Notes on Lattice Graphics

J H Maindonald

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Lattice (trellis) graphics functions allow the use of the layout on the page to reflect meaningful aspects of data structure. Different levels of a factor may appear in different panels. Or they may appear in the same panel, distinguished by color and/or symbol. If lines or smooth curves are added, there is a different line or curve for each different group.

Similar considerations apply when columns of data are plotted in parallel. Different columns may appear in different panels. Or they may appear in the same panel, distinguished by color and/or symbol.

To see some of the possibilities that lattice graphics offers, enter

```
library(lattice)
demo(lattice)
```

1 Lattice Graphics vs Base Graphics

Contrast the different ways that base and lattice graphics are designed to operate.

- In base graphics, a graphics page (possibly the first of a sequence of pages) opens when a device is opened. Plots then go to the page or pages. For a screen device, plots go to the screen. For a hardcopy device, plots usually go, in the first place, to a file.

- Lattice functions create trellis objects. Objects can be created even if no device is open. Such objects can be updated. Objects are plotted (by this time, a device must be open), either when output from a lattice function goes to the command line (thus implicitly invoking the `print()` command), or by the explicit use of `print()`.

The updating feature allows the graphics object to be built up in steps, or even modified. Additionally, abilities that were added relatively late in lattice’s development make it possible to adds new features to the “printed” page, after a style of use that is common in base graphics.

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1 © J. H. Maindonald 2008. Permission is given to make copies for personal study and class use. (June 9, 2008)
The lattice package comes already installed with all the binary distributions that are supplied from CRAN (Comprehensive R Archive Network: \url{http://mirror.aarnet.edu.au/pub//CRAN/}). For use in an R session, it must first be attached.

```r
text <- "library(lattice)

Now compare:

plot(ACT ~ year, data=austpop)  # Base graphics
xyplot(ACT ~ year, data=austpop) # Lattice graphics"
```

In both cases, if these are typed from the command line, a graph is plotted. The reason is different in the two cases:

- `plot()` gives a graph as a side effect of the command.
- `xyplot()` generates a graphics object. As this is output to the command line, the object is "printed", i.e., a graph appears.

The following makes this clear: The following makes clear the difference between the two functions:

```r
invisible(plot(ACT ~ year, data=austpop))  # A graph is plotted
invisible(xyplot(ACT ~ year, data=austpop)) # Graph does appear
```

The function `invisible()` suppresses the command line printing. Hence `invisible(xyplot(...))` does not yield a graph.

Inside a function, `xyplot(...)` prints a graph only if it appears as the return value from the function, i.e., usually, as the final line. In a file that is sourced, no graph will appear. Inside a function (except as mentioned), or in a file that is sourced, there must be an explicit `print()`, i.e.

```r
print(xyplot(ACT ~ year, data=austpop))
```

## 2 Groups within Data, and/or Columns in Parallel

Here are selected lines from the data set `grog` (\textit{DAAGxtras} package):

<table>
<thead>
<tr>
<th></th>
<th>Beer</th>
<th>Wine</th>
<th>Spirit</th>
<th>Country</th>
<th>Year</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>5.24</td>
<td>2.86</td>
<td>1.81</td>
<td>Australia</td>
<td>1998</td>
</tr>
<tr>
<td>2</td>
<td>5.15</td>
<td>2.87</td>
<td>1.77</td>
<td>Australia</td>
<td>1999</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>4.57</td>
<td>3.11</td>
<td>2.15</td>
<td>Australia</td>
<td>2006</td>
</tr>
<tr>
<td>10</td>
<td>4.50</td>
<td>2.59</td>
<td>1.77</td>
<td>NewZealand</td>
<td>1998</td>
</tr>
<tr>
<td>11</td>
<td>4.28</td>
<td>2.65</td>
<td>1.64</td>
<td>NewZealand</td>
<td>1999</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>18</td>
<td>3.96</td>
<td>3.09</td>
<td>2.20</td>
<td>NewZealand</td>
<td>2006</td>
</tr>
</tbody>
</table>

There are three drinks (liquor products), shown in different columns, and two countries, occupying rows that are indexed by the factor `Country`. The lattice function `xyplot()` can accommodate any of the following possibilities:

- Different symbols and/or colors are used for different drinks, within the one panel. Different panels must then be used for different countries, as in Figure 1. Or if different countries are shown in the same panel, then different panels must be used for the different drinks.

---

2 The data (dataset `grog`, from \textit{DAAGxtras}) are 1998 – 2006 Australian and New Zealand apparent per person annual consumption (in liters) of the pure alcohol content of Beer, Wine and Spirit. Data, based on Australian Bureau of Statistics and Statistics New Zealand figures, are obtained by dividing estimates of total available alcohol by number of persons aged 15 or more.
Use a 3 drinks × 2 countries, or 2 countries × 3 drinks layout of panels.

Where plots are superposed in the one panel and, e.g., regression lines or smooth curves are fitted, this will be done separately for each different set of points. The separate sets may be distinguished by colour, and/or they may be distinguished by different symbols and/or line styles.

Figure 1: Australian and New Zealand apparent per person annual consumption (in liters) of the pure alcohol content of liquor products, for 1998 to 2006.

Simplified code for Figure 1 is:

```r
xyplot(Beer + Spirit + Wine ~ Year | Country, data=grog, outer=FALSE,
      auto.key=list(columns=3))
```

To obtain various enhancements that give Figure 1 specify:

```r
grogplot <-
  xyplot(Beer + Spirit + Wine ~ Year | Country, data=grog, outer=FALSE,
         auto.key=list(columns=3))
update(grogplot, ylim=c(0,5.5),
      xlab="", ylab="Amount consumed (per person)",
      par.settings=simpleTheme(pch=c(1,3,4)))
```

The footnote has alternative code that updates the object, then uses an explicit print(). Observe that:

- Use of `Beer + Spirit + Wine` gives plots for each of `Beer`, `Spirit` and `Wine`. With `outer=FALSE`, these appear in the same panel.
- Conditioning by country (`| Country`) gives separate panels for separate countries.
- The function `simpleTheme()` is convenient for setting or changing point and line settings.

The plot superimposes the separate plots (two panels each):

```r
xyplot(Beer ~ Year | Country, data=grog)  # Plot for Beer
xyplot(Spirit ~ Year | Country, data=grog)  # Plot for Spirit
xyplot(Wine ~ Year | Country, data=grog)   # Plot for Wine
```

For separate panels for the three liquor products (different levels of `Country` can now use the same panel), specify `outer=TRUE`:

```r
xyplot(Beer + Spirit + Wine ~ Year, groups=Country, outer=TRUE,
       data=grog, auto.key=list(columns=2) )
```

---

33# Update trellis object, then print
```
frillyplot <-
  update(grogplot, ylim=c(0,5.5),
         xlab="", ylab="Amount consumed (per person)",
         par.settings=simpleTheme(pch=c(1,3,4)))
print(frillyplot)
```
Here is a summary of the syntax:

<table>
<thead>
<tr>
<th>Levels of a factor</th>
<th>Overplot (a single panel)</th>
<th>Separate panels (conditioning)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beer ~ Year, groups=Country</td>
<td>Beer ~ Year</td>
<td>Beer ~ Year</td>
</tr>
<tr>
<td>Columns in parallel</td>
<td>outer=FALSE</td>
<td>outer=TRUE</td>
</tr>
</tbody>
</table>

3 Lattice Parameters and Graphics Features

### Lattice parameter settings

1. Changes to the defaults for points and lines are most easily made using the function `simpleTheme()` (in recent versions of `lattice`).

2. Axis, axis tick, tick label and axis label parameters are conveniently set using the parameter `scales` in the function call.

3. Lattice objects can be created, then updated to incorporate changes to parameter settings.

4. Note also the parameters `aspect` (aspect ratio) and `layout` (# rows × # columns × # pages).

3.1 Point, line and fill color settings

**Lattice point, line & related settings**

First use `simpleTheme()` to create a “theme” with the new settings:

```r
miscSettings <- simpleTheme(pch = c(1,3,4), cex=1.25)
```

Alternatives are then:

(i) Supply the “theme” to `par.settings` in the function call.

```r
xyplot(Beer+Spirit+Wine ~ Year | Country, outer=FALSE, 
auto.key=list(columns=3), data=grog, 
par.settings=miscSettings)
```

[This stores the settings with the object. These stored settings over-ride the global settings at the time of printing.]

(ii) Supply the “theme” to `trellis.par.set()`, prior to plotting:

```r
trellis.par.set(miscSettings)
xyplot(Beer+Spirit+Wine ~ Year | Country, outer=FALSE, 
auto.key=list(columns=3), data=grog)
```

[Makes the change globally, until a new trellis device is opened]

The function `simpleTheme()` creates a “theme”, i.e., a list of parameter settings, in a form that can be supplied: (i) in the argument `par.settings` in the graphics function call; or (ii) in the argument `theme` in a call to `trellis.par.set()`, prior to calling the graphics function; or (iii) in the argument `theme` to `trellis.device()`.

Note the use of the function `trellis.device()` to open a new graphics device. By default, it has `retain=FALSE`, so that parameters are reset to their defaults for the relevant device.

The following changes the plotting symbols to symbols 1, 3 and 4, as in Figure 1. It also increases the size of points by 25%:

```r
miscSettings <- simpleTheme(pch = c(1,3,4), cex=1.25)
```
Where there are a small number of points, it can be helpful to show them as large solid dots. The following affects all subsequent plots, until changed or until a new device is opened:

```r
trellis.par.set(simpleTheme(pch = 16, cex = 2))
```

When there are a large number of points, it may be helpful to set the background transparency alpha (c.f., also, alpha.points and alpha.line) to a value less than 1, so that regions where there are many overlapping points can be readily identified.

Where changes go beyond what `simpleTheme()` allows, it is necessary to know the names under which settings are stored. To inspect these, type:

```r
> names(trellis.par.get())
[1] "fontsize" "background" "clip" ...
[28] "par.sub.text"
```

The settings that are of interest can then be inspected individually. Section 14.12 of DAAGUR has brief details. For a visual display that shows default settings for points, lines and fill colour, try the following:

```r
trellis.device(color = FALSE)
show.settings()
trellis.device(color = TRUE)
show.settings()
```

The following sets the fontsize. Note that there are separate settings for text and symbols:

```r
trellis.par.set(list(fontsize = list(text = 7, points = 4)))
```

### 3.2 Parameters that affect axes, tick marks, and axis labels

**Axis, tick, tick label and axis label settings – the `scales` argument**

- Tick positions and tick labels:

```r
jobplot <- xyplot(Ontario+BC ~ Date, data = jobs)
## Half-length ticks, each quarter, Label years, Add key
tpos <- seq(from = 95, by = 0.25, to = 97)
tlabs <- rep(c("Jan95", "", "Jan96", "", "Jan97"),
c(1, 3, 1, 3, 1))
update(jobplot, auto.key = list(columns = 2), xlab = "",
scales = list(tck = 0.5, x = list(at = tpos, labels = tlabs)))
```

**A logarithmic scale, and/or relation="sliced"**

- Use a Logarithmic scale (here, natural logarithmic)

```r
logplot <- xyplot(Ontario+BC ~ Date, data = jobs, outer = TRUE,
                   xlab = "", scales = list(y = list(log = "e")))
```

- Slice the scale

```r
update(logplot, scales = list(y = list(relation = "sliced")))
```

Scales may have relation="fixed", or relation="sliced", or relation="free"
Figure 2: Labor force numbers (1000s) for various regions of Canada. Labels on the vertical axis show both numbers and log of numbers. Distances between ticks are 0.02 on the log scale, i.e., a change of almost exactly 2%.

The data frame jobs (DAAG) has numbers in the Canadian labour force, for each of six different regions, by month over January 1995 to December 1996. The regions appear as columns of the data frame jobs. The following plots these in parallel, on the one panel:

```R
xyplot(Ontario+Quebec+BC+Alberta+Prairies+Atlantic ~ Date, data=jobs, ylab="Number of jobs", type="b", outer=FALSE, auto.key=list(space="right", lines=TRUE))
```

To get a good visual indication of relative changes over time, however, a “sliced” logarithmic scale is needed. The following saves for later enhancement a simplified of the plot shown in Figure 2 giving it the name jobs.xyplot:

```R
## Save the graphics object, for later updating
jobs.xyplot <-
  xyplot(Ontario+Quebec+BC+Alberta+Prairies+Atlantic ~ Date, data=jobs, type="b", layout=c(3,2), ylab="Number of jobs", scales=list(y=list(relation="sliced", log=TRUE)), outer=TRUE)
```

The sliced scale gives each panel the slice of the scale that is needed for points in that panel. A logarithmic scale makes equal relative changes equidistant.

The labeling can be greatly improved. In Figure 3 the y-axis label shows number of jobs, with the logarithms of the numbers given in parentheses. Additionally, dates of the form Jan95 label the x-axis. In the following code, observe the use of update() to specify tick positions and tick labels for the graphics object jobs.xyplot.

```R
ylabpos <- exp(pretty(log(unlist(jobs[, -7])), 100))
ylabels <- paste(round(ylabpos), "\n(\n(log(ylabpos), ")", sep="")
## Create a date object ‘startofmonth’; use this instead of ‘Date’
atdates <- seq(from=95, by=0.5, length=5)
datelabs <- format(seq(from=as.Date("1 Jan1995", format="%d%b%Y"), by="6 month", length=5), "%b%Y")
update(jobs.xyplot, xlab="", between=list(x=0.5, y=1),
```
### 3.3 Further example

The dataset ais (DAAG) has a number of physical and biological measurements on 202 athletes at the Australian Institute of Sport. See help(ais) for details of the measurements, which include a variety of blood cell counts. Data are for ten different sports. Here is a breakdown of numbers:

```r
> with(ais, table(sex, sport))

            B_Ball Field Gym Netball Row Swim T_400m T_Sprint Tennis W_Polo
   sex
   f 13  7  4 23 22  9 11  4  7  0
   m 12 12  0  0 15 13 18 11  4 17
```

The data were collected with the aim of examining possible differences in blood characteristics, between athletes in endurance-related events and those in power-related events.

Figure 3 plots blood cell to plasma ratio (%) against red cell count, for two sports only. The two sports appear within the one panel, distinguished by different symbols and/or colours. Females and males appear in separate panels. Figure 3 shows a suitable plot, adding also regression lines. Again, note the creation of an initial basic plot, which is then updated. Code is:

```r
aisBS <- subset(ais, 
    sport %in% c("B_Ball", "Swim"))
basic.xyp <- 
    xyplot(hg ~ rcc | sex, 
        groups=sport[drop=TRUE], 
        data=aisBS)
## Simplified Code
update(basic.xyp, 
    type=c("p", "r"), 
    auto.key=list(lines=TRUE, 
        columns=2))
# For a smooth curve, specify 
# type=c("p", "smooth")

basic1 <- xyplot(hc ~ rcc | sex, 
    groups=sport[drop=TRUE], 
    data=subset(ais, 
        sport %in% c("B_Ball", "Swim")), 
    xlab="", ylab="Blood cell to plasma ratio (%)")
basic2 <- update(basic1, par.settings=simpleTheme(pch = c(1,3), 
    scales=list(tck=0.5), lty=1:2, lwd=1.5))
update(basic2, type=c("p", "r"), auto.key=list(columns=2, lines=TRUE), 
    xlab=expression("Red cell count (10^{12}L^{-1})"))
```

Again, there are details that require explanation:
• type=c("p","r") gives both points and fitted regression lines.

• In groups=sport[drop=TRUE], the drop=TRUE is optional. If not included there will be one legend item for each of the 10 sports. Subsetting a factor leaves the levels attribute unchanged, even if some of the levels are no longer present in the data.

• As in base graphics, graphical annotation (tick labels, axis labels, labels on points, etc.) can be given using the function expression(). In this context, “expression” is broadly defined; thus expressions can have terms that are character strings. See help(plotmath).

3.4 Keys – auto.key, key & legend

The argument auto.key=TRUE gives a basic key that identifies colors, plotting symbols and names for the groups. For greater flexibility, auto.key can be a list. Settings that are often useful are:

• points, lines: in each case set to TRUE or FALSE.

• columns: number of columns of keys.

• x and y, which are coordinates with respect to the whole display area. Use these with corner, which is one of c(0,0) (bottom left corner of legend), c(1,0), c(1,1) and c(0,1).

• space: one of "top", "bottom", "left", "right".

Use of auto.key sets up the call key=simpleKey(). If not otherwise specified, colors, plotting symbols, and line type use the current trellis settings for the device. Unless text is supplied as a parameter, levels(groups) provides the legends.

When updating, use legend=NULL to remove an existing key, prior to adding a different key.

4 Panel Functions and Interaction with Plots

Further flexibility is added, in the creation of plots, by the use of a user’s own panel functions. A number of panel functions are provided that can be incorporated. A further possibility is interaction with the panels, or other graphics features, of a graph that has just been printed.

4.1 Panel functions

Each lattice command that creates a graph has its own panel function. Thus xyplot() has the panel function panel.xyplot(). The following are equivalent:

```
xyplot(ACT ~ year, data=austpop)
xyplot(ACT ~ year, data=austpop, panel=panel.xyplot)
```

The user’s own function can be substituted for panel.xyplot(). Panel functions that may be used, either in combination with functions such as panel.xyplot() or separately, include:

• panel.points, panel.lines() and a number of other such functions that are documented on the same help page as panel.points;

• panel.abline(), panel.curve(), panel.rug(), panel.average() and a number of other functions that are documented on the same help page as panel.abline().

The following gives a version of Figure 3 in which the lines for the two sports are parallel:

```
xypoti(hg ~ rcc | sex, groups=sport[drop=TRUE], data=aisBS,
        auto.key=list(lines=TRUE, columns=2), aspect=1,
        strip=strip.custom(factor.levels=c("Female","Male")),
        # In place of level names c("f", "m"), use c("Female", "Male")
        panel=function(x, y, groups, subscripts, ...){
```
When there are groups within panels, panel.xyplot() calls panel.superpose(). The customized panel function has the structure:

```r
panel = function(x, y, groups, subscripts, ...){
  panel.superpose(x, y, groups = groups, subscripts = subscripts, ...)
  . . .
  panel.abline(b[1], b[3], col=lcol[1], lty=lty[1])
  panel.abline(b[1]+b[2], b[3], col=lcol[2], lty=lty[2])
}
```

As the function panel.superpose() lacks an option to fit and display multiple parallel lines, the user must supply the needed code. The following calculates the regression slope estimates:

```r
b <- coef(lm(y ~ groups[subscripts] + x))
# NB: groups (but not x and y) must be subscripted
```

The lines are then drawn one at a time, taking care that the line settings agree with those that will appear in the key.

A further enhancement (omitted from the above code) adds axis labels, using an expression for the x-axis label.

```
xlab = expression("Red cell count (10^{12}.*L^{-1}.*")
ylab = "Blood cell to plasma ratio (%)"
```

### 4.2 Interaction with Lattice Plots

**Focusing and unfocusing:**

- Following the plot, call `trellis.focus()`.
- In a multi-panel display, click on a panel to select it.
- Use functions such as `panel.points()`, `panel.text()`, `panel.abline()`, `panel.identify()`.
- Call `trellis.focus()`, as needed, to switch panels.
- When finished, call `trellis.unfocus()`.

For non-interactive use of `trellis.focus()`, turn off highlighting, i.e., the call becomes `trellis.focus(highlight=FALSE)`.

Use the call `trellis.panelArgs()` to identify the arguments that are available to panel functions following a call to `trellis.focus()`.
**Viewports:**

A lattice plot is made up of a number of “viewports”. In the call to `trellis.focus()`, the default is `name="panel"`.

Other choices of name include "panel", "strip", name="legend" and "toplevel". For name="legend"; side should be indicated.

Here is an example of the interactive labeling of points:

```r
xyplot(log(Time) ~ log(Distance), groups=roadORtrack,
data=worldRecords)
trellis.focus()
## Now click (maybe twice) on a panel
panel.identify(labels=worldRecords$Place)
## Click near to points that should be labeled
## Right click to terminate
trellis.unfocus()
```

Lattice is built on top of the `grid` package. This implements viewports, which are arbitrary rectangular regions within which plotting takes place. In the course of plotting, the focus moves from one viewport to the next, as needed to build up the plot.

The function `trellis.focus()` can, once the printing is complete, be used to restore focus to a viewpoint within one of the current panels, or to the whole panel. Common choices for the parameter name are "panel" and "strip", with column and row (by default, counting from the bottom up) identifying the column and row in the layout. For name="legend": side must be indicated. The argument name="toplevel" gives access to the rectangular region within which the panels are placed.

For interactive use, the function `trellis.focus()` can be called without parameters. In a single panel display, this highlights the panel. In a multi-panel display, clicking on a panel will select it. The function `trellis.unfocus()` removes the highlighting and makes "toplevel" the current viewport.

Once the focus is on a panel, the user has access to the functions that were noted in the previous subsection, and to many others besides.

The functions `trellis.focus()` and `trellis.unfocus()` can be used in a non-interactive mode.

The following prints the stripplot and a boxplot objects created in Subsection 5.1 one under the other on the same graphics page. Following the printing of each plot, the focus is placed on the top level viewport, and the function `grid.text()` (from the `grid` package) used to add a label:

```r
library(DAAG)
library(grid)
## Positioning will be (xmin=0, ymin=0.46, xmax=1, ymax=1)
print(update(cuckoostrip, xlab=""), position=c(0, .46, 1,1))
trellis.focus("toplevel", highlight=FALSE)
grid.text("A", x=0.05, y=0.935, gp=gpar(cex=1.15))
trellis.unfocus()
print(cuckoobox, position=c(0, 0, 1, 0.54), newpage=FALSE)
trellis.focus("toplevel", highlight=FALSE)
grid.text("B", x=0.05, y=0.935, gp=gpar(cex=1.15))
trellis.unfocus()
```

Observe that the rectangular regions on which the objects are printed have been chosen so that they overlap somewhat, reducing the space between.
5 Displays of Distributions

5.1 Stripplots, dotplots and boxplots

Because the syntax for stripplot() and boxplot() are very similar, we demonstrate suitable code side by side. (The function dotplot() is very similar to stripplot(), with differences that are mainly cosmetic.) The following code creates a stripplot object and a boxplot object, for the cuckoos data (from DAAG):

```r
cuckoostrip <- stripplot(species ~ length, aspect=0.5, 
                          xlab="Cuckoo egg length (mm)", data=cuckoos)
cuckoobox <- bwplot(species ~ length, aspect=0.5, 
                    data=cuckoos, xlab="Cuckoo egg length (mm)"
```

The `aspect` argument determines the ratio of distance in the y-direction to distance in the x-direction.

The following demonstrates the use of dotplot():

```r
dotplot(variety ~ yield | site, data = barley, groups = year, 
        xlab = "Barley Yield (bushels/acre)", ylab = NULL, 
        layout = c(1, 6), aspect = 0.5, 
        auto.key=list(labels=levels(barley$year), space = "right"))
```

Try stretching the plot vertically so that the labels do not overlap.

The argument `type="h"` gives a line from the origin to the point. Both a line and a point may be given. This can be used to quite striking effect, as in the following:

```r
deathrate <- c(40.7, 36, 27, 30.5, 27.6, 83.5)
hosp <- c("Cliniques of Vienna (1834-63) (> 2000 cases pa)", 
          "Enfans Trouves at Petersburg (1845-59, 1000-2000 cases pa)", 
          "Pesth (500-1000 cases pa)", 
          "Edinburgh (200-500 cases pa)", 
          "Frankfort (100-200 cases pa)", "Lund (< 100 cases pa)"
)
hosp <- factor(hosp, levels=hosp[order(deathrate)])
dotplot(hosp ~ deathrate, xlab="("Sexes per 1000 "", cex=1.5, 
        xlab=list("Death rate per 1000 ", cex=1.5), 
        sub="From Nightingale (1871) - data from Dr Le Fort")
```

5.2 Lattice Style Density Plots

![Lattice style density plot](image)

Figure 4: Lattice style density plot comparing possum earconch measurements, separately for males and females, between Victorian and other populations. Observe that the scatter of data values is shown along the horizontal axis.

Here is a density plot (Figure 4), for data from the possum data set (DAAG), that compares sexes and Vic/other populations.

---

## For slightly improved labeling, precede with:
```
levels(cuckoos$species) <- sub("."," ", levels(cuckoos$species), fixed=T)
```

## Data are from Nightingale, F. (1871): Notes on Lying-in Institutions.
densityplot(~ earconch | sex, groups=Pop, data=possum, 
par.settings=simpleTheme(col=c("gray","black"),
auto.key=list(columns=2))

Where densityplot() (and histogram()) have a formula as argument, a name is not allowed on the left of the $\sim$ symbol. For histogram(), the groups argument is not available.

6 Lattice graphics functions – Further Points

6.1 Help on lattice functions

For an overview, type help(Lattice). For help on the graphical parameters used by lattice functions, see help(trellis.par.set) and help(simpleTheme). For other settings, see help(lattice.options).

Several of the help pages for lattice functions are shared between more than one function. For example, xyplot(), dotplot(), barchart(), stripplot() and bwplot() share the same help page. As a consequence, typing example(bwplot) has the same effect as typing example(xyplot).

6.2 Selected Lattice Functions

Functions that have already been demonstrated are xyplot(), stripplot(), dotplot(), densityplot() and bwplot(). Other "high level" functions include:

barchart(character ~ numeric, ...) 
histogram(~ numeric, ...) # NB: does not accept groups parameter
densityplot(~ numeric, ...) # Density plot; does allow groups 
bwplot(factor ~ numeric, ...) # Box and whisker plot 
qqmath(factor ~ numeric, ...) # normal probability plots 
## Bivariate
qq(factor ~ numeric, ...) # comparing two empirical distributions 
## Multivariate
cloud(numeric ~ numeric * numeric, ...) # 3D surface
wireframe(numeric ~ numeric * numeric, ...) # 3D scatterplot
levelplot(numeric ~ numeric * numeric, ...) # cf image() in base graphics
contourplot(numeric ~ numeric * numeric, ...) # contour plot
## Hypervariate
splom(~ dataframe,..) # Scatterplot matrix 
parallel(~ dataframe,..) # Parallel coordinate plots 
## Miscellaneous
rfs() # Residual and fitted value plot (also see 'oneway')
tmd() # Tukey Mean-Difference plot

In each instance, users can add conditioning variables.

Reference

This is the definitive account of the lattice implementation of trellis graphics. It merits careful study.
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