R Graphics

Deepayan Sarkar

introduction

Origins

- History of the R graphics model goes back to S.
- The S language was from the very beginning designed to be interactive.
- Graphics was naturally an essential component of the system.
- The model adopted was the GRZ model (already in use at Bell Labs).
- May be described as a “painter’s model”:
  - a graphic was built out of a small set of primitives such as line segments, polygons, text, etc., and
  - later elements are drawn on top of earlier ones.
  - no provision for deleting an element once it was drawn
  - except to start a completely new graphic.

GRZ model

- both input and output could be abstracted.
- Graphics functions that were meant for users would internally call these primitives.
- For output, the primitives could be implemented differently depending on the target "device", which could be
    - Postscript or PDF files for printing,
    - hardware devices such as pen plotters,
    - on-screen devices for interactive viewing.
- The device-specific implementations of the primitives are known as device drivers
- new drivers can be written to support new kinds of output formats.
- See `?Devices` for more details.

Traditional graphics model

- The painter's model naturally led to a mental approach that viewed a plot as a work-in-progress, always with the possibility of adding something more to it.
- This attitude pervades much of the graphics functionality written for S in its early days, and is still popular due to its simplicity, familiarity, and the availability of a large variety of graphic designs implemented using this model.
- We will loosely refer to this model of graphics as the *traditional graphics* model.

Trellis graphics

- In the 1990s S introduced a new approach to graphics, which was called Trellis graphics, meant to substitute the traditional graphics tools rather than to complement it.
- The most prominent feature of Trellis graphics was the notion of *conditioning* (also known as “small multiples” or “faceting”) which allowed subsets of data to be intelligently visualized so as to enable effective comparison between those subsets.
- The way this was done necessitated a departure from the “work-in-progress” model, and required the user to completely specify the details of the plot in one go. This was not really a departure from the painter’s model in terms of implementation, but rather a change in the mental approach to plotting.

Grid graphics

- R followed S in implementing the traditional graphics model first.
- When it came to Trellis graphics, it took a slightly different approach that had important repurcussions.
- Instead of implementing Trellis graphics using the tools provided by the traditional model, as S had done, the R developers first introduced a layer of abstraction called *Grid graphics*.
- Grid was designed to be a low-level tool, which provided graphical elements as objects that could be manipulated to a considerable extent, and sophisticated viewport and layout capabilities to use these elements to construct complicated plots.
- Grid was used to implement two important general high-level graphics packages, as well as many other specialized packages.
  - One was lattice , which implemented the functionality of Trellis graphics in R.
  - The other was ggplot2 , which adapted ideas from to provide another alternative graphics system.
- We will discuss both systems

Principles of data graphics

- A discussion of why graphics are important in statistical analysis and what makes good graphics good is beyond the scope of this chapter, and we refer the reader to for an excellent introduction and further references.
- If there is one single underlying principle, it is that good graphics should enable comparison. Starting from this principle, performed a series of perceptual experiments that indicated, for instance, that the human eye can judge the difference in positions along a common axis better than it can judge differences in lengths of line segments, and that it is worse than either in judging quantitative differences based on a color scale.
- Based on such experiments, discusses principles that when used systematically should yield effective visualizations, and these principles played an important role in the evolution of S graphics.
- The same principle of enabling comparison is also the basis of Trellis graphics, which grew out of ideas in .
- Overall, the work of Cleveland, and before him, , has been extremely influential in shaping the direction and visual feel of traditional S and R graphics.

traditional graphics

Traditional graphics

- The core of the traditional R graphics system is the suite of functions available in the graphics package,
- with various add-on packages providing further functionality.
- The full list of functions can be seen using

```
library(help = graphics)
```

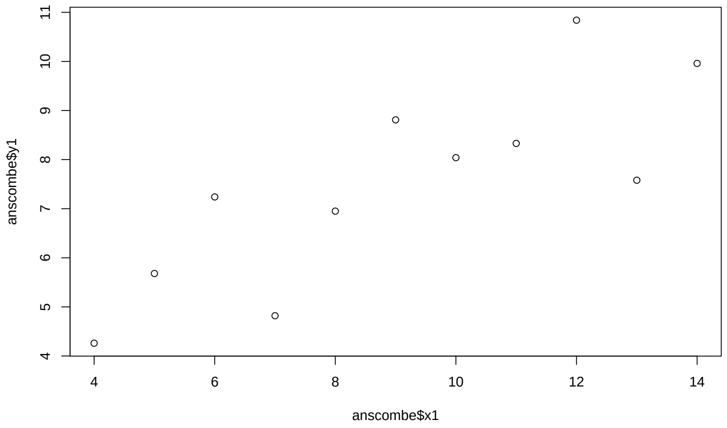
- The listed functions can be roughly categorized into two groups:
  - High-level functions are those that are intended to produce a complete plot by themselves.
  - Low-level functions are those that are intended to add elements to existing plots.
- Of course, high-level functions are themselves built up from low-level functions.

Example: Anscombe's data

- Let us look at an example. The simplest and most common type of statistical plot is the scatterplot, which depicts bivariate numeric data as points in a Cartesian coordinate system.
- The high-level function that produces scatterplots is `plot()` (although that is not all `plot()` does).
- We use R's built-in dataset, `anscombe`, for illustration.
- The dataset contains Anscombe's well-known quartet of bivariate datasets that are quite different from each other, yet have the same traditional statistical summaries (mean, variance, correlation, least squares regression line, etc.).
- The first dataset can be plotted as follows:

```
> plot(x = anscombe$x1, y = anscombe$y1)
```

Example: Anscombe's data



Details

- What low-level functions could have created this plot?
- The plot consists of
  - the points,
  - the box surrounding the plot,
  - the axes,
  - the axis labels.
- All these elements can be suppressed by `plot()` as follows.

```
> plot(x = anscombe$x1, y = anscombe$y1,
+      type = "n", axes = FALSE, xlab = "", ylab = "")
```

- This produces a completely blank page
- but performs one important task: it sets up the coordinate system for subsequent low-level calls.

Details

- The extent of this coordinate system can be obtained using

```
> par("usr")
```

```
[1] 0 1 0 1
```

- This is the range of the data that was supplied to `plot()`, with a padding of 4% on both sides

```
> range(anscombe$x1)
```

```
[1]  4 14
```

```
> range(anscombe$y1)
```

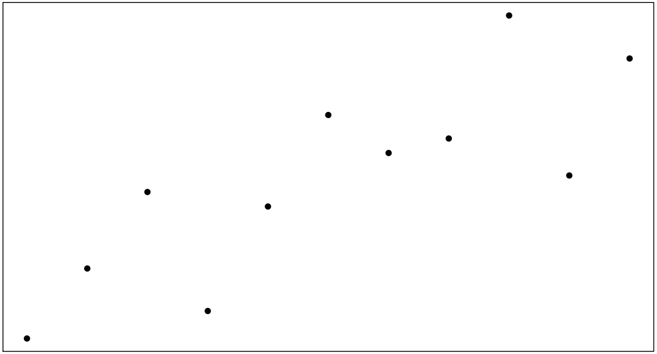
```
[1]  4.26 10.84
```

Details

- This rectangular region does not occupy the full figure area, only a part of it.
- This is referred to as the *plot region*
- We can now draw a box around the plot region and add the data points as follows.

Details

```
> box()
> points(anscombe$x1, anscombe$y1, pch = 16)
```

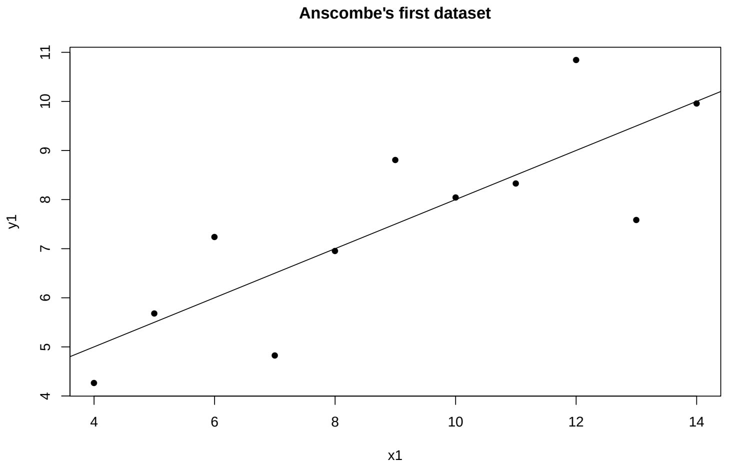


Details

- The area outside the plot region is known as the margin, and is used for axis annotation and labels.
- The following low-level calls complete the plot and adds a linear regression line.

```
> axis(side = 1)
> axis(side = 2)
> title(main = "Anscombe's first dataset",
+       xlab = "x1", ylab = "y1")
> abline(lm(y1 ~ x1, anscombe))
```

Details

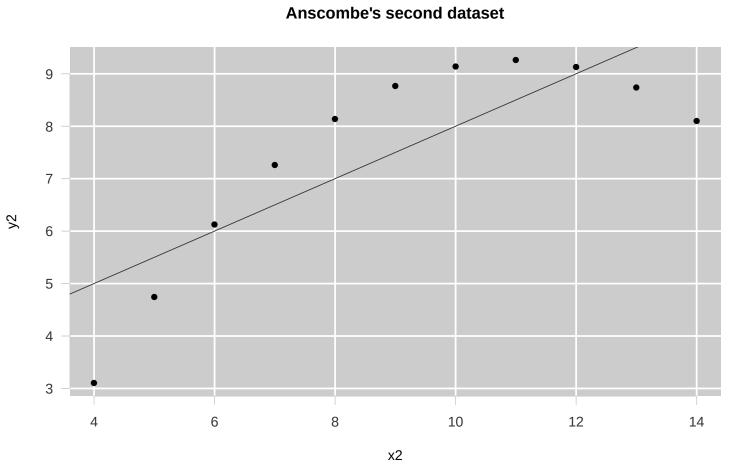


Why are these details important?

- Is this relevant for routine use? Consider this code:

```
> plot(anscombe$x2, anscombe$y2,
+      type = "n", axes = FALSE, xlab = "", ylab = "")
> lims <- par("usr")
> rect(lims[1], lims[3], lims[2], lims[4],
+      col = "grey80", border = NA)
> abline(v = pretty(lims[1:2]), h = pretty(lims[3:4]),
+        col = "white", lwd = 2)
> axis(side = 1, col = "grey80", col.axis = "grey20")
> axis(side = 2, col = "grey80", col.axis = "grey20",
+      las = 1)
> points(anscombe$x2, anscombe$y2, pch = 16)
> title(main = "Anscombe's second dataset",
+       xlab = "x2", ylab = "y2", col = "grey20")
> abline(lm(y2 ~ x2, anscombe), col = "grey20")
```

Why are these details important?



Why are these details important?

- This kind of customization is often desirable,
- making use of low-level functions as above is the standard approach with traditional graphics
- Most other high-level traditional graphics functions follow this structure
- We will not discuss low-level structure of traditional graphics

Some useful low-level functions

`text()`	Add Text to a Plot
`lines()`	Add Connected Line Segments to a Plot
`points()`	Add Points to a Plot
`polygon()`	Polygon Drawing
`rect()`	Draw One or More Rectangles
`segments()`	Add Line Segments to a Plot

Some useful low-level functions

`abline()`	Add Straight Lines to a Plot
`arrows()`	Add Arrows to a Plot
`axis()`	Add an Axis to a Plot
`box()`	Draw a Box around a Plot
`grid()`	Add Grid to a Plot
`legend()`	Add Legends to Plots
`title()`	Plot Annotation

The `plot()` function I

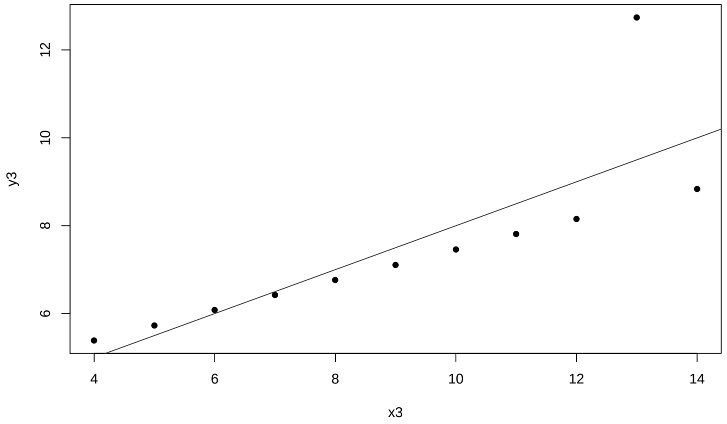
- The `plot()` function is actually a generic function that can deal with the task of plotting several types of R objects.
- The most common method is the default method `plot.default()`, which can be used to plot
  - paired numeric data
  - univariate numeric data, plotted against serial number
- See `?plot` and `?plot.default` for details, including
  - logarithmic scales using the `log` argument
  - the `type` argument for controlling display

The `plot()` formula method

- Another common method for bivariate data: use a formula
- Similar to various statistical modeling functions
- Allows cleaner specification of the plot
- Leads to better default axis labels

The plot() formula method

```
> plot(y3 ~ x3, data = anscombe, pch = 16)
> abline(lm(y3 ~ x3, anscombe), col = "grey20")
```



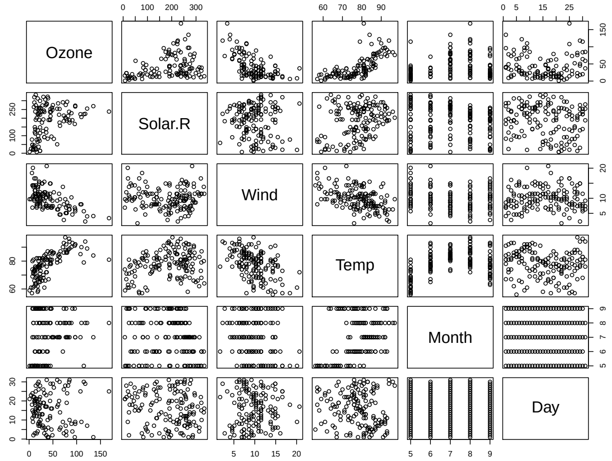
Other plot methods

Full list of available methods for the `plot()` generic can be listed by

```
> methods("plot")
```

```
 [1] plot.acf*           plot,ANY-method
 [3] plot,color-method   plot.data.frame*
 [5] plot.decomposed.ts* plot.default
 [7] plot.dendrogram*    plot.density*
 [9] plot.ecdf           plot.factor*
[11] plot.formula*       plot.function
[13] plot.ggplot*        plot.gtable*
[15] plot.hclust*        plot.histogram*
[17] plot.HoltWinters*   plot.isoreg*
[19] plot.lm*            plot.medpolish*
[21] plot.mlm*           plot.ppr*
[23] plot.prcomp*        plot.princomp*
[25] plot.profile.nls*   plot.raster*
[27] plot.shingle*       plot.spec*
[29] plot.stepfun        plot.stl*
[31] plot.table*         plot.trellis*
[33] plot.ts             plot.tskernel*
[35] plot.TukeyHSD*
```

Other plot methods: “data.frame”



Other plot methods: “data.frame”

- Actually, the `plot()` method in this case simply calls `pairs()`, the function designed to draw scatterplot matrices
- The previous figure could also have been produced by

```
> pairs(airquality)
```

Other plot methods: "factor"

Similarly, the "factor" method for `plot()` may call

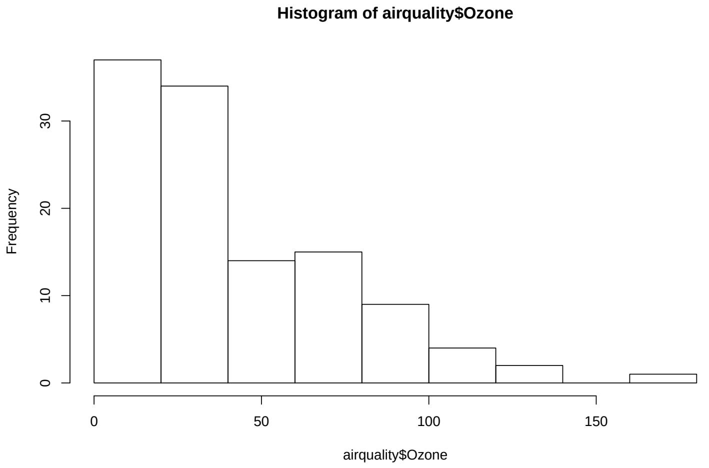
- `barplot()` to show a bar chart of the frequency distibution (if the input is a single "factor" variable)
- `boxplot()` to show box-and-whisker plots (if an additional numeric variable is provided)

We discuss these specialized high-level functions next

Specialized functions: histogram

Histograms are produced by the `hist()` function

```
> hist(airquality$Ozone)
```



Specialized functions: kernel density estimate

First step: compute density estimate as a “density” object

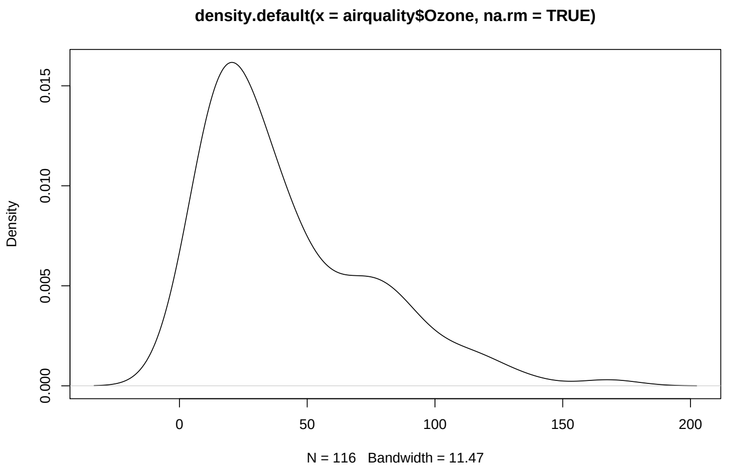
```
> d <- density(airquality$Ozone, na.rm = TRUE)
> str(d)
```

```
List of 7
 $ x        : num [1:512] -33.4 -33 -32.5 -32 -31.6 ...
 $ y        : num [1:512] 1.08e-05 1.24e-05 1.41e-05 1.62e-05 1.85e
 $ bw       : num 11.5
 $ n        : int 116
 $ call     : language density.default(x = airquality$Ozone, na.rm 
 $ data.name: chr "airquality$Ozone"
 $ has.na   : logi FALSE
 - attr(*, "class")= chr "density"
```

Common high-level functions for specific displays

Second step: plot it with the suitable `plot()` method

```
> plot(d)
```



Return values of specialized plotting functions

- density() returns object with information about calculations
- Similarly, hist() return a "histogram" object containing details

```
> h <- hist(airquality$Ozone, plot = FALSE)
> str(h)
```

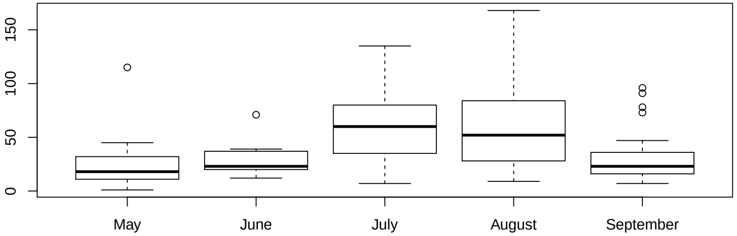
```
List of 6
 $ breaks  : num [1:10] 0 20 40 60 80 100 120 140 160 180
 $ counts  : int [1:9] 37 34 14 15 9 4 2 0 1
 $ density : num [1:9] 0.01595 0.01466 0.00603 0.00647 0.00388 ...
 $ mids    : num [1:9] 10 30 50 70 90 110 130 150 170
 $ xname   : chr "airquality$Ozone"
 $ equidist: logi TRUE
 - attr(*, "class")= chr "histogram"
```

- Such objects can also be plotted using plot()
- More useful because it allows customization (examples later)

Quantile-based plots: box plots

`boxplot()` produce comparative box-and-whisker plots

```
> airquality$fmonth <- with(airquality,
+   droplevels(factor(Month, levels = 1:12, labels = month.name)))
> boxplot(Ozone ~ fmonth, data = airquality)
```

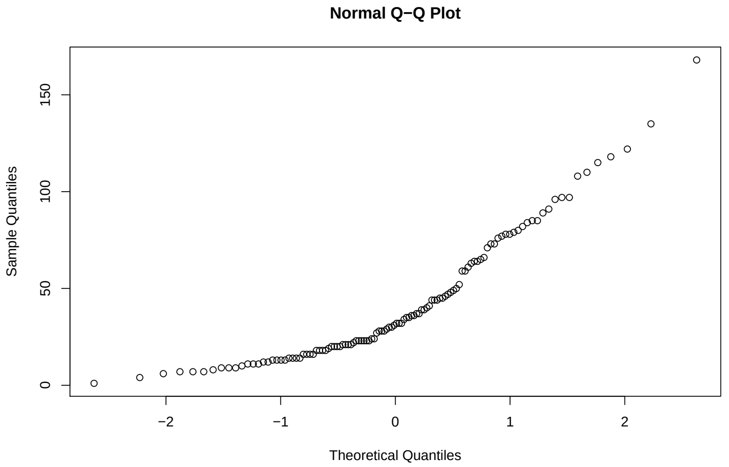


As with `hist()` and `density()`, these functions also have useful return values.

Quantile-based plots: Q-Q plots

`qqnorm()` produces Normal Q-Q plots

```
> qqnorm(airquality$Ozone)
```



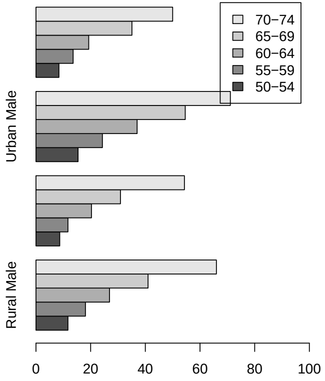
Displaying tabular data

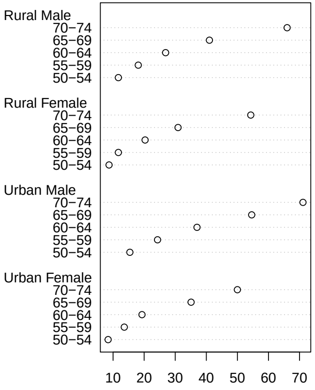
- Common visualizations: bar plots and dot plots
- Bar plots are produced by `barplot()`
- Dot plots by the `dotchart()` function.
- Example using dataset on death rates in different population subgroups in the US state of Virginia in 1940

```
> barplot(VADeaths, beside=TRUE, horiz=TRUE,
+         legend.text=TRUE, xlim = c(0, 100))
> dotchart(VADeaths)
```

- Note use of `xlim` to fit legend

Displaying tabular data

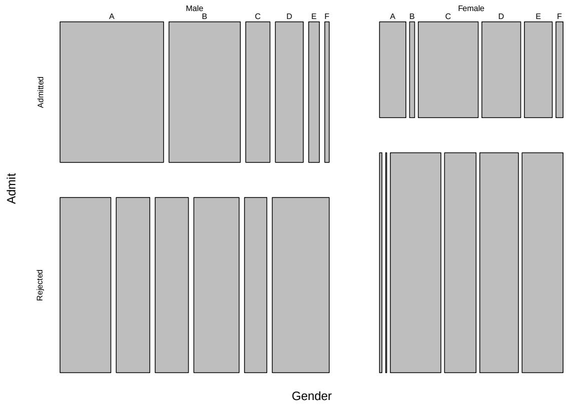


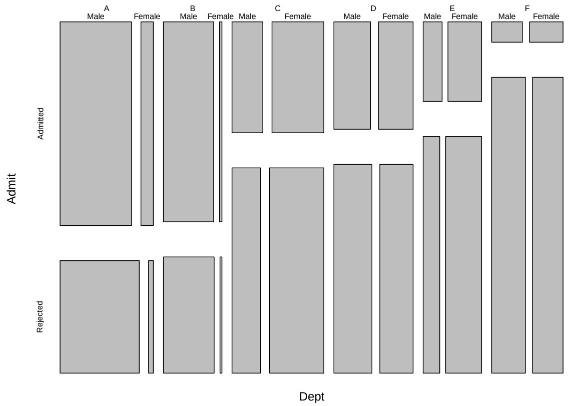


Displaying tabular data: mosaic plots

- Less common visualization
- Useful for tabular higher dimensional tables
- Example: Simpson's paradox in Berkeley admissions data:
  - aggregate number of applicants to at Berkeley in 1973
  - six largest departments (labeled A-F)
  - classified by gender and whether they were admitted.

UCB Admissions, 1973




UCB Admissions, 1973
A
B
C
D
E
F
Male
Female
Admitted
Rejected
Admit
Dept

Displaying tabular data: mosaic plots

- The plots are produced by the following calls
- Uses `aperm()` to rearrange the dimensions of the `UCBAdmissions` array to achieve the desired hierarchy of groups.

```
> mosaicplot(aperm(UCBAdmissions, c(2, 1, 3)),
+            main = "UCB Admissions, 1973")
> mosaicplot(aperm(UCBAdmissions, c(3, 1, 2)),
+            main = "UCB Admissions, 1973")
```

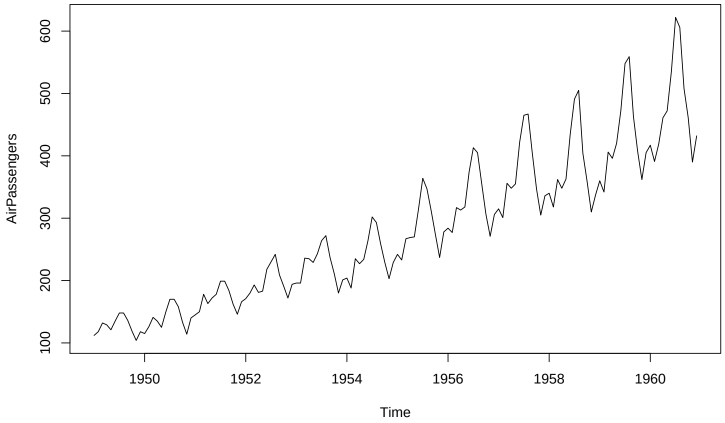
Visualizations for time series data

- R comes with many specialized graphical designs
- Those used for time series data deserve special mention because of their ubiquity.
- Time series data are typically represented in R as objects of class “ts”.
- Corresponding `plot()` method produces a standard time series plot, which is essentially a scatterplot with points joined by lines.

Typical plot of time series data

A time series plot of the `AirPassengers` data

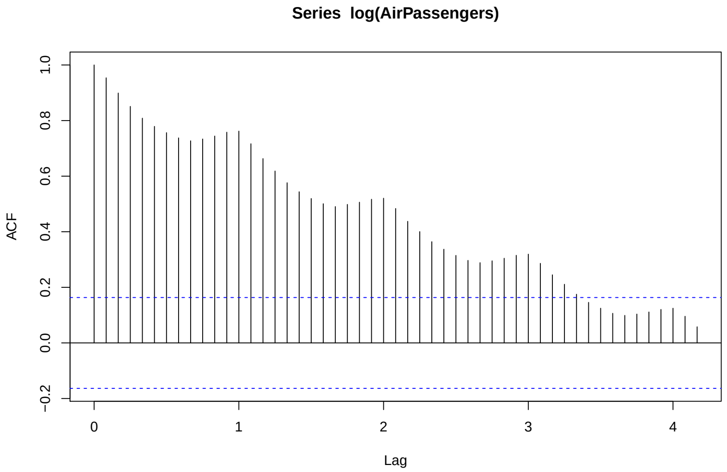
```
> plot(AirPassengers)
```



Time series data: ACF plot

Plot of estimated autocorrelation function (of log-transformed data)

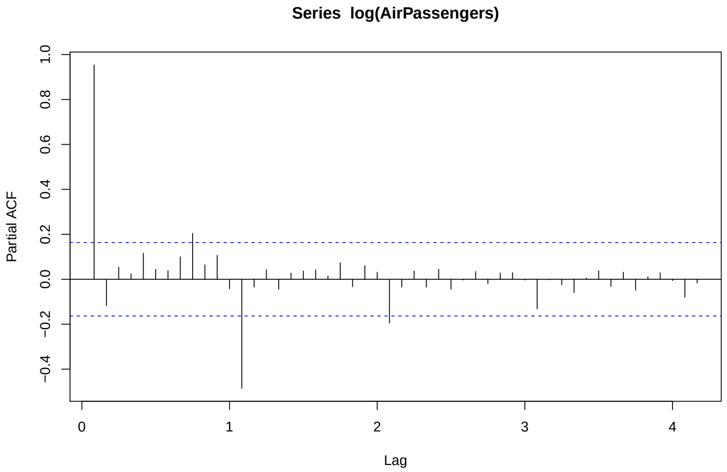
```
> acf(log(AirPassengers), lag.max = 50)
```



Time series data: ACF plot

Plot of partial autocorrelation function by

```
> pacf(log(AirPassengers), lag.max = 50)
```

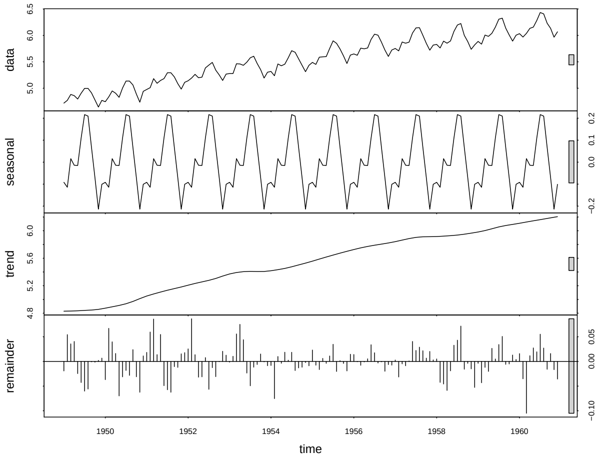


Time series decompositions I

- In addition to these basic plots, R provides functions for various time series decompositions that can be plotted.
- For example, an STL decompositionof the `AirPassengers` data is produced by

```
> plot(stl(log(AirPassengers), "periodic"))
```

Time series decompositions II



- Other decomposition methods are implemented in the `decompose()` and `StructTS()` functions.

Time series decompositions III

- A number of contributed R packages substantially enhance the time series analysis capabilities of R; see `http://cran.r-project.org/web/views/TimeSeries.html`

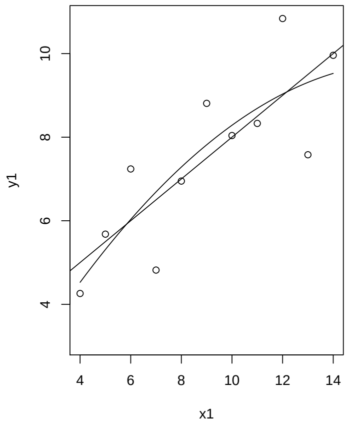
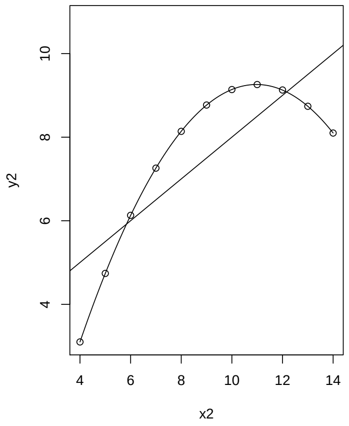
Customizing plots using low-level functions

- High-level graphics functions produce basic versions of common statistical graphs
- Often we want to fine-tune them in different ways to get something more relevant to our purposes.
- We have seen a somewhat extreme example before (Anscombe's data), starting from a blank plot
- More common to start with a complete high-level plot
- Incrementally add components to customize it

Customizing plots using low-level functions

- Common use: add representation of some model fit
- Example: side-by-side scatterplots of Anscombe's first two datasets, with the least squares fits from a linear and quadratic model.

```
> lims <- with(anscombe, list(x = range(x1, x2),
+                             y = range(y1, y2)))
> par(mfrow = c(1, 2))
> plot(y1 ~ x1, data = anscombe,
+      xlim = lims$x, ylim = lims$y)
> abline(lm(y1 ~ x1, data = anscombe))
> f1 <- function(x) predict(lm(y1 ~ poly(x1, 2), data = anscombe),
+                          newdata = list(x1 = x))
> curve(f1, add = TRUE)
> plot(y2 ~ x2, data = anscombe,
+      xlim = lims$x, ylim = lims$y)
> abline(lm(y2 ~ x2, data = anscombe))
> f2 <- function(x) predict(lm(y2 ~ poly(x2, 2), data = anscombe),
+                          newdata = list(x2 = x))
> curve(f2, add = TRUE)
```


y1
x1
4
6
8
10
12
14

y2
x2
4
6
8
10
12
14

Customizing plots using low-level functions

- Linear fit easily added using `abline()`
- Quadratic fit needs more general `curve()` function.
- Second approach works for any other modeling function that has a suitable `predict()` method.
- The `par(mfrow=)` construct is used to enable a “multiple figure" layout (see `?par`).

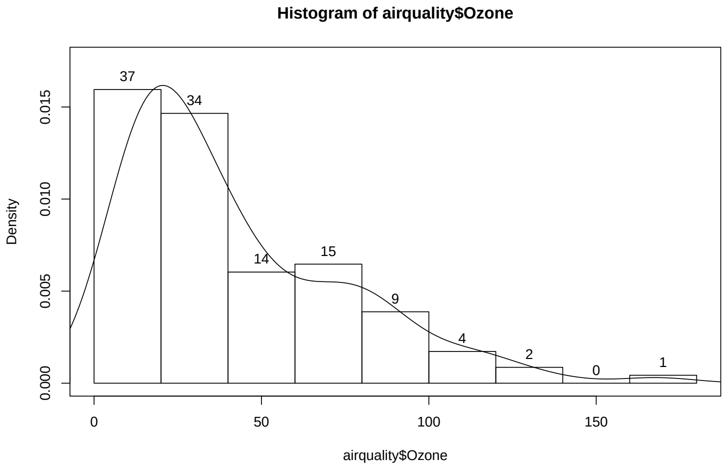
Customizing plots: histogram

- As noted before, many high-level graphics functions (e.g., `hist()`, `boxplot()`, `barplot()`) return objects containing intermediate computations.
- These are useful for customizations.
- Example: annotates a density histogram of Ozone concentration (the `airquality` data) with the bin frequencies, and adds a kernel density estimate for comparison.

```
> h <- hist(airquality$Ozone, plot = FALSE)
> d <- density(airquality$Ozone, na.rm = TRUE)
> plot(h, freq = FALSE, ylim = c(0, 1.1 * max(h$density)))
> box()
> text(h$mids, h$density, labels = h$counts, pos = 3)
> lines(d)
```

Note the need to increase the y-axis range slightly to accommodate the label for the highest bin.

Customizing plots: histogram

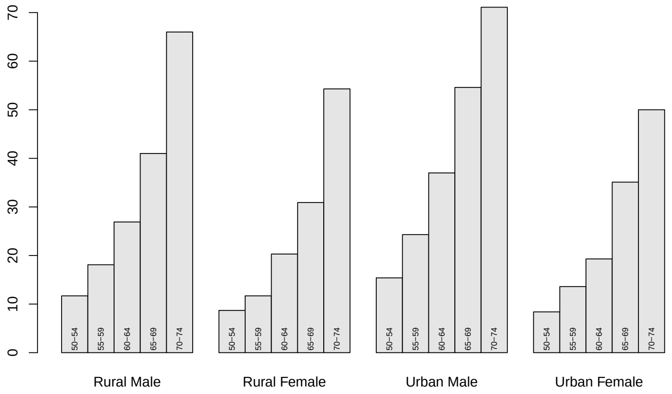


Customizing plots: bar plots

- barplot() returns coordinates of the bar midpoints, allows similar annotation to be added to bar charts.
- Example: age groups in the VADeaths data are indicated using text labels rather than a legend

```
> b <- barplot(VADeaths, beside = TRUE, col = "grey90")
> text(b, 0, labels = rownames(VADeaths), srt = 90, adj = -0.1, cex
```

Customizing plots: bar plots



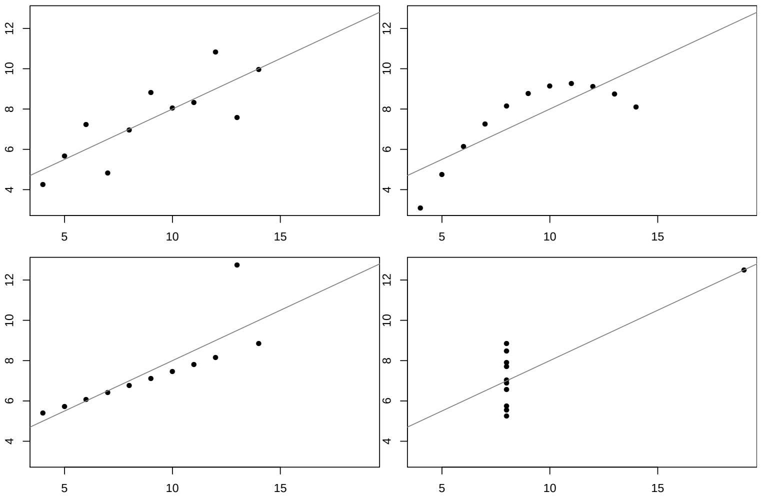
Limitations of traditional graphics

- Traditional graphics model is considerably limited by its design.
- Basic Assumption: a single plot area in the center, and margins will be used for axis annotation and labels.
- Not all graphical designs fit this paradigm.
- One important class of such examples: “small multiples” or “conditioned plots”, where one page contains multiple plots grouped by some categorical variable.

Limitations of traditional graphics

Example using traditional graphics:

```
> lims <- with(anscombe, list(x = range(x1, x2, x3, x4),
+                             y = range(y1, y2, y3, y4)))
> par(mfrow = c(2, 2), mar = c(2, 2, 1, 0))
> plot(y1 ~ x1, data = anscombe, pch = 16, xlim = lims$x, ylim = li
> abline(lm(y1 ~ x1, data = anscombe), col = "grey50")
> plot(y2 ~ x2, data = anscombe, pch = 16, xlim = lims$x, ylim = li
> abline(lm(y2 ~ x2, data = anscombe), col = "grey50")
> plot(y3 ~ x3, data = anscombe, pch = 16, xlim = lims$x, ylim = li
> abline(lm(y3 ~ x3, data = anscombe), col = "grey50")
> plot(y4 ~ x4, data = anscombe, pch = 16, xlim = lims$x, ylim = li
> abline(lm(y4 ~ x4, data = anscombe), col = "grey50")
```



4
6
8
10
12
5
10
15

More realistic example: `airquality` data

- Compare the distributions of `Ozone` across months
- With density plots or histograms
- Density estimates can be superposed in the same plot, with a little work to ensure adequate axis limits.

More realistic example: airquality data

We first use the split() function to divide up the Ozone observations by month.

```
> s <- with(airquality, split(Ozone, fmonth))
> str(s)
```

```
List of 5
 $ May      : int [1:31] 41 36 12 18 NA 28 23 19 8 NA ...
 $ June     : int [1:30] NA NA NA NA NA NA 29 NA 71 39 ...
 $ July     : int [1:31] 135 49 32 NA 64 40 77 97 97 85 ...
 $ August   : int [1:31] 39 9 16 78 35 66 122 89 110 NA ...
 $ September: int [1:30] 96 78 73 91 47 32 20 23 21 24 ...
```

Next, we call density() on each component using lapply().

```
> dlist <- lapply(s, density, na.rm = TRUE)
```

More realistic example: airquality data

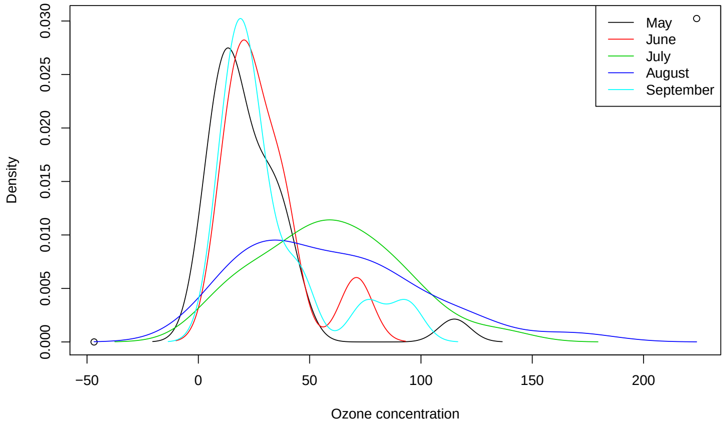
Each component of dlist now contains a “density” object with components x and y giving the estimated density function. We can compute the range needed to contain all the densities as follows.

```
> dxrng <- range(unlist(lapply(dlist, function(d) d$x)))
> dyrng <- range(unlist(lapply(dlist, function(d) d$y)))
```

More realistic example: airquality data

We then create a blank plot (using `type="n"`) and add the densities one by one, followed by a legend.

```
> plot(dxrng, dyrng, xlab = "Ozone concentration", ylab = "Density"
> for (i in seq_along(dlist)) lines(dlist[[i]], col = i)
> legend("topright", legend = names(dlist),
+         lty = 1, col = seq_along(dlist))
```



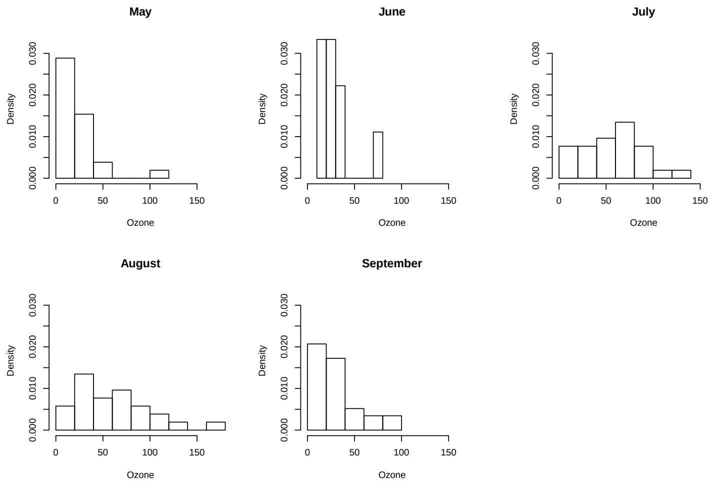
Density
0.000
0.005
0.010
0.015
0.020
0.025
0.030
−50
0
50
100
150
200
Ozone concentration
May
June
July
August
September

More realistic example: comparative histogram

Histograms are not easily amenable to superposition, but they can be juxtaposed.
Using similar tricks along with the multiple figure approach we obtain

```
> par(mfrow = c(2, 3))
> hlist <- lapply(s, hist, plot = FALSE)
> hxrng <- range(unlist(lapply(hlist, function(h) h$breaks)))
> hyrng <- range(unlist(lapply(hlist, function(h) h$density)))
> invisible(lapply(names(s),
+                  function(nm) {
+                      plot(hlist[[nm]], main = nm, freq = FALSE,
+                           xlim = hxrng, ylim = hyrng, xlab = "Ozo
+                  }))
```

More realistic example: comparative histogram



Limitations

- Although not very difficult, obtaining these plots is not simple either, and the results leave a lot to be desired.
- It is precisely the need to deal with these kinds of graphic designs that Trellis graphics as implemented in the lattice package, and more recently the ggplot2 package, was developed.
- Before we move on to these, we will briefly discuss the low-level system these packages are based on, namely, Grid graphics.

grid

Grid graphics

Viewports I

Viewports are a central concept in Grid graphics. They are essentially rectangular subregions of the plotting area. They can be nested within other viewports, forming a tree of viewports. The initial blank graphics area is the ROOT viewport. New viewports can be defined relative to parent either by position, or in terms of a layout. Viewports are created by the `viewport()` function, and made active by `pushViewport()`. The `upViewport()` function is used to navigate to the parent of the current viewport. Viewports support several coordinate systems that can be used to specify locations within the viewport. Of these, the most useful is the *native coordinate system*, which is determined by specifying x-axis and y-axis extents when creating the viewport using the arguments `xscale` and `yscale`.

Coordinate systems in grid

`"native"`	Native coordinates
`"npc"`	Normalized Parent Coordinates
`"snpc"`	‘Square’ NPC
`"inches"`, `"cm"`, `"points"`, etc.	absolute lengths
`"char"`	Character size
`"lines"`	Height of a lines of text
`"strwidth"`, `"strheight"`	Width or height of a string
`"grobwidth"`, `"grobheight"`	Width or height of a ‘grid object’ (details later)

Units and primitives

- Another fundamental concept is that of units of length
- Grid can specify lengths in various ways
- The basic low-level primitive functions in traditional graphics have analogs in grid.
- There are two versions of each function, one that produces output, and one that produces an object without actually plotting it.
- These objects can eventually be plotted, but they can also be queried to determine their height and width, so that appropriate space can be allocated for them.

Common primitive objects in grid

Type	Function producing output	Function producing object
Points	grid.points	pointsGrob
Lines	grid.lines	linesGrob
Text	grid.text	textGrob
Rectangles	grid.rect	rectGrob
Circles	grid.circle	circleGrob
Polygons	grid.polygon	polygonGrob
Segments	grid.segments	segmentsGrob
X-axis	grid.xaxis	xaxisGrob
Y-axis	grid.yaxis	yaxisGrob
Arrows	grid.arrows	arrowsGrob

Simple attempt I

The data we will use for our example is the `faithful` dataset, which contains eruption times and inter-eruption intervals lengths for the famous Old Faithful geyser in Yellowstone national park. We first compute some summaries that will be required to set up the plot.

```
> str(faithful)
```

```
'data.frame':   272 obs. of  2 variables:
 $ eruptions: num  3.6 1.8 3.33 2.28 4.53 ...
 $ waiting  : num  79 54 74 62 85 55 88 85 51 85 ...
```

Simple attempt II

```
> x <- faithful$eruptions
> y <- jitter(faithful$waiting)
> xrng <- range(x)
> yrng <- range(y)
> xlim <- extendrange(xrng, f = 0.1)
> ylim <- extendrange(yrng, f = 0.1)
> xdens <- density(x)
> ydens <- density(y)
> xdens.max <- max(xdens$y)
> ydens.max <- max(ydens$y)
```

We can now use these to take a shot at our desired plot. First we create a viewport for the central plot area with a suitable native coordinate system that covers the range of the data. The location of the viewport itself is specified in terms of the parent (root) viewport. By default, the coordinate system used to specify the location of a viewport is the *normalized parent coordinate* (NPC) system, which assigns the range $[0, 1]$ to both coordinate axes.

Simple attempt III

```
> library(grid)
> pushViewport(viewport(x = 0.45, y = 0.45, width = 0.7, height = 0
+                       xscale = xlim, yscale = ylim))
```

Next we add the data points using the native coordinate system and add the x- and y-axes.

```
> grid.points(x, y, default.units = "native")
> grid.xaxis()
> grid.yaxis()
```

For the rugs, we use line segments whose locations along the axes are specified using the native coordinate system, but whose lengths are specified using the NPC system to be exactly 3% of the range of the corresponding axis.

```
> grid.segments(x0 = unit(x, "native"), y0 = unit(0, "npc"),
+               x1 = unit(x, "native"), y1 = unit(0.03, "npc"))
> grid.segments(x0 = unit(0, "npc"), y0 = unit(y, "native"),
+               x1 = unit(0.03, "npc"), y1 = unit(y, "native"))
```

Simple attempt IV

Finally, we can add axis labels, and then the densities by creating two new viewports and plotting the densities inside.

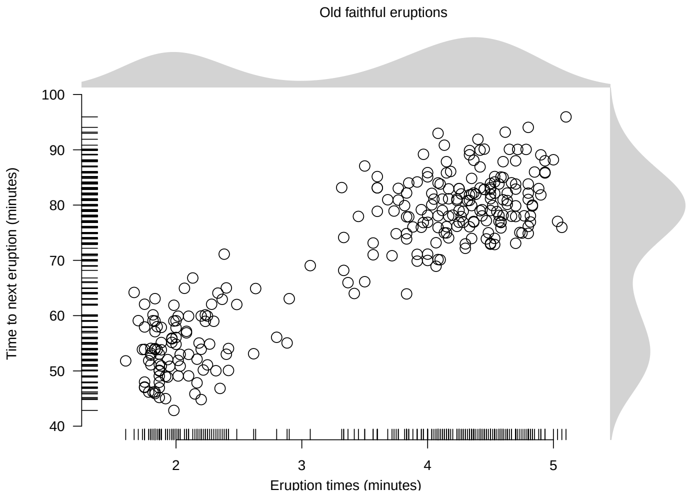
```
> upViewport(1)
> grid.text("Eruption times (minutes)", x = 0.45, y = 0,
+           just = c("centre", "bottom"))
> grid.text("Time to next eruption (minutes)", x = 0, y = 0.45,
+           rot = 90, just = c("centre", "top"))
> pushViewport(viewport(x = 0.45, y = 0.85, width = 0.7, height = 0
+                       xscale = xlim, yscale = c(0, xdens.max),
+                       clip = "on"))
> grid.polygon(x = xdens$x, y = xdens$y, default.units = "native",
+              gp = gpar(fill = "lightgrey", col = "transparent"))
> upViewport(1)
> pushViewport(viewport(x = 0.85, y = 0.45, width = 0.1, height = 0
+                       xscale = c(0, ydens.max), yscale = ylim,
+                       clip = "on"))
> grid.polygon(x = ydens$y, y = ydens$x, default.units = "native",
+              gp = gpar(fill = "lightgrey", col = "transparent"))
> upViewport(1)
```

Simple attempt V

We finish by adding a main label on top.

```
> pushViewport(viewport(x = 0.5, y = 0.95, width = 1, height = 0.1)
> grid.text("Old faithful eruptions", x = 0.5, y = 0.5)
```

Simple attempt VI



Further improvements

- This approach can be easily generalized to work with other datasets
- Several improvements could be desirable:
  - space for the axes, main title, etc., are proportions of the total figure area
  - instead, could want to use only as much space as necessary
  - can be done by specifying viewports are using "*layouts*"
- Will not go into that approach
- Such advanced features of grid are used by the lattice and ggplot2 packages (discussed next)

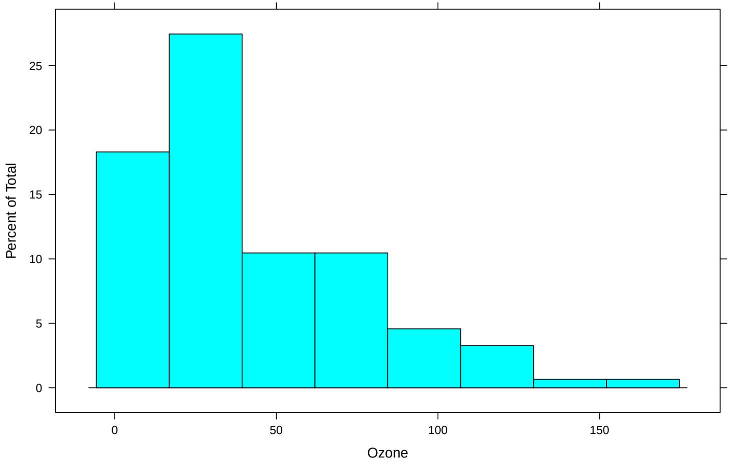
lattice

Lattice

- lattice: add-on package that implements Trellis graphics in R.
- Powerful high-level data visualization system with an emphasis on multivariate data.
- Typical usage: revisit histograms for the ozone concentration data
- Function used: `histogram()`

```
> library(lattice)
> histogram(~ Ozone, data = airquality)
```

Histogram (without conditioning)

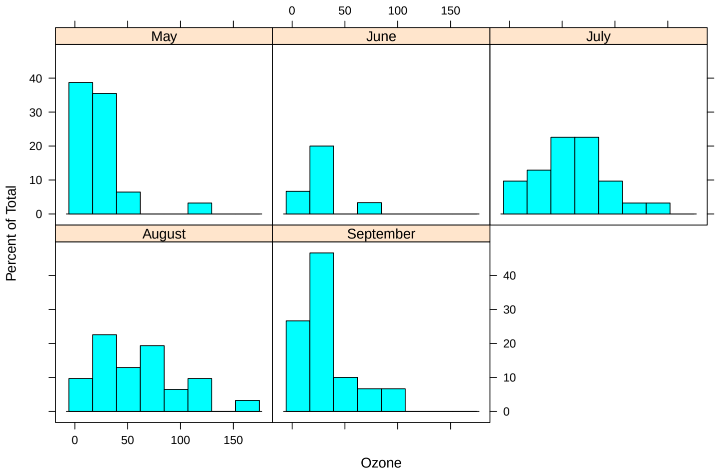


Histogram

- Note that Ozone is specified in a formula.
- All high-level functions in lattice support formulas
- The formula language allows us to elegantly express *conditioning variables* that are used to subdivide the data into subgroups that are plotted in "panels" juxtaposed to enable comparison.
- To see the distribution of Ozone across different months, we can simply use

```
> histogram(~ Ozone | fmonth, data = airquality)
```

Histogram (with conditioning)

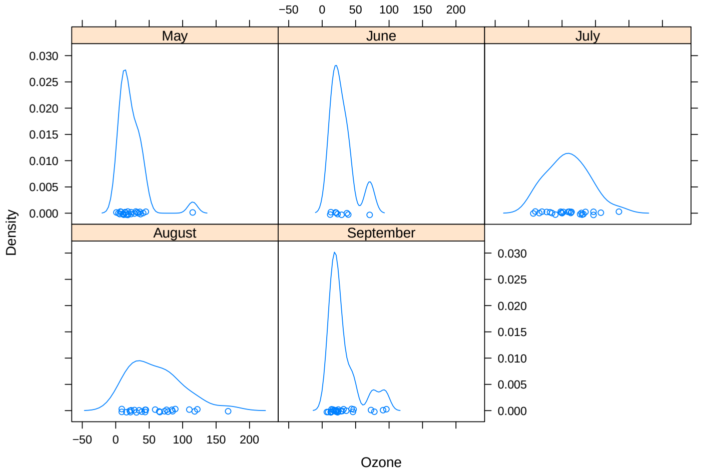


Features

- Panels share the same data ranges
- Axes are labeled only along the boundaries of the whole plot
- Optimal use of available space while making comparison easier

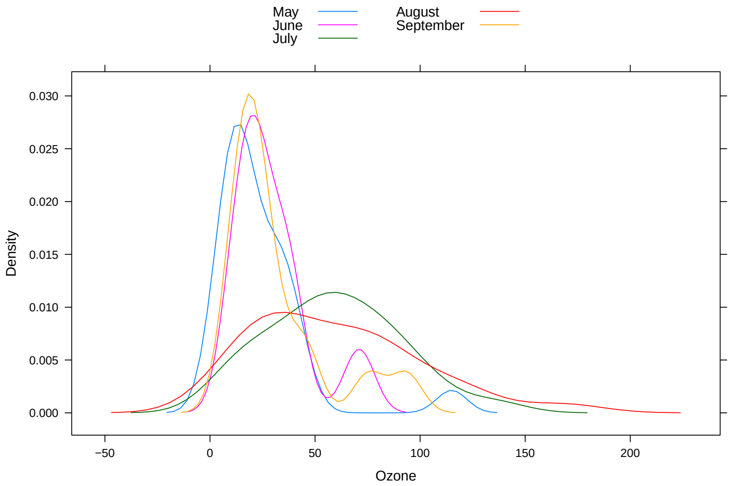
Kernel density plots (with conditioning)

```
> densityplot(~ Ozone | fmonth, data = airquality,
+                 as.table = TRUE)
```



Kernel density plots (with grouping)

```
> densityplot(~ Ozone, data = airquality, groups = fmonth,
+         plot.points = FALSE, auto.key = list(columns = 2))
```



Features

- Conditioning gives juxtaposition with common axes
- Even better comparison by superposition (grouping)
- `plot.points` and `auto.key` control further details

General overview

- High-level system for statistical graphics
- Independent of traditional R graphics
- Modeled on the Trellis suite in S

General overview

- High-level system for statistical graphics
- Independent of traditional R graphics
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- Displays defined by *type* of graphic and *role* different variables play in it
- Function name indicates type of graphic: `histogram`, `densityplot`
- Typical roles are:
  - *primary variables* define the main display (e.g., `Ozone`)
  - *conditioning variables* divide data into subgroups displayed in different panels
  - *grouping variables* divide data into subgroups contrasted within panels

High-level functions

Function	Default Display
`histogram()`	Histogram
`densityplot()`	Kernel density plot
`qqmath()`	Theoretical quantile plot
`qq()`	Two-sample quantile plot
`stripplot()`	Stripchart (comparative 1-D scatterplots)
`bwplot()`	Comparative box-and-whisker plot
`dotplot()`	Cleveland dot plot
`barchart()`	Bar plot
`xyplot()`	Scatterplot and time-series plot
`splom()`	Scatterplot matrix
`contourplot()`	Contour plot of surfaces
`levelplot()`	False-color level plot of surfaces
`wireframe()`	Three-dimensional perspective plot of surfaces
`cloud()`	Three-dimensional scatterplot
`parallelplot()`	Parallel coordinates plot

Design features

- Overall goal: make comparison easier
- Use as much of the available space as possible
- Force direct comparsion by superposition (grouping) when possible
- Encourage comparison when juxtaposing (conditioning): use common axes, add common reference objects such as grids.

Design features: implications

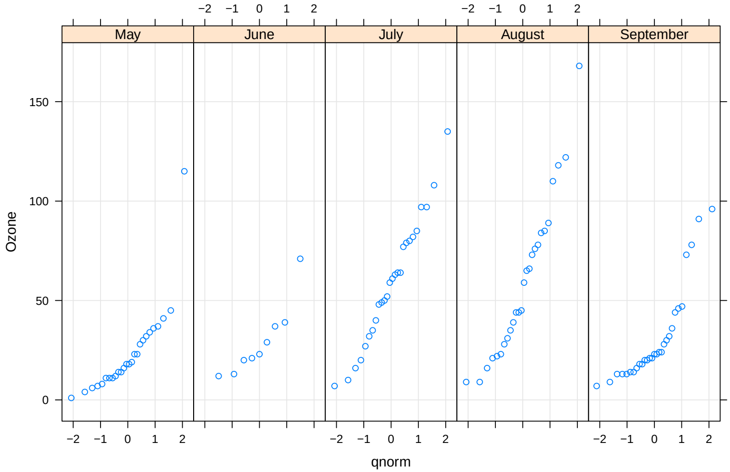
- Avoid empty space: no space for labels/legends if they are absent
- To implement this, all details need to be known when plotting begins
- Implication: incremental approach common in traditional R doesn't work
- Lattice approach:
  - plots are R objects (of class "trellis")
  - incremental updates are performed by modifying and re-plotting

Extensions / customizations

- Within overall structure, components can be customized
- The main components are
  - the primary (panel) display
  - axis annotation
  - strip annotation (describing the conditioning process)
  - legends (typically describing the grouping process)
- Most common: customized panel display

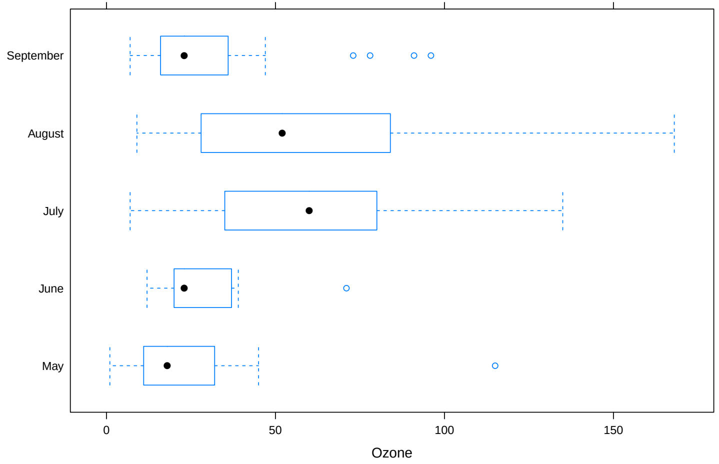
Common high-level displays: Q-Q plots

```
> qqmath(~ Ozone | fmonth, data = airquality, grid = TRUE,
+        layout = c(5, 1))
```



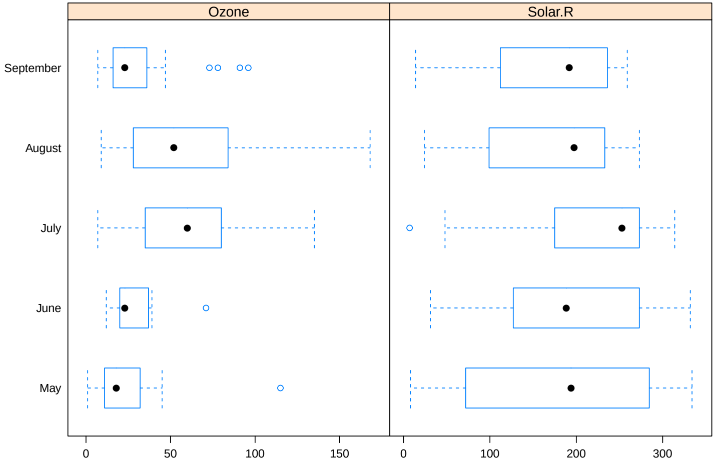
Common high-level displays: Comparative box-and-whisker plots

```
> bwplot(fmonth ~ Ozone, data = airquality)
```



Common high-level displays: different scales

```
> bwplot(fmonth ~ Ozone + Solar.R, data = airquality,
+        outer = TRUE, scales = list(x = "free"), xlab = NULL)
```



Bar charts and dot plots for tabular data

- We will use the `VADeaths` dataset again
- `VADeaths` is a matrix, but need a data frame to use the formula interface

```
> VADeathsDF <-
+     as.data.frame.table(VADeaths, responseName = "Rate")
> str(VADeathsDF)
```

```
'data.frame':   20 obs. of  3 variables:
 $ Var1: Factor w/ 5 levels "50-54","55-59",..: 1 2 3 4 5 1 2 3 4 5
 $ Var2: Factor w/ 4 levels "Rural Male","Rural Female",..: 1 1 1 1
 $ Rate: num  11.7 18.1 26.9 41 66 8.7 11.7 20.3 30.9 54.3 ...
```

Bar charts and dot plots for tabular data

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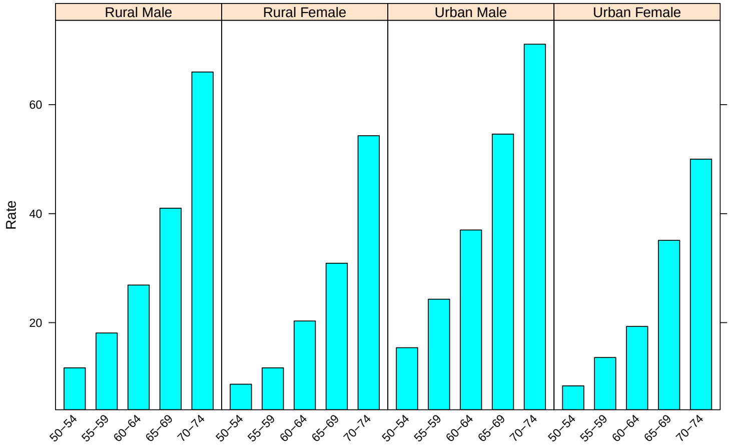
```

```
'data.frame':   20 obs. of  3 variables:
 $ Var1: Factor w/ 5 levels "50-54","55-59",..: 1 2 3 4 5 1 2 3 4 5
 $ Var2: Factor w/ 4 levels "Rural Male","Rural Female",..: 1 1 1 1
 $ Rate: num  11.7 18.1 26.9 41 66 8.7 11.7 20.3 30.9 54.3 ...
```

- TO produce a bar chart:

```
> barchart(Rate ~ Var1 | Var2, VADeathsDF, layout = c(4, 1),
+          scales = list(x = list(rot = 45)))
```

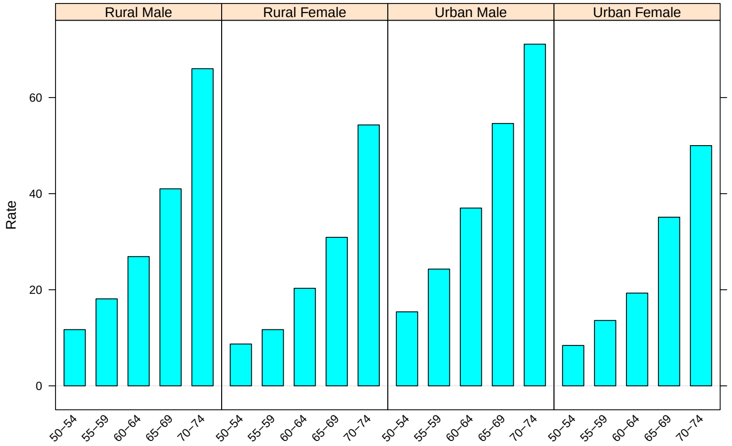

Rural Male
Rural Female
Urban Male
Urban Female
Rate
20
40
60
50–54
55–59
60–64
65–69
70–74

Bar charts

Potentially misleading, because

- strong visual comparison: areas of the shaded bars
- areas do not mean anything here
- can be addressed by making the bars start at 0.

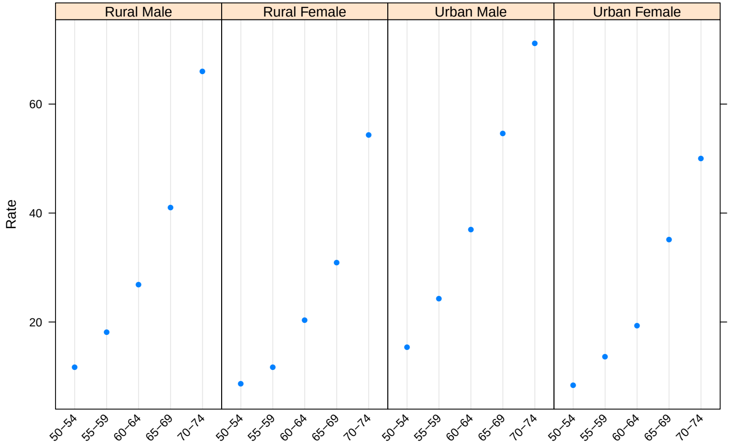
```
> barchart(Rate ~ Var1 | Var2, VADeathsDF, layout = c(4, 1),
+          origin = 0,
+          scales = list(x = list(rot = 45)))
```



Rural Male
Rural Female
Urban Male
Urban Female
Rate
0
20
40
60
50–54
55–59
60–64
65–69
70–74

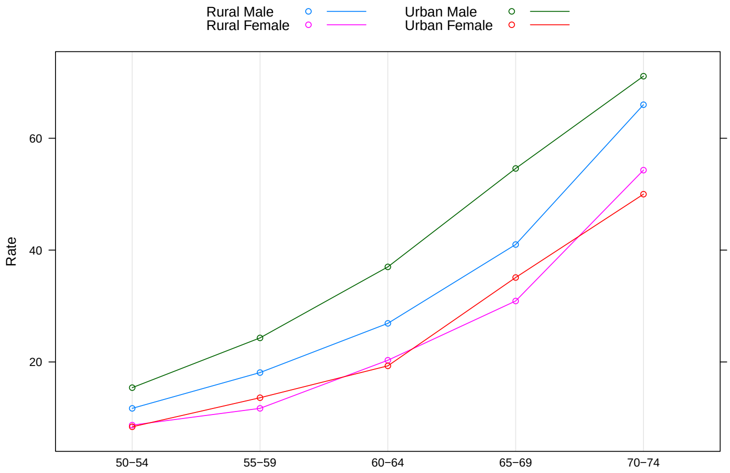
Dot plots: compare only location

```
> dotplot(Rate ~ Var1 | Var2, VADeathsDF, layout = c(4, 1),
+         scales = list(x = list(rot = 45)))
```



Dot plots (grouped)

```
> dotplot(Rate ~ Var1, VADeathsDF, groups = Var2, type = "o",
+         auto.key = list(columns = 2, points = TRUE, lines = TRUE))
```



Methods

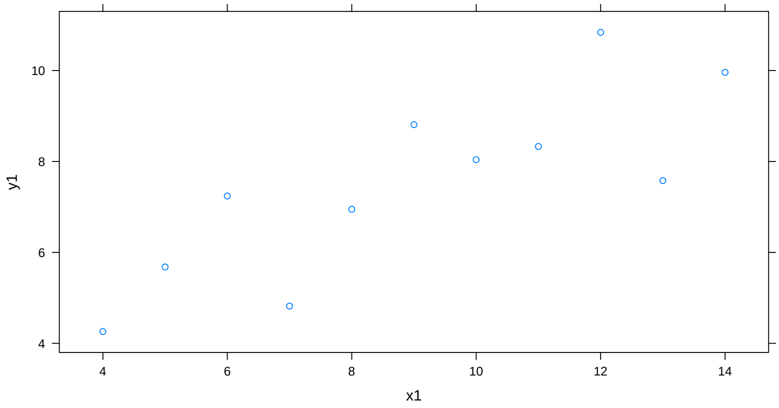
- High-level lattice functions are actually generic
- Specific methods do the actual work
- Examples seen so far are “formula” methods
- `barchart()` and `dotplot()` also have “table” methods

```
> dotplot(VADeaths, type = "o", ylab = "Rate", horizontal = FALSE,
+         auto.key = list(columns = 2, points = TRUE, lines = TRUE)
```

Scatter plots

Produced using `xyplot()`

```
> xyplot(y1 ~ x1, data = anscombe)
```



Scatter plots

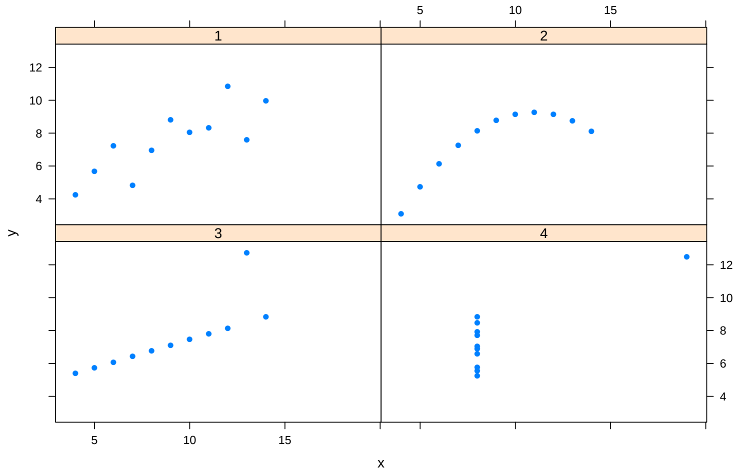
To show all four datasets, need to rearrange data

```
> anscombe.long <-
+     with(anscombe, data.frame(x = c(x1, x2, x3, x4),
+                               y = c(y1, y2, y3, y4),
+                               which = gl(4, nrow(anscombe))))
```

Scatter plots

A conditional plot can now be created using

```
> xyplot(y ~ x | which, data = anscombe.long, pch = 16)
```



Customization

- Suppose we want to add linear and quadratic regression lines
- Similar idea: fit models, add lines or curves representing the fits
- However, this cannot be done after the basic plot is already drawn
- Solution:
    - provide a function that implements procedure to display data
    - executed once for every panel (data subset)
    - known as the *panel function*
    - supplied as the `panel` argument to high-level calls

Customization

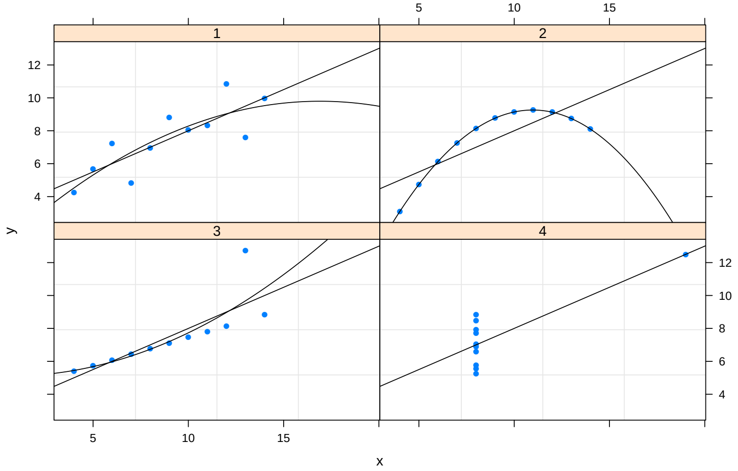
Such a function might look like:

```
> panel.lq <- function(x, y, ...)
+ {
+     panel.grid()
+     panel.xyplot(x, y, ...)
+     fm1 <- lm(y ~ x)
+     panel.abline(fm1)
+     try({
+         fm2 <- lm(y ~ poly(x, 2))
+         f <- function(x) predict(fm2, newdata = list(x = x))
+         panel.curve(f)
+     }, silent = TRUE)
+ }
```

- Uses lattice analogues of functions such as `abline()` and `curve()`
- The `panel.xyplot()` function represents the default panel function
- The quadratic model fit is wrapped inside `try()` because the fit fails for the fourth dataset which has only two unique values

Customization

```
> xyplot(y ~ x | which, data = anscombe.long, pch = 16,
+         as.table = TRUE, panel = panel.lq)
```

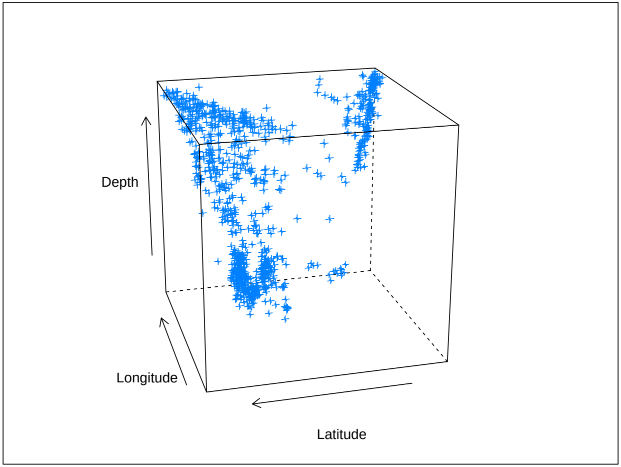


Three-dimensional plots

- Three-dimensional scatterplots supported by the `cloud()` function
- Example: scatter plot of latitude, longitude, and depth of earthquake epicenters

```
> cloud(depth ~ lat * long, data = quakes,
+       zlim = rev(range(quakes$depth)),
+       screen = list(z = 105, x = -70), panel.aspect = 0.75,
+       xlab = "Longitude", ylab = "Latitude", zlab = "Depth")
```

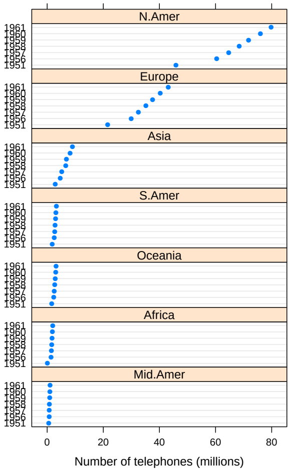
Three-dimensional plots



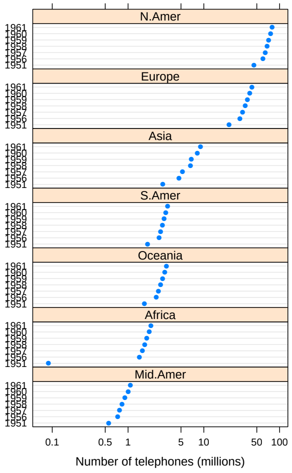
The "trellis" object

- Important feature of lattice:
  - high-level functions do not plot anything.
  - they return an object of class "trellis"
  - must be `print()`-ed or `plot()`-ed (not necessary in interactive use due to R's automatic printing rule)
  - can be useful to display multiple plots:

```
> dp.wp <- dotplot(WorldPhones/1000, groups = FALSE,
+                  layout = c(1, NA),
+                  xlab = "Number of telephones (millions)")
> dp.wp.log <-
+     dotplot(WorldPhones/1000, groups = FALSE, layout = c(1, NA),
+             scales = list(x = list(log = TRUE,
+                                    equispaced.log = FALSE)),
+             xlab = "Number of telephones (millions)")
> plot(dp.wp,     split = c(1, 1, 2, 1))
> plot(dp.wp.log, split = c(2, 1, 2, 1), newpage = FALSE)
```



N.Amer
Europe
Asia
S.Amer
Oceania
Africa
Mid.Amer
1961
1960
1959
1958
1957
1956
1951
0
20
40
60
80
Number of telephones (millions)



N.Amer
Europe
Asia
S.Amer
Oceania
Africa
Mid.Amer
1961
1960
1959
1958
1957
1956
1951
0.1
0.5
1
5
10
50
100
Number of telephones (millions)

ggplot2

Grammar of graphics

Traditional and trellis graphics both have the same basic approach:

- functions are written to implement specific graphical designs
- usually these designs have already been established as beingu useful
- customization is achieved through a procedural approach.

The ggplot2 package takes a different approach:

- defines a “layered grammar” for defining graphical designs
- defines various components of a graphical display
- final display is a composition of various independent components
- grammar is used to specify the composition
- can be used to create novel displays easily
- plots consist of one or more layers
  (e.g., raw data could be one layer, model fits another)

Grammar of graphics

The main components of the grammar are:

- *aesthetic mappings* that map data values to some aspect in the displayed graph, such as coordinate positions, color, shape, size, group, etc.
- geometric types used to render the mapped data, e.g., by points, lines, polygons, or something more complex such as a box-and-whisker plot.
- statistical transformations that are applied to the data beforehand, such as binning for histograms, or computation of kernel density estimates.
- Scales that give a visual indication of the aesthetic mappings, e.g., axis annotation for position mapping, legends for mapping to color, size, etc.
- Faceting (conditioning in Trellis terminology) to produce small multiples.

Example: Air quality data

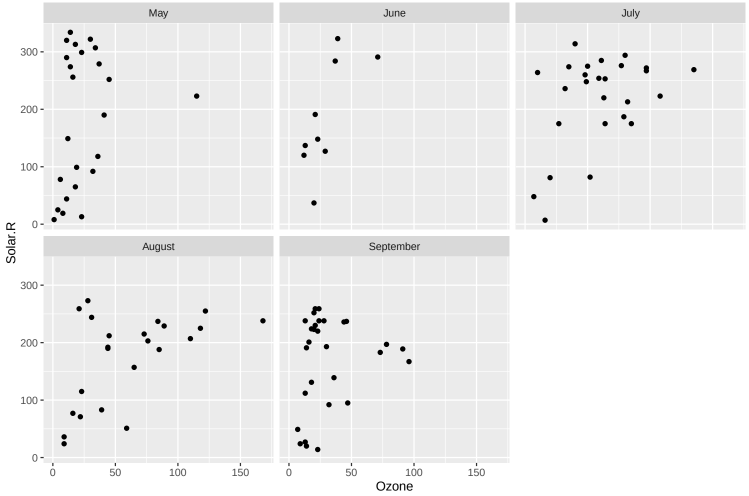
- Goal: produce histograms and kernel density plots conditioned on `fmonth`.
- Common data source and faceting, so capture these aspects first.

```
> library(ggplot2)
> p <- ggplot(airquality, aes(x = Ozone)) + facet_wrap(~ fmonth)
```

- `aes()` specifies the aesthetic mapping: saying in this case that `Ozone` variable should be mapped to x-coordinates in the plot.
- p is not yet a valid plot, because it doesn't yet have any layers.
- To create a scatterplot, we can add a point "geom" (short for geometric type), but to do so, we also need to specify a variable that will map to the y-coordinates.

Example: scatter plot

```
> p + geom_point(aes(y = Solar.R))
```

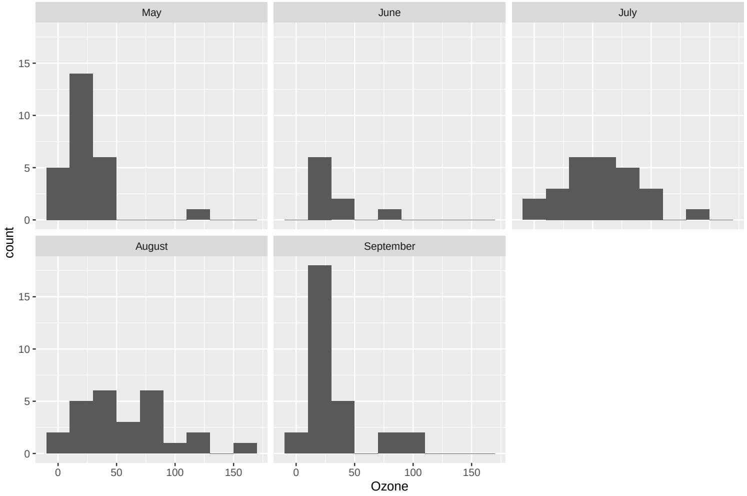


Example: histogram

- adding a geom is not enough for histogram
- we first need to transform the data by binning it
- we add a new “stat” layer created by `stat_bin()`
- we can also specify the geom to be used for rendering the transformed data.

Example: histogram

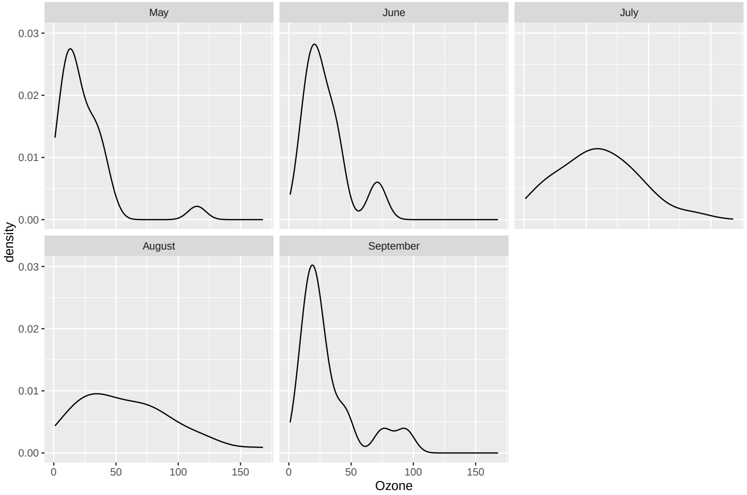
```
> p + stat_bin(binwidth = 20, geom = "bar")
```



Example: kernel density plots

- similarly produced using `stat_density()`.

```
> p + stat_density(geom = "path")
```



Simpler interface

- For these standard graphical designs, the calls above are too verbose
- `qplot()` offers a simpler interface for common designs
- The previous plots can be produced directly using

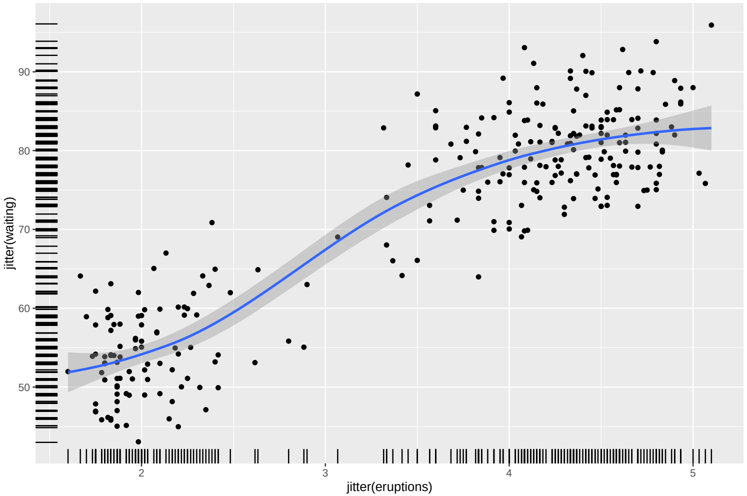
```
> qplot(x = Ozone, y = Solar.R, data = airquality,
+       facets = ~ fmonth)
> qplot(x = Ozone, data = airquality, facets = ~ fmonth,
+       stat = "bin", binwidth = 20)
> qplot(x = Ozone, data = airquality, facets = ~ fmonth,
+       stat = "density", geom = "line", binwidth = 20)
```

Layers

- Full potential of the layered approach becomes apparent when we need to add more elements to a plot.
- The following call creates a scatterplot of the `faithful` data with a LOESS fit and rugs on the margin.

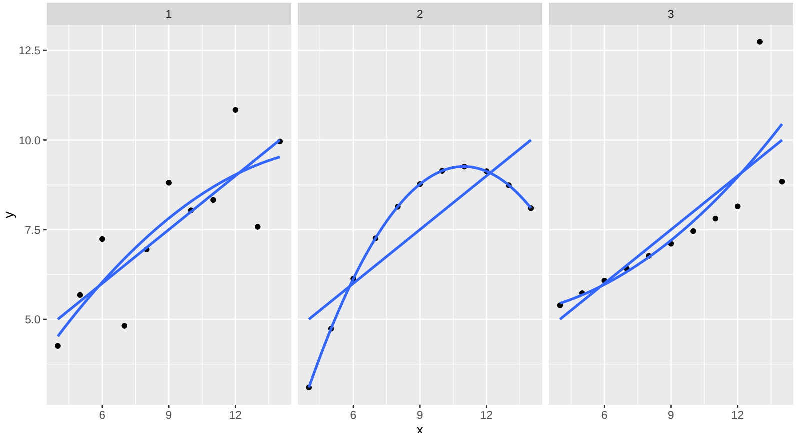
Layers

```
> qplot(x= jitter(eruptions), y= jitter(waiting), data= faithful) +
+     stat_smooth(method = "loess") + geom_rug()
```



Layers: another example

```
> anscombe.123 <- subset(anscombe.long, which != "4")
> qplot(x = x, y = y, data = anscombe.123, facets = ~ which) +
+   stat_smooth(method = "lm", se=FALSE) +
+   stat_smooth(method = "lm", formula = y ~ poly(x, 2), se=FALSE)
```



References

- Anscombe, F.J., 1973. *Graphs in statistical analysis. The American Statistician* 27:1, 17–21. Link
- Murrell, P., *R Graphics* (second edition), 2011. Chapman & Hall/CRC. `https://www.stat.auckland.ac.nz/~paul/RG2e/`
- Sarkar, D., 2008. *Lattice: Multivariate Data Visualization with R*. Springer, New York. `lmdvr.r-forge.rproject.org`
- Tukey, J.W., 1977. *Exploratory Data Analysis*. Addison-Wesley, Menlo Park, CA.
- Wickham, H., 2009. *ggplot2: Elegant Graphics for Data Analysis*. Springer, New York. `http://ggplot2.org/`
- Wilkinson, L., 1999. *The Grammar of Graphics*. Springer, New York.