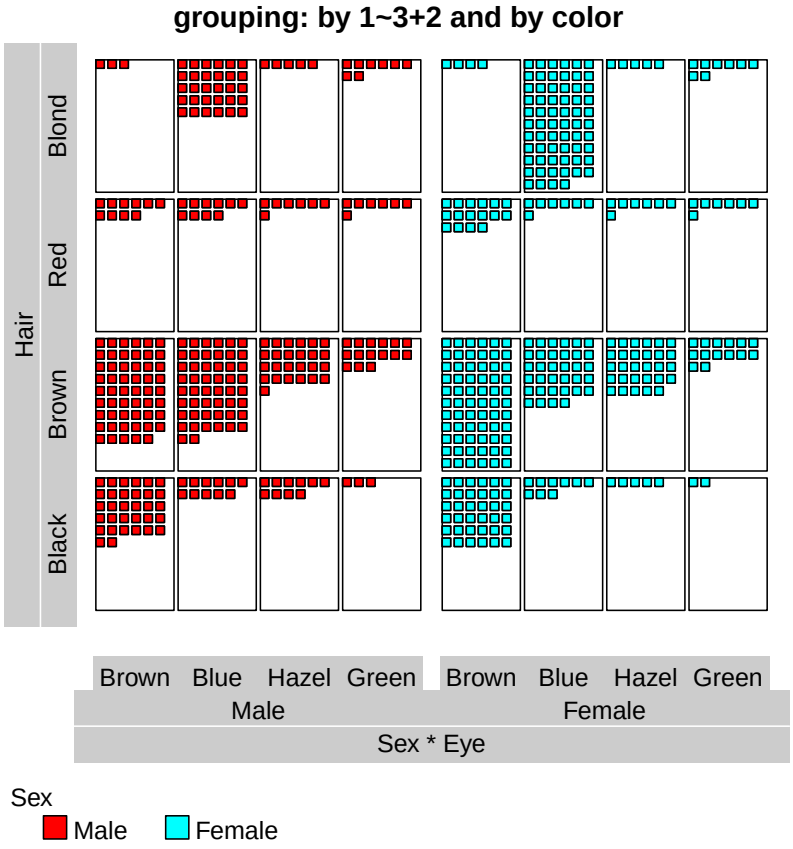
Remarks: Five of the arguments control the layout of the labels. Now the labels for the y-groupings are on the right side. By `lab.boxes = 1, lab.color = "lightgreen"` the names of the variables are placed in a green box.

A more complicated case emerges if we split one range by two and the other one by one variable.

grp.xy=1~3+2

33

```
> pic.plot(HairEyeColor,
           grp.xy          = 1 ~ 3 + 2,
           grp.color       = 3,
           main = "grouping: by 1~3+2 and by color")
>
```

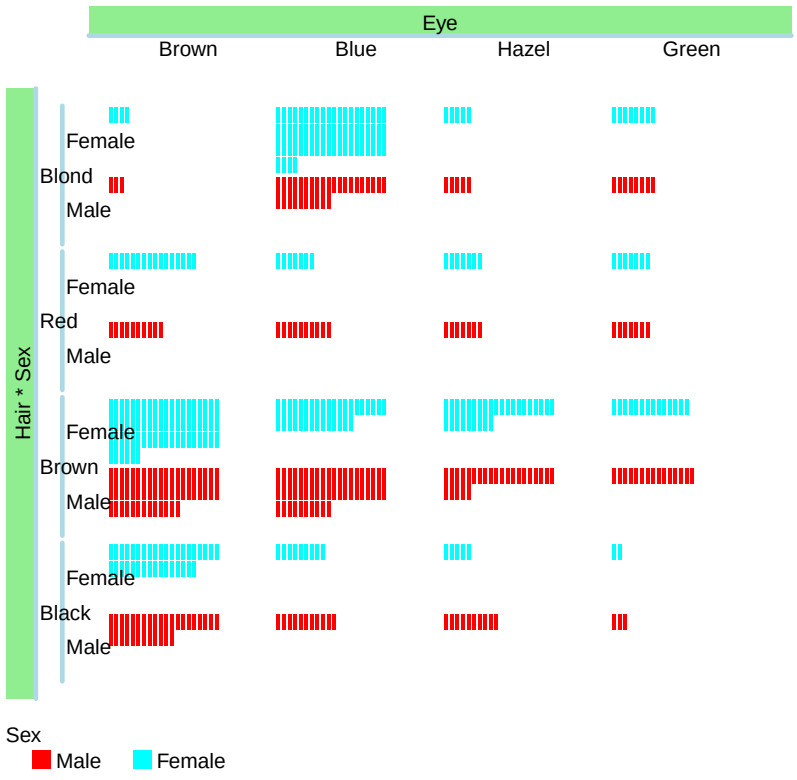


Remarks: You get this interesting plot by using three arguments of `pic.plot()` only.

Here is a variation of the groupings. By the color of the eyes the x-range is split. Sex and hair colors define the y-groupings.

grp.xy=1+3~2
pic.stack.len
lab.boxes=1.3
34

```
> pic.plot(HairEyeColor,
           grp.xy           = 1 + 3 ~ 2,
           grp.color        = 3,
           pic.aspect       = 0.25,
           pic.stack.len    = 20,
           pic.frame        = FALSE,
           pic.space.factor = c(0.3, 0.05),
           panel.frame      = FALSE,
           lab.side         = "tl",
           lab.boxes        = 1.3,
           lab.color        = c("lightgreen", "lightblue"),
           lab.parallel     = c(TRUE, FALSE),
           lab.cex          = 0.8,
           main = "grouping: 1+3~2 and by color, margin labs variations")
```



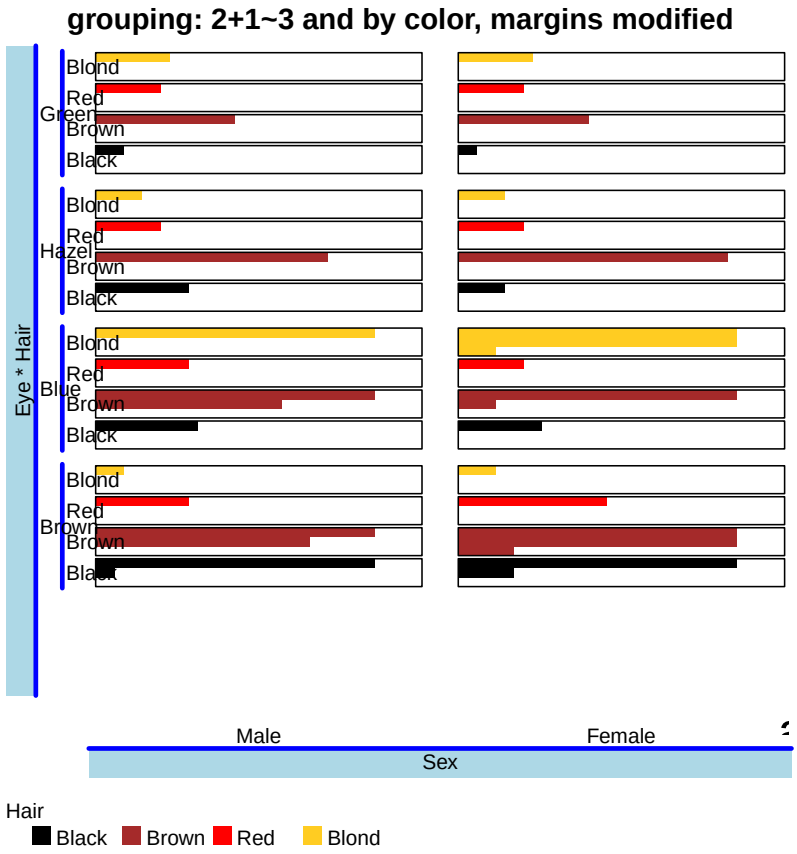
grouping: 1+3~2 and by color, margin labs variations

Remark: The margins on the left and on the top side are filled by labels. The stack length is limited to 20 so that the appearance of a table for counting scores occurs. `lab.boxes` and `lab.color` define sizes and coloring of the margin areas.

Sometimes you need some space to write additional information into the plot. By argument `panel.margin` you can set margins around the area of the panels.

grp.xy=2+1~3
panel.space.factor
panel.margin
35

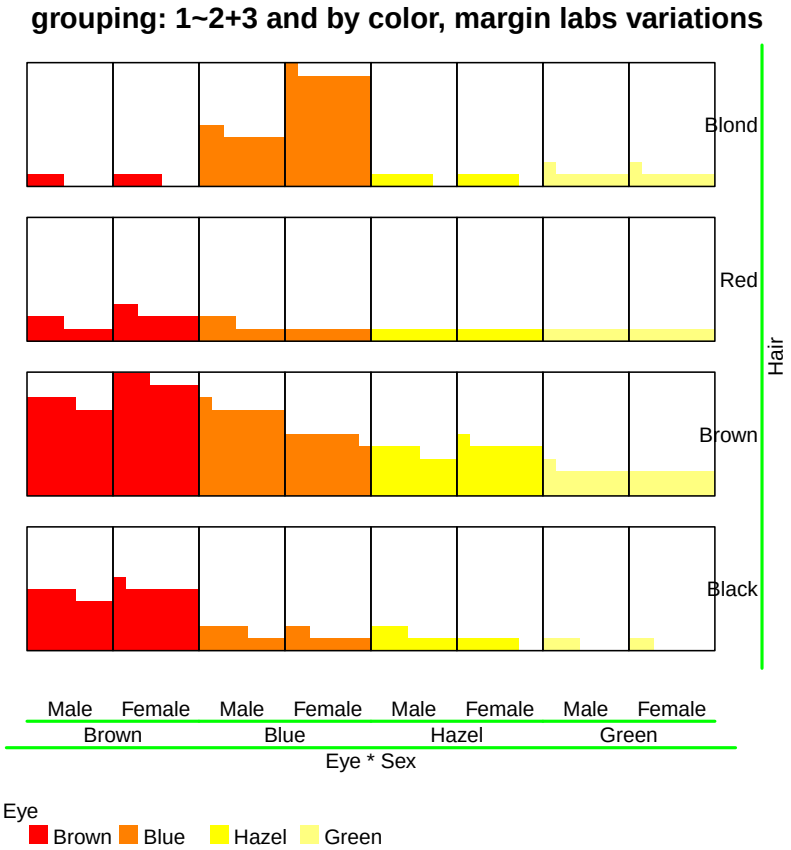
```
> pic.plot(HairEyeColor,
           grp.xy             = 2 + 1 ~ 3,
           grp.color          = 1,
           colors             = c("black", "brown", "red", "#FFCC22"),
           pic.stack.type     = "lt",
           pic.frame          = FALSE,
           pic.stack.len      = 30,
           pic.space.factor   = 0.0,
           panel.space.factor = c(0.1, 0.1),
           panel.margin       = c(0.2, 0.01, 0.01, 0.01),
           lab.parallel       = c(TRUE, FALSE),
           lab.color          = c("lightblue", "blue"),
           lab.side           = "bl",
           lab.boxes          = 1.3,
           lab.cex            = 0.8,
           main = "grouping: 2+1~3 and by color, margins modified")
> text(1.5, 0, "additional info in additional space", cex = 2)
```



Remarks: Additional information has been added by `text()`. You can call `axis()` to get an idea of the coordinate system at work. By the call of `locator()` you are able to find x and y values of suitable positions.

The next example looks like a profile or a time series plot. The color encoding of variable 2 is defined by `heat.colors()`.

```
> pic.plot(HairEyeColor,
           grp.xy             = 1 ~ 2 + 3,
           grp.color          = 2,
           colors             = heat.colors(4),
           pic.stack.type     = "lb",
           pic.stack.len      = 7,
           pic.space.factor   = 0.0,
           pic.frame          = FALSE,
           panel.space.factor = c(0, 0.2),
           lab.parallel       = c(TRUE, FALSE),
           lab.color          = c("lightblue", "green"),
           lab.side           = "br",
           lab.boxes          = 0.2,
           lab.cex            = 0.8,
           main = "grouping: 1~2+3 and by color, margin labs variations")
```



Remarks: Sometimes it is necessary to make a few experiments to find out which combinations of parameter settings work well. You have to consider that the graphical device has a great influence on sizes. Therefore, it is not sufficient to decide on the output in an `x11` device for example.

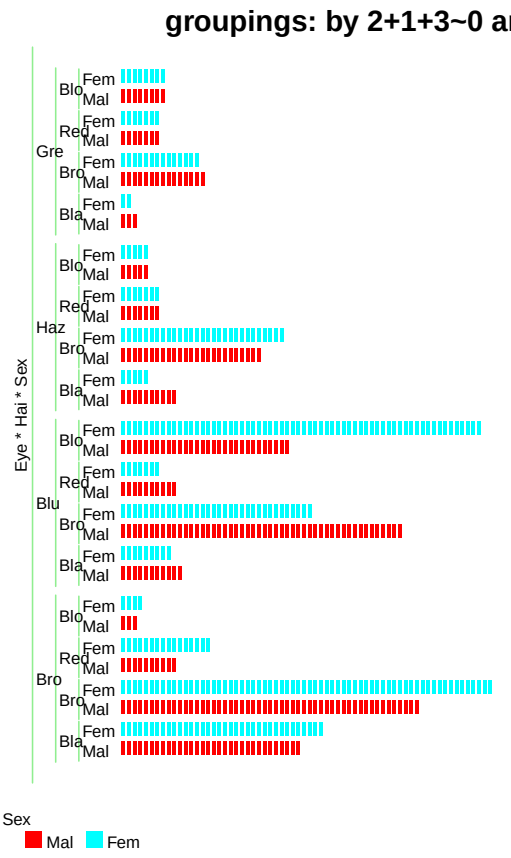
lab.side="br"
pic.stack.type="lb"

36

Now the y-range is split three times by three variables. `pic.plot` is able to handle more than three y-groupings. But usually this isn't a good idea because mostly the plotting area is to small or the size of the elements gets too tiny.

`grp.xy=2+1+3~0`
`lab.n.max`
37

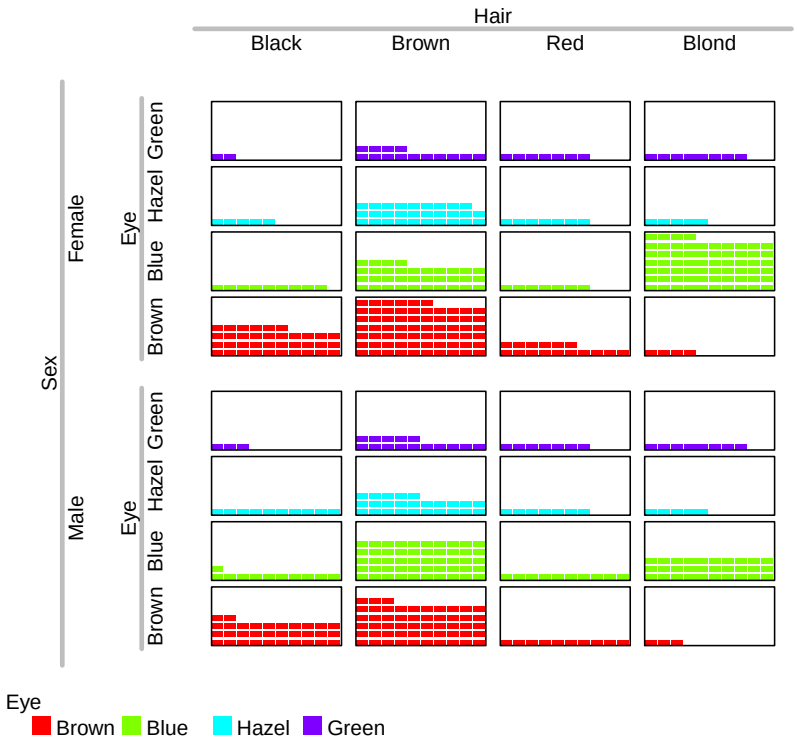
```
> pic.plot(HairEyeColor,
           grp.xy         = 2 + 1 + 3 ~ 0,
           grp.color      = 3,
           pic.aspect     = 0.3,
           pic.stack.type = "lt",
           pic.frame      = FALSE,
           panel.frame    = FALSE,
           lab.parallel   = c(FALSE, FALSE),
           lab.color      = "lightgreen",
           lab.boxes      = FALSE,
           lab.cex        = 0.7,
           lab.n.max      = c(3, 32),
           main = "groupings: by 2+1+3~0 and by col")
```



Remarks: The formula describing the xy-grouping is of the pattern already known. To control the number of characters of the levels we use argument `lab.n.max`: The names of levels should be cut after the third character. The second element of the argument limits the number of level entries on the last stage. For we know that there are $4 \times 2 \times 4 = 32$ cells we choose this value as the second element of `lab.n.max`.

The following example is the last one discussing the xy-groupings.

```
> pic.plot(HairEyeColor,
           grp.xy              = 3 + 2 ~ 1,
           grp.color           = 2,
           pic.stack.type      = "lb",
           pic.horizontal      = TRUE,
           pic.stack.len       = 10,
           pic.space.factor    = c(.1, .3),
           pic.aspect          = NA,
           pic.frame           = FALSE,
           panel.space.factor = 0.1,
           lab.boxes           = 0.3,
           lab.color           = "grey",
           lab.side            = "tl",
           lab.parallel        = TRUE,
           lab.cex             = 0.8,
           lab.type            = "expanded",
           main = "groupings: 3 + 2 ~ 1 and by color")
```



groupings: 3 + 2 ~ 1 and by color

Remarks: Inspecting the labeling of the margin of the left side you see another type of labeling (`expanded`). Moreover, `pic.aspect` is set to `NA` which causes the function to select an optimal aspect ratio. As a consequence some of the panels are filled almost completely.

`lab.type="expanded"`
`pic.aspect=NA`

8 Data Input and Transformations

`pic.plot()` aims at visualizing data matrices or contingency tables. During the checking of arguments tables are expanded to data frames keeping the original observations. By default the variables of the data frames will be converted to factors by calling `factor()`.

Using argument `vars.to.factors` you can control the process of transformation. Element `i` of this variable defines how variable `i` of the data is treated. A value of 0 (or `FALSE`) skips the transformation step. A value greater 1 invokes the functions `cut()` and the range of the variable is cut in `floor(vars.to.factors)` intervals of equal size. A value lower 1 leads to classes each containing approximately `vars.to.factors * 100` percent of the data. The default case corresponds to a value of 1 (or `TRUE`). If numerical data are not transformed to factors strange results may be occur. For more information see the help page of `pic.plot()`.

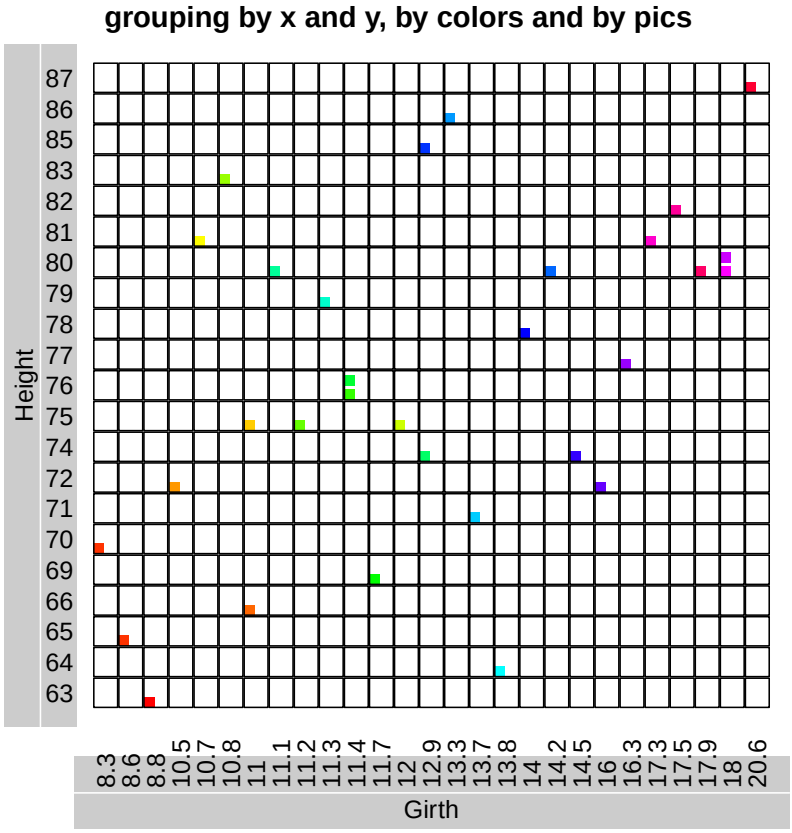
In this section we use the data set `trees` usually available in R. This data frame shows the values of the variables `Girth`, `Height` and `Volume` of 31 trees.

In the first example of this section we apply `pic.plot()` to the numerical matrix `tree` without specifying `vars.to.factors`. Therefore, the variables are transformed by `factor` and we get a lot of levels.

`vars.to.factors`

39

```
> pic.plot(trees,
           grp.xy         = Height ~ Girth,
           grp.color      = Volume,
           pic.stack.type = "b",
           pic.frame      = FALSE,
           lab.parallel   = c(FALSE, FALSE),
           main = "grouping by x and y, by colors and by pics")
```



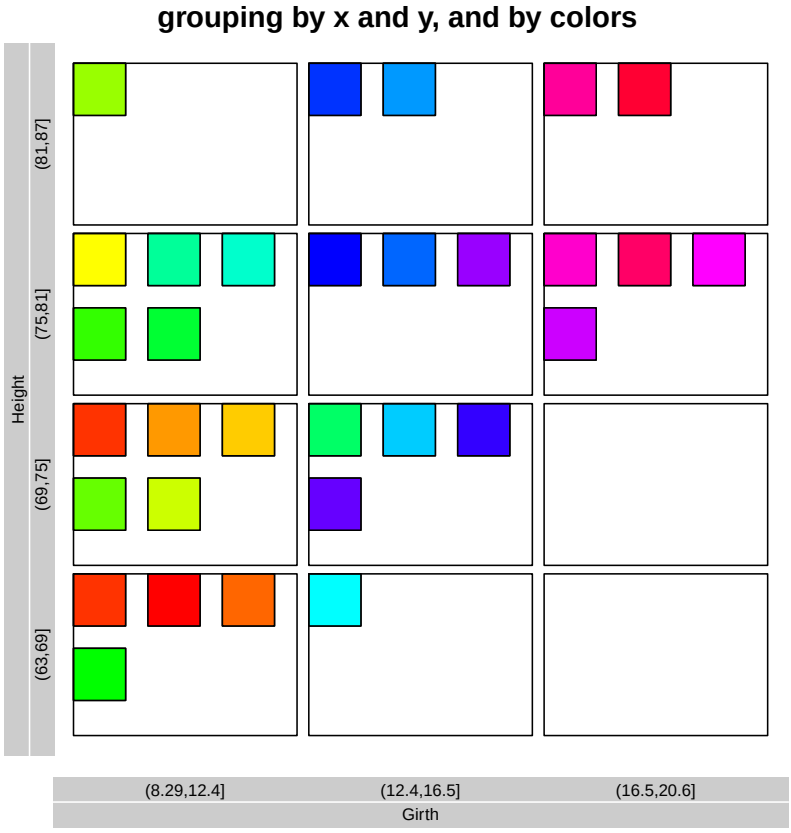
Remarks: Without setting `vars.to.factors` we get a plot that looks like a scatterplot. However it is a pictogram plot showing 27×21 panels and 31 observations. Each panels belongs to a combination of two levels of two factor variables arisen from the variables `Girth` and `Height`. To reduce the number of fewer empty panels we can envoke `vars.to.factors`.

As a consequence of the last example we split the range of the first variable into three intervals and the other one into four subranges.

vars.to.factors = c(3, 4)

40

```
> pic.plot(trees,
           grp.xy         = Height ~ Girth,
           grp.color      = Volume,
           vars.to.factor = c(3, 4),
           lab.cex        = 0.7,
           main = "grouping by x and y, and by colors")
```



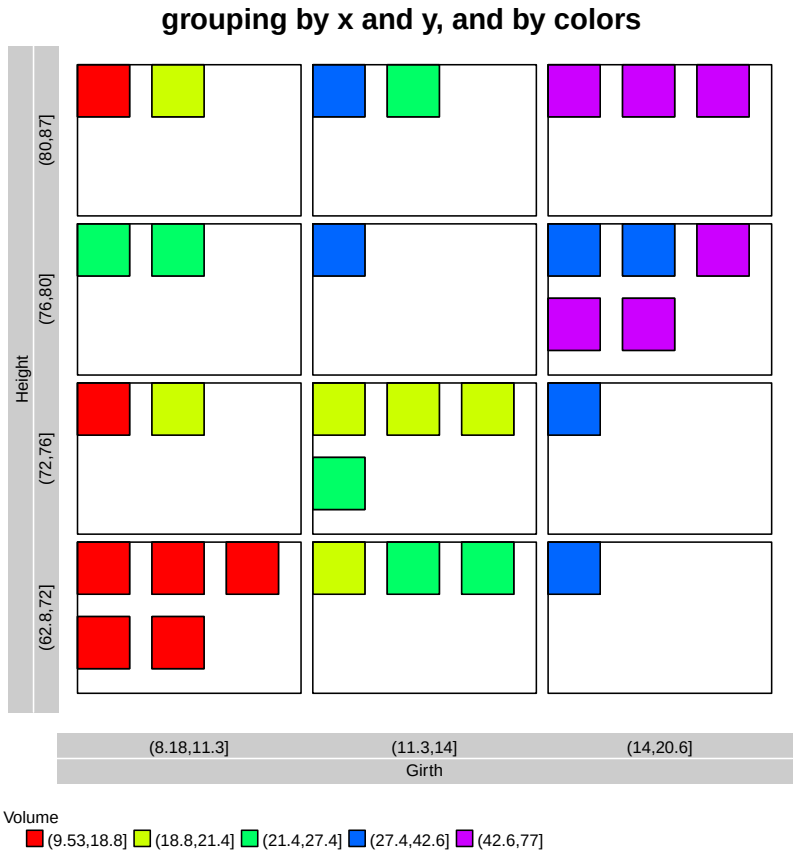
Remarks: Now we have a nice summary of the data in form of a graphical table. You see there are a lot of colors. Maybe you miss the legend explaining the colors. It has been decided to skip the legend in case of too many entries.

Now let's see what happens if the number of elements in the intervals is nearly the same. For this we assign fractions to the `vars.to.factor` argument and get a slightly modified output. In this example the third variable is split into `5 = 1/.2` intervals. You can check that there are approximately 6 ($\approx 31/5$) pictogram elements of each color.

`vars.to.factors = 1 / c(3, 4, 5)`

41

```
> pic.plot(trees,
           grp.xy         = Height ~ Girth,
           grp.color      = Volume,
           vars.to.factor = 1 / c(3, 4, 5),
           lab.cex        = 0.7,
           main = "grouping by x and y, and by colors")
```

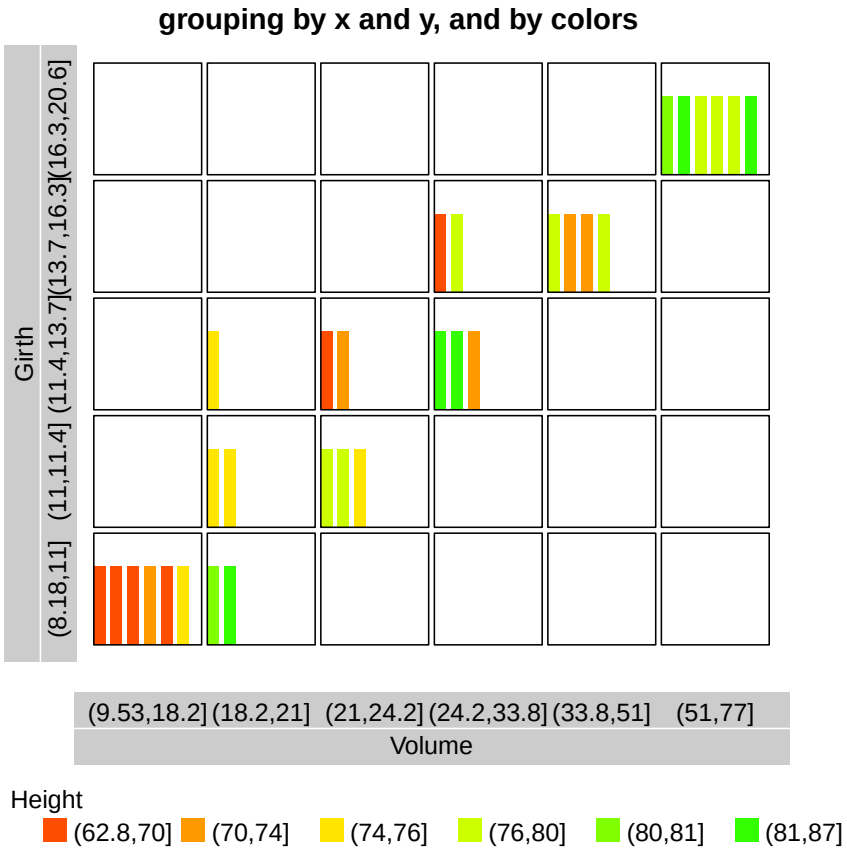


Remarks: We recognize the obvious dependencies of the three variables. Usually a scatterplot offers the structure within the data in a better way. However, sometimes the reduction of precision may help to see the point.

In the last example of this section we split the horizontal range by variable `Volume` and the y-range by `Girth`. The colors are defined by `Height`.

42

```
> pic.plot(trees,
           grp.xy          = Girth ~ Volume,
           grp.color       = Height,
           vars.to.factors = 1/c(5, 6, 6),
           colors          = rainbow(6, start = 0.05, end = 0.3),
           pic.frame       = FALSE,
           pic.stack.type  = "b",
           pic.aspect      = 0.15,
           panel.frame     = TRUE,
           main = "grouping by x and y, and by colors")
```



Remarks: We see the dependency between `Volume` and `Girth`. It is interesting that there are two tall trees belonging to the class of the smallest `Girth`.

9 Panels proportional to frequencies

Up to now we have constructed panels of equal sizes. But there are arguments that the sizes of the panels should sometimes differ. At first the number of pictograms in the panels may be very unbalanced. In such a case it may be preferred to modify the heights and the widths of the panels. Secondly, referring to the statistical concept of expectation we can propose panel sizes that are proportional to the expected numbers presuming independent variables. Then we are able to see in which of the fields size and number of pictogram don't fit very well.

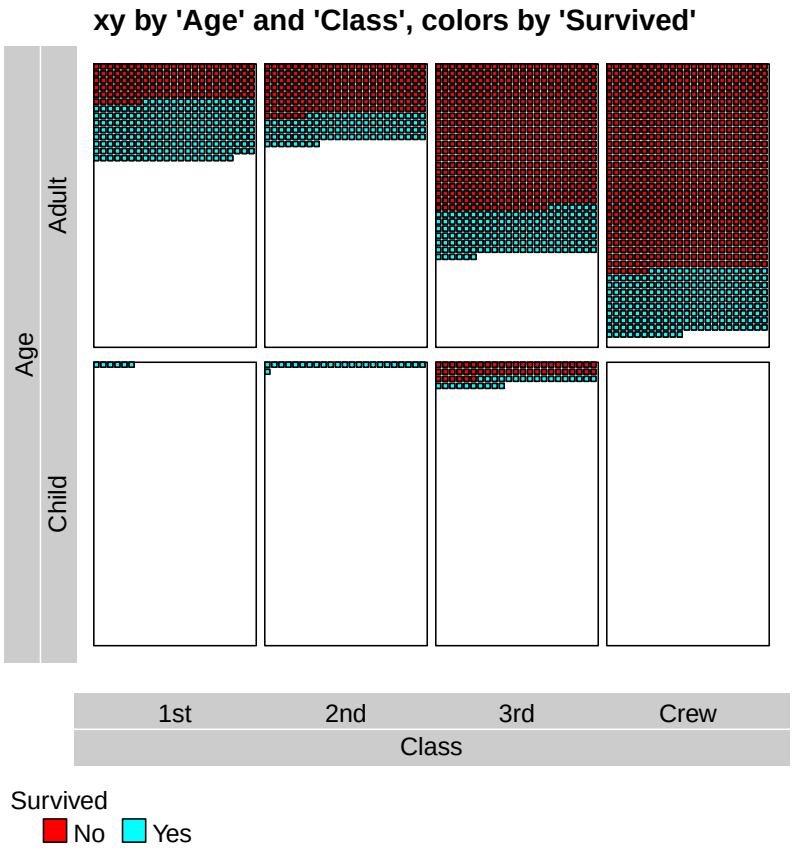
The famous Titanic data set works fine to demonstrate this idea. This contingency table consists of dimensions `"Class", "Sex", "Age", "Survived"`:

```
$Class
[1] "1st"  "2nd"  "3rd"  "Crew"

$Sex
[1] "Male"   "Female"

$Age
[1] "Child" "Adult"

$Survived
[1] "No"  "Yes"
```

Let's start with a simple `pic.plot()` of the data set `Titanic`.

`Titanic`
43

```
> pic.plot(Titanic,
           grp.xy          = Age ~ Class,
           grp.color       = Survived,
           main = "xy by 'Age' and 'Class', colors by 'Survived'")
```



Remarks: Three of the four dimensions of the data set are represented in the pictogram plot. The color `red` has been choosen for persons not having survived the disaster. Four of the eight panels are nearly empty. Therefore, we would like to be able to control the sizes of the panels.

In the second example all of the four variables have been used in defining `grp.xy` and `grp.color`.

`pic.stack.type="b"`

44

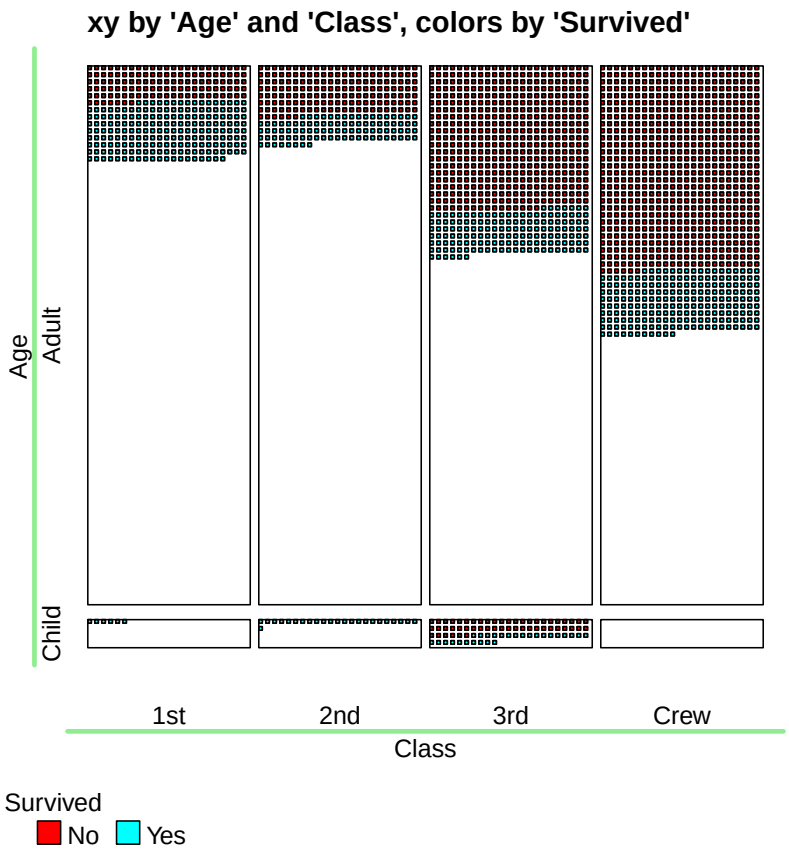
```
> pic.plot(Titanic,
           grp.xy          = Survived ~ Class + Sex,
           grp.color       = Age,
           colors          = c("red", "lightblue"),
           pic.stack.type  = "b",
           pic.frame       = FALSE,
           pic.space.factor= 0.5,
           panel.frame     = FALSE,
           lab.boxes       = 0.3,
           lab.color       = "lightgreen",
           main = "x by 'Class*Sex', y by 'Survived', colors by 'Age'")
```

Remarks: The data set contains 2201 elements. Therefore, the space to represent a single one is very small. Additionally you may want to divide the whole plotting region in a different way. For there are more people that didn't survive the upper row of panels could be a little bit smaller.

Now we tackle the first problem by changing the sizes of the panels. In the x-direction the panels should remain of equal size. However, the heights are chosen in a way that ratios are equal to the ratios of children and adults in the data set. To meet this requirement we set `panel.prop.to.size = c(FALSE,TRUE)`. The first entry defines the treatment of the widths and the second one that of the heights.

`panel.prop.to.size = c(FALSE,TRUE)`
45

```
> pic.plot(Titanic,
           grp.xy             = Age ~ Class,
           grp.color          = Survived,
           pic.space.factor   = 0.5,
           panel.prop.to.size = c(FALSE, TRUE),
           lab.boxes          = 0.3,
           lab.color          = "lightgreen",
           main = "xy by 'Age' and 'Class', colors by 'Survived'")
```



Remarks: Indeed, now the layout of the plot is much better and the pictogram elements are somewhat increased.

Assuming independent variables the expected numbers of a two dimensional table are proportional to the product of the margin entries:

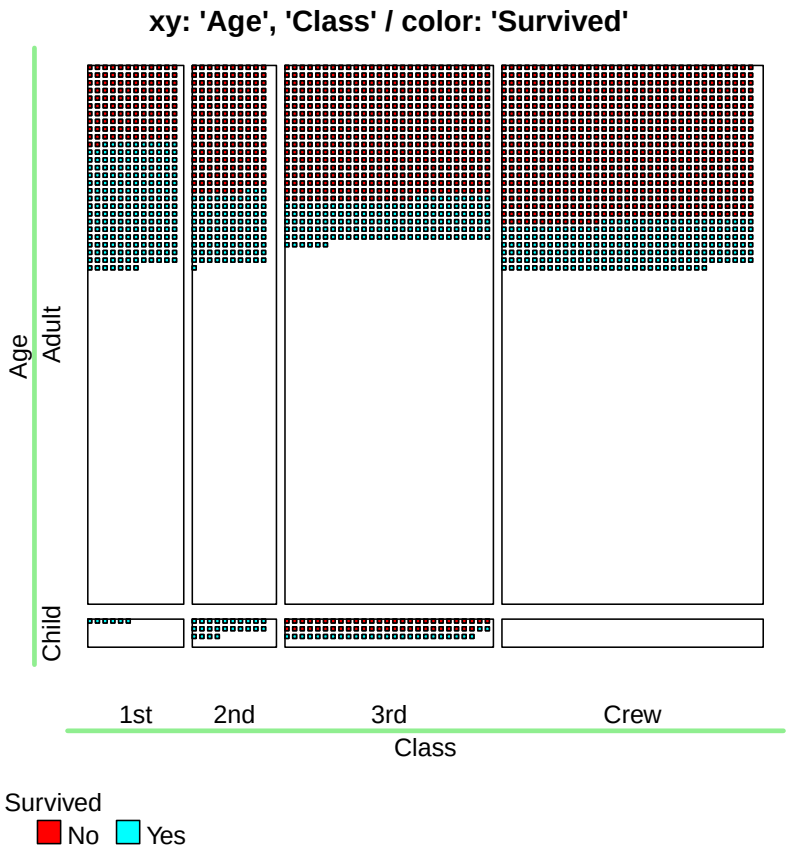
$$\tilde{n}_{ij} = \frac{n_{i\bullet} n_{\bullet j}}{n}$$

Therefore, if we choose the heights and the widths proportional to the margin entries we get panels whose areas are proportional to the expectations in case of independence. By setting both elements of `panel.prop.to.size` to `TRUE` we can implement this idea. Let's check the effect by a minimal modification of the last example.

`panel.prop.to.size = c(TRUE,TRUE)`

46

```
> pic.plot(Titanic,
           grp.xy             = Age ~ Class,
           grp.color          = Survived,
           pic.space.factor   = 0.5,
           panel.prop.to.size = c(TRUE, TRUE), # <-
           lab.boxes          = 0.3,
           lab.color          = "lightgreen",
           main = "xy: 'Age', 'Class' / color: 'Survived'")
```

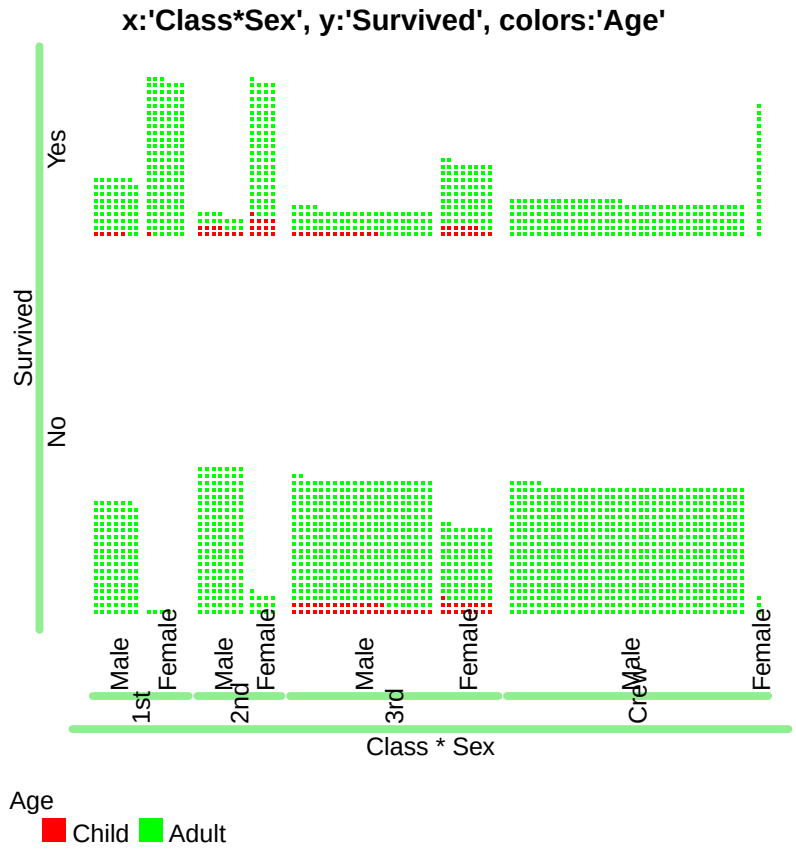


Remarks: Boxes being filled nearly completely contain numbers that are above the expectation. A box with a lot of white space indicates that the number of elements is lower than expected under the assumption of independent variables. As an extreme example the field (Crew × Child) is empty. Based on the assumption and the margins we would expect a positive number. But knowing the semantic background of the variables it is clear that there are no children among the members of the crew.

What happens if there are more than two dimensions? To answer this question we modify the second example of this section.

grp.xy=4~1+2
panel.prop.to.size
47

```
> pic.plot(Titanic,
           grp.xy             = Survived ~ Class + Sex,
           grp.color          = Age,
           colors             = c("red", "green"),
           pic.stack.type     = "b",
           pic.frame          = FALSE,
           pic.space.factor   = 0.5,
           panel.prop.to.size = c(TRUE, TRUE, TRUE),
           panel.frame        = FALSE,
           lab.boxes          = 0.5,
           lab.parallel       = c(FALSE, TRUE, TRUE),
           lab.color          = "lightgreen",
           main = "x:'Class*Sex', y:'Survived', colors:'Age'")
```



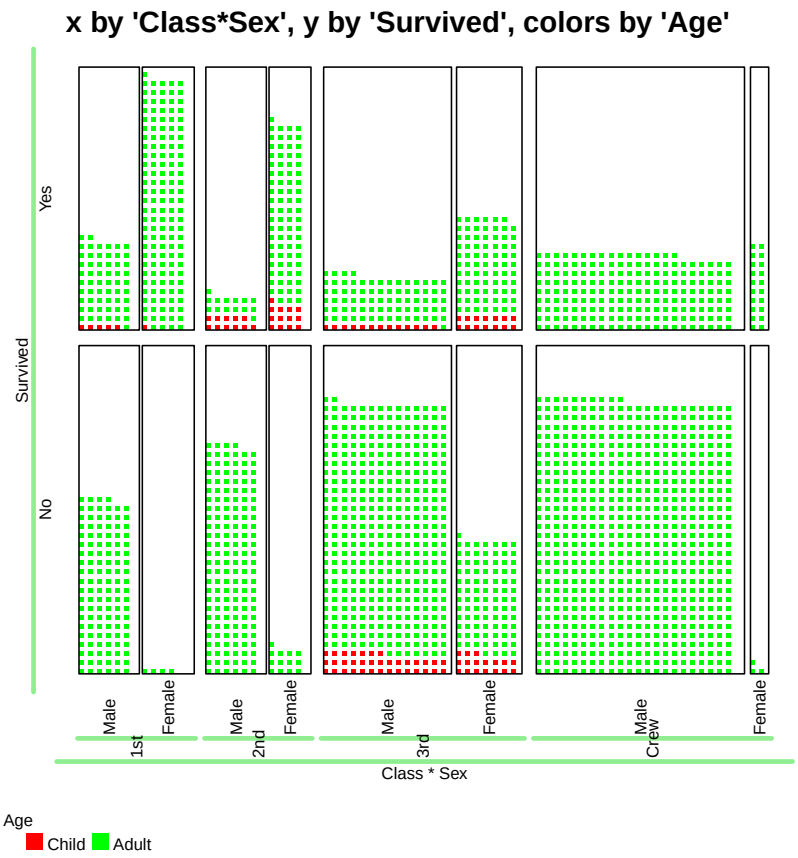
Remarks: We wonder why there is so much white space in the plot. But an inspection reveals that the second and fourth panel in the upper line of panels are nearly filled up to their limits. If you are not convinced set `panel.frame = TRUE` and you get the argument.

Often you are not driven questions of expectations but arguments of the layout matter. Then you can supply `panel.prop.to.size` with numerical values. A value out of the interval (0,1) results in a compromise between equal sizes and sizes induced by expectation values. Values greater one increase the boxes of the panels. Have a look at the following plot:

`panel.prop.to.size = c(0.7, 0.3)`

48

```
> pic.plot(Titanic,
           grp.xy              = Survived ~ Class + Sex,
           grp.color           = Age,
           colors              = c("red", "green"),
           pic.stack.type      = "b",
           pic.frame           = FALSE,
           pic.space.factor    = 0.5,
           panel.prop.to.size  = c(0.7, 0.3),              # <- changed
           panel.frame         = TRUE,                     # <- changed
           lab.boxes           = 0.3,
           lab.parallel        = c(FALSE, TRUE, TRUE),
           lab.color           = "lightgreen",
           lab.cex             = 0.7,
           main = "x by 'Class*Sex', y by 'Survived', colors by 'Age'")
```

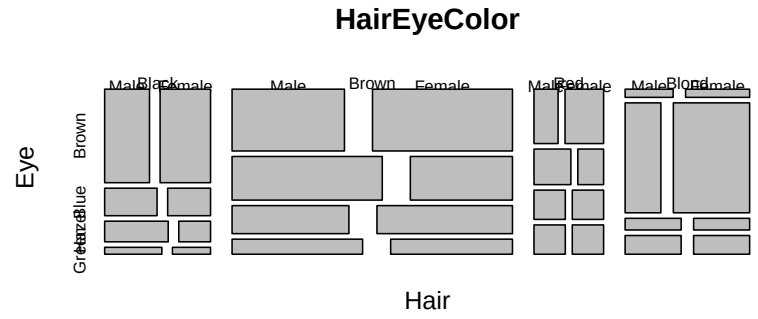


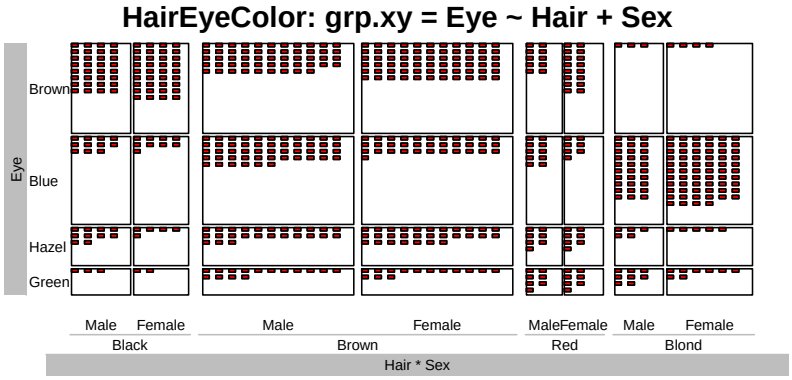
Remarks: The lines of the call containing a comment character have been changed. Now the panels are filled quite good. You are welcome to play with the arguments to get improved diagrams of the data set.

As a last application in this section we construct a pictogram plot and compare it to a simple `mosaicplot()`. The good old `HairEyeColor` serves as data source.

mosaicplot()
49

```
> par(mfrow = 2:1)
> mosaicplot(HairEyeColor)
> pic.plot(HairEyeColor,
           grp.xy             = Eye ~ Hair + Sex,
           lab.parallel       = c(TRUE, FALSE),
           colors             = "red",
           pic.space.factor   = 0.5,
           pic.aspect         = 2,
           panel.reverse.y    = TRUE,
           panel.prop.to.size = TRUE,
           lab.cex            = 0.6,
           lab.boxes          = 1,
           lab.color          = "grey",
           panel.margin       = c(0.00,.035,0.0,.050),
           main = 'HairEyeColor: grp.xy = Eye ~ Hair + Sex')
> par(mfrow=c(1,1))
```





Remarks: The arguments of `pic.plot` have been chosen in a way that the size and appearance fits to the properties of the Mosaic-Plot. Maybe friends of Mosaic-Plots prefer them. But on the other side a lot of people may like to see the sets of individuals. Anyway, with the function `pic.plot()` they can now use the pictogram approach or both of the proposals. Perhaps the expectation arguments support the new approach.

10 Larger units and fractional numbers

Sometimes the numbers of elements in the cells of a table are very huge. The Titanic data contain a cell with entry 670. Counts belonging to the subpopulations of a country often exceed 1.000.000. In these cases it is helpful to change the units. E. g. you can count members of nations in millions. Or for the Titanic data we can choose a unit of 10 people.

As a consequence fractional numbers occur in the cells of a table. The function `pic.plot()` is able to handle fractional numbers of tables. The representation of the fractional parts of numbers is realized by scaling the pictogram elements.

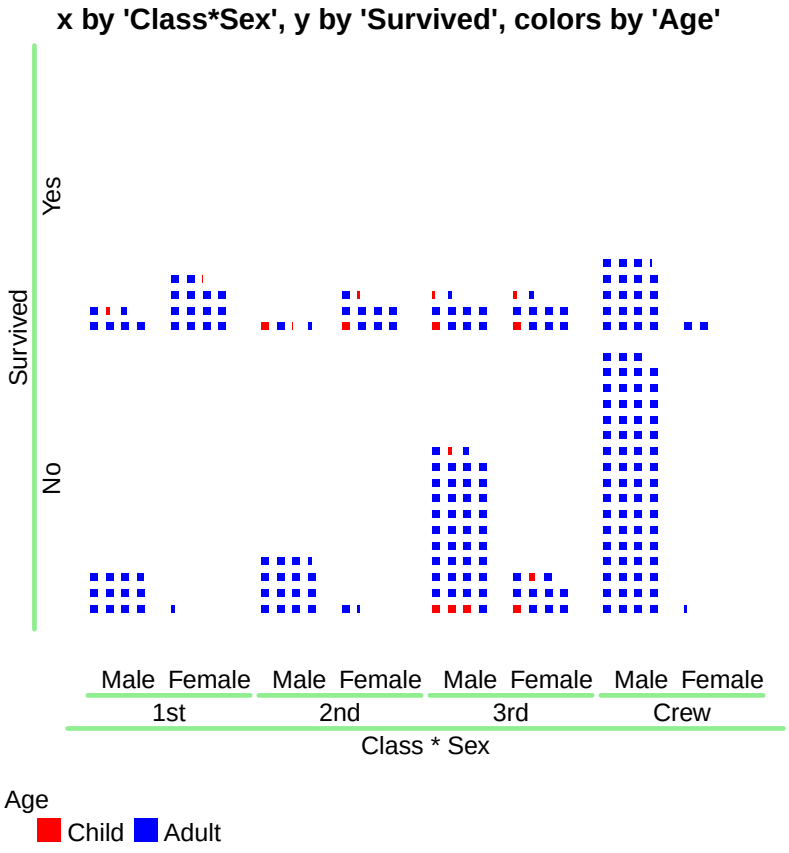
First, we see an application based on the Titanic data set whose entries are divided by 10.

Let's recall the second example of the last section using unit *10 persons*.

```
Titanic / 10
```

```
50
```

```
> pic.plot(Titanic / 10,
           grp.xy          = Survived ~ Class + Sex,
           grp.color       = Age,
           colors          = c("red", "blue"),
           pic.stack.type  = "b",
           pic.frame       = FALSE,
           pic.space.factor= 0.5,
           panel.frame     = FALSE,
           lab.boxes       = 0.3,
           lab.color       = "lightgreen",
           main = "x by 'Class*Sex', y by 'Survived', colors by 'Age'")
```

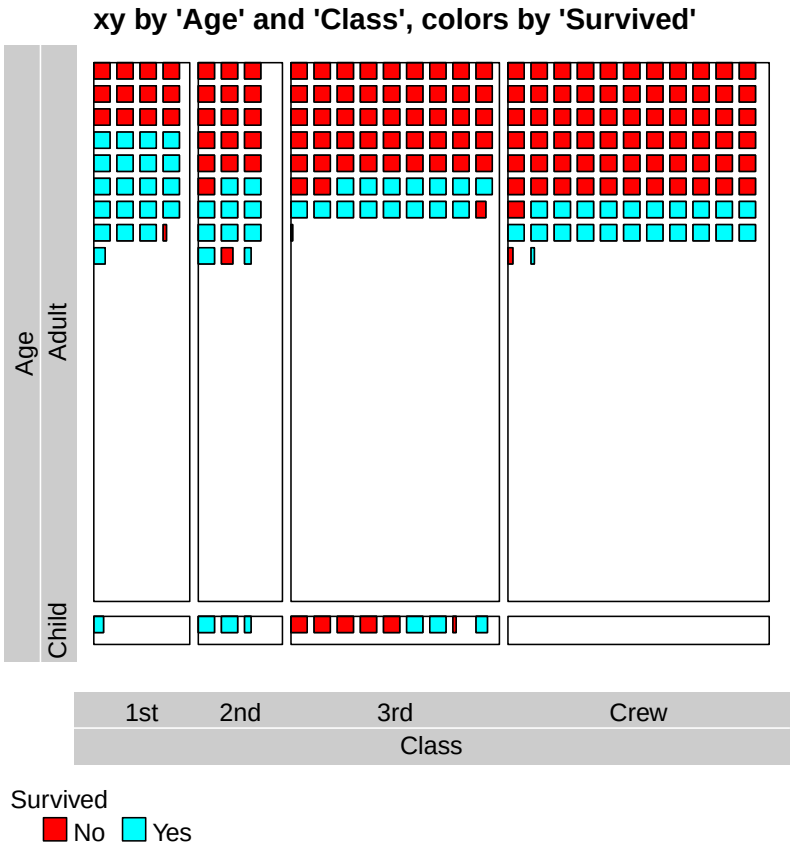


Remarks: We get the same structure as with the unit *1 person*. But now the number of pictogram elements is smaller and the single elements are distinguishable to a larger extent. The fractional parts are represented by pictograms with smaller widths. For in each of the panels we summarize the entries of the two levels of variable `Age` there are two fractional numbers and two smaller pictograms per panel. Even if we don't set `grp.color = 3` the number of (fractional) pictogram elements remains. If you want to join the smaller elements, you have to find the proper marginal table (by `margin.table()`) and use the reduced table as input of `pic.plot()`.

As a second example we modify the call of the first example of the last section. Setting the `panel.prop.to.size` and using the data of the previous data set we get:

`Titanic / 10`
`panel.prop.to.size`
51

```
> pic.plot(Titanic / 10,
           grp.xy             = Age ~ Class,
           grp.color          = Survived,
           panel.prop.to.size = c(TRUE, TRUE),
           main = "xy by 'Age' and 'Class', colors by 'Survived'")
```

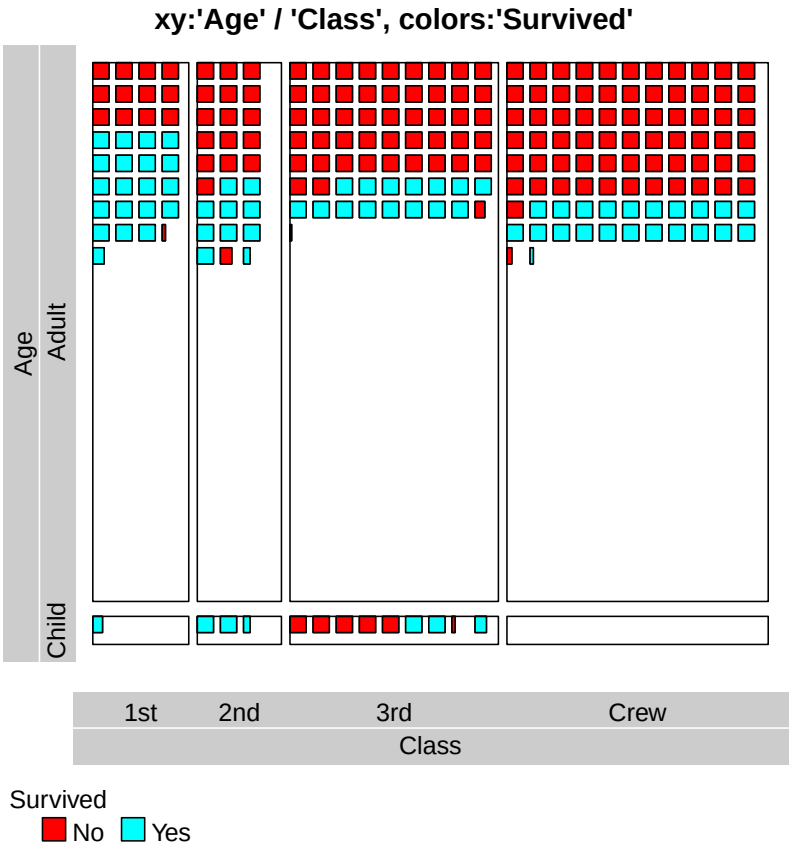


Remarks: Now in each of the eight panels four combinations of the levels of two variables (`Sex, Survived`) are combined. Therefore, we get up to four smaller pictograms per panel.

An alternative approach is to compute a suitable margin table at first. We proceed in this way and set `panel.prop.to.size` again:

`margin.table(..)` 52

```
> pic.plot(margin.table(Titanic / 10, c(1, 3, 4)),
           grp.xy             = Age ~ Class,
           grp.color          = Survived,
           panel.prop.to.size = c(TRUE, TRUE),
           main = "xy:'Age' / 'Class', colors:'Survived'")
```



Remarks: For the dimension 2 has been removed we have to modify the assignments of `grp.xy` (`2~1` instead of `3~1`) and `grp.color` (3 instead of 4). Using variable names we can avoid any confusion caused by the numbers encoding the variables. Now there are one or two smaller elements per panel.

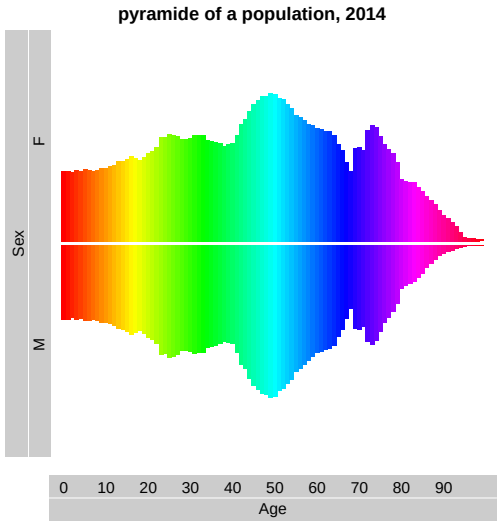
In the next example you see a pictogram plot of some age pyramid data. This plot looks nice. However, other representation may be superior.[1] 53

```
> mw <- c(350, 351, 345, 354, 349, 358, 358, 352, 356, 366, 366, 373,
    383, 399, 401, 409, 423, 417, 408, 419, 437, 446, 468, 519, 516,
    534, 526, 518, 501, 501, 503, 515, 509, 510, 487, 482, 479, 469,
    458, 463, 468, 511, 565, 587, 634, 665, 684, 705, 709, 722, 716,
    691, 679, 655, 637, 600, 585, 566, 545, 529, 509, 506, 495, 492,
    475, 433, 403, 348, 300, 399, 402, 385, 458, 471, 452, 410, 369,
    342, 314, 276, 208, 192, 180, 172, 151, 133, 106, 86, 69, 50,
    39, 33, 26, 19, 10, 5, 3, 2, 2, 2, 333, 333, 328, 337, 331, 341,
    339, 333, 338, 347, 348, 354, 362, 379, 379, 389, 401, 394, 385,
    395, 416, 427, 447, 494, 493, 508, 500, 496, 481, 482, 487, 500,
    500, 503, 480, 474, 471, 464, 451, 459, 464, 504, 555, 577, 619,
    649, 668, 687, 688, 703, 699, 679, 672, 650, 633, 598, 586, 571,
    557, 551, 535, 534, 523, 522, 503, 458, 431, 376, 333, 442, 447,
    432, 526, 552, 541, 498, 460, 439, 415, 376, 294, 284, 279, 281,
    258, 239, 211, 194, 176, 147, 124, 107, 91, 71, 42, 20, 14, 11, 10, 9)
> mw <- as.table(matrix(mw, ncol = 2,)/10)
> dimnames(mw) <- list(Age = as.character((1:nrow(mw))-1), Sex = c("M","F"))
```

pic.stack.type=
rep(c("t","b"),nrow(mw)

54

```
> pic.plot(mw,
           grp.xy             = Sex ~ Age,
           grp.color          = Age,
           pic.aspect         = 2,
           pic.stack.type     = rep(c("t", "b"), nrow(mw)),
           pic.horizontal     = FALSE,
           pic.space.factor   = 0,
           pic.frame          = FALSE,
           panel.frame        = FALSE,
           panel.space.factor = c(.0, .02),
           lab.n.max          = c(3, 10),
           main = paste("pyramide of a population, 2014"))
```



Remarks: Most of the arguments of the call have been explained above. However, a vector is assigned to argument `pic.stack.type`. The panels of the males are filled from top (`t`) whereas the others are placed beginning from the bottom side (`b`).

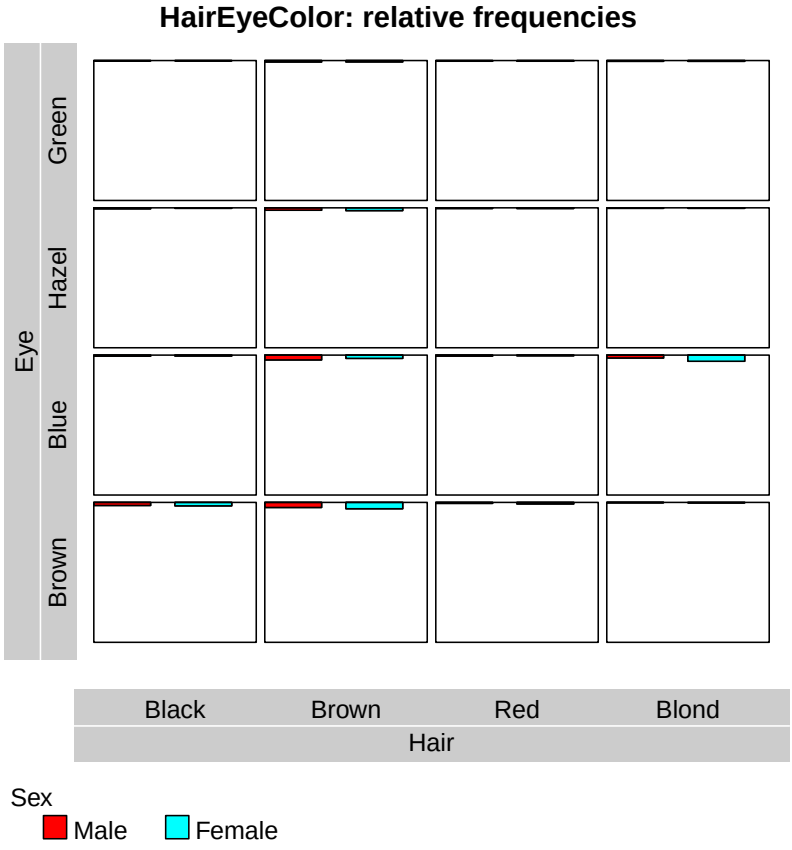
[1] Data are downloadable from page https://www.destatis.de/bevoelkerungspyramide/bev13te_v1236.csv via https://www.destatis.de/bevoelkerungspyramide/#!v=2 of the *Statistisches Bundesamt*.

A more serious question is how to represent a table containing relative frequencies. Coming back to the data set `HairEyeColor` we now show the result of handing a table with numbers out of $[0, 1]$ over to `pic.plot()`

relative frequencies

55

```
> pic.plot(HairEyeColor / sum(HairEyeColor),
           grp.xy         = Eye ~ Hair,
           grp.color      = Sex,
           pic.horizontal = FALSE,
           main = paste("HairEyeColor: relative frequencies"))
```



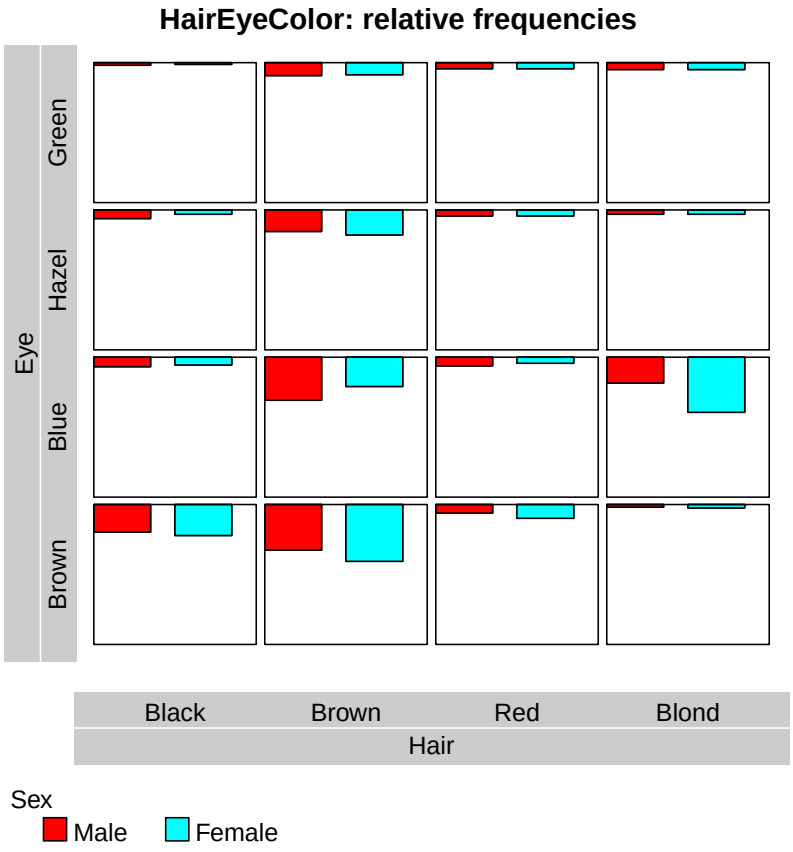
Remarks: The algorithm that looks for the best size of pictograms is based on the pictograms representing one unit and not fractional parts of a unit. Therefore, the pictograms of the values lower one often are of very tiny size. To overcome this fact you can adjust some of the arguments to get an improved output.

Instead of experimenting with different combinations of argument settings it is recommendable to scale the data:

dividing by max(data)

56

```
> pic.plot(HairEyeColor / max(HairEyeColor),
           grp.xy         = Eye ~ Hair,
           grp.color      = Sex,
           pic.horizontal = FALSE,
           main = paste("HairEyeColor: relative frequencies"))
```

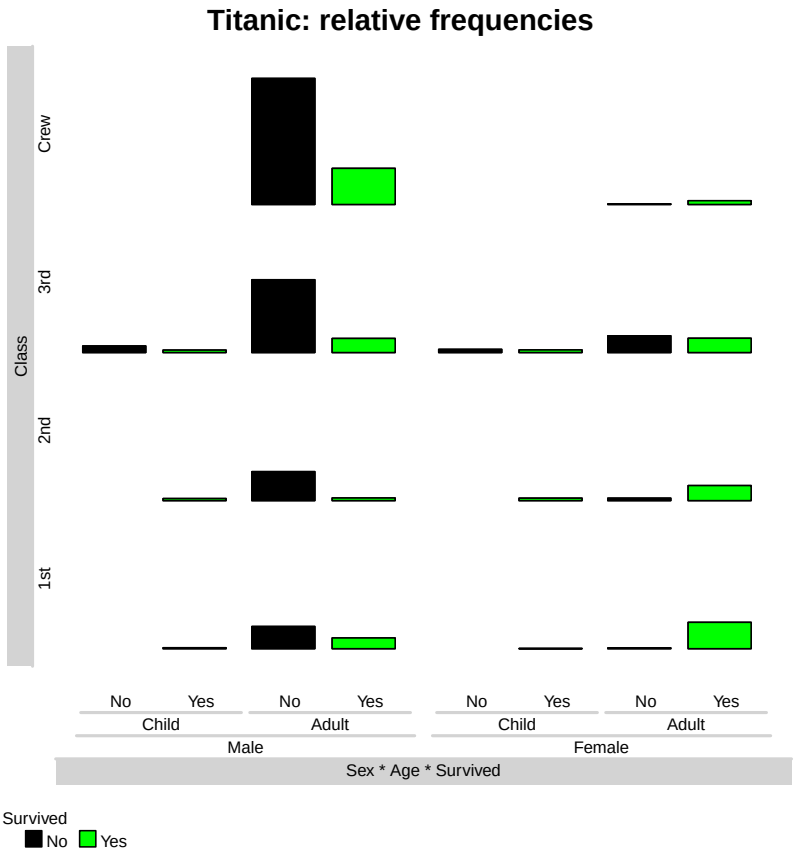


Remarks: As you can see the scaling trick works. By the way: for the stacks of pictograms are placed vertically into the panel fields the sizes of the fractions result in different heights of the pictogram elements and not in different widths.

We finish this section by an example computed from the Titanic data.

Titanic
dividing by max(data)
57

```
> pic.plot(Titanic / max(Titanic),
           grp.xy             = Class ~ Sex + Age + Survived,
           grp.color          = Survived,
           colors             = c("black", "green"),
           pic.stack.type     = "b",
           pic.horizontal     = FALSE,
           panel.frame        = FALSE,
           panel.space.factor = 0.05,
           pic.space.factor   = 0.103,
           pic.aspect         = 0.5,
           lab.box            = 1.2,
           lab.color          = c("lightgrey", "lightgrey"),
           lab.cex            = 0.7,
           main = "Titanic: relative frequencies")
```



Remarks: An interesting homework is to modify the data set in a way that the *bars* show the conditional distributions of the four *columns* `Child, Adult, Child, Adult`.

11 Negative frequencies

Negative frequencies can occur in a table after computing differences; e. g. if somebody computes the differences between observations and expected values. In this section we try to represent the deviations from expectations based on the data set `HairEyeColor`. 58

```
> data <- HairEyeColor
> data.exp <- margin.table(data, 1)
> for( d in 2:length(dim(data)) ){
    data.exp <- outer( data.exp, margin.table(data, d) ) / sum(data)
  }
> cat("=== observed ===\n"); print(data)

=== observed ===

, , Sex = Male

       Eye
Hair    Brown Blue Hazel Green
  Black    32   11    10     3
  Brown    53   50    25    15
  Red      10   10     7     7
  Blond     3   30     5     8

, , Sex = Female

       Eye
Hair    Brown Blue Hazel Green
  Black    36    9     5     2
  Brown    66   34    29    14
  Red      16    7     7     7
  Blond     4   64     5     8

> cat("=== expected ===\n"); print(round(data.exp, 3))

=== expected ===

, , Sex = Male

       Eye
Hair     Brown   Blue  Hazel  Green
  Black 18.915 18.485  7.996  5.503
  Brown 50.090 48.951 21.174 14.572
  Red   12.435 12.152  5.257  3.617
  Blond 22.243 21.737  9.403  6.471

, , Sex = Female

       Eye
Hair     Brown   Blue  Hazel  Green
  Black 21.220 20.738  8.970  6.173
  Brown 56.194 54.917 23.755 16.347
  Red   13.950 13.633  5.897  4.058
  Blond 24.953 24.386 10.548  7.259
```

1 The deviations follow immediately. 59

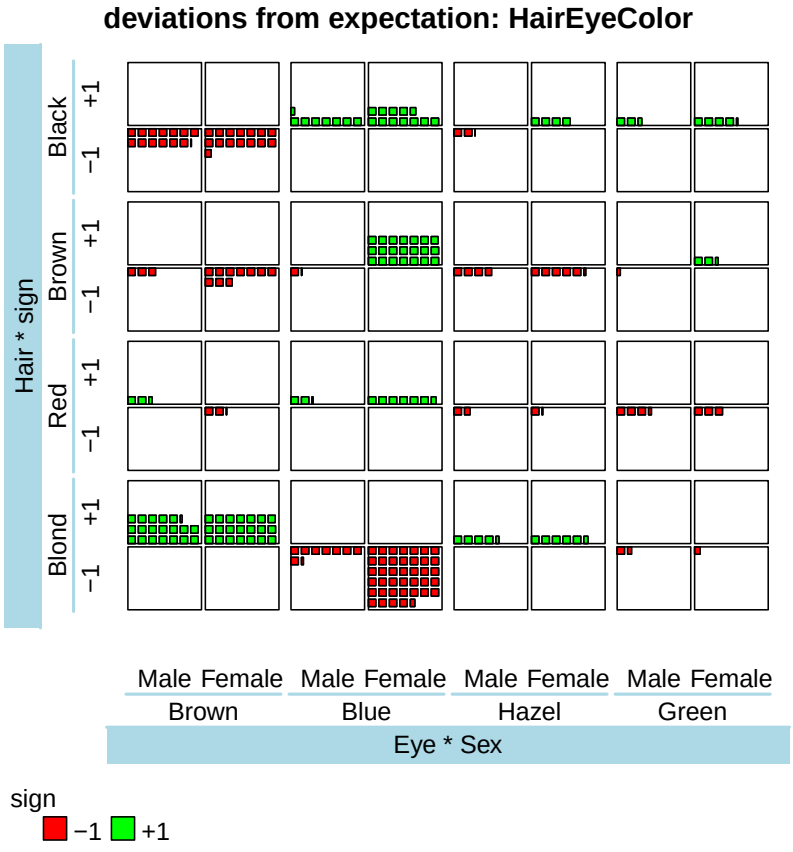
```
> data.diff <- data.exp - data
> cat("=== deviation: expected - observed ===\n"); print(round(data.diff, 3))

=== deviation: expected - observed ===

, , Sex = Male

       Eye
Hair      Brown    Blue   Hazel   Green
  Black -13.085   7.485  -2.004   2.503
  Brown  -2.910  -1.049  -3.826  -0.428
  Red     2.435   2.152  -1.743  -3.383
  Blond  19.243  -8.263   4.403  -1.529

, , Sex = Female

       Eye
Hair      Brown    Blue   Hazel   Green
  Black -14.780  11.738   3.970   4.173
  Brown  -9.806  20.917  -5.245   2.347
  Red    -2.050   6.633  -1.103  -2.942
  Blond  20.953 -39.614   5.548  -0.741
```

Now let's study how `pic.plot()` finds a nice representation of the deviations. If `pic.plot()` discovers negative cell entries it creates a new dimension with name `sign` and levels `c(+1, -1)`. Then the absolute values of the entries of the cells are assigned according to their signs in the sign dimension. These internal arguments don't matter. However, you are allowed to use the variable `sign` in assigning `grp.xy` and `grp.color`. Have a look at the following example:

```
negative frequencies
residuals
variable:  sign
```

60

```
> pic.plot(data.diff,
           grp.xy          = Hair + sign ~ Eye + Sex,
           grp.color       = sign,
           colors          = c( "red", "green"),
           pic.stack.type  = c("t","b"),
           panel.reverse.y = TRUE,
           lab.boxes       = 1.2,
           lab.color       = "lightblue",
           main = "deviations from expectation: HairEyeColor")
```



Remarks: Negative entries are painted using color `red` and the other entries are green. The order of the panels is similar to the order of the printed output of `data.diff`. Please check whether the plot is correct. Zero entries in one of the sign levels lead to short thin lines. The stacks of the negative entries are filled from the top side and the others from the bottom side.

12 Raster and PPM Graphics

In newspapers we often find some statistical graphics which are designed to attrack attention. And sometimes nice little pictures of different sizes are drawn to represent the magnitudes of the observed values of some variables. Therefore, `pic-plot()` should also be able to generate small pictures within its panels. In this section we discuss how raster graphics can be used as pictograms elements.

For we use different data sets we don't make an assignment to `data` here. However, we need some objects stored on the server `www.wiwi.uni-bielefeld.de`. 61

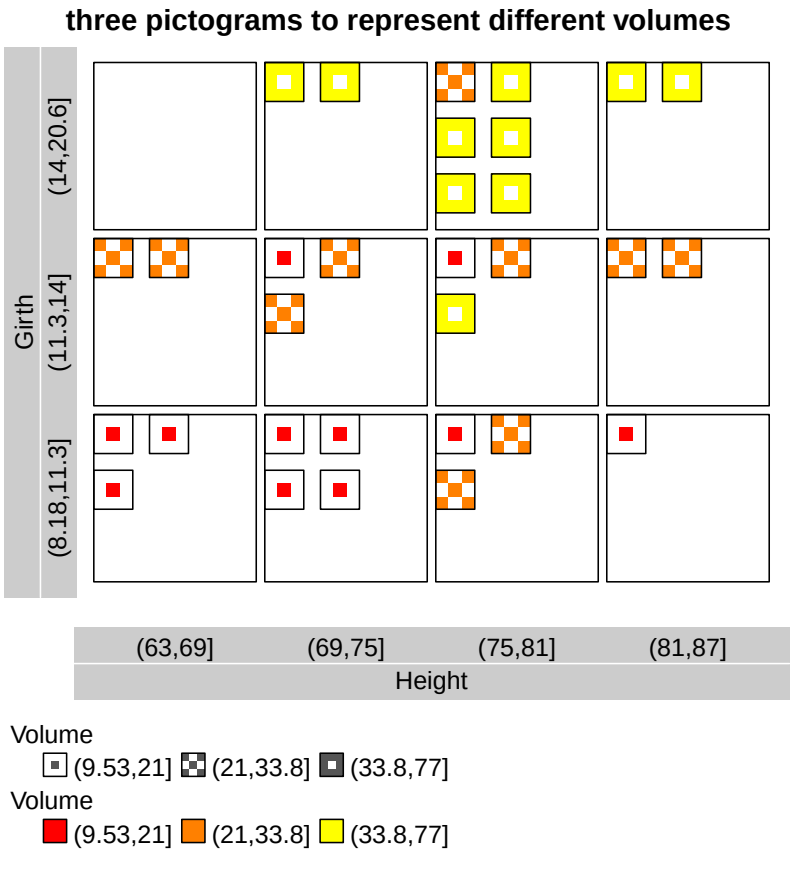
```
> # get file some files
> #   This chunk loads the graphics files "R.pnm", "tm.pnm", "m2.pnm" and "f2.pnm"
> #   and the data set "goettingen-niedersachs" via internet into the R environment.
> #   If you forget to activate these statements some of the following chunks don't work!!!
> url <- "http://www.wiwi.uni-bielefeld.de/lehrbereiche/statoekoinf/comet/wolf/pw_files/files/"
> tmp.pic <- readBin(paste(sep="", url, "R.pnm"),  what="raw", n=51315); writeBin(tmp.pic, "R.pnm")
> tmp.pic <- readBin(paste(sep="", url, "m2.pnm"), what="raw", n=89435); writeBin(tmp.pic, "m2.pnm")
> tmp.pic <- readBin(paste(sep="", url, "f2.pnm"), what="raw", n=83393); writeBin(tmp.pic, "f2.pnm")
> tmp.pic <- readBin(paste(sep="", url, "tm.pnm"), what="raw", n=22514); writeBin(tmp.pic, "tm.pnm")
> source(paste(sep="/", url, "goettingen-niedersachs.R")); require(tcltk)
```

In the fourth section we demonstrated that by assigning numbers to argument `pics` plotting characters are used. In the first application we construct some variables of class `raster` and then use them as pictograms. Raster variables contain a matrix of rgb color values and are of the `raster` class.

constructed raster

62

```
> image1 <- as.raster(  matrix( c(1,1,1,1,0,1,1,1,1), ncol = 3, nrow = 3))
> image2 <- as.raster(  matrix( c(0,1,0,1,0,1,0,1,0), ncol = 3, nrow = 3))
> image3 <- as.raster(  matrix( c(0,0,0,0,1,0,0,0,0), ncol = 3, nrow = 3))
> p.set <- list(image1, image2, image3)
> pic.plot(trees,
           grp.xy          = 1 ~ 2,
           grp.color       = 3,
           grp.pic         = 3,
           colors          = heat.colors(3),
           pics            = p.set,
           pic.draft       = FALSE,
           vars.to.factors = c(.3, 4, .3),
           lab.parallel    = c(TRUE, TRUE, FALSE),
           main            = "three pictograms to represent different volumes")
```

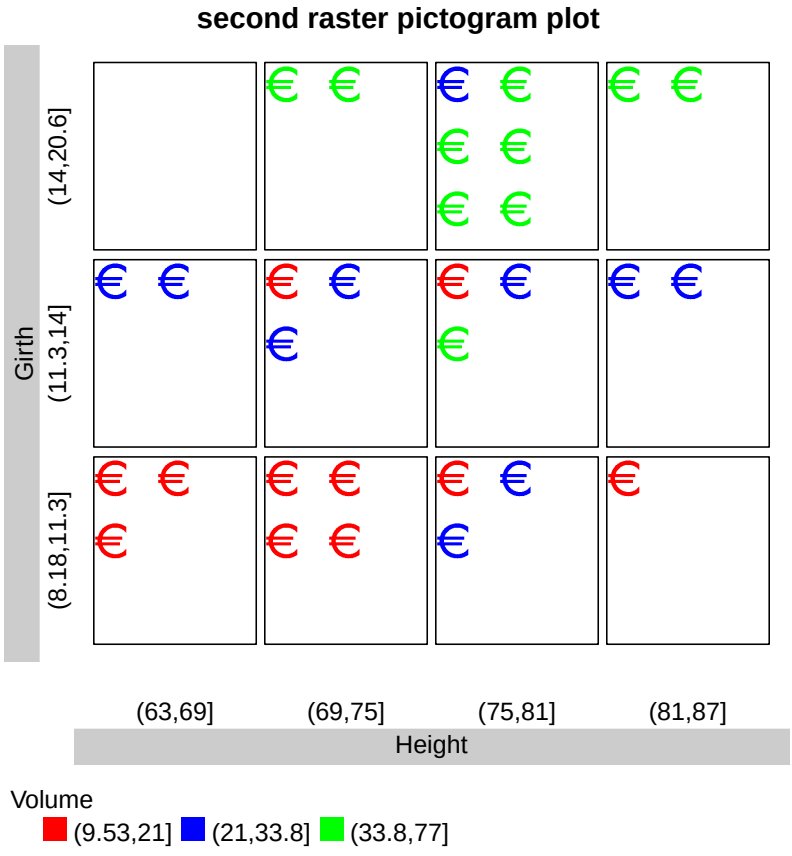


Remarks: You see the raster graphics have been combined in a list. The argument `pic.draft` is set to FALSE to get sharp borders. Otherwise some interpolation operations take place. Check the effect of `pic.draft = TRUE`.

Here is almost the same plot, but now we use an Euro raster image built by some geometrical elements.

Euro icon
pics=image
63

```
> n <- 200; m <- n/2; x <- y <- seq(n <- 200); f <- floor
> image1 <- (outer( (x-m)^2, (y-m)^2, FUN="+") > (.8*m)^2 )
> image2 <- (outer( (x-m)^2, (y-m)^2, FUN="+") > (.6*m)^2 )
> image3 <- image1 | !image2; image3[,f(.75*n):n] <- 1
> image3[f(0.47*n):f(0.4*n), f(.05*n):f(.65*n)] <- 0
> image3[f(0.53*n):f(0.6*n), f(.05*n):f(.60*n)] <- 0
> image <- as.raster(image3)
> pic.plot(trees,
           grp.xy          = 1 ~ 2,
           grp.color       = 3,
           grp.pic         = 3,
           colors          = c("red", "blue", "green"),
           pics            = image,
           pic.draft       = FALSE,
           pic.frame       = FALSE,
           vars.to.factors = c(.3, 4, .3),
           lab.boxes       = 1,
           main            = "second raster pictogram plot")
```

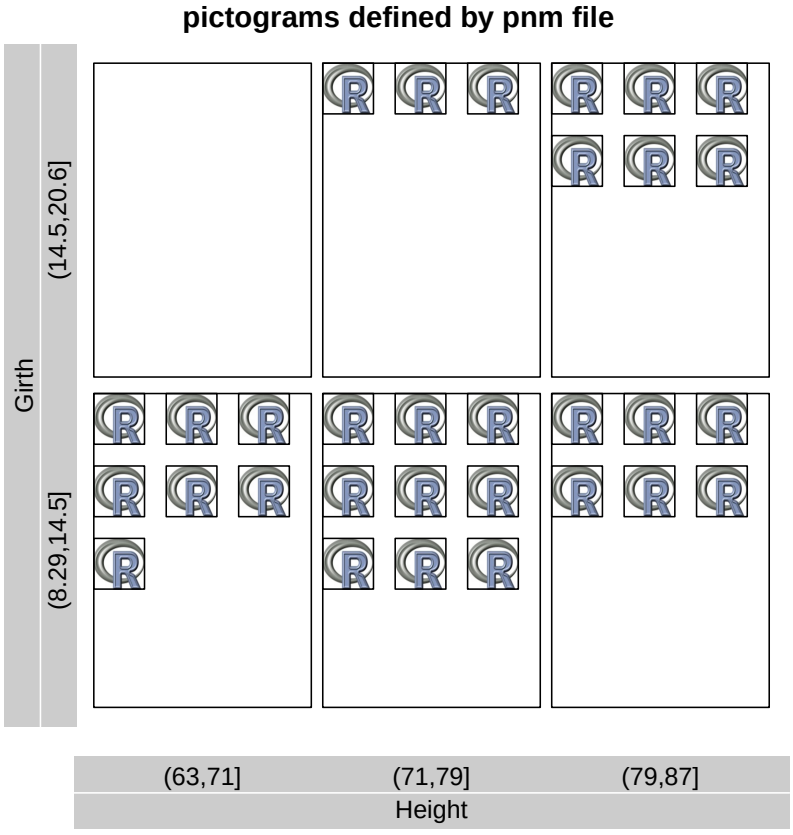


Remarks: For the variable `Volume` has been cut into three intervals the list of images must have a length of three, too. Otherwise `pic.plot()` selects plotting characters to complete the number of pictograms.

Because the construction of raster images may be boring programming work you can use ppm files as pictograms. These bitmap graphics types have a simple structure and `pic.plot()` is able to read them. The user has to assign the concatenated file names to the argument `pics`. As an example we catch the R logo and convert it to a pnm file by `convert` outside of R.

R-logo: file "R.pnm"
pics="R.pnm"
64

```
> pic.plot(trees,
           grp.xy          = 1 ~ 2,
           grp.pic         = 3,
           pics            = "R.pnm",
           vars.to.factors = c(2, 3, .9),
           main            = "pictograms defined by pnm file")
```

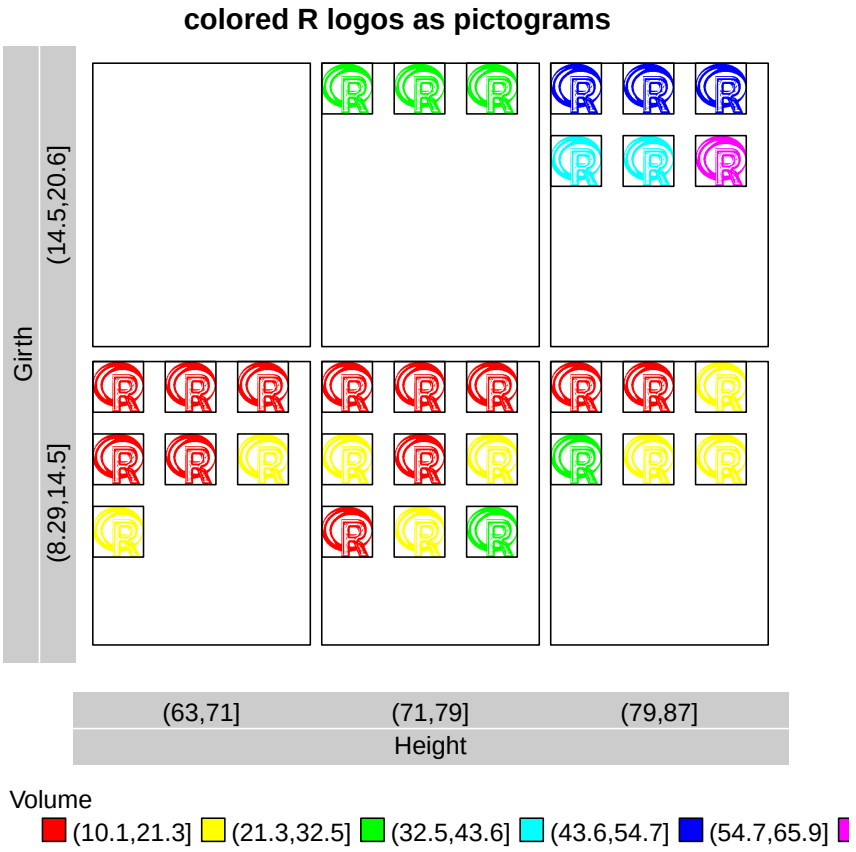


Remarks: Because we want to represent all the trees by the same pictogram we define one interval for the values of the third variable. The entry 0.9 of `vars.to.factors` means *put 90% of the data in each of the intervals* and the requirement can only be met by one interval. The R icon is stored within the package `jpeg`. Therefore, we have to load this package.

Now we extend the last example by coloring the pictograms according to the values of the third variable.

colored logo
pics="R.pnm"
vars.to.factors
65

```
> pic.plot(cbind(trees, pic = 1),
           grp.xy          = 1 ~ 2,
           grp.color       = 3,
           grp.pic         = "pic",
           pics            = "R.pnm",
           vars.to.factors = c(2, 3, 6),
           lab.parallel    = c(TRUE, TRUE, FALSE),
           main            = "colored R logos as pictograms")
>     par(pin = c(10, 10) / 2.54)
```

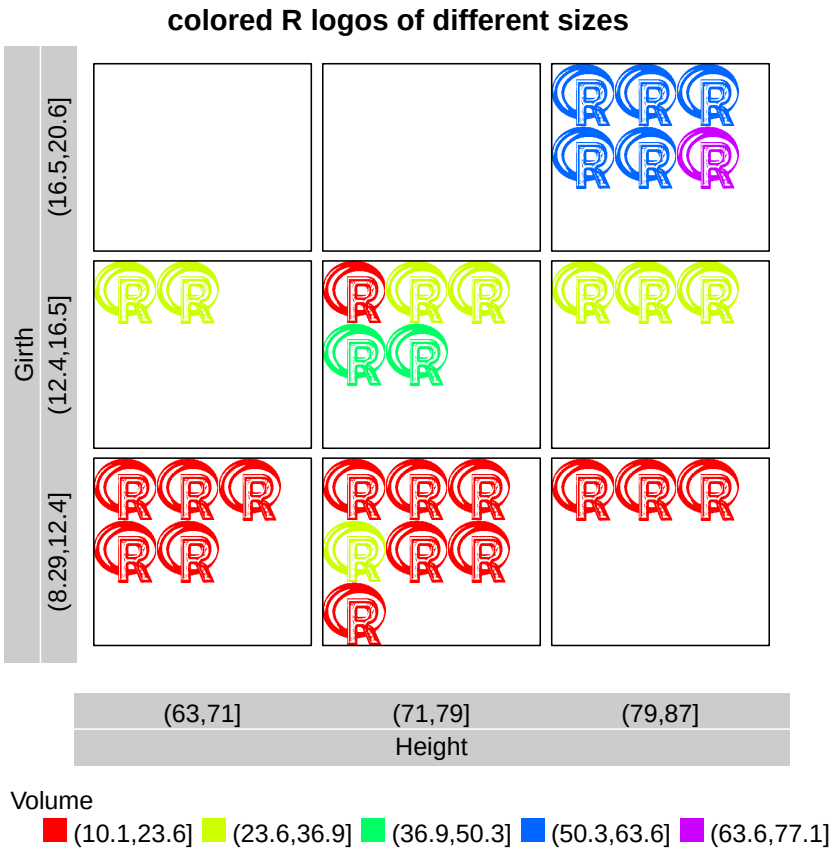


Remarks: Before we call `pic.plot()` we expand the data frame by a new variable called `pic`. The values of the new column are `1`. Therefore, we need one pictogram file only and deliver `R.pnm` via `pics`. Because of `grp.color = 3` the colors of the pictograms are modified depending on the value of variable 3. Check what happens if `pic` isn't appended and `grp.pic = 3`. Notice that the name of the variable doesn't matter at all.

Maybe you want to construct pictograms whose sizes depend on the value of a variable. Here we show a trick to realize this idea.

new variable
fraction.1
pic.stack.type="tls"
66

```
> data <- cbind(trees, pic = 1,
                fraction.1 = trees[,3] / max(trees[,3]) )
> pic.plot(data,
           grp.xy           = 1 ~ 2,
           grp.color        = Volume,
           grp.pic          = pic,
           pics             = "R.pnm",
           vars.to.factors  = c(3, 3, 5),
           pic.stack.type   = "tls",
           pic.space.factor = 0.0,
           pic.frame        = FALSE,
           lab.parallel     = c(TRUE, TRUE, FALSE),
           main = "colored R logos of different sizes")
```

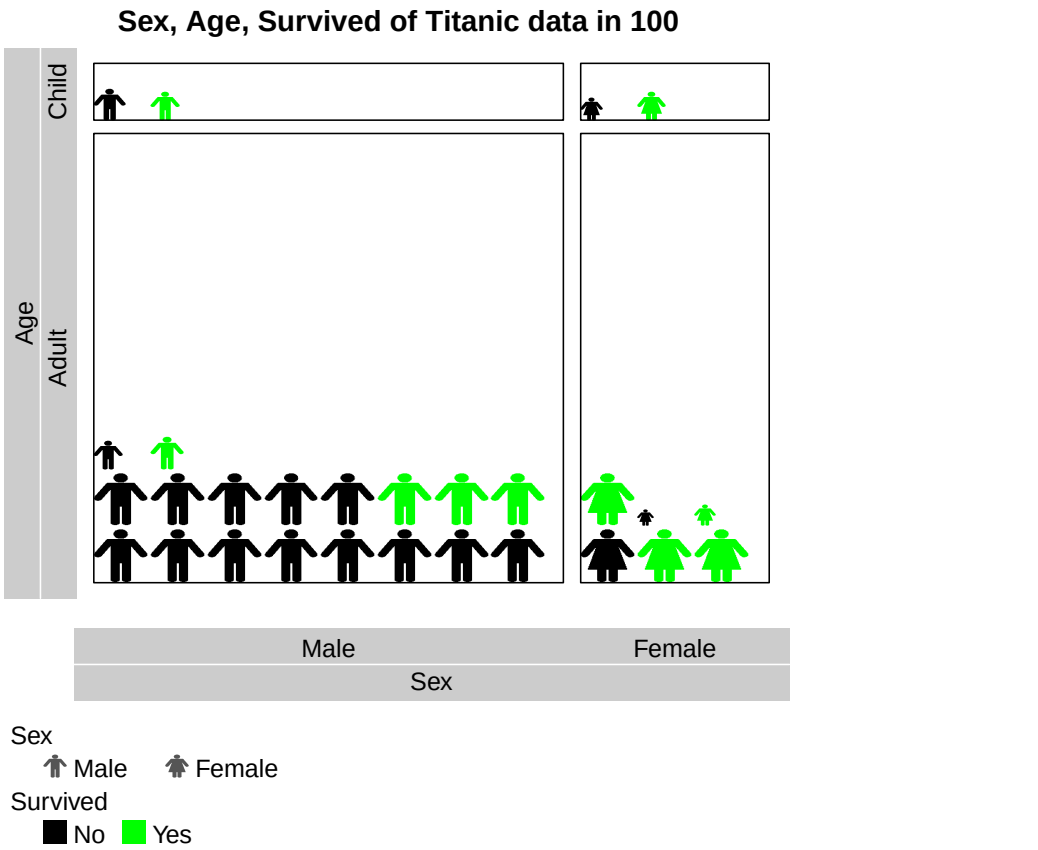


Remarks: The trick consists of appending a column of fractions to the data matrix. The fractions are built by dividing the values of `Volume` by their maximal entry. It is important to name the column by `fraction.1` because this is the internal name to store decimal parts. Hereby the divided volumes are interpreted as fractions of a unit. As further remarks we have split the range of the variable `Girth` into three intervals and set `pic.stack.type = "tls"`. The meaning of `"s"` is short for *shrinking* and leads to a proportional shrinking of the pictograms. Without this setting the width of the pictograms will only be reduce.

Usually you have different image files at hand so you can represent different levels of a variable by suitable icons. For example in the case of the Titanic data we can show the levels of Sex by male and female icons:

icons from file 67

```
> p.set <- c("m2.pnm", "f2.pnm")
> data <- margin.table(Titanic/100, 2:4)
> pic.plot(data,
           grp.xy             = Age ~ Sex,
           grp.color          = Survived,
           grp.pic            = Sex,
           colors             = c("black", "green"),
           pics               = p.set,
           vars.to.factors    = c(2, 3, 6),
           panel.prop.to.size = 0.7,
           panel.reverse.y    = TRUE,
           pic.stack.type     = "s",
           pic.frame          = FALSE,
           pic.space.factor   = 0.05,
           lab.parallel       = c(TRUE, TRUE, FALSE),
           main               = "Sex, Age, Survived of Titanic data in 100")
```

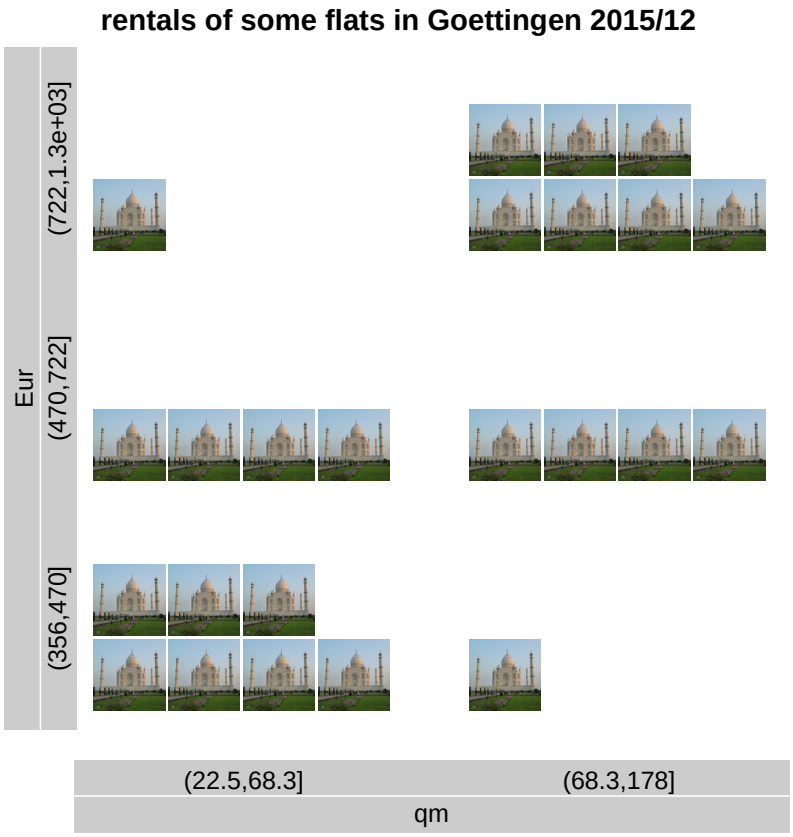



```
       Sex
Age      Male Female
  Child  0.64   0.45
  Adult 16.67   4.25
```

The user may ask whether pictures can be used as icons. The following example visualizes rentals of flats in Göttingen. As an adequate icon we use a pictures of the Taj Mahal.

photograph as icon
pic.stack.type="s"
68

```
> data <- goettingenniedersachs
> data <- cbind(data, fraction.1 = (data[,3] / max(data[,3]))^.5)
> pic.plot(data,
           grp.xy             = Eur ~ qm ,
           grp.pic            = qm,
           pics               = "tm.pnm",
           vars.to.factors    = c(1, .5, .3),
           pic.stack.type     = "s",
           pic.frame          = FALSE,
           pic.space.factor   = 0.05,
           panel.frame        = FALSE,
           panel.space.factor = 0.2,
           panel.prop.to.size = 0.7,
           lab.parallel       = c(TRUE, TRUE, FALSE),
           main = "rentals of some flats in Goettingen 2015/12")
```

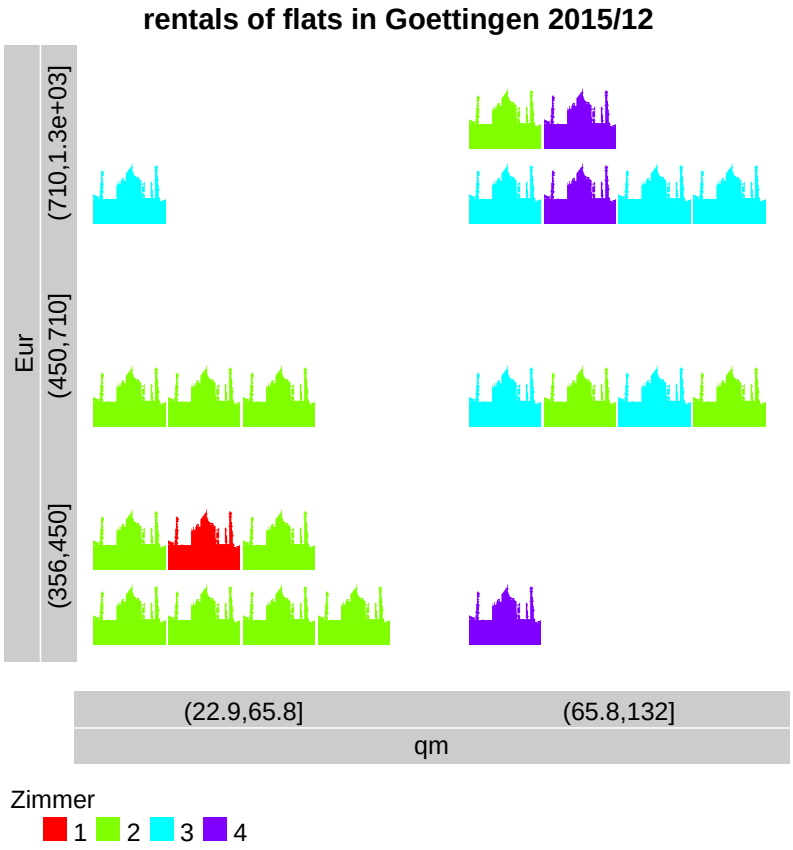


Remarks: `grp.color` and `colors` have not been set. So the original raster image is used in the plot.

Now we repeat the last example with the same settings but add `grp.color = "Zimmer"`. Hence the colors represent the numbers of rooms in the flats.

colored photograph 69

```
> pic.plot(data,
           grp.xy             = Eur ~ qm ,
           grp.pic            = qm,
           grp.color          = Zimmer,
           pics               = "tm.pnm",
           vars.to.factors    = c(1, .5, .3),
           pic.stack.type     = "s",
           pic.frame          = FALSE,
           pic.space.factor   = 0.05,
           panel.frame        = FALSE,
           panel.space.factor = 0.2,
           panel.prop.to.size = 0.7,
           lab.parallel       = c(TRUE, TRUE, FALSE),
           main = "rentals of flats in Goettingen 2015/12")
```



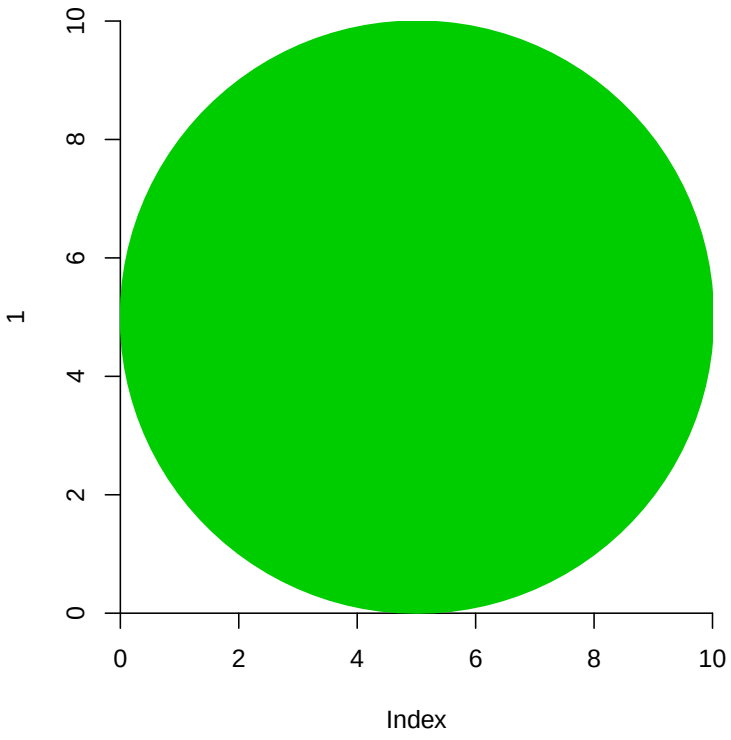
Remark: Because of coloring (`grp.color=Zimmer`) the pictograms are not multicolored but monochrome. It is clear that not all pictures are suitable as pictogram elements and it is recommended to choose pictures which are rich in contrast. Maybe you have to modify your pictures and transform the format to `pnmraw`.

13 Picture Generating Functions

All around the world a lot of R freaks like to implement ideas by programming. They will wonder whether pictograms can also be described by sequences of R statements. In this section we show how to write icon generating functions and their usage within `pic.plot()`.

Let's study an example. In a simple case an icon generating function defines an icon by a set of segments and stores the segments in a matrix or data frame. Then the functions must return a matrix of five or six columns and its class attribute has to be set to `"segments"`. The first four columns contain vectors of the coordinates of the segments as it is known from calls of `segments()`: `x0, y0, x1, y1`. The fifth column fixes the line width of the segments and the last one the colors. The coordinates and line widths must be set in a way that they generate a suitable icon on a graphics device with a world window of the size of $[0, 10] \times [0, 10]$ and a viewport of *10cm* $\times$ *10cm*. So you are able to check the generator function quickly. 70

```
> circle.simple <- function(){
    res <- rbind( c( 5,5,5,5, lwd.mm = 100, NA)); class(res) <- "segments"; res }
> xyxylc <- circle.simple(); xyxylc[ is.na(xyxylc[, 6]), 6] <- 3
> dev.fac <- 1; mm.to.lwd <- function(lwd.mm) lwd.mm * 3.787878 * dev.fac
> par(pin = c(10, 10) / 2.54);  plot(1, type = "n", axes = FALSE);
> par(usr = c(0,10,0,10)); axis(1); axis(2)
> segments(xyxylc[,1], xyxylc[,2], xyxylc[,3], xyxylc[,4],
           lwd = mm.to.lwd(xyxylc[,5]), col = xyxylc[,6])
```

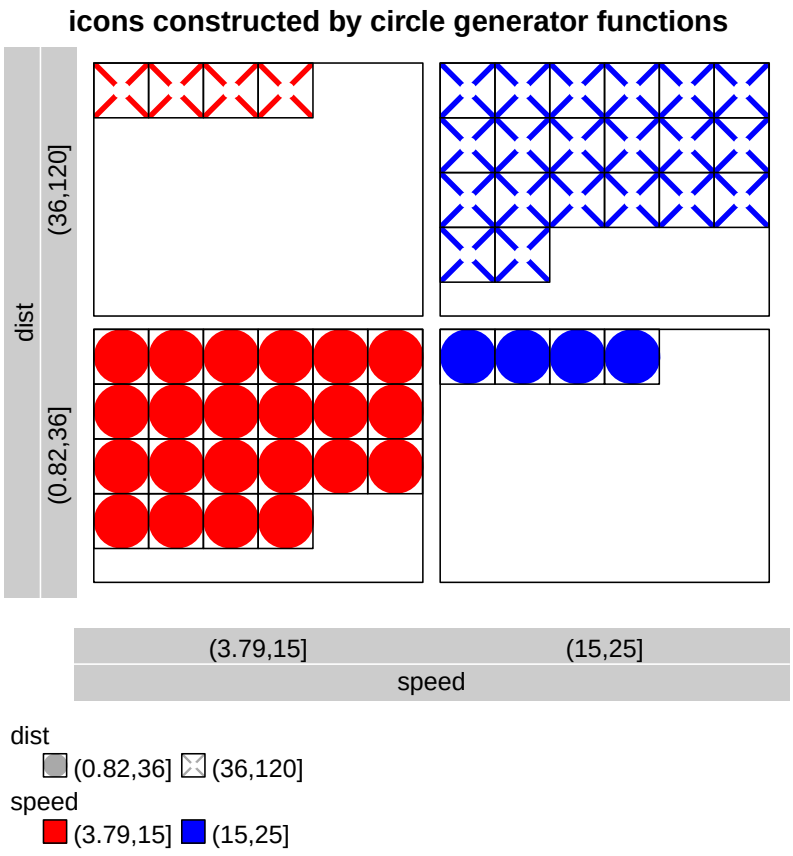


Remarks: The color column is set by `circle.simple()` to `NA`. Segments of this *color* will be recolored according to the `colors` argument of `pic.plot()`. A value of 0 indicates color `white`.

Now we define a second generator function and call `pic.plot()` with data set `cars`.

icons by functions 71

```
> cross.simple <- function(data.row = NULL){
    res <- rbind( c( 0.5, 0.5, 9.5, 9.5, lwd.mm = 10, NA),
                  c( 0.5, 9.5, 9.5, 0.5, lwd.mm = 10, NA),
                  c( 5,   5,   5,   5,   lwd.mm = 30, 0 ))
    class(res) <- "segments"; res
  }
> pic.plot(cars,
           grp.color        = 1,
           grp.pic          = 2,
           colors           = c("red", "blue", "green"),
           pics             = c(circle.simple, cross.simple),
           vars.to.factors  = c(.5, .5),
           pic.space.factor = 0,
           main = "icons constructed by circle generator functions",
  )
```



Remarks: The generated crosses consist of two crossing segments. In the center a white point (see color code 0 in `cross.simple`) recolors some fragments of the segments. Within the center of the white point we add a small point of color code 3. Furthermore, in both functions we use a local one to scale the line width easier.

Following an idea of Mazziotta and Pareto we will now construct some *traveller icons*. These icons represent non-compensatory aggregation of social indicators.[2] Here is the data matrix to demonstrate the implementation of the proposal.

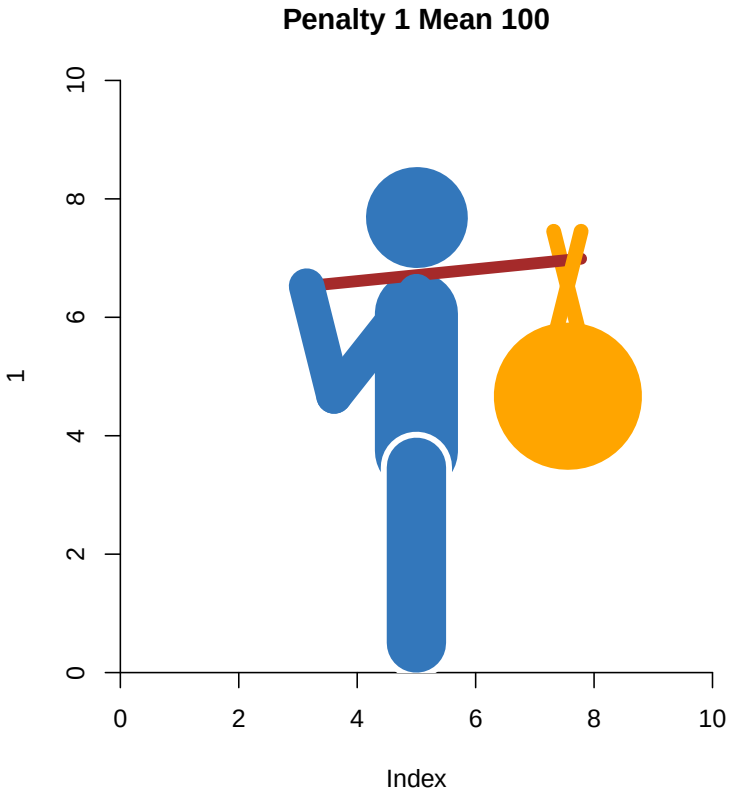
```
                 Region   Mean Penalty    MPI
1              Piemonte  98.74    0.43  98.30
2          Valle d'Aosta 104.07    4.23  99.84
3              Lombardia 101.38    0.64 100.74
4    Trentino-Alto Adige 106.10    0.63 105.47
5                 Veneto 104.38    0.77 103.61
6  Friuli-Venezia Giulia 105.55    0.34 105.21
7                Liguria 102.76    0.29 102.47
8         Emilia-Romagna 103.62    0.46 103.16
9                Toscana 101.84    0.27 101.57
10                Umbria 103.52    0.22 103.30
11                Marche 102.05    0.15 101.90
12                 Lazio  97.88    0.82  97.06
13               Abruzzo 102.90    1.30 101.60
14                Molise  91.43    1.02  90.42
15              Campania  94.12    0.37  93.75
16                Puglia  96.78    0.21  96.58
17            Basilicata  93.55    2.37  91.18
18              Calabria  92.59    0.51  92.08
19                Sicilia  96.29    0.31  95.98
20              Sardegna 100.45    0.76  99.69
```

At first we define a function which constructs a standardized traveller man. To check it call the function with the option `plot=TRUE`.

travaller icon by lines 72

```
> mazz.man <- function(Mean = 100, expo = 1/(1:3)[3], Mean.max = 107, Mean.half = 90,
    Penalty = 1, Penalty.max = 5, Penalty.min = 0, plot = FALSE){
    # compute factor of traveller man
    Mean.min <- Mean.half - (Mean.max - Mean.half) / ((h <- 2^(1/expo)) - 1)
    Mean.min <- min(Mean.min, Mean)
    fac      <- 0.95 * ((h * (Mean - Mean.min)) / Mean.max) ^ expo
    bag.size <- 0.80 * ((Penalty - Penalty.min) / Penalty.max )^expo /2
    res <- rbind(c(5,            7.75*fac + .5, 5,           7.75*fac + .5), #head
                 c(5,            3.5 *fac + .5, 5,           6   *fac + .5), #body
                 c(5,            3.2 *fac + .5, 5,           0   *fac + .5), #leg in white
                 c(5,            3.2 *fac + .5, 5,           0   *fac + .5), #leg
                 c(5 + 3*fac,    5.5 *fac + .5, 5 + 2.5*fac, 7.5 *fac + .5), #tape2
                 c(5 - 2*fac,    6.5 *fac + .5, 5 + 3  *fac, 7   *fac + .5), #stick
                 c(5,            6.4 *fac + .5, 5 - 1.5*fac, 4.5 *fac + .5), #arm one
                 c(5 - 2*fac,    6.5 *fac + .5, 5 - 1.5*fac, 4.5 *fac + .5), #arm
                 c(5 + 2.75*fac, 5   *fac + .5 - 2*bag.size ,
                   5 + 2.75*fac, 5   *fac + .5 - 2*bag.size),                #bag
                 c(5 + 2.5*fac,  5.5 *fac + .5, 5 + 3  *fac, 7.5 *fac + .5)) #tape1
    lwd.mm <-  c( c(17, 14, 12, 10, 2.5, 2, 6, 6) * fac / 0.927042
              ,   31 * bag.size / 0.2924,     2.5 * fac / 0.927042 )
    colors <- c("#3377BB", "white", "brown", "orange")[c(1,1,2,1,4,3,1,1,4,4)]
    if( plot ){
      dev.fac <- 1; mm.to.lwd <- function(lwd.mm) lwd.mm * 3.787878 * dev.fac
      par(pin = c(10, 10) / 2.54);  plot(1, type = "n", axes = FALSE);
      par(usr = c(0,10,0,10)); axis(1); axis(2)
      title(paste("Penalty", Penalty, "Mean", Mean))
      segments(res[,1], res[,2], res[,3], res[,4], lwd = mm.to.lwd(lwd.mm), col = colors)
    }
    res <- cbind(data.frame(res, lwd.mm = lwd.mm, colors))
    class(res) <- c(class(res), "segments"); res
  }
> mazz.man(plot = TRUE)
```

[2] M. Mazziotta, A. Pareto (2014): Non-compensatory Aggregation of Social Indicators: An Icon Representation. In: F. Crescenzi and S. Mignnani (eds.), Statistical Methods and Applications from a Historical Perspective, Studies in Theoretical and Applied Statistics, DOI 10.1007/978-3-319-05552-7_33



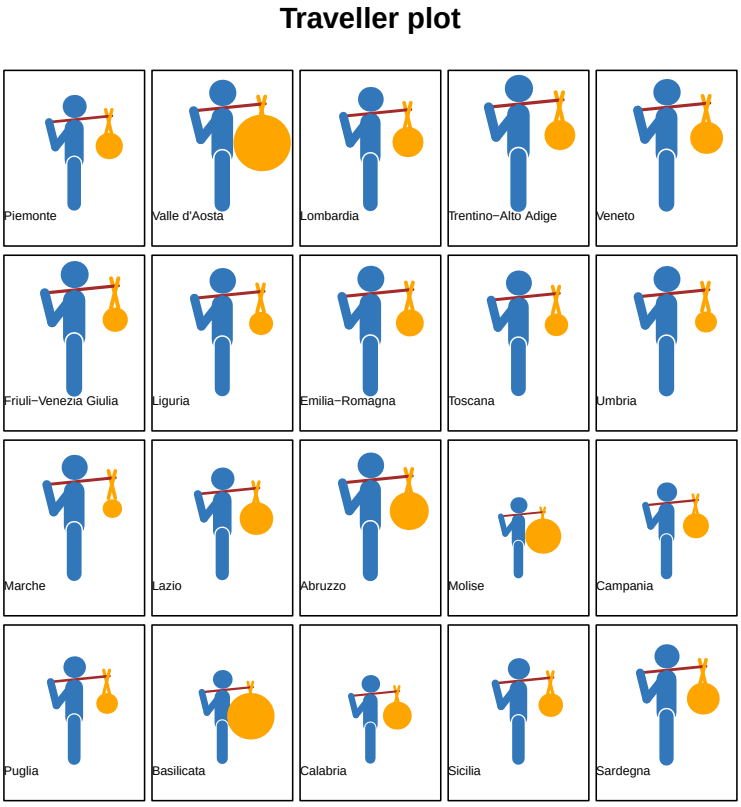
Remarks: The output of the function `mazz.man()` is a data frame and consists of six columns. We will not comment on the boring work of composing the lines of the function.

Now we can use this function to create a suitable traveller plot. To this end we first modify the data frame a little bit. Then we write a second function as an interface between `mazz.man()` and the requirements of `pic.plot()`. The third step is to call `pic.plot()`. These three steps we summarize in the function `traveller.plot()`. 73

```
> mazz.man.gen <- function(data.row = NULL){
    if(0 < length(data.row)){
      idx <- as.numeric(rownames(data.row))
      text(data.row$x0, data.row$y0, data.row$Region, cex = 0.5, adj = c(0,1))
      mazz.man(Mean = data.row$Mean, Penalty = data.row$Penalty)
    } else { mazz.man() }
  }
> Mazziotta.Pareto <-
   structure(list(Region = c("Piemonte", "Valle d'Aosta", "Lombardia",
   "Trentino-Alto Adige", "Veneto", "Friuli-Venezia Giulia", "Liguria",
   "Emilia-Romagna", "Toscana", "Umbria", "Marche", "Lazio", "Abruzzo",
   "Molise", "Campania", "Puglia", "Basilicata", "Calabria", "Sicilia",
   "Sardegna"), Mean = c(98.74, 104.07, 101.38, 106.1, 104.38, 105.55,
   102.76, 103.62, 101.84, 103.52, 102.05, 97.88, 102.9, 91.43,
   94.12, 96.78, 93.55, 92.59, 96.29, 100.45), Penalty = c(0.43,
   4.23, 0.64, 0.63, 0.77, 0.34, 0.29, 0.46, 0.27, 0.22, 0.15, 0.82,
   1.3, 1.02, 0.37, 0.21, 2.37, 0.51, 0.31, 0.76), MPI = c(98.3,
   99.84, 100.74, 105.47, 103.61, 105.21, 102.47, 103.16, 101.57,
   103.3, 101.9, 97.06, 101.6, 90.42, 93.75, 96.58, 91.18, 92.08,
   95.98, 99.69)), .Names = c("Region", "Mean", "Penalty", "MPI"
   ), row.names = c(NA, -20L), class = "data.frame")
> dm <- Mazziotta.Pareto
> dm <- cbind(dm, fraction.1 = dm[, "Mean"] / max(dm[, "Mean"]),
              col = as.factor(rep(1:5,4)),         # as.factor!!
              row = as.factor(rep(1:4, each = 5))) # as.factor!!
```

travallers by generator functions 74

```
> pic.plot(dm,
           grp.xy           = row ~ col,
           grp.pic          = 0 | Mean + Penalty + Region,
           vars.to.factor   = FALSE,
           pics             = mazz.man.gen,
           pic.space.factor = 0,
           pic.frame        = FALSE,
           panel.reverse.y  = TRUE,
           lab.parallel     = TRUE,
           lab.side         = c("",""),
           main = "Traveller plot")
```



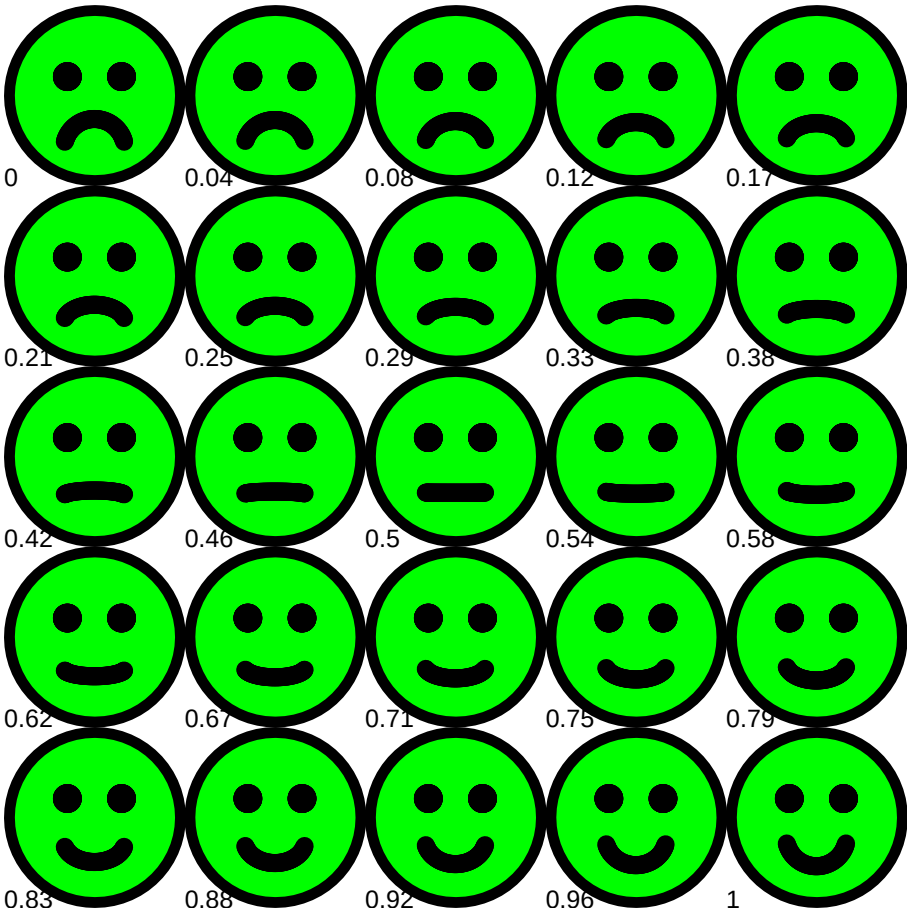
Remarks: In the function `mazz.man.gen()` we shift and scale the sizes of bag.size. Furthermore, we add the names of the Italian regions to the plot. We added a column and a row variable to control the positions of the traveller man in the plot. By this trick we get a (4×5)-facet layout for the vector of 16 pictograms. To suppress margin legend argument `lab.side` is set to `c("","")`. These complicated ingredients are necessary to get a 4x5 table of pictograms as we see in the paper of Mazziotta and Pareto.

The traveller icons are tuned by choosing suitable parameters within the function `mazz.man()`. However, you like to drive some attributes of your icons by some of the data variables. As a demonstration we represent the trees of data set `trees` by smileys whose volume entries determine the intensity of laughing.

At first we need a function for defining the general plot of a smiley. The grade of smiling is delivered by argument `smile` $\in [0, 1]$.

smileys by function 75

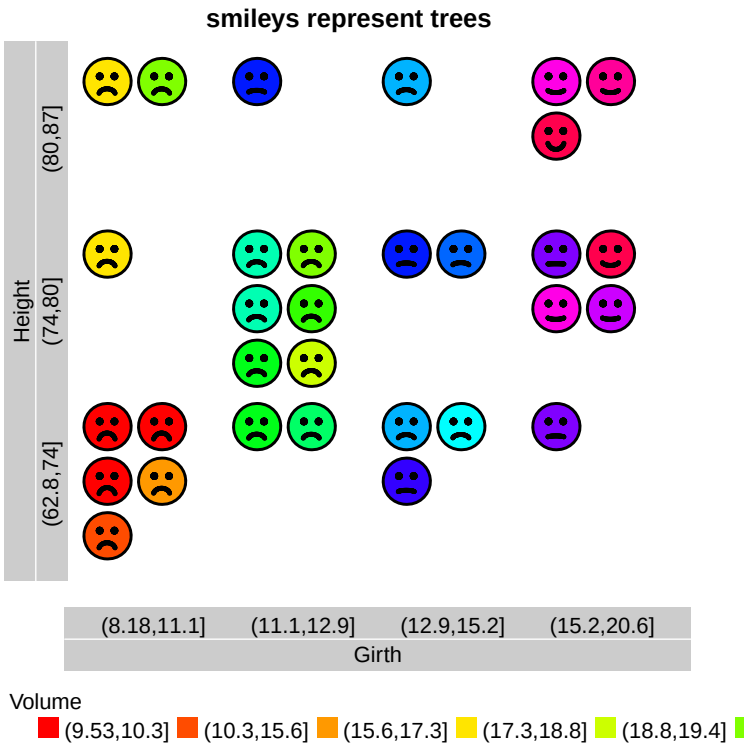
```
> smiley <- function(smile = 0, plot = FALSE){
    circle <- function(x0 = 1, y0 = 1, a = 3, lwd = 5,
                       time.0 = 0, time.1 = 12, n = 60){
      alpha <- seq(time.0, time.1, length = n); alpha <- alpha * (2*pi/12)
      x <- a * sin(alpha) + x0;               y <- a * cos(alpha) + y0
      cbind(x[-n],y[-n], x[-1],y[-1], lwd)
    }
    res <- NULL
    res <- rbind( res, cbind(5, 5, 5, 5, 100, 1 )) # face+rand
    res <- rbind( res, cbind(5, 5, 5, 5,  88, NA)) # face
    res <- rbind( res, cbind(circle(3.5,6.05,.30, 10), 1) ) # eye
    res <- rbind( res, cbind(circle(6.5,6.05,.30, 10), 1) ) # eye
    if(is.na(smile)){
      res <- rbind( res, cbind(circle(5,5, 2.7,  7.5, 7.50, 4.50),1) ) # mouse
    } else {
      #            x0 y0            a lwd  time.0  time.1
      hs <- circle( 5, 4,         1.7, 10,    8.5,    3.5) # mouse laughing
      hn <- circle( 5, 2,         1.7, 10,    9.5,   14.5) # mouse not laughing
      s <- smile; n <- 1-s
      h <- cbind( hs[,1], s*hs[,2]+n*hn[,2], hs[,3], s*hs[,4]+n*hn[,4], hs[,5])
      res <- rbind( res, cbind(h, 1) )                    # mouse
    }
    class(res) <- "segments"
    if(plot){
      plot(1, type = "n", axes = FALSE); par(usr = c(0,10,0,10)) # ; axis(1); axis(2)
      plot.dim.fac <- par()$pin[1] * 2.54 / 10; dev.fac <- 1
      mm.to.lwd <- function(lwd.mm) lwd.mm * 3.787878 * dev.fac * plot.dim.fac
      col <- ifelse( is.na(res[,6]), "green",  res[,6])
      segments(res[,1], res[,2], res[,3], res[,4], lwd = mm.to.lwd(res[,5]), col = col )
      text(0, 0, as.character(round(smile,2)), xpd = NA, cex = 1.5, adj = c(0,0) )
    }
    return(res)
  }
> oldpar <- par(mfrow = c(5,5), mar = c(0,0,0,0))
> for(smile in seq(0,1, length = 25)){
    smiley(smile, TRUE)
  }; par(oldpar)
```


0
0.04
0.08
0.12
0.17
0.21
0.25
0.29
0.33
0.38
0.42
0.46
0.5
0.54
0.58
0.62
0.67
0.71
0.75
0.79
0.83
0.88
0.92
0.96
1

Now we are able to define an icon generating function and to call `pic.plot()`.

smiley generator function 76

```
> smiley.gen <- function(data.row = NULL){
    if(0 < length(data.row)){
      idx <- as.numeric(data.row["idx"])
      h <- min(trees[, "Volume"])
      smile <-     (trees[idx, "Volume"]  - h)/
               (max(trees[   , "Volume"]) - h)
      res <- smiley(smile = smile)
    } else { res <- smiley() }
    return(res)
  }
> pic.plot(trees,
           grp.xy           = Height ~ Girth,
           grp.pic          = Volume,
           grp.color        = Volume,
           vars.to.factor   = c(.25, .3, .05),
           pics             = smiley.gen,
           pic.space.factor = 0.1,
           pic.frame        = FALSE,
           panel.frame      = FALSE,
           main = "smileys represent trees")
```



Remarks: The icon generating function `smiley.gen()` serves as interface between the function `smiley()` which constructs normal-sized smileys and the values of data set `trees`. You see that the values of the volumes are mapped to the interval $[0, 1]$. To implement this approach at first the number of the tree is identified (`idx`). Then the `smile` is found by substracting the minimum and dividing by the span of the values of the variable `Volume`. For there are a lot of different volumes no legends concerning variable `Volume` are added.

In the last example of this section `faces()` of package `aplpack` is used to get *face* icons. At first we call `faces()` and get a data structure describing the line segments of the faces. Then we define standardized icons within a function (`generate.fns()`). The xy values of the output of faces are rearranged, shifted, scaled and stored in the local object `b`. By evaluating suitable character strings we get some icon generating functions and gather them in the list `f.list`.

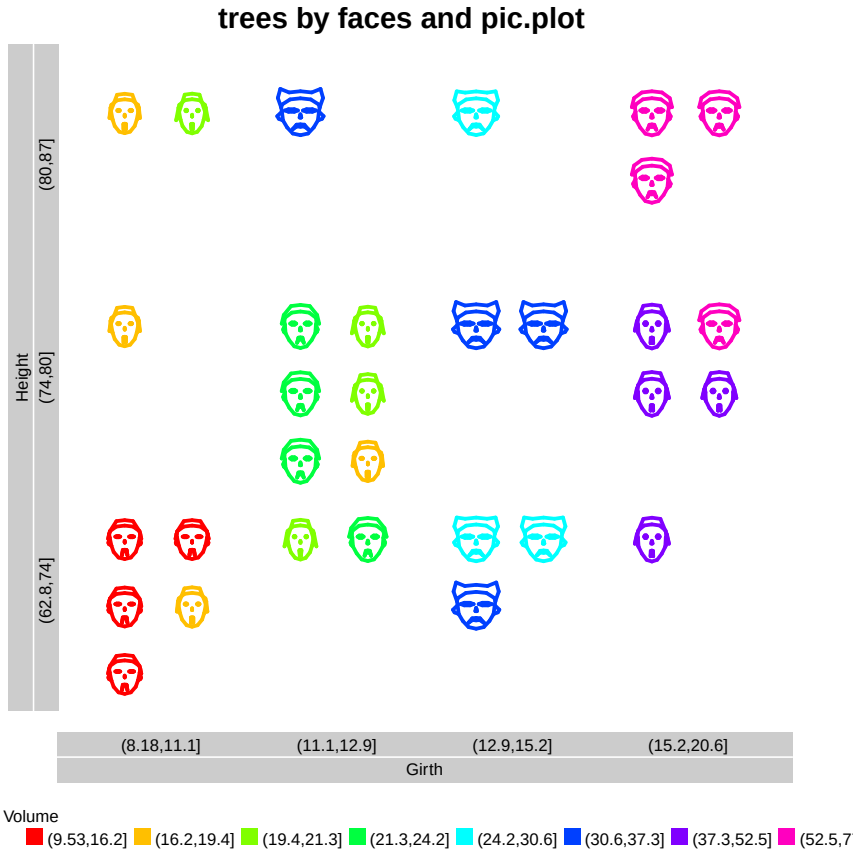
Before calling `pic.plot()` we extend data set `trees` by a column containing the numbers 1, ..., 31. This column is used to find the correct face or icon generating function.

`faces()` 77

```
> generate.fns <- function(set.of.faces, i.set = 16){
    a <- set.of.faces[[1]]; f.list <- NULL
    for(i in i.set){
      ai <- a[[i]];     b <- NULL
      for(k in seq(along=ai)){
        b <- rbind(b, cbind( ai[[k]][ -dim(ai[[k]])[1],, drop=FALSE ],
                             ai[[k]][ -1,, drop=FALSE ], 8, NA))
      }
      b[, 1:4] <- b[, 1:4]/15; b[, c(1,3)] <- b[, c(1,3)] + 10
      class(b) <- "segments"
      fname <- paste(sep = "", "f", i)
      f <- eval(parse(text = c(paste(fname, "<- function()"), deparse(b))))
      f.list <- c(f.list, f)
    }
    f.list
  }
```

78

```
> library(aplpack, lib.loc = "~/lib")
> faces.of.trees <- faces(trees, plot.faces = FALSE)
> f.list <- generate.fns(faces.of.trees, 1:31)
> pic.plot(trees,
           grp.pic          = 3,
           grp.col          = 3,
           vars.to.factors  = c(.25, .3, .12),
           pics             = f.list,
           pic.space.factor = 0.3,
           pic.frame        = FALSE,
           panel.frame      = FALSE,
           lab.cex          = 0.7,
           lab.parallel     = c(TRUE, TRUE, FALSE),
           main = "trees by faces and pic.plot")
```



Remarks: To invoke `faces` it is necessary to load the package `aplpack`. `faces()` is called with the argument `plot.faces=FALSE` to suppress the generation of faces by `faces()`. For we have split the variable `Volume` into 8 ($\approx 1/12$) we get a color legend in contrast to the example with the smileys. The most complicated part of this example solves the task to reorganize the data computed by `faces()` and to define the icon generating functions. Maybe this is only interesting for R users who have a larger amount of experience in R programming. The rest of it is business as usual.

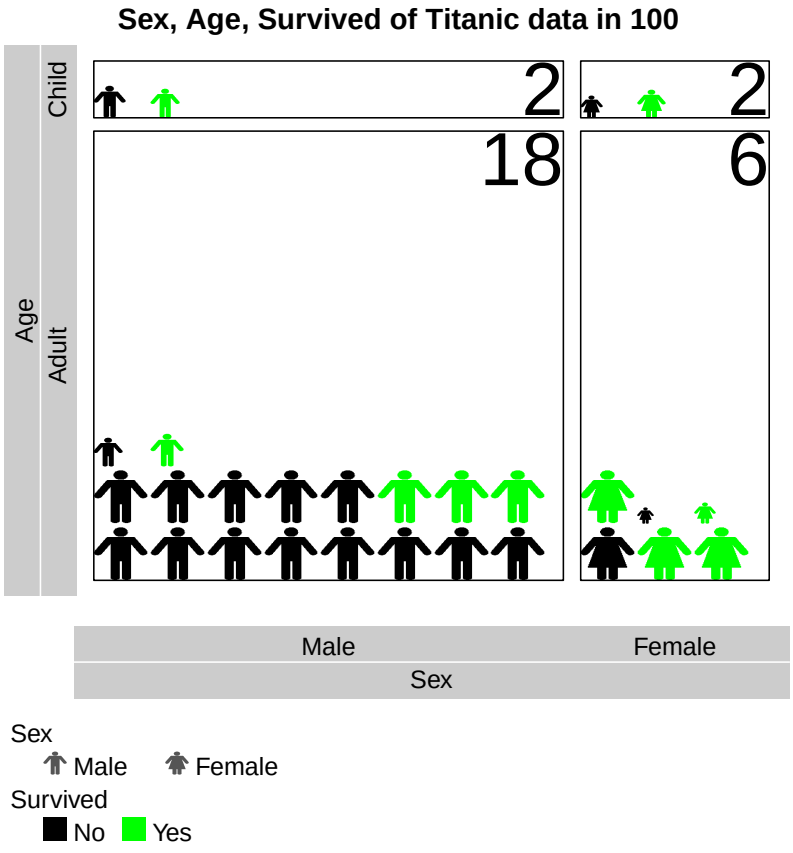
14 Graphical Add-ons for Pictogram Plots

After calling a high-level plotting function you often invoke some low-level plotting function to tune the plot. Therefore you wonder whether you can add some graphical elements to a pictogram plot. Indeed `pic.plot()` returns a list of three elements: The first element is a matrix and characterizes the panels whose columns have the names `xmins, xmaxs, ymins, ymaxs, job.no, counts, row, col`. So the first four columns store the coordinates of the world windows of the panels. `counts` show the number of elements drawn in the panels and `row` and `col` tell you the indices of the panels in a matrix like interpretation of a panel grid. Column five holds `job.no` which links the panels to the elements of the data matrix stored in the second element of the list. By the way, the data matrix is expanded by some additional variables showing `sign, fraction.1, color, pic, job.no, x0, y0` – all the information that may be interesting concerning a single pictogram element.

In the first example of this section we want to add the number of cells to the panels and recall an example of a prior section.

additional elements 79

```
> p.set <- c("m2.pnm", "f2.pnm")
> data <- margin.table(Titanic/100, 2:4)
> result <- pic.plot(data,
            grp.xy             = Age ~ Sex,
            grp.color          = Survived,
            grp.pic            = Sex,
            colors             = c("black", "green"),
            pics               = p.set,
            vars.to.factors    = c(2, 3, 6),
            panel.prop.to.size = 0.7,
            panel.reverse.y    = TRUE,
            pic.stack.type     = "s",
            pic.frame          = FALSE,
            pic.space.factor   = 0.05,
            lab.parallel       = c(TRUE, TRUE, FALSE),
            main               = "Sex, Age, Survived of Titanic data in 100")
> coor   <- result[[1]][,1:4]; counts <- result[[1]][,"counts"]
> old <- par(result$newpar)
> text(coor[,2], coor[,4], as.character(counts), cex = 3, adj = c(1,1))
> par(result$old)
```



Remarks: You see there is no magic in adding some graphical elements to pictogram plot. The

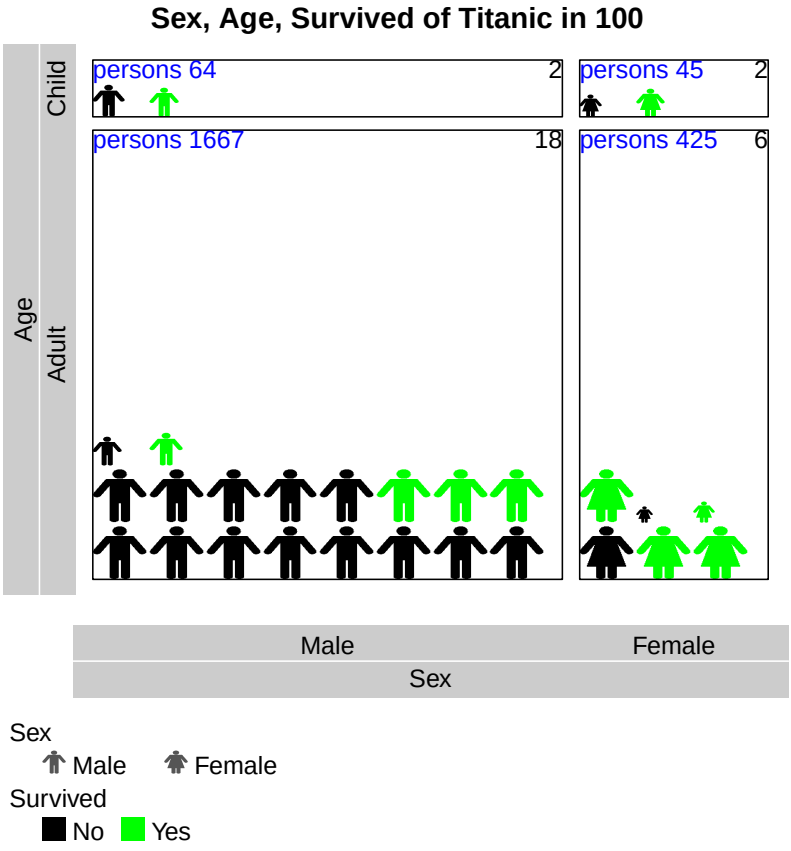
argument `xpd` has been set to prevent clipping.

You may argue that you aren't interested in the number of pictogram icons but in the real number of passengers in the panels. Therefore, you have to compute these numbers from the information of the result or you have to extract them from the data input. A solution is presented in the next example:

using output of pic.plot()

80

```
> p.set <- c("m2.pnm", "f2.pnm")
> data <- margin.table(Titanic/100, 2:4)
> result <- pic.plot(data,
            grp.xy             = Age ~ Sex,
            grp.color          = "Survived",
            grp.pic            = "Sex",
            colors             = c("black", "green"),
            pics               = p.set,
            vars.to.factors    = c(2, 3, 6),
            panel.prop.to.size = 0.7,
            panel.reverse.y    = TRUE,
            pic.stack.type     = "s",
            pic.frame          = FALSE,
            pic.space.factor   = 0.05,
            lab.parallel       = c(TRUE, TRUE, FALSE),
            main               = "Sex, Age, Survived of Titanic in 100")
> coor <- result[[1]][,1:4]; counts <- result[[1]][,"counts"]
> old <- par(result$newpar)
> text(coor[,2], coor[,4], as.character(counts), cex = 1, adj = c(1,1))
> dm <- result[[2]]
> no <- 100 * sapply(split(dm[,"fraction.1"], dm[,"job.no"]), sum)
> idx <- rank(result[[1]][,"job.no"])
> text(coor[idx, 1], coor[idx, 4], paste("persons", no),
       cex = 1, adj = c(0,1), col = "blue")
> par(result$old); margin.table(Titanic, c(3:2))

named list()

       Sex
Age     Male Female
  Child   64     45
  Adult 1667    425
```



Remarks: Observing the marginal contingency table we see the trick works: After splitting the variable `fraction.1` according to the `job.no` we sum up the numbers and multiply them by 100. To find the correct panel we have to evaluate the link information between the data matrix and the matrix carrying the coordinate information.

The results of `pic.plot()` can be used by other functions. In a more complicated example we demonstrate this point. The main idea is to use the framework of `pic.plot()` but ignore the drawing of pictogram elements. Instead of packing icons other *packers* can be defined and activated.

For a demonstration we created the function `grp.plot()` which calls the pictogram function and constructs within the panels xy-plots of groups of data. Have a look at the structure of the function:

```
grp.plot <- function( <arguments skipped> ){
  <call [[pic.plot()]]>
  <split [[pic.plot.result]]>
  <set environment for [[panel.function()]]>
  <set graphics parameters>
  <initialize plot>
  for(j in seq(dim(jobs)[1])){
    <choose data ([[dm]]) and graphics parameter for panel [[j]]>
    <activate packer>
    <active panel function and draw box>
  }
}
```

You see that `pic.plot` is invoked and after organizing some graphical parameters we fill the panels in a loop along the *jobs*. How the groups are represented is defined by a panel function. The panel function of the following example is defined by: 81

```
> my.panel.function <- function(){
    if(0 == length(dm)) return()
    xx <- dm[, panel.x]; yy <- dm[, panel.y]
    points(xx, yy, col = "green", pch = 16, cex = 2)
    if(length(xx) < 2) return()
    abline(lm(yy ~ xx)$coef, col = "red", lwd = 4)
  }
```

Obviously the function should plot some points. If there is more than one data point a regression line should be added.

For the demonstration we use the data set `USJudgeRatings`. Here are the first lines of it: 82

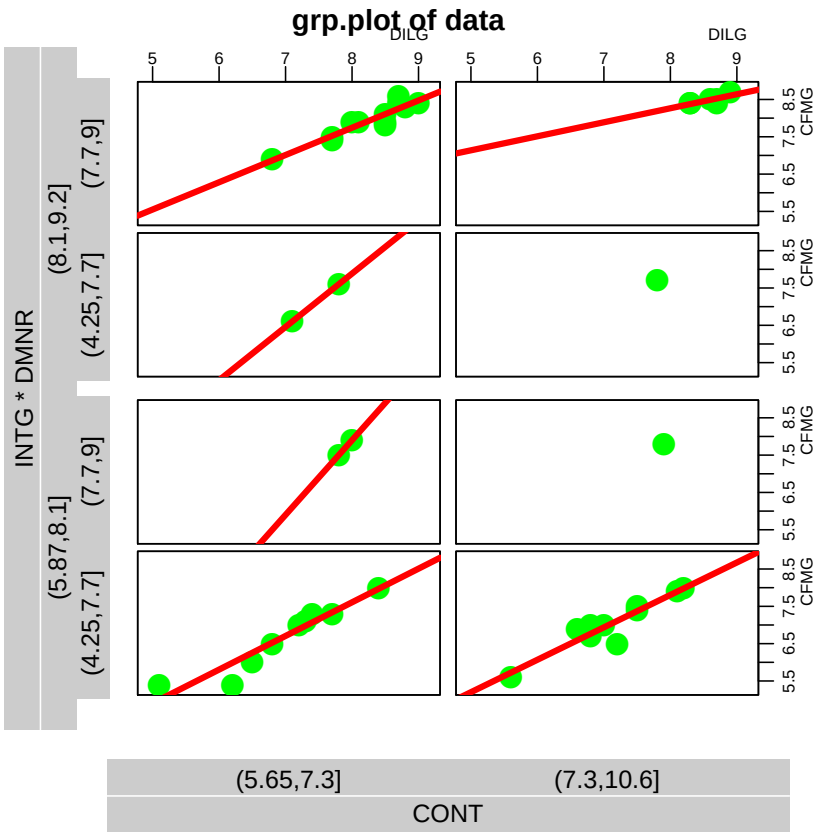
```
> USJudgeRatings[1:5,]
```

	CONT	INTG	DMNR	DILG	CFMG	DECI	PREP	FAMI	ORAL	WRIT	PHYS	RTEN
AARONSON,L.H.	5.7	7.9	7.7	7.3	7.1	7.4	7.1	7.1	7.1	7.0	8.3	7.8
ALEXANDER,J.M.	6.8	8.9	8.8	8.5	7.8	8.1	8.0	8.0	7.8	7.9	8.5	8.7
ARMENTANO,A.J.	7.2	8.1	7.8	7.8	7.5	7.6	7.5	7.5	7.3	7.4	7.9	7.8
BERDON,R.I.	6.8	8.8	8.5	8.8	8.3	8.5	8.7	8.7	8.4	8.5	8.8	8.7
BRACKEN,J.J.	7.3	6.4	4.3	6.5	6.0	6.2	5.7	5.7	5.1	5.3	5.5	4.8

Now, the call of `grp.plot()` contains some arguments known from function`pic.plot()`. The other ones are arguments specifying the task to be done.

grp.plot() scatterplots within panels 83

```
> grp.plot(USJudgeRatings,
           grp.xy             = 2 + 3 ~ 1,
           vars.to.factors    = c(.5, .5, .5),
           panel.space.factor = 0.05,
           packer             = "xy.plot",
           panel.x            = "DILG",
           panel.y            = "CFMG",
           panel.axes         = c("lb","rt")[2],
           panel.function     = my.panel.function
  )
```

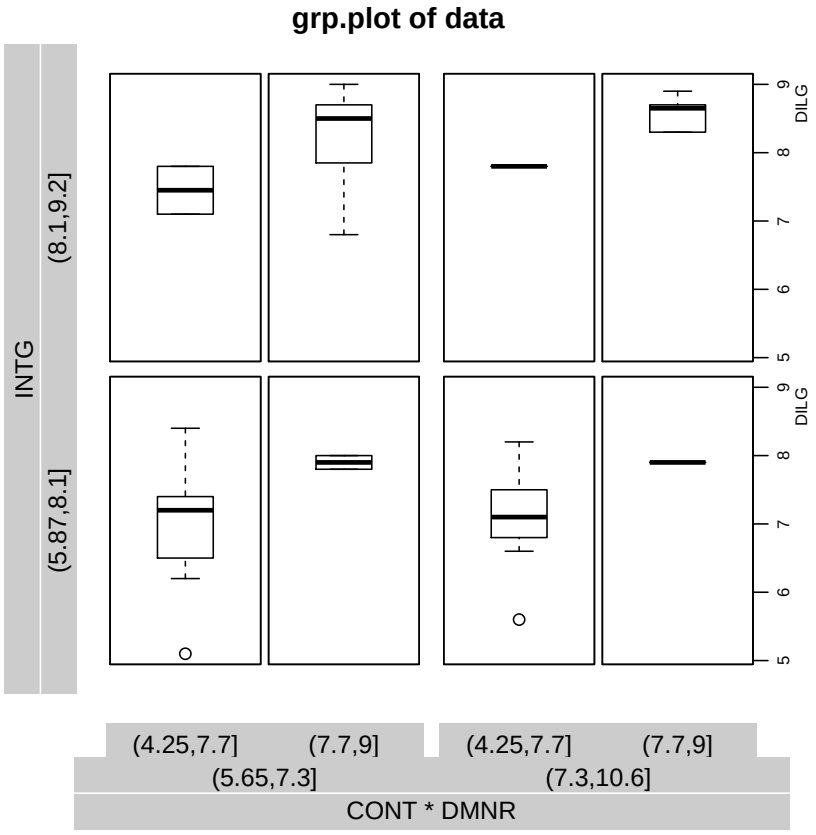


Remarks: Let's study the statement and the result. The first four arguments are forwarded to `pic.plot()`. `grp.plot()` catches the results of the call and uses the attributes of the 12 panels to create xy-plots of the data belonging to the panels.

It is obvious to invoke other packers and we present you a packer packing boxplots into the areas of the panels.

boxplots within panels 84

```
> grp.plot(USJudgeRatings,
           grp.xy             = 2 ~ 1 + 3,
           vars.to.factors    = c(.5, .5, .5),
           panel.space.factor = 0.05,
           packer             = "boxplot",
           panel.x            = "DILG",
           panel.axes         = c("lb","rt")[2]
  )
```



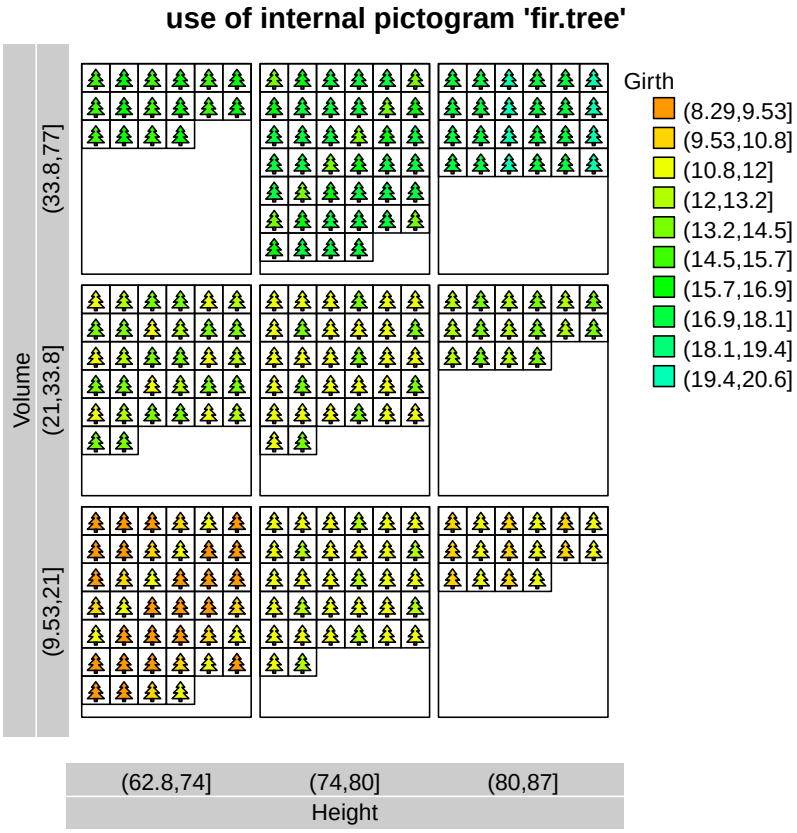
Remarks: The results will remember you at graphics produced by the packages `lattice graphics` or `ggplot2`. Both of them have a special approach to organize the elements of graphics. The same is true for `pic.plot()`. Maybe an advantage of the new approach is that it is based on the standard graphics system of R. These short explanations should be enough as a demonstration of the idea of using the framework of `pic.plot()`. Now you are welcome to develop your own applications with `pic.plot()`.

15 Built-in generating pictograms

The programming of new icons or pictograms may be a boring talk. Therefore, an internal pictogram generator has been defined which allows to use some built-in pictograms. To reference an internal pictogram you have to deliver its name by argument `pics`, too. Here is a simple example representing trees by `fir.trees`.

built-in pictograms 85

```
> data <- rbind(trees,trees,trees,trees,trees,trees,trees,trees)
> pic.plot(data, vars.to.factors = c(10, .33, .33),
           grp.xy           = Volume ~ Height,
           grp.color        = Girth,
           grp.pic          = 0,
           pics             = "fir.tree",
           colors           = rainbow(10, start = .1, end = .45),
           lab.legend = "vertical", pic.space.factor = 0, lab.cex = 0.9,
           main       = "use of internal pictogram 'fir.tree'")
```

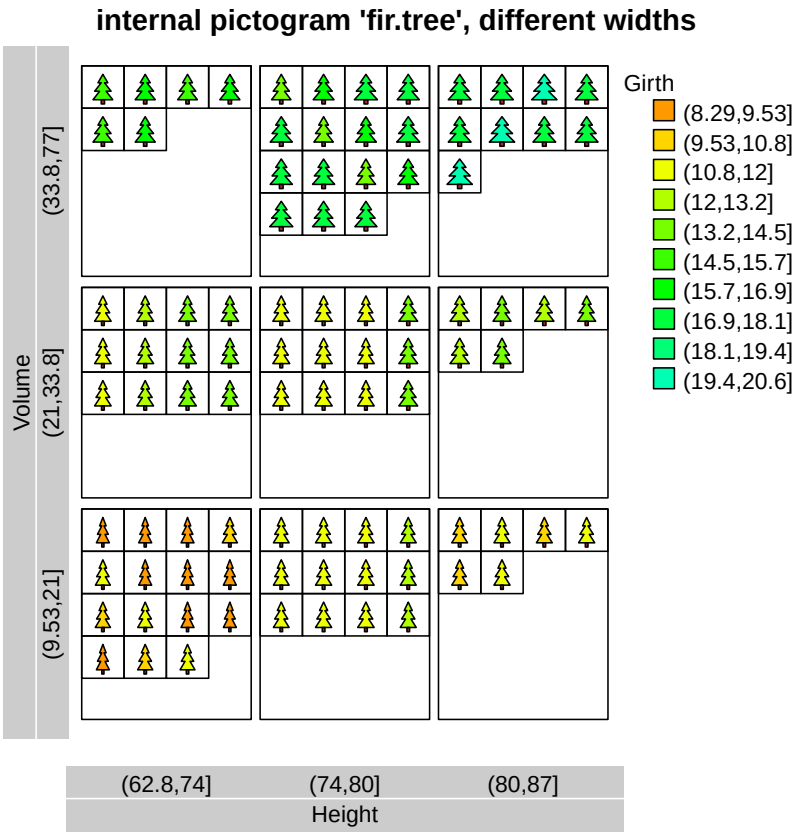


Remarks: Each of the pictograms represents a single tree and the colors are defined by variable `Girth`. The setting `grp.pic = .` indicates that there is no variable responsible for choosing a special pictogram out of a set and there is used one symbol only. This assignment can be omitted.

The 'fir.tree' pictogram allows you to modify its width and height by a variable of the data set. Here is an example showing smaller and bigger trees and the widths of the trees are defined by the variable Width of the data set. To get the desired effect in the call . | Width is assigned to pics.

modifying characteristics 86

```
> data <- rbind(trees,trees,trees)
> w <- data$Volume^(1/3); w <- w/max(w)
> data <- cbind(data, Width = w)
> pic.plot(data, vars.to.factors = c(10, .33, .33, FALSE),
           grp.xy           = Volume ~ Height,
           grp.color        = Girth,
           grp.pic          = 0 | Width,
           pics             = "fir.tree",
           colors           = rainbow(10, start = .1, end = .45),
           lab.legend = "vertical", pic.space.factor = 0, lab.cex = 0.9,
           main       = "internal pictogram 'fir.tree', different widths")
```

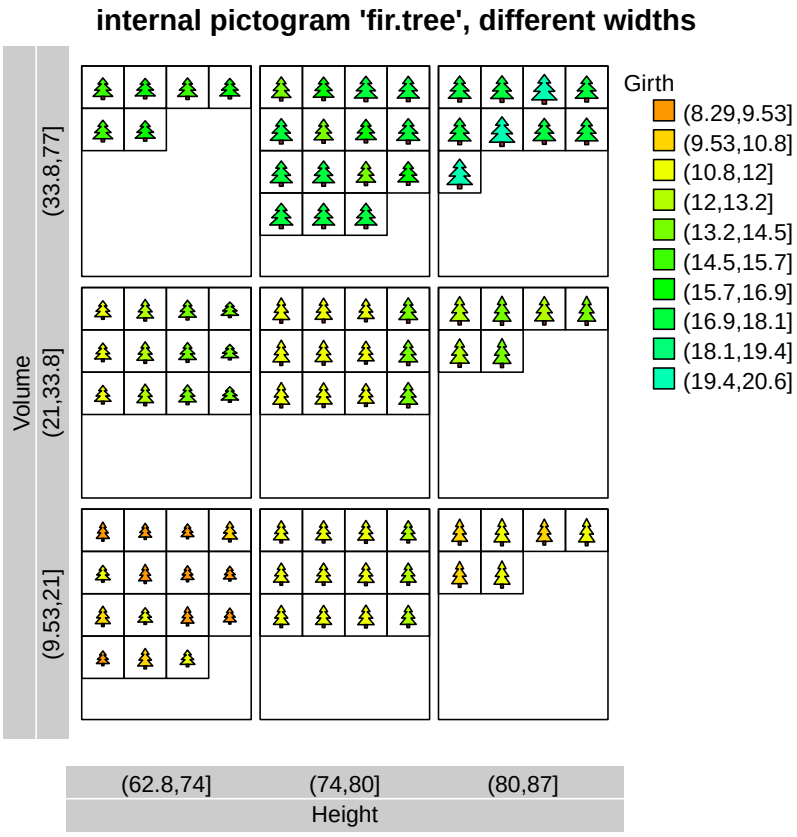


Remarks: The vector of values defining the widths of the trees has to lie within the interval [0,1]. Greater values are replaced by 1 and negative ones by 0. Note that the fourth variable isn't converted to a factor variable because the fourth element of vars.to.factors is set to FALSE. The pipe character divides the variable responsible for choosing the pictogram from further specifications. This kind of notation is known from other contexts like setting parameters of a function.

To get trees of different heights we have to deliver another variable to argument `pics`. This is shown by the following example.

trees of different widths and heights 87

```
> data <- rbind(trees,trees,trees)
> w <- data$Volume^(1/3); w <- w/max(w)
> s <- data$Height; s <- s - min(s); s <- s/max(s); s <- (s + 1)/2
> data <- cbind(data, Width = w, Size = s)
> pic.plot(data, vars.to.factors = c(10, .33, .33, FALSE, FALSE),
           grp.xy           = Volume ~ Height,
           grp.color        = Girth,
           grp.pic          = 0 | Width + Size,
           pics             = "fir.tree",
           colors           = rainbow(10, start = .1, end = .45),
           lab.legend = "vertical", pic.space.factor = 0, lab.cex = 0.9,
           main       = "internal pictogram 'fir.tree', different widths")
```

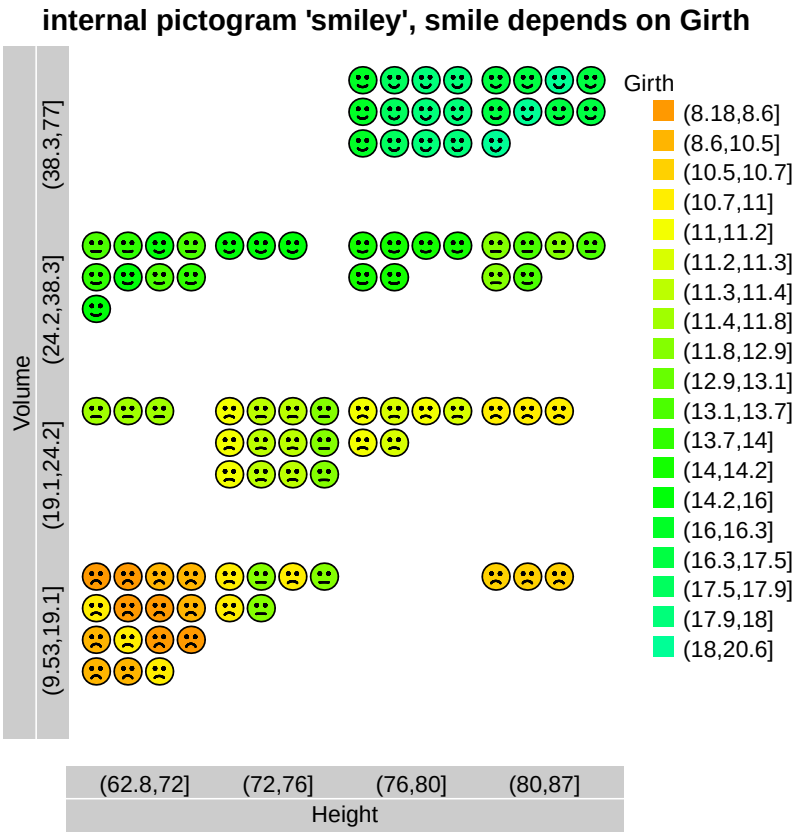


Remarks: The variable `Size` is constructed in a way that its values fall into the interval [0.5, 1]. Therefore, the height of the tallest tree is equal to the height of the smallest tree times two. Note that the point before the pipe character must not be removed.

There is a set of pictograms integrated within `pic.plot()`. The number of characteristics that can be changed by variables varies: The `fir.tree` pictogram has two properties to be modified and the integrated `smiley` pictogram has one slot to change the layout of its smile.

`internal smiley pictogram` 88

```
> data <- rbind(trees,trees,trees)
> pic.plot(data, vars.to.factors = c(.05, .25, .25),
           grp.xy           = Volume ~ Height,
           grp.color        = Girth,
           grp.pic          = 0 | Girth,
           pics             = "smiley",
           colors           = rainbow(20, start = .1, end = .45),
           pic.frame        = FALSE,
           panel.frame      = FALSE,
           lab.legend = "vertical", pic.space.factor = 0.1, lab.cex = 0.9,
           main       = "internal pictogram 'smiley', smile depends on Girth")
```



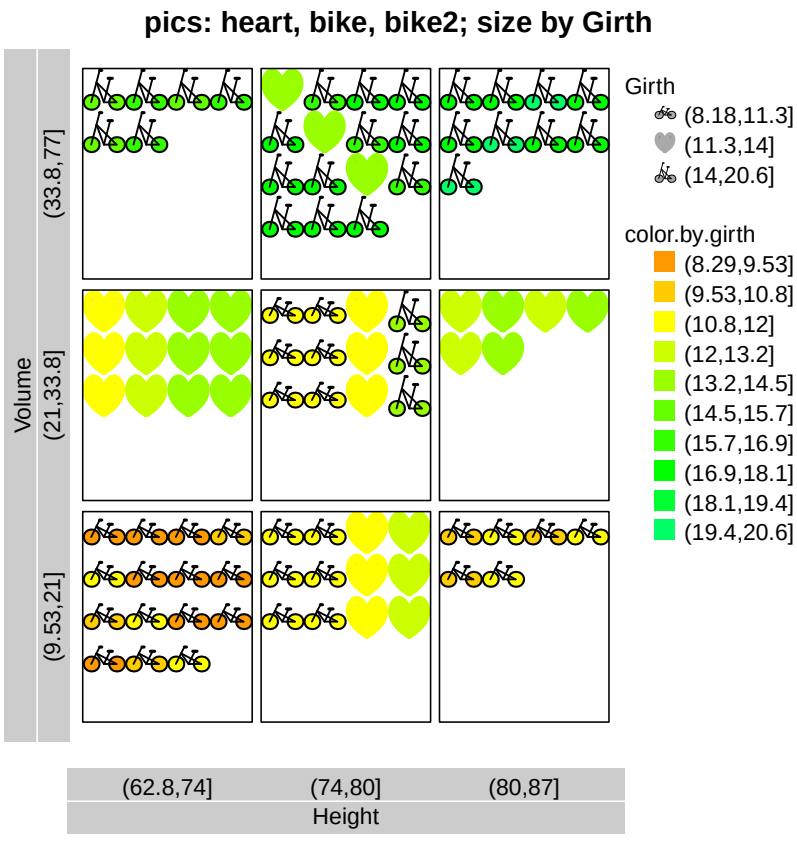
Remarks: The smiling and the color of the pictograms depend on the same variable `Girth`. However, in this version of `pic.plot()` the controlled layouts of the pictograms are not explained by a legend. Therefore, the user has to comment on it in the paper which includes the pictogram.

Now we split the range of one variable into three parts (see: `vars.to.factors[1]`) and represent the items by three different pictograms (`grp.pic = Girth`). The color should also depend on variable `Girth`. But as we want to have 10 different colors we build the new variable (`color.by.grith`) and convert it to get 10 different levels (see: `vars.to.factors[4]`). Furthermore, we want to fix the sizes of the elements by `Girth` and we transform the first column whose result is appended to our data set.

`heart, bike, bike2`

89

```
> data <- rbind(trees, trees, trees)
> s <- data$Girth; s <- s - min(s); s <- s/max(s); s <- (s + 1)/2
> data <- cbind(data, color.by.girth = data[,"Girth"], fraction.1 = s)
> pic.plot(data, vars.to.factors = c(.33, .33, .33, 10),
           grp.xy           = Volume ~ Height,
           grp.color        = color.by.girth,
           grp.pic          = Girth,
           pics             = c("bike", "heart", "bike2"),
           colors           = rainbow(10, start = .1, end = .40),
           pic.frame        = FALSE,
           lab.legend = "vertical", pic.space.factor = 0, lab.cex = 0.9,
           main       = "pics: heart, bike, bike2; size by Girth")
```



Remarks: The fifth column gets the name `fraction.1` because this is the special name for the column defining the sizes of the pictograms.

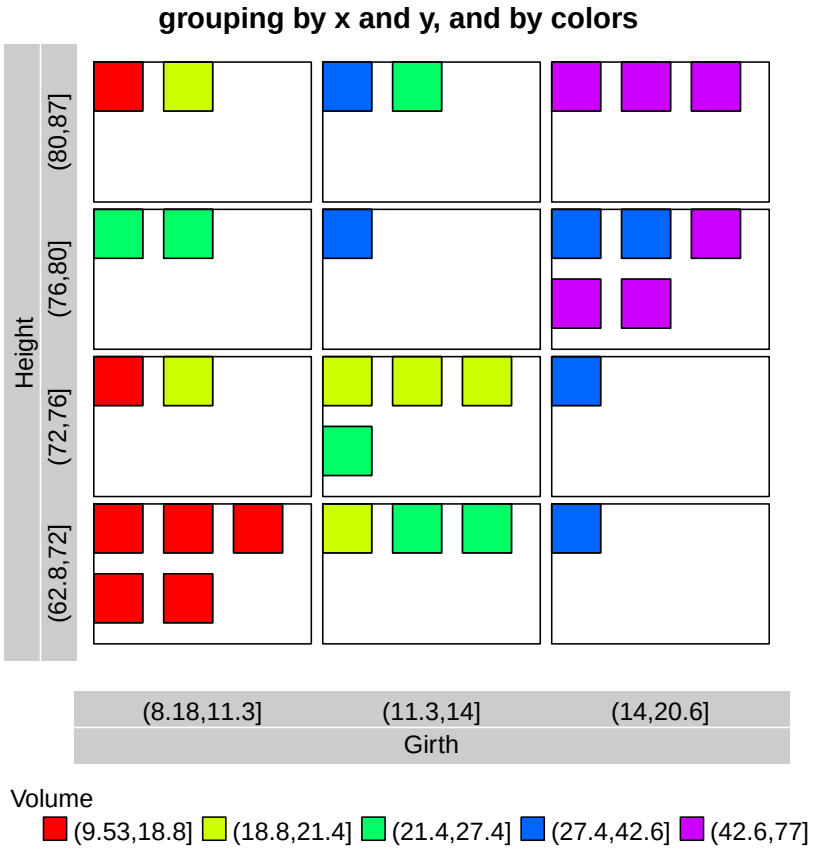
16 Different Color and Pictogram Legends

A color legend will be constructed if the set of colors used contains more than one and less than `lab.n.max[3] + 1` elements. The same condition holds for pictogram legends. In this section we present the different types of legends of `pic.plot()` which are called `cols, rows, skewed, horizontal, vertical`. The default type is `rows` and is changed by setting argument `lab.legend`.

At first we show the five different layouts concerning the color legends. In the following example the third variable of the data set `trees` is used to define the colors of the pictograms.

`color legend`
`default: rows`
90

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.2),
           main = "grouping by x and y, and by colors")
```



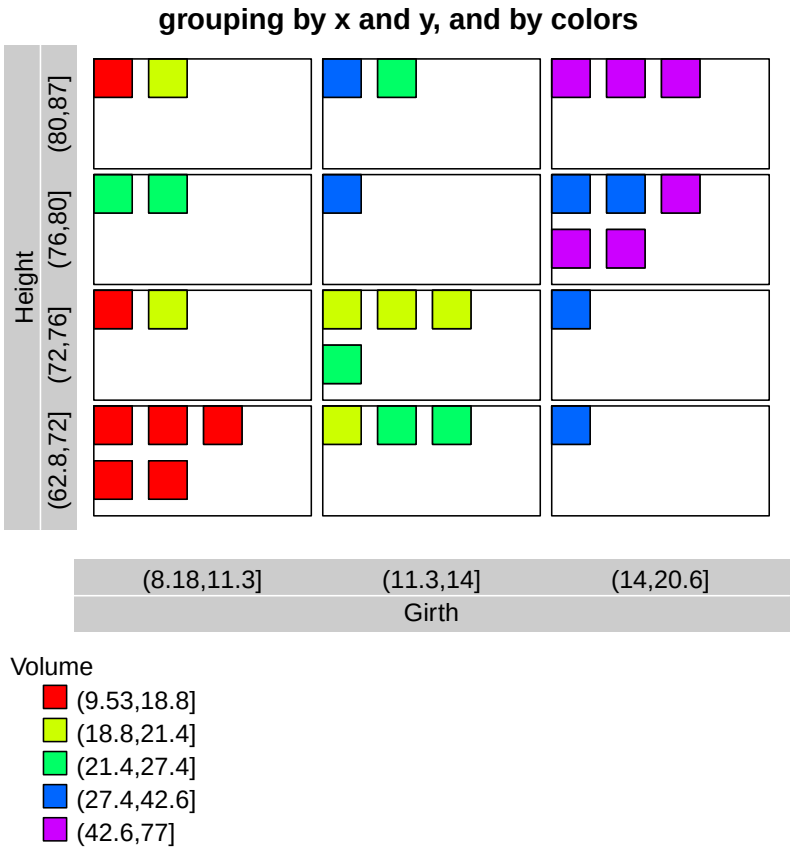
Remarks: For the argument `lab.legend` hasn't been set in the call we get the default legend type. The different colors and the labels of the levels are arranged side by side and build a *row*. A pictogram legend isn't needed and is missing.

To get a legend in a column we choose the option *cols*:

```
color legend
type:  rows
```

91

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.2),
           lab.legend     = "cols",
           main = "grouping by x and y, and by colors")
```



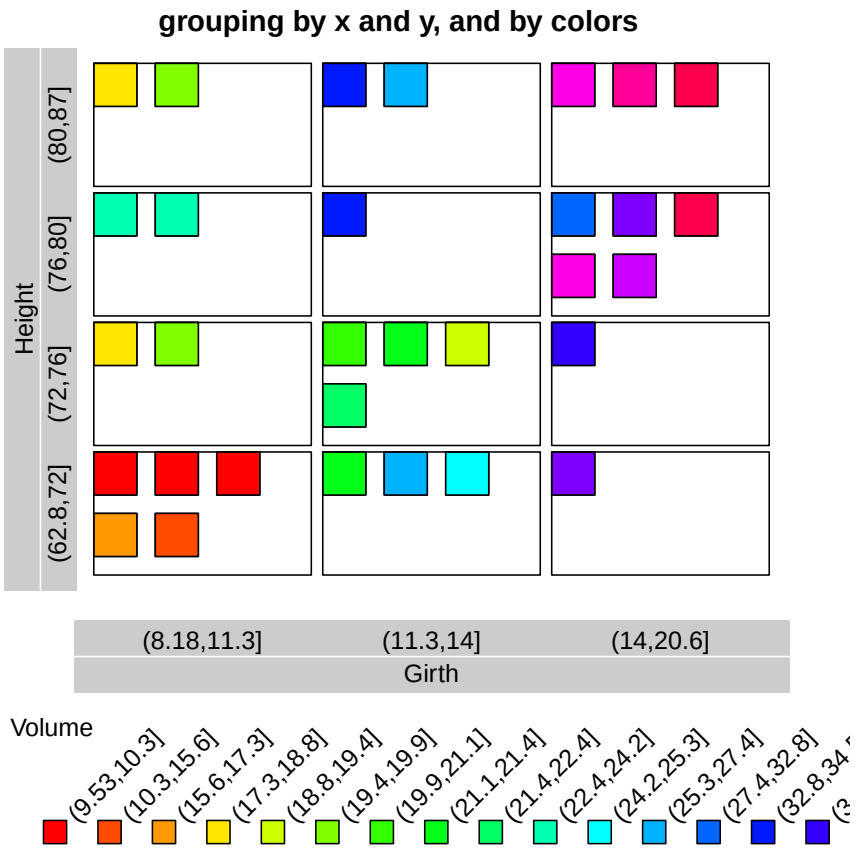
Remarks: This arrangement is advisable if the labels of the variable are very long and the list of the colors is short.

If there are a lot of items the types *skewed* or *horizontal* are preferable. Here is an example for *skewed*. By the third element of `vars.to.factor = c(0.333, 0.25, 0.05)` we split the range of variable `Volume` in 20 areas and the color legend has to explain 20 colors.

`color legend type skewed`

92

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.legend     = "skewed",
           main = "grouping by x and y, and by colors")
```

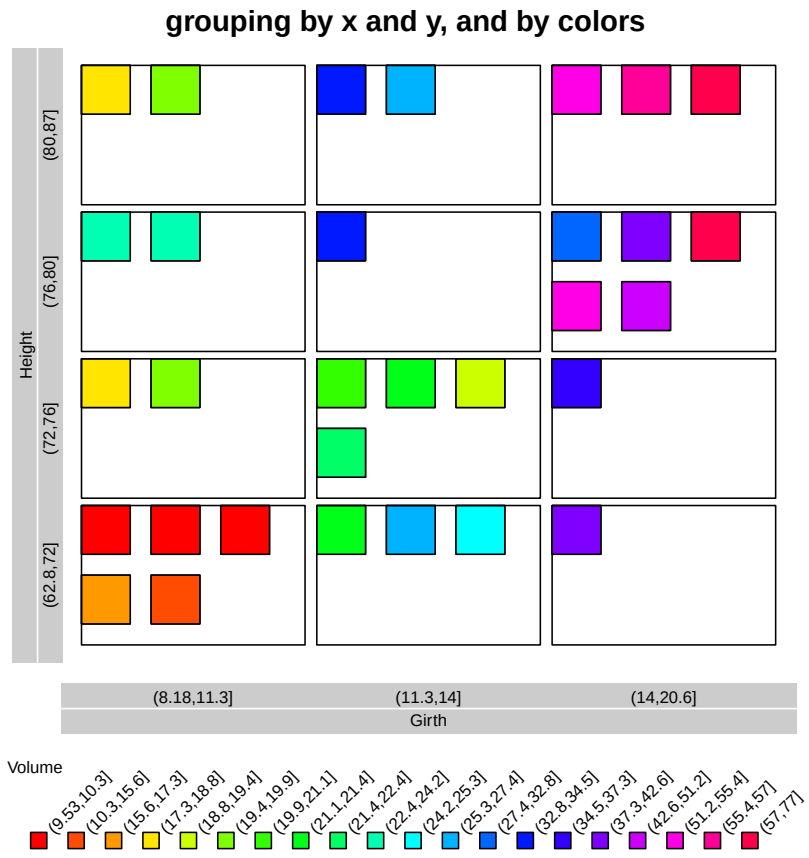


Remarks: This type is called *skewed* because the labels have been rotated. Check if your graphics device is able to plot rotated texts. An inspection of the result shows that the space for the legend is too small and the legend is clipped by the device.

To reduce the space needed for the color legend we reduce the size of the labels by argument `lab.cex`.

color legend
lab.cex = 0.7
93

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.legend     = "skewed",
           lab.cex        = 0.7,
           main = "grouping by x and y, and by colors")
```

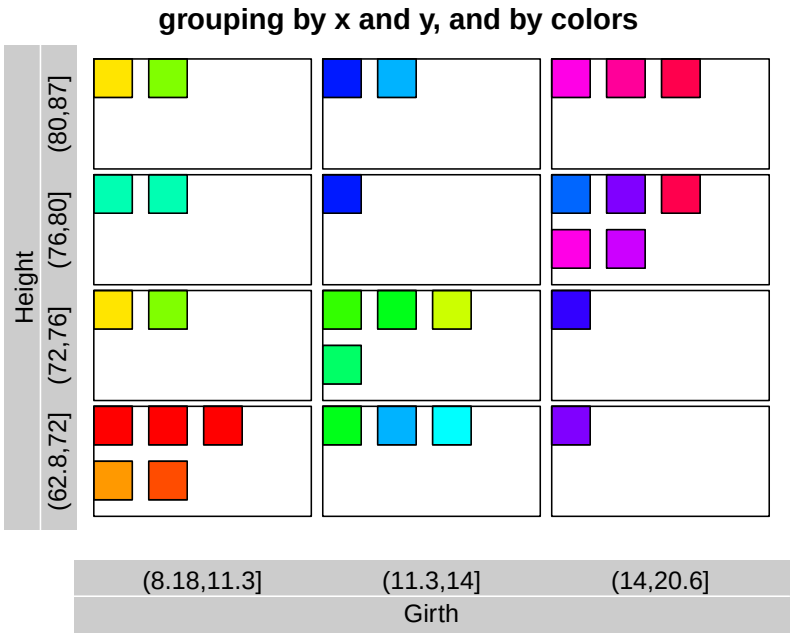


Remarks: By reducing the text size all level labels fit into the space scheduled for the legend.

The *horizontal* option results in a *horizontal* legend with vertical labels.

color legend horizontal
94

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.legend     = "horizontal",
           main = "grouping by x and y, and by colors")
```

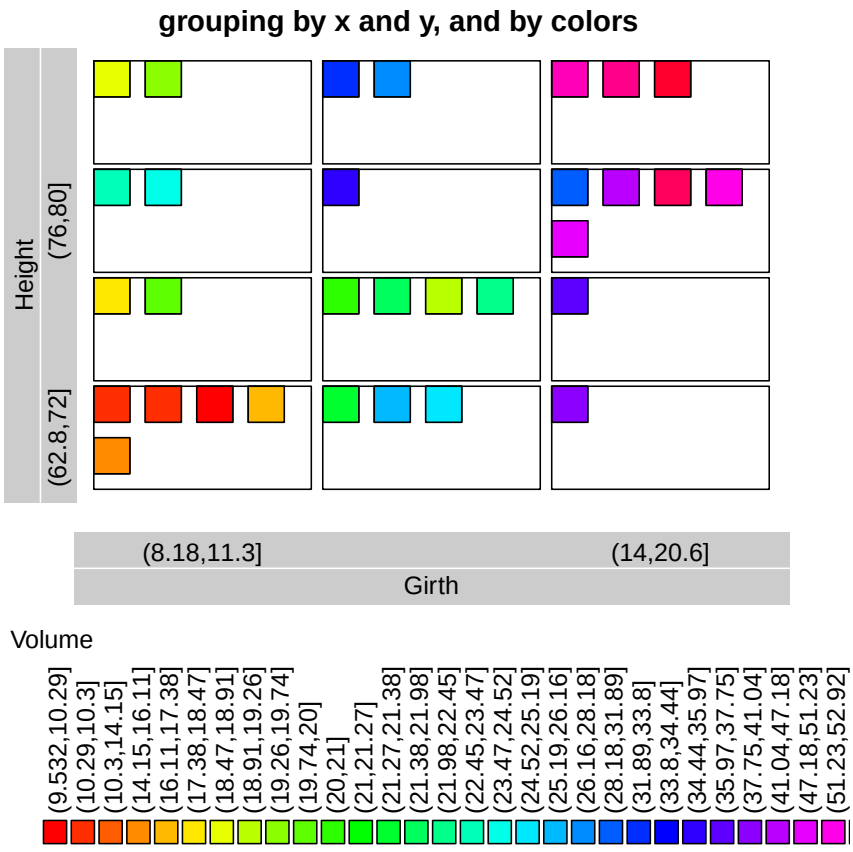


Remarks: Now the legend is parallel to the x-axis. This types allows to deal with a large number of items.

If the number of items exceeds 20 the legend is suppressed by default. To increase the limit of 20 you have to choose a suitable value for the third element of `lab.n.max`.

color legend
lab.n.max
95

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.03),
           lab.legend     = "horizontal",
           lab.n.max      = c(15, 2, 33),
           main = "grouping by x and y, and by colors")
```

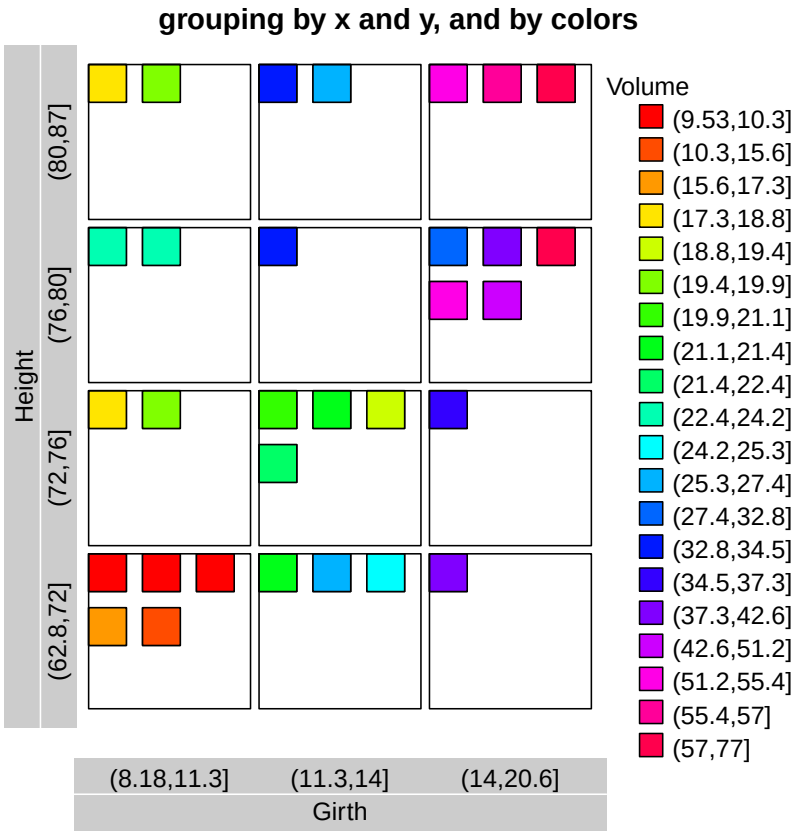


Remarks: The range of variable `Volume` is now split into 33 areas. Therefore, setting `lab.n.max[3] = 33` works. By the way the first element of `lab.n.max` defines the maximal number of characters of the labels and the second one limits the number of items of the xy-labels – you see that two intervals of `Girth` are labeled in margin just below the plot.

The option *vertical* constructs the fifth type.

color legend vertical 96

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.legend     = "vertical",
           main = "grouping by x and y, and by colors")
```

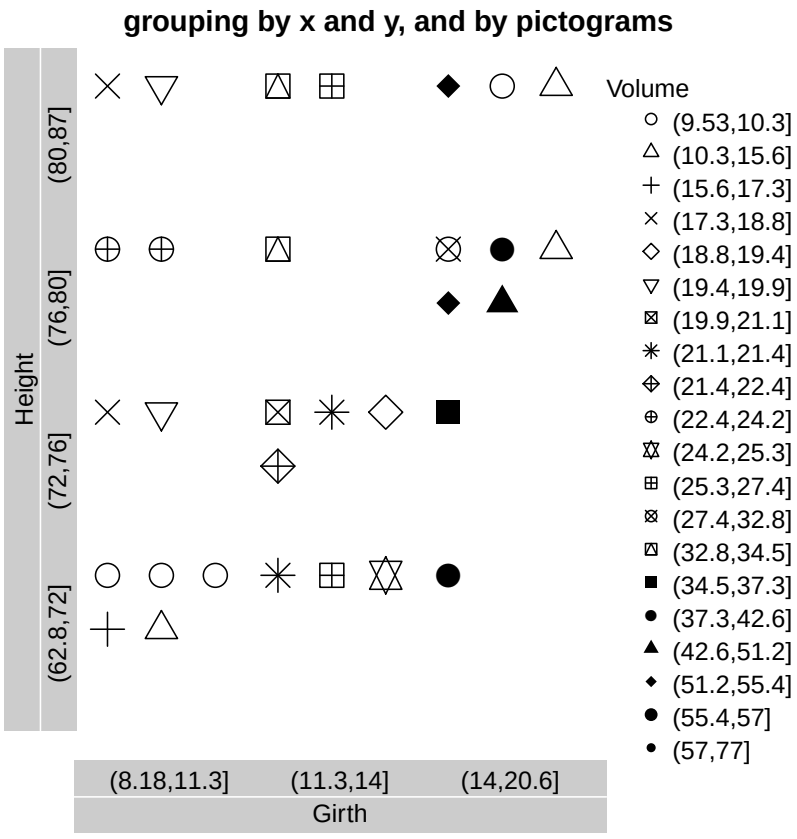


Remarks: Now the right-hand margin is increased and a vertical legend is plotted on the right side of the plot. Especially if there are many short labels this type is preferable.

We modify the last example and set `grp.pic` instead of `grp.color`. To get a new appearance we suppress the frames around the panels and pictogram elements.

pic legend vertical 97

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.pic        = 3,
           vars.to.factor = c(0.333, 0.25, 0.05),
           panel.frame    = FALSE,
           pic.frame      = FALSE,
           lab.legend     = "vertical",
           main = "grouping by x and y, and by pictograms")
```

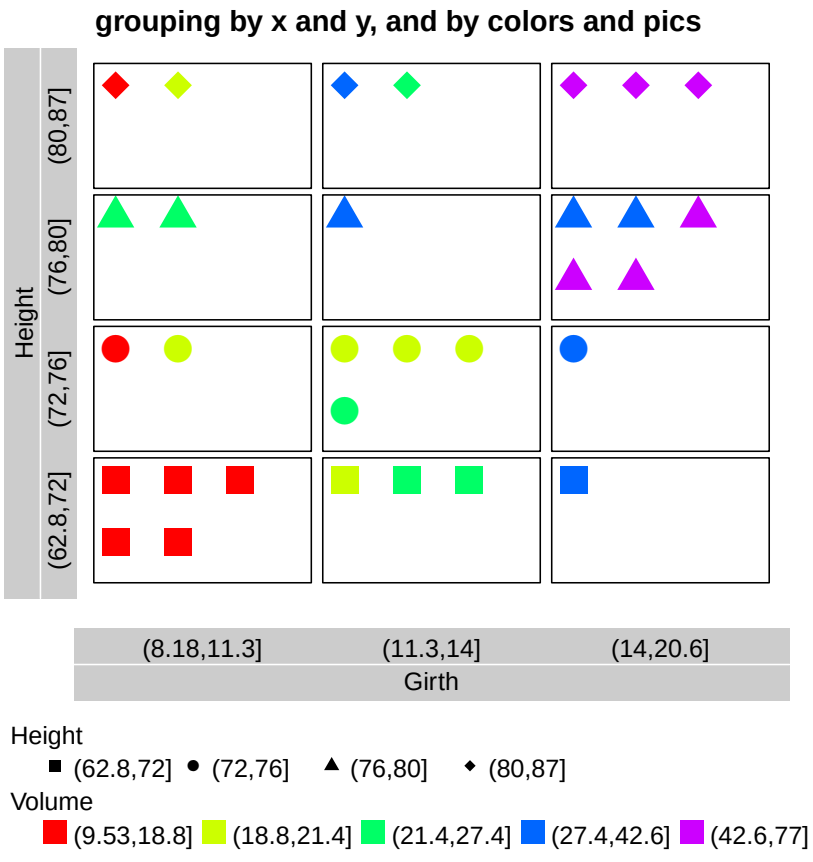


Remarks: You see that the layout of the legend has not been changed.

two legends default 98

Now let us have a look at a pictogram plot with two legends.

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           grp.pic        = 2,
           pics           = 15:18,
           pic.frame      = FALSE,
           vars.to.factor = c(0.333, 0.25, 0.2),
           lab.legend     = "rows",
           main = "grouping by x and y, and by colors and pics")
```

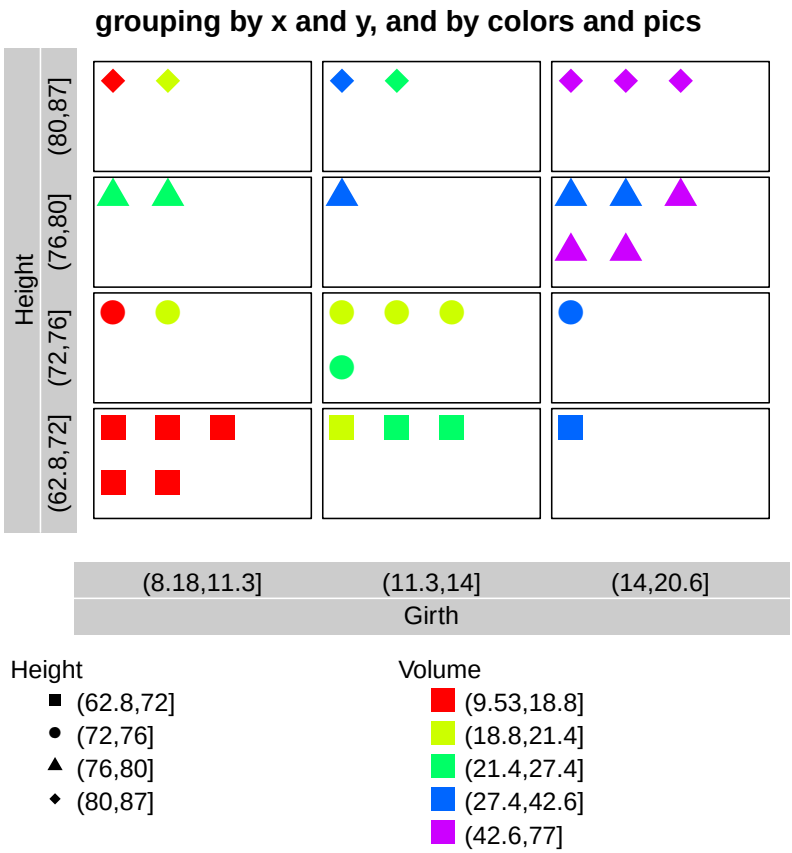


Remarks: The default setting results in two legends at the bottom side of the plot which looks like two *rows*.

1 To get two legends in a layout consisting of two columns we choose the type *cols*.

two legends
type cols
99

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           grp.pic        = 2,
           pics           = 15:18,
           pic.frame      = FALSE,
           vars.to.factor = c(0.333, 0.25, 0.2),
           lab.legend     = "cols",
           main = "grouping by x and y, and by colors and pics")
```



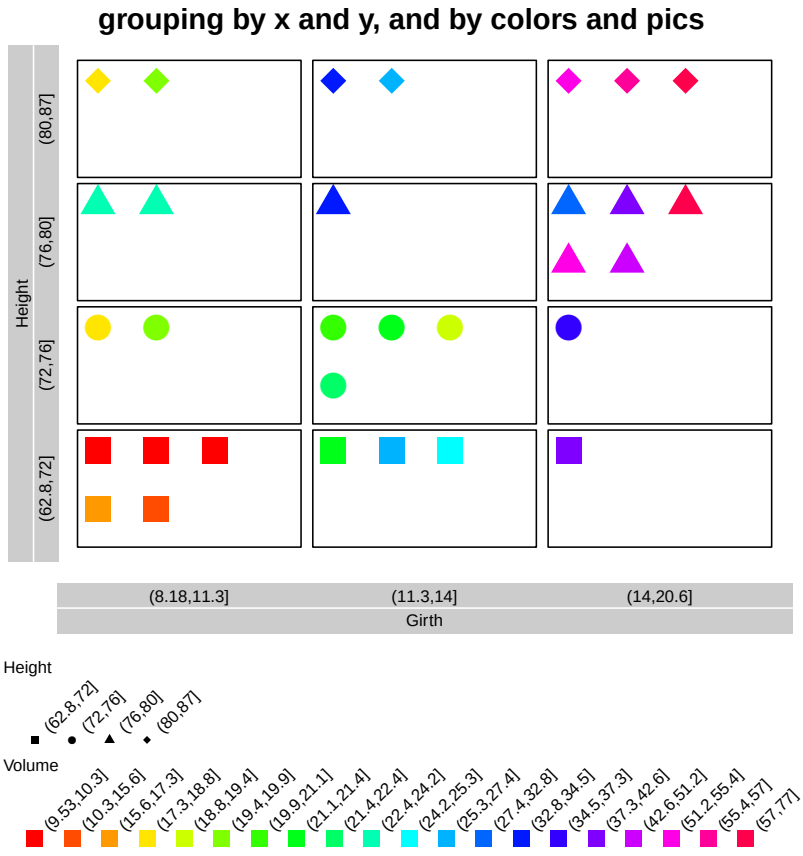
2

3 Remarks: We get a clear arrangement which may be fine for sheets of paper.

two legends
skewed
100

If we have a lot of items the *skewed* type may be a good alternative.

```
> pic.plot(trees,
           grp.xy          = 2 ~ 1,
           grp.color       = 3,
           grp.pic         = 2,
           pics            = 15:18,
           pic.frame       = FALSE,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.legend      = "skewed",
           lab.cex         = 0.7,
           main = "grouping by x and y, and by colors and pics")
```

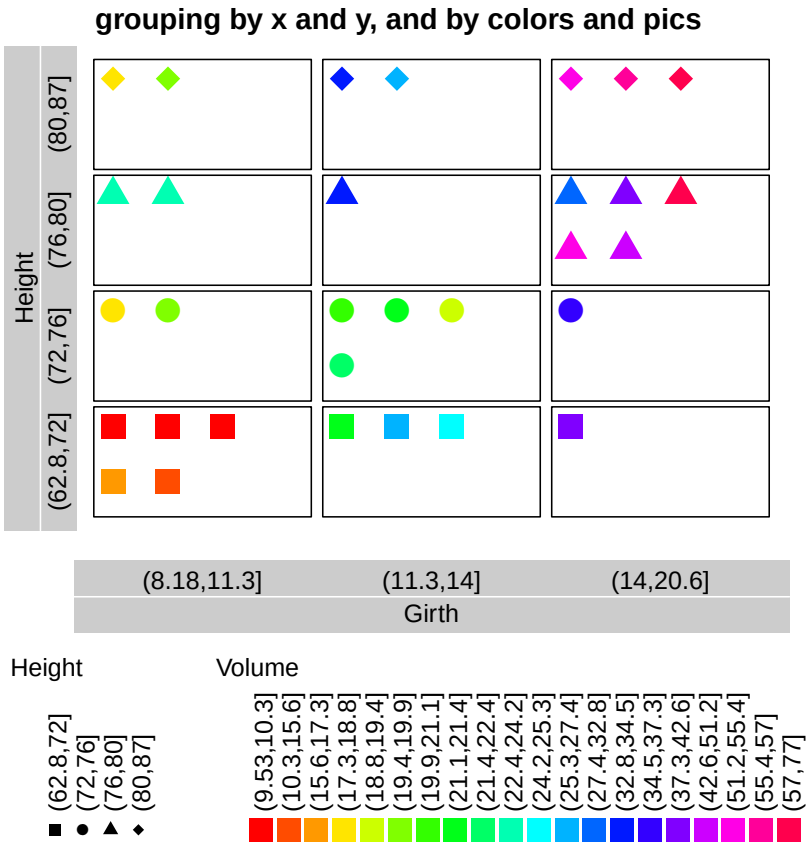


Remarks: In this example we see again that the size of labels has to be reduced. Otherwise the legend of the colors is clipped.

The *horizontal* type is the second answer to the problem of space.

two legends
horizontal
101

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           grp.pic        = 2,
           pics           = 15:18,
           pic.frame      = FALSE,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.cex        = 1,
           lab.legend     = "horizontal",
           main = "grouping by x and y, and by colors and pics")
```

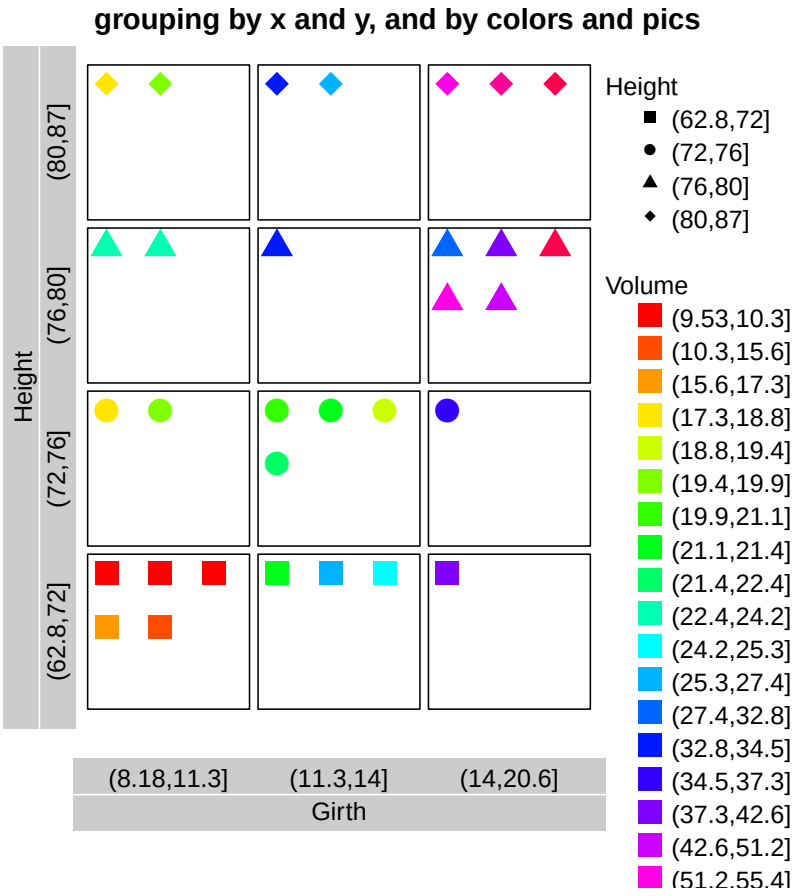


Remarks: The space on the bottom side of the plot is horizontally divided into two parts. The first one is filled by the pictogram legend and the second one by the color legend.

Transparency slides usually offer more vertical space. Therefore, the type *vertical* is a good idea very often.

two legends
vertical
102

```
> pic.plot(trees,
           grp.xy         = 2 ~ 1,
           grp.color      = 3,
           grp.pic        = 2,
           pics           = 15:18,
           pic.frame      = FALSE,
           vars.to.factor = c(0.333, 0.25, 0.05),
           lab.cex        = 1,
           lab.legend     = "vertical",
           main = "grouping by x and y, and by colors and pics")
```



Remarks: You see, there are a lot of possibilities to design the legends. We hope that the user will find a suitable one for his data set.