Stat 5810, Section 003
Statistical Visualization I
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Contents

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Jürgen Symanzik, September 10, 2018.

1 Univariate Plots

1.1 Histograms

Example 1:

Four histograms of the same data set, showing the weights in pounds of 132 professional male athletes.

Question:

What can we conclude about the underlying data? And which of these four histograms best reveals this fact?

Example 2:

An interactive applet that allowed to change the number of classes in a histogram via a slider could be found at `http://www.stat.sc.edu/~west/javahtml/Histogram.html`:

> "**Histogram Applet:**
>
> This applet is designed to teach students how bin widths (or the number of bins) affect a histogram. The histogram below is for the Old Faithful data set. The observations are the duration (in minutes) for eruptions of the Old Faithful geyser in Yellowstone National Park. Students should interactively change the bin width by dragging the arrow underneath the bin width scale. For large bin widths, the bimodal nature of the dataset is hidden, and for small bin widths the plot reduces to a spike at each data point. What bin width do you think provides the best picture of the underlying data?"

While the URL above no longer exists, the following applet from the Rossman and Chance Applet Collection has a similar functionality: `http://www.rossmanchance.com/applets/Dotplot.html`

First prepare the *faithful* data in R so it appears in a single column without any additional spaces before/after the values:

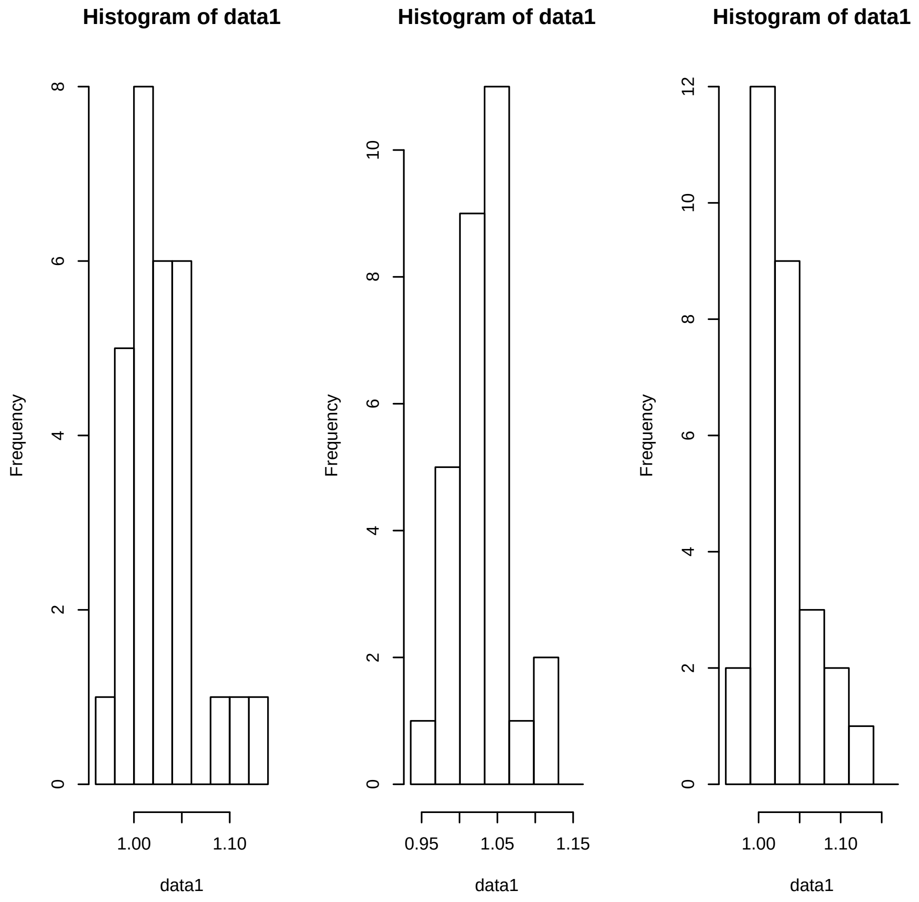
```
> for (i in 1:length(faithful$eruptions)) {
+       cat(paste0(faithful$eruptions[i], "\n"))
+ }
```

Then copy the data from your R console and paste them into the "Sample data" box on the web site. Click on "Use data" and select "Histogram". Use the slider and change the "Number of bins". What happens when this number increases?

Example 3:

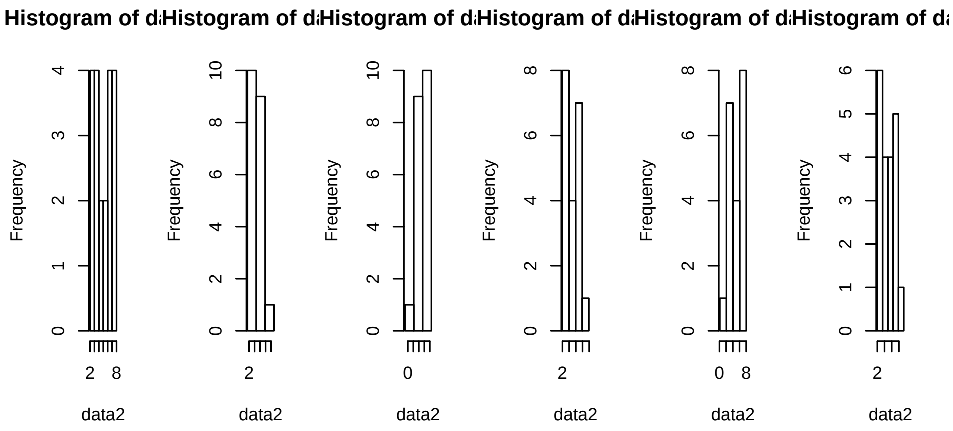
Example data sets from **?**:

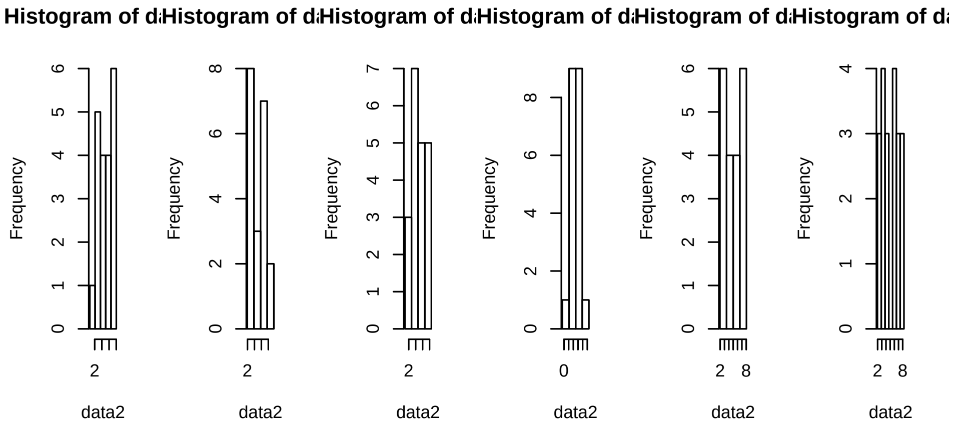
```
> # Weber (2008), Set 1:
>
> data1 <- c(.968, .982, .991, .993, .998, .999, 1.004, 1.004,
+   1.007, 1.010, 1.012, 1.015, 1.017, 1.019, 1.021,
+   1.035, 1.037, 1.037, 1.039, 1.039, 1.042, 1.042,
+   1.047, 1.053, 1.055, 1.059, 1.081, 1.107, 1.1305)
> par(mfrow = c(1, 3))
> hist(data1) #Default
> hist(data1, breaks = 0.9356 + (0:7) * 0.0325) #A
> hist(data1, breaks = 0.9600 + (0:7) * 0.0300) #B
> summary(data1)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  0.968   1.004   1.021   1.029   1.042   1.131
```



```
> # Weber (2008), Set 2:
>
> data2 <- c(2.05, 2.27, 2.50, 2.95, 3.18, 3.41, 3.64, 3.86, 4.09, 4.32,
+   5.68, 5.91, 6.14, 6.36, 6.59, 6.82, 7.05, 7.50, 7.73, 7.95)
> par(mfrow = c(2, 6))
> hist(data2)
> hist(data2, breaks = 1.425 + (0:3) * 3.2075) #C
> hist(data2, breaks = -1.048 + (0:3) * 3.2075) #D
> hist(data2, breaks = 1.9767 + (0:4) * 1.9789) #E
> hist(data2, breaks = 0.1078 + (0:4) * 1.9789) #F
> hist(data2, breaks = 1.9829 + (0:5) * 1.4750) #G
> hist(data2, breaks = 0.6421 + (0:5) * 1.4750) #H
> hist(data2, breaks = 1.9619 + (0:4) * 1.9060) #I
> hist(data2, breaks = 0.8944 + (0:4) * 1.9060) #J
> hist(data2, breaks = -0.6800 + (0:4) * 2.8400) #K
> hist(data2, breaks = 1.9542 + (0:4) * 1.5229) #L
> hist(data2, breaks = 1.9619 + (0:7) * .9060) #New 1
> summary(data2)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  2.050   3.353   5.000   5.000   6.647   7.950
```





Conclusion: “Never believe any statistics you haven’t falsified yourself.”

(http://sanmateorealestateblog.com/real-estate/statistics-real-estate/never-believe-any-statistics-you-havent-falsified-yourself/)

The R help page for hist indicates:

> "The generic function hist computes a histogram of the given data values."

The R help page for the Iris data set indicates:

> "This famous (Fisher's or Anderson's) iris data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are *Iris setosa*, *versicolor*, and *virginica*.
>
> iris is a data frame with 150 cases (rows) and 5 variables (columns) named Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, and Species."

Choosing the number of classes for a histogram:

As seen in the previous three examples, a bad choice for the number of classes (nclass or breaks in the R command) in a histogram or the starting point of an interval and its width can almost entirely hide the most interesting information of the underlying data.

Several suggestions for the number of classes exist and are summarized in **?**, p. 112. We define range $= x_{(n)} - x_{(1)}$, where n represents the number of observations.

- Sturges' formula (default in R):

$$\text{nclass} = \lceil \log_2 n + 1 \rceil, \quad \text{bin width} = \frac{\text{range}}{\text{nclass}},$$

  where $\lceil \ldots \rceil$ indicates the ceiling function.

- Scott's 1979 formula ("scott" in R):

$$\text{bin width} = 3.5\ \hat{\sigma}\ n^{-1/3}, \quad \text{nclass} = \frac{\text{range}}{\text{bin width}},$$

  where $\hat{\sigma}$ is the estimated standard deviation.

- Freedman and Diaconis 1981 formula ("fd" in R):

$$\text{bin width} = 2\ \text{IQR}\ n^{-1/3}, \quad \text{nclass} = \frac{\text{range}}{\text{bin width}},$$

  where IQR is the inter–quartile range.

- Sometimes, the use of nclass $\approx \sqrt{n}$ is suggested:

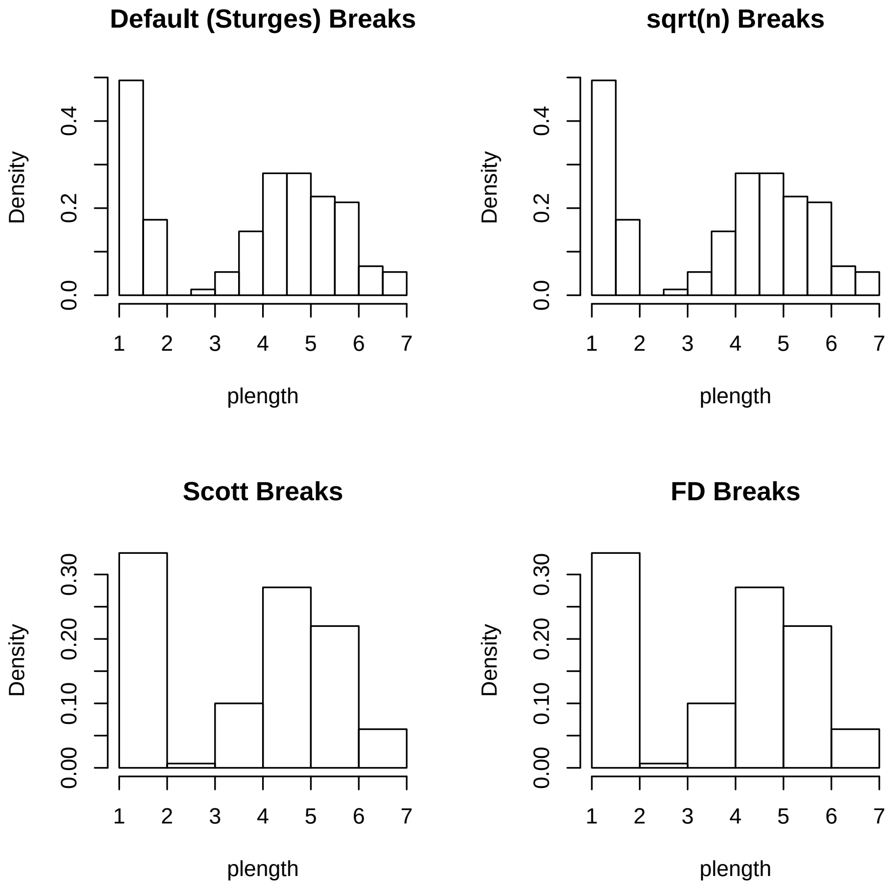
  `http://www.qimacros.com/qiwizard/how-to-determine-histogram-bin-interval.htm` suggests: *"Take the square root of the number of data points and round up to determine the number of bins required."*

  `http://www.moresteam.com/toolbox/t417.cfm` suggests: *"Calculate the square root of the number of data points and round to the nearest whole number. In the case of our height example, the square root of 50 is 7.07, or 7 when rounded.*

  `http://www.micquality.com/introductory_statistics/int08.htm` states: *"There are various ways of calculating the number of bins. I find that using the square root of the number of data values gives as good a result as the more complicated methods. The value is usually on the low side, but you can adjust it upwards to get convenient bin boundaries. Treat the calculated number of bins as a starting point, and adjust it as necessary to give the result you prefer."*

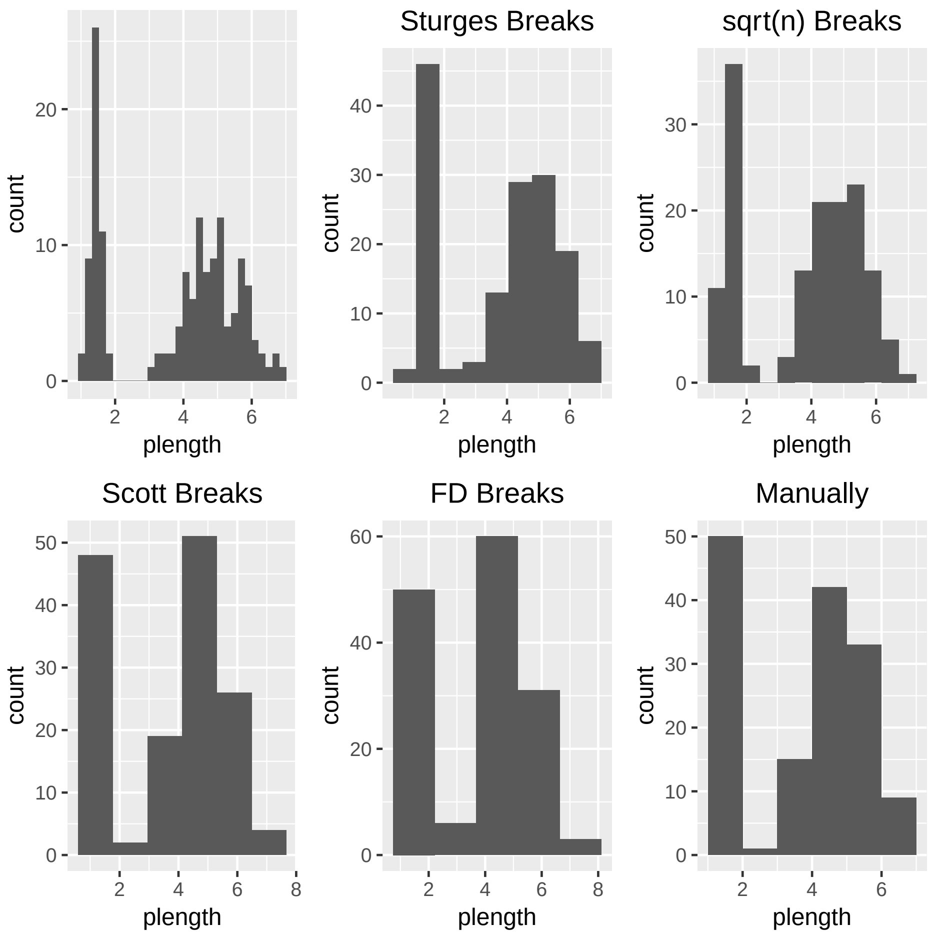
Example:

```
> head(iris)

  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa

> plength <- iris[, 3]
> n <- length(plength)
> par(mfrow = c(2, 2))
> hist(plength, freq = FALSE,
+      main = "Default (Sturges) Breaks")
> hist(plength, breaks = as.integer(sqrt(n)), freq = FALSE,
+      main = "sqrt(n) Breaks")
> hist(plength, breaks = "scott", freq = FALSE,
+      main = "Scott Breaks")
> hist(plength, breaks = "fd", freq = FALSE,
+       main = "FD Breaks")
> nclass.Sturges(plength)

[1] 9

> sqrt(n)

[1] 12.24745

> nclass.scott(plength)

[1] 6

> nclass.FD(plength)

[1] 5
```



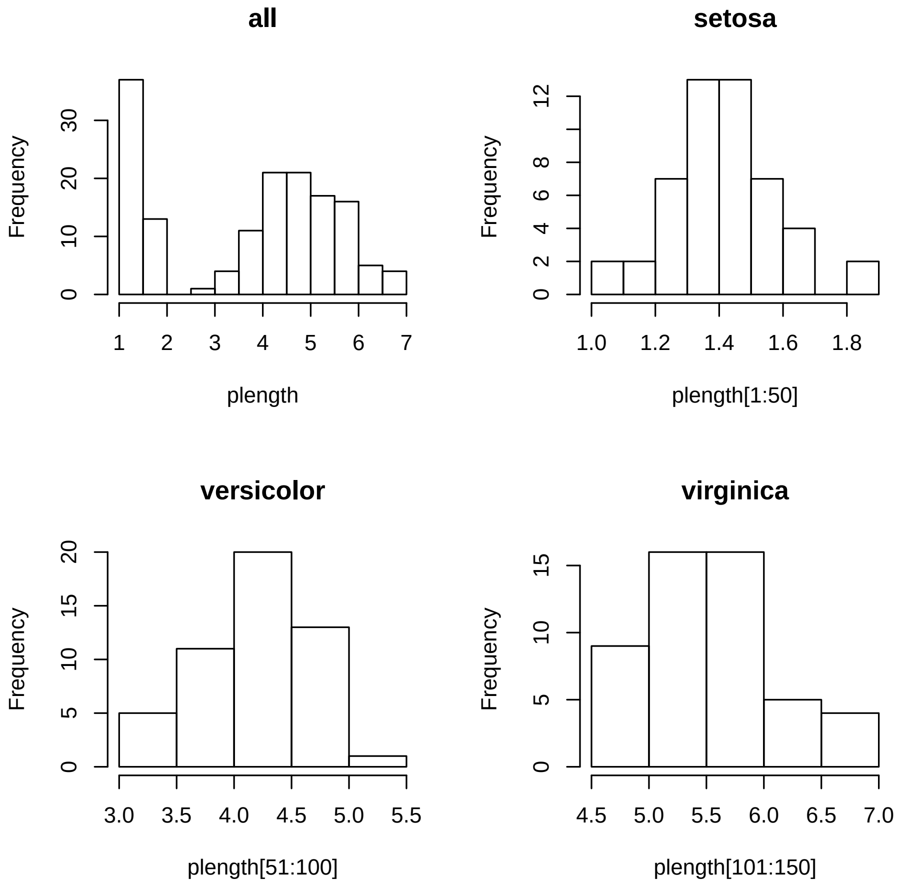
Now in ggplot2:

```
> library(ggplot2)
> library(gridExtra)
> h1 <- ggplot(iris, aes(x = plength)) +
+   geom_histogram()
> h2 <- ggplot(iris, aes(x = plength)) +
+   geom_histogram(bins = nclass.Sturges(plength)) +
+   ggtitle("Sturges Breaks") +
+   theme(plot.title = element_text(hjust = 0.5))
> h3 <- ggplot(iris, aes(x = plength)) +
+   geom_histogram(bins = as.integer(sqrt(n))) +
+   ggtitle("sqrt(n) Breaks") +
+   theme(plot.title = element_text(hjust = 0.5))
> h4 <- ggplot(iris, aes(x = plength)) +
+   geom_histogram(bins = nclass.scott(plength)) +
+   ggtitle("Scott Breaks") +
+   theme(plot.title = element_text(hjust = 0.5))
> h5 <- ggplot(iris, aes(x = plength)) +
+   geom_histogram(bins = nclass.FD(plength)) +
+   ggtitle("FD Breaks") +
+   theme(plot.title = element_text(hjust = 0.5))
> h6 <- ggplot(iris, aes(x = plength)) +
+   geom_histogram(binwidth = 1.0, center = 0.5) +
+   ggtitle("Manually") +
+   theme(plot.title = element_text(hjust = 0.5))
> grid.arrange(h1, h2, h3, h4, h5, h6,  nrow = 2)
```



Finally, how do the histograms for the three species look like?

```
> par(mfrow = c(2, 2))
> hist(plength, main = "all")
> hist(plength[1:50], main = "setosa")
> hist(plength[51:100], main = "versicolor")
> hist(plength[101:150], main = "virginica")
```



Note:

- These various methods (Sturges, Scott, FD, sqrt) provide suggestions for the number of classes only. To enforce particular breaks, we have to provide a vector giving the exact break points between the histogram cells. However, good software will use the suggestions and then make further adjustments to obtain meaningful class breaks for a human reader, e.g., use integers (and multiples of 5 or 10, etc.) as the boundaries.

- Carefully check whether class intervals are left–open or right–open. R class intervals by default are left–open whereas most readers prefer right–open intervals. Also, check in which class interval the minimum and maximum of a data set are included. For continuous data, there will be little differences in the appearance of a histogram, but for discrete data, different settings may result in a dramatically different visual appearance of a histogram. R provides arguments (include.lowest and right) to adjust these options.

- **?**, p. 30, state: **“Since it is relatively complicated both to draw and to read histograms with classes of different size we recommend that, as far as possible, both tables and charts should be made with classes of equal length.”**

1.2 Averaged Shifted Histograms

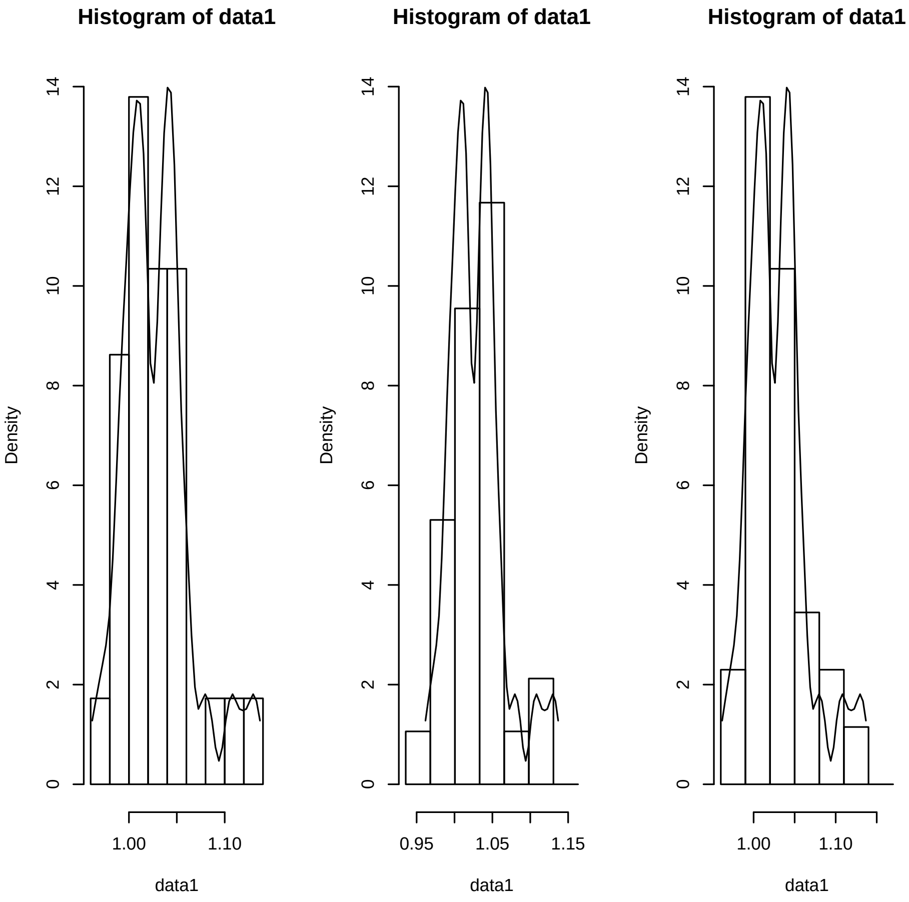
?, p. 307, states:

> “**?** provides a general overview on techniques for density estimation, including averaged shifted histograms (ASH) and kernel density estimators, including possible visualization techniques via contour surfaces, (transparent) α–level contours, and contour shells.”

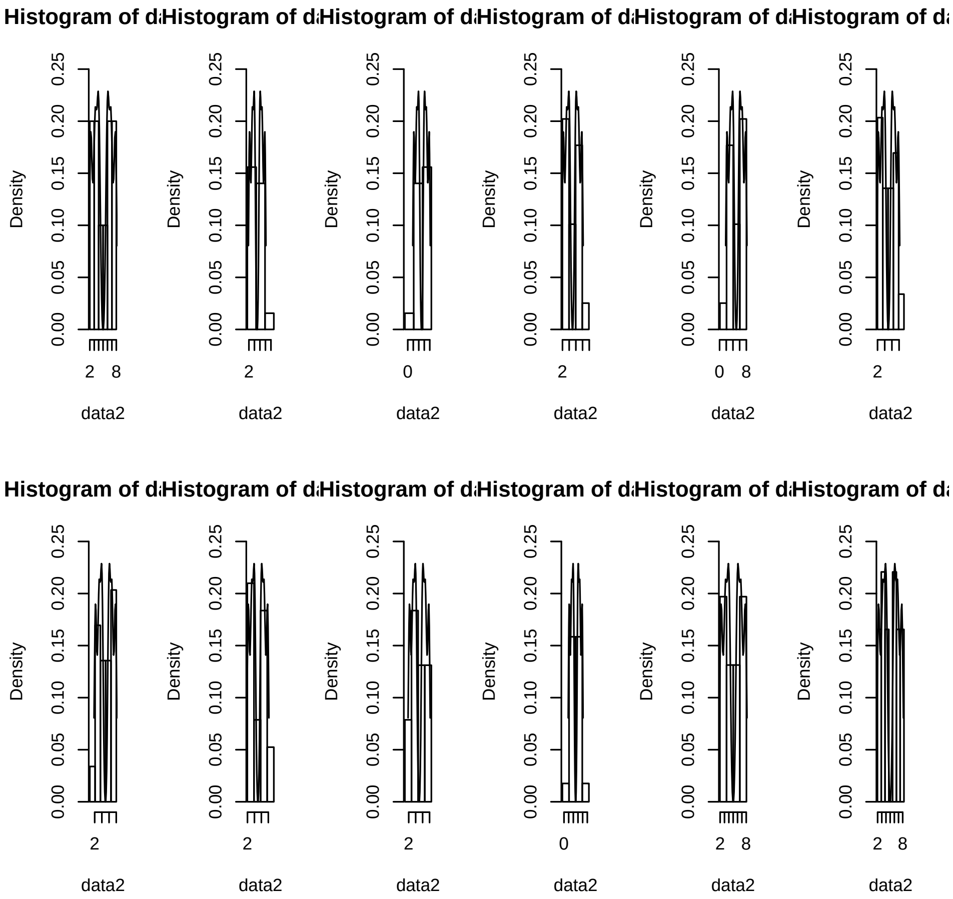
ASH plots were originally introduced in **?**. They are created by averaging several shifted histograms and further smoothing the result. Details are provided in Chapter 5 of **?**.

ASH plots may not be easy to explain to non–statisticians, but they may help to determine which histograms may be closest to the underlying data.

```
> # Weber (2008), Set 1:
>
> data1 <- c(.968, .982, .991, .993, .998, .999, 1.004, 1.004,
+   1.007, 1.010, 1.012, 1.015, 1.017, 1.019, 1.021,
+   1.035, 1.037, 1.037, 1.039, 1.039, 1.042, 1.042,
+   1.047, 1.053, 1.055, 1.059, 1.081, 1.107, 1.1305)
> library(ash)
> f1 <- ash1(bin1(data1, nbin = 50), 5) # compute ash estimate

[1] "ash estimate nonzero outside interval ab"

> par(mfrow = c(1, 3))
> hist(data1, freq = FALSE, ylim = c(0, 14)) #Default
> lines(f1 , type = "l") # line plot of estimate
> hist(data1, breaks = 0.9356 + (0:7) * 0.0325, freq = FALSE, ylim = c(0, 14)) #A
> lines(f1 , type = "l") # line plot of estimate
> hist(data1, breaks = 0.9600 + (0:7) * 0.0300, freq = FALSE, ylim = c(0, 14)) #B
> lines(f1 , type = "l") # line plot of estimate
```



```
> # Weber (2008), Set 2:
>
> data2 <- c(2.05, 2.27, 2.50, 2.95, 3.18, 3.41, 3.64, 3.86, 4.09, 4.32,
+   5.68, 5.91, 6.14, 6.36, 6.59, 6.82, 7.05, 7.50, 7.73, 7.95)
> f2 <- ash1(bin1(data2, nbin = 50), 5) # compute ash estimate

[1] "ash estimate nonzero outside interval ab"

> par(mfrow = c(2, 6))
> hist(data2, freq = FALSE, ylim = c(0, 0.25))
> lines(f2 , type ="l") # line plot of estimate
> hist(data2, breaks = 1.425 + (0:3) * 3.2075, freq = FALSE, ylim = c(0, 0.25)) #C
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = -1.048 + (0:3) * 3.2075, freq = FALSE, ylim = c(0, 0.25)) #D
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 1.9767 + (0:4) * 1.9789, freq = FALSE, ylim = c(0, 0.25)) #E
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 0.1078 + (0:4) * 1.9789, freq = FALSE, ylim = c(0, 0.25)) #F
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 1.9829 + (0:5) * 1.4750, freq = FALSE, ylim = c(0, 0.25)) #G
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 0.6421 + (0:5) * 1.4750, freq = FALSE, ylim = c(0, 0.25)) #H
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 1.9619 + (0:4) * 1.9060, freq = FALSE, ylim = c(0, 0.25)) #I
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 0.8944 + (0:4) * 1.9060, freq = FALSE, ylim = c(0, 0.25)) #J
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = -0.6800 + (0:4) * 2.8400, freq = FALSE, ylim = c(0, 0.25)) #K
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 1.9542 + (0:4) * 1.5229, freq = FALSE, ylim = c(0, 0.25)) #L
> lines(f2 , type = "l") # line plot of estimate
> hist(data2, breaks = 1.9619 + (0:7) * .9060, freq = FALSE, ylim = c(0, 0.25)) #New 1
> lines(f2 , type = "l") # line plot of estimate
```


Histogram of d
Histogram of d
Histogram of d
Histogram of d
Histogram of d
Histogram of d
Density
0.00
0.05
0.10
0.15
0.20
0.25
2
8
2
0
2
0
8
2
data2
data2
data2
data2
data2
data2
Histogram of d
Histogram of d
Histogram of d
Histogram of d
Histogram of d
Histogram of d
Density
0.00
0.05
0.10
0.15
0.20
0.25
2
2
2
0
2
8
2
8
data2
data2
data2
data2
data2
data2

1.3 Stem–and–Leaf Plots

The R help page for stem indicates:

> “stem produces a stem-and-leaf plot of the values in x.”

?, p. 113, further specify: *“A stem–and–leaf plot is an enhanced histogram. The data are divided into bins, but the ‘height’ is replaced by the next digits in order.”*

While stem–and–leaf plots show more details than histograms, they are rarely used in practice, in particular not for larger data sets. However, they are a useful first step to the creation of histograms and therefore appear in many introductory statistics textbooks, e.g., **?**, pp. 9–12, and **?**, pp. 46–49.

```
> sort(plength)

  [1] 1.0 1.1 1.2 1.2 1.3 1.3 1.3 1.3 1.3 1.3 1.3 1.4 1.4 1.4 1.4 1.4 1.4 1.4
 [19] 1.4 1.4 1.4 1.4 1.4 1.4 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5 1.5
 [37] 1.5 1.6 1.6 1.6 1.6 1.6 1.6 1.6 1.7 1.7 1.7 1.7 1.9 1.9 3.0 3.3 3.3 3.5
 [55] 3.5 3.6 3.7 3.8 3.9 3.9 3.9 4.0 4.0 4.0 4.0 4.0 4.1 4.1 4.1 4.2 4.2 4.2
 [73] 4.2 4.3 4.3 4.4 4.4 4.4 4.4 4.5 4.5 4.5 4.5 4.5 4.5 4.5 4.5 4.6 4.6 4.6
 [91] 4.7 4.7 4.7 4.7 4.7 4.8 4.8 4.8 4.8 4.9 4.9 4.9 4.9 4.9 5.0 5.0 5.0 5.0
[109] 5.1 5.1 5.1 5.1 5.1 5.1 5.1 5.1 5.2 5.2 5.3 5.3 5.4 5.4 5.5 5.5 5.5 5.6
[127] 5.6 5.6 5.6 5.6 5.6 5.7 5.7 5.7 5.8 5.8 5.8 5.9 5.9 6.0 6.0 6.1 6.1 6.1
[145] 6.3 6.4 6.6 6.7 6.7 6.9

> stem(plength)

  The decimal point is at the |

  1 | 0122333333344444444444444
  1 | 55555555555556666666777799
  2 |
  2 |
  3 | 033
  3 | 55678999
  4 | 000001112222334444
  4 | 5555555566677777888899999
  5 | 000011111111223344
  5 | 55566666677788899
  6 | 0011134
  6 | 6779

> stem(data1)

  The decimal point is 2 digit(s) to the left of the |

   96 | 8
   98 | 21389
  100 | 44702579
  102 | 157799
  104 | 227359
  106 |
  108 | 1
  110 | 7
  112 | 1

> stem(data1, scale = 2)

  The decimal point is 2 digit(s) to the left of the |

   96 | 8
   97 |
   98 | 2
   99 | 1389
  100 | 447
  101 | 02579
  102 | 1
  103 | 57799
  104 | 227
  105 | 359
  106 |
  107 |
  108 | 1
  109 |
  110 | 7
  111 |
  112 |
  113 | 1

> stem(data2)

  The decimal point is at the |

  2 | 13502469
  4 | 1379
  6 | 1468157
  8 | 0

> stem(data2, scale = 2)

  The decimal point is at the |

  2 | 135
  3 | 02469
  4 | 13
  5 | 79
  6 | 1468
  7 | 157
  8 | 0

> stem(data2, scale = 4)

  The decimal point is at the |

  2 | 13
  2 | 5
  3 | 024
  3 | 69
  4 | 13
```

```
4 |
5 |
5 | 79
6 | 14
6 | 68
7 | 1
7 | 57
8 | 0
```

1.4 Boxplots (or Box–and–Whisker Plots)

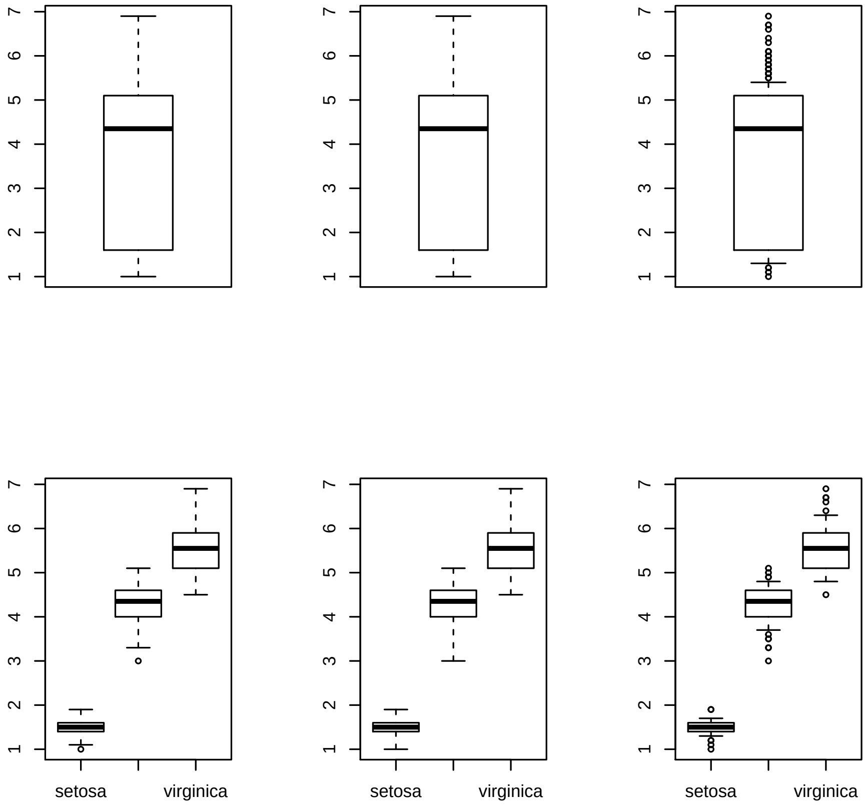
The R help page for boxplot indicates:

> "Produce box-and-whisker plot(s) of the given (grouped) values.
>
> range: this determines how far the plot whiskers extend out from the box. If range is positive, the whiskers extend to the most extreme data point which is no more than range times the interquartile range from the box. A value of zero causes the whiskers to extend to the data extremes."

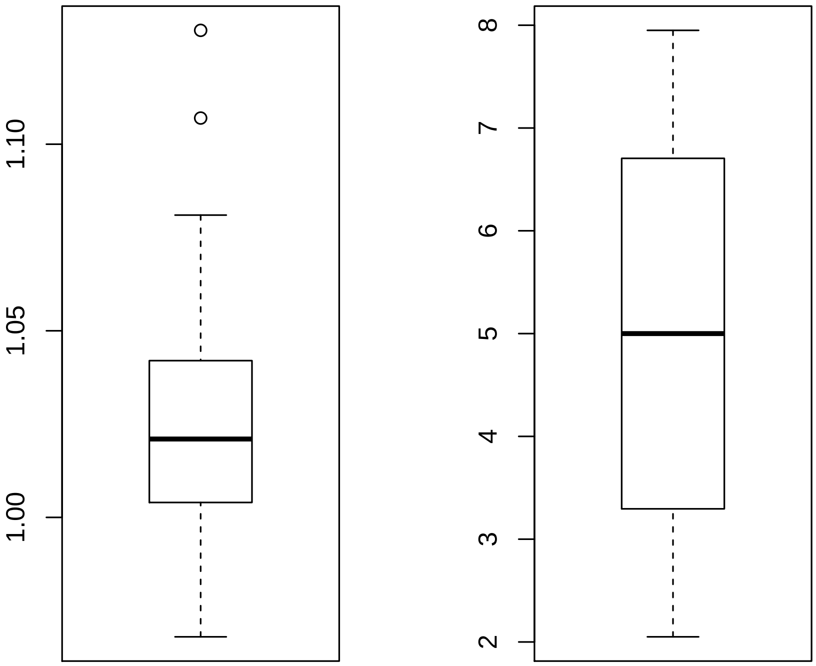
The default for range is 1.5.

?, p. 115, further specify: *"A boxplot is a way to look at the overall shape of a set of data. The central box shows the data between the 'hinges' (roughly quartiles), with the median represented by a line. 'Whiskers' go out to the extremes of the data, and very extreme points are shown by themselves."*

```
> par(mfrow = c(2, 3))
> boxplot(plength)
> boxplot(plength, range = 0)
> boxplot(plength, range = 0.1)
> boxplot(plength ~ iris$Species)
> boxplot(plength ~ iris$Species, range = 0)
> boxplot(plength ~ iris$Species, range = 0.5)
```



```
> par(mfrow = c(1, 2))
> boxplot(data1)
> boxplot(data2)
```

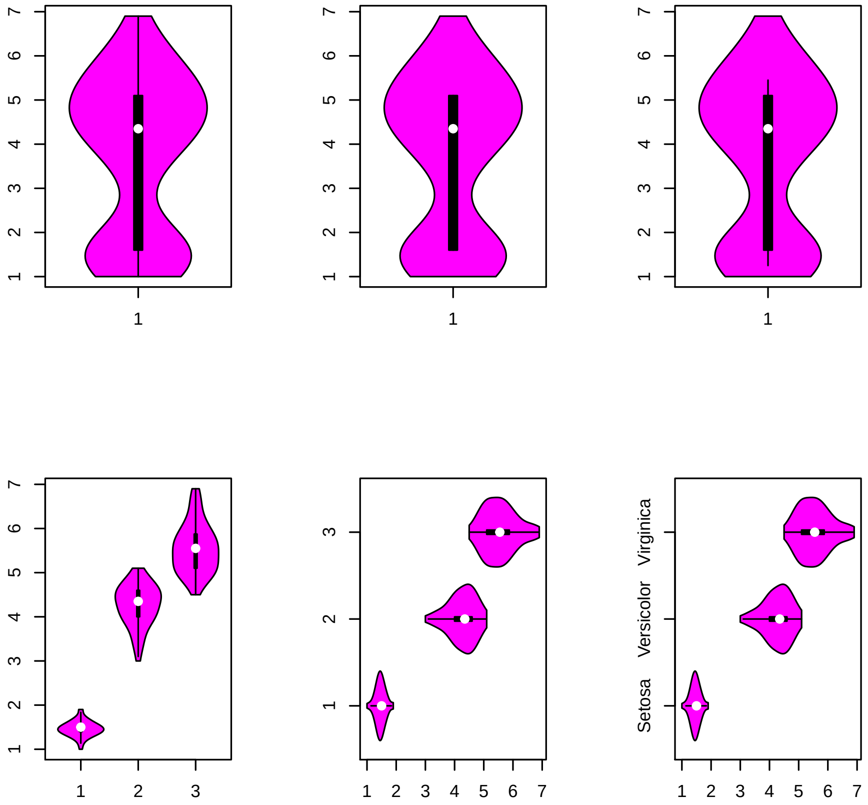

1.00
1.05
1.10
2
3
4
5
6
7
8

1.5 Violin Plots

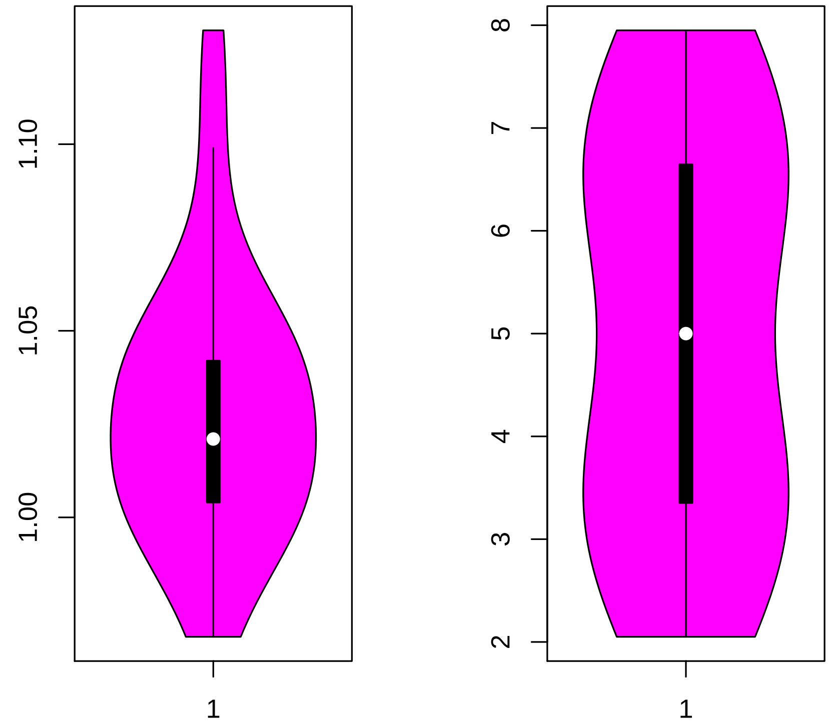
The R help page for vioplot indicates:

> “Produce violin plot(s) of the given (grouped) values.
>
> A violin plot is a combination of a box plot and a kernel density plot. Specifically, it starts with a box plot. It then adds a rotated kernel density plot to each side of the box plot.”

```
> library(vioplot)
> par(mfrow = c(2, 3))
> vioplot(plength)
> vioplot(plength, range = 0)
> vioplot(plength, range = 0.1)
> vioplot(plength[iris$Species == "setosa"],
+         plength[iris$Species == "versicolor"],
+         plength[iris$Species == "virginica"])
> vioplot(plength[iris$Species == "setosa"],
+         plength[iris$Species == "versicolor"],
+         plength[iris$Species == "virginica"],
+         horizontal = TRUE)
> vioplot(plength[iris$Species == "setosa"],
+         plength[iris$Species == "versicolor"],
+         plength[iris$Species == "virginica"],
+         horizontal = TRUE,
+         names = c("Setosa", "Versicolor", "Virginica"))
```



```
> par(mfrow = c(1, 2))
> vioplot(data1)
> vioplot(data2)
```

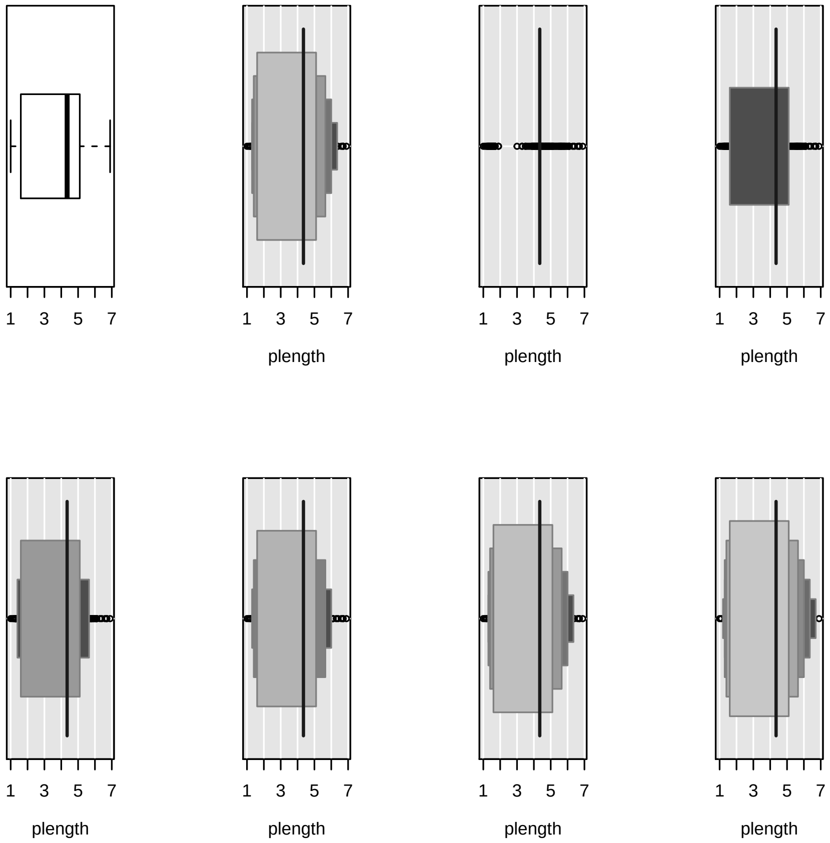

1.10
1.05
1.00
1
8
7
6
5
4
3
2
1

1.6 Letter Value Boxplots

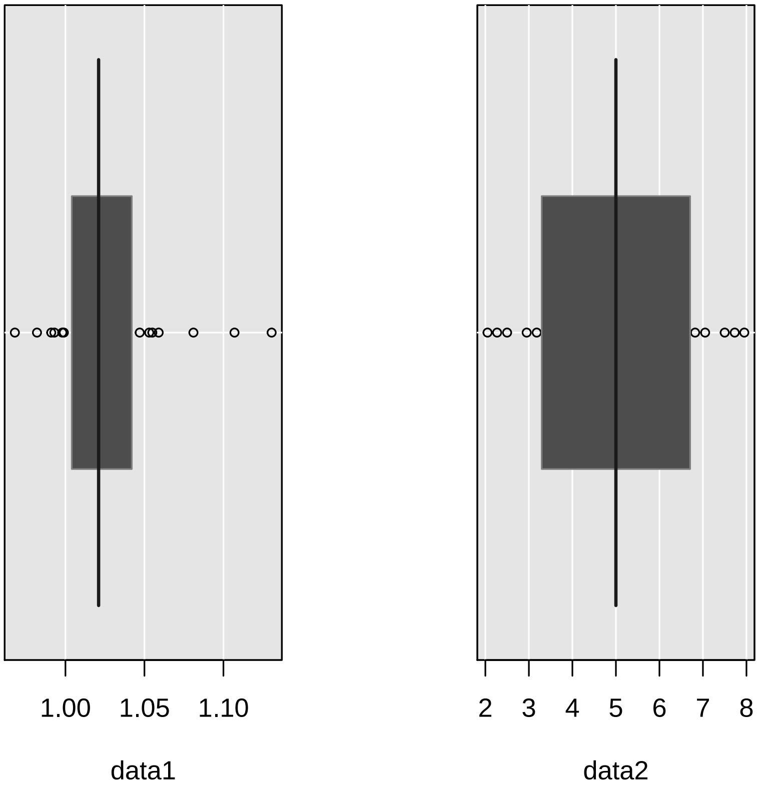
The R help page for LVboxplot indicates:

> "An extension of standard boxplots which draws k letter statistics. Conventional boxplots (Tukey 1977) are useful displays for conveying rough information about the central 50% of the data and the extent of the data.
>
> For moderate-sized data sets (n < 1000), detailed estimates of tail behavior beyond the quartiles may not be trustworthy [...]. Large data sets [...] can be expected to present a large number of 'outliers' [...]."

```
> library(lvplot)
> par(mfrow = c(2, 4))
> boxplot(plength, horizontal = TRUE)
> LVboxplot(plength)
> LVboxplot(plength, k = 1)
> LVboxplot(plength, k = 2)
> LVboxplot(plength, k = 3)
> LVboxplot(plength, k = 4)
> LVboxplot(plength, k = 5)
> LVboxplot(plength, k = 6)
```

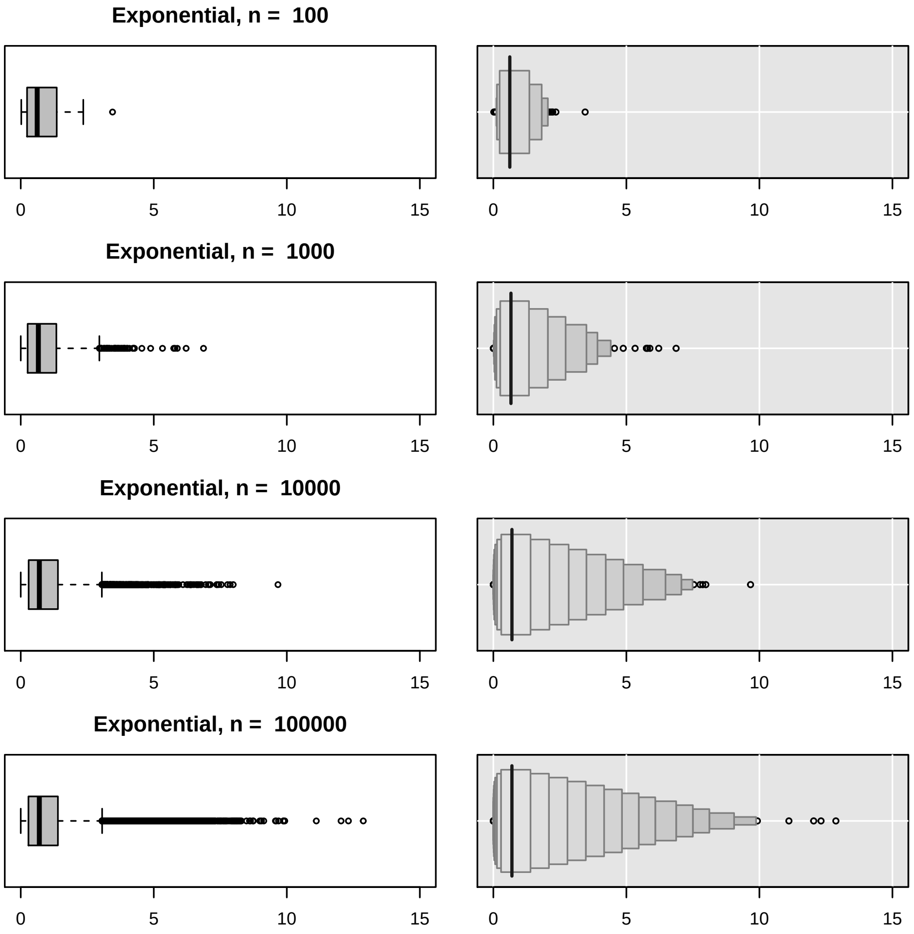


```
> par(mfrow = c(1, 2))
> LVboxplot(data1)
> LVboxplot(data2)
```



Additional example for samples from an exponential distribution, based on LVboxplot help page:

```
> par(mfrow = c(4, 2), mar = c(2, 1, 3, 1))
> for (i in 1:4) {
+   x <- rexp(10^(i + 1))
+   boxplot(x, col = "grey", horizontal = TRUE,
+           ylim = c(0, 15))
+   title(paste("Exponential, n = ", length(x)))
+   LVboxplot(x, col = "grey", xlab = "",
+             xlim = c(0, 15))
+ }
```



Exponential, n = 100

Exponential, n = 1000

Exponential, n = 10000

Exponential, n = 100000

1.7 Dot Charts for Univariate Data

The R help page for dotchart indicates:

> "Draw a Cleveland dot plot."

The R help page for UScereal(MASS) indicates:

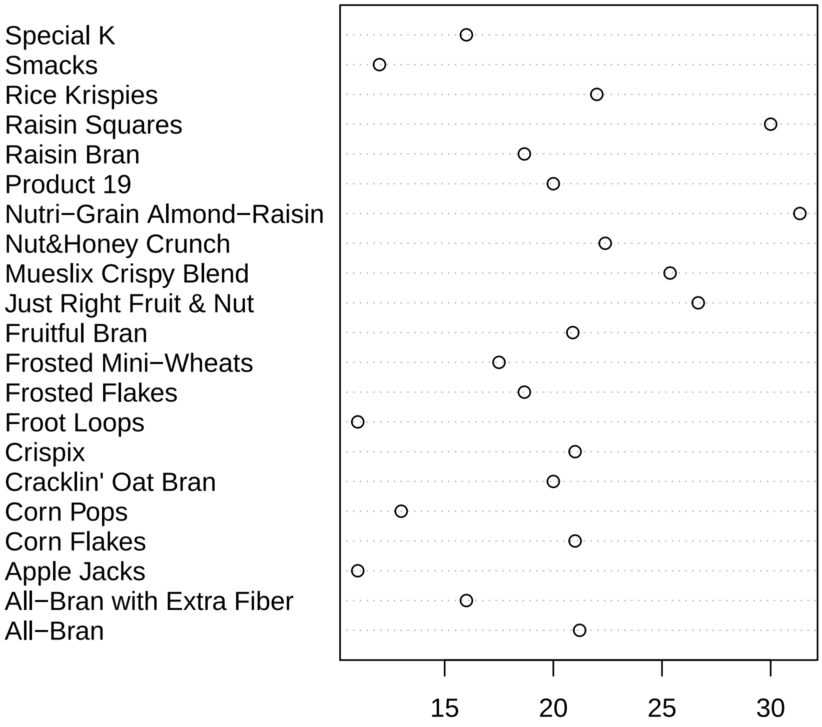
> "**Nutritional and Marketing Information on US Cereals:**
>
> The UScereal data frame has 65 rows and 11 columns. The data come from the 1993 ASA Statistical Graphics Exposition, and are taken from the mandatory F&DA food label. The data have been normalized here to a portion of one American cup. "

```
> library(MASS)  # for cereal data
> data(UScereal)
> head(UScereal)
```

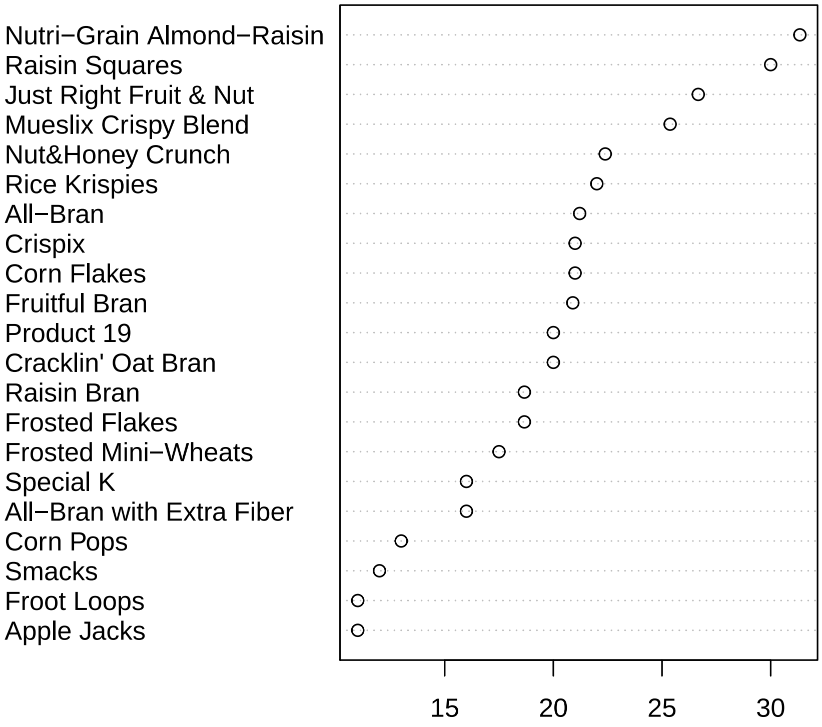
```
                          mfr calories   protein      fat   sodium     fibre
100% Bran                   N 212.1212 12.121212 3.030303 393.9394 30.303030
All-Bran                    K 212.1212 12.121212 3.030303 787.8788 27.272727
All-Bran with Extra Fiber   K 100.0000  8.000000 0.000000 280.0000 28.000000
Apple Cinnamon Cheerios     G 146.6667  2.666667 2.666667 240.0000  2.000000
Apple Jacks                 K 110.0000  2.000000 0.000000 125.0000  1.000000
Basic 4                     G 173.3333  4.000000 2.666667 280.0000  2.666667
                             carbo   sugars shelf potassium vitamins
100% Bran                 15.15152 18.18182     3 848.48485 enriched
All-Bran                  21.21212 15.15151     3 969.69697 enriched
All-Bran with Extra Fiber 16.00000  0.00000     3 660.00000 enriched
Apple Cinnamon Cheerios   14.00000 13.33333     1  93.33333 enriched
Apple Jacks               11.00000 14.00000     2  30.00000 enriched
Basic 4                   24.00000 10.66667     3 133.33333 enriched
```

```
> Kel.carbs <- UScereal[UScereal$mfr == "K", 7]
> Kel.carbs
```

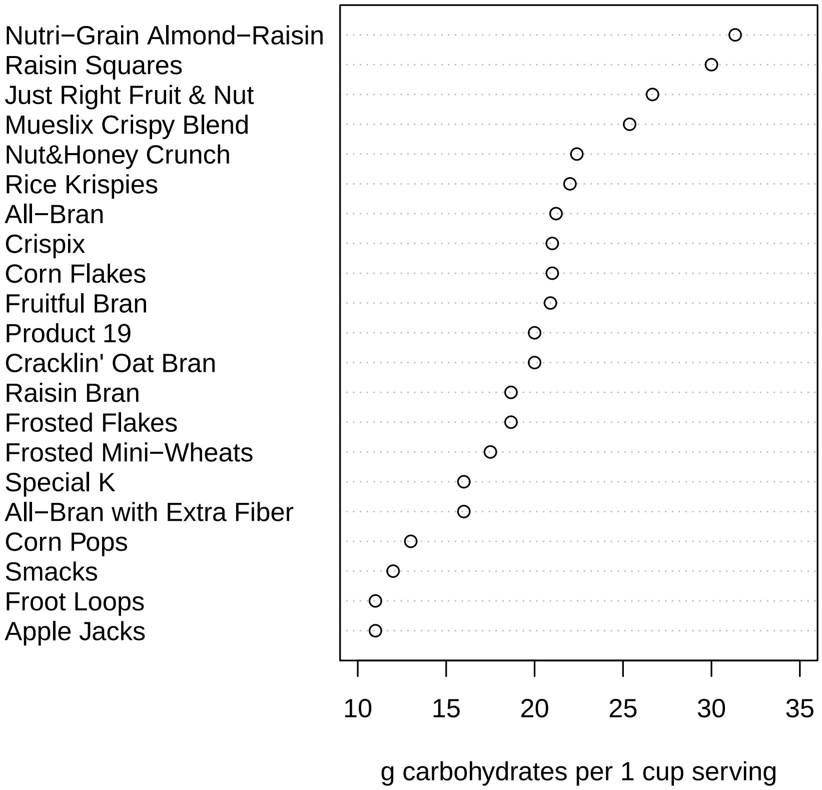
```
 [1] 21.21212 16.00000 11.00000 21.00000 13.00000 20.00000 21.00000 11.00000
 [9] 18.66667 17.50000 20.89552 26.66667 25.37313 22.38806 31.34328 20.00000
[17] 18.66667 30.00000 22.00000 12.00000 16.00000

> names(Kel.carbs) <- row.names(UScereal[UScereal$mfr == "K", ])
> Kel.carbs

            All-Bran All-Bran with Extra Fiber               Apple Jacks
            21.21212                  16.00000                  11.00000
         Corn Flakes                 Corn Pops        Cracklin' Oat Bran
            21.00000                  13.00000                  20.00000
             Crispix               Froot Loops            Frosted Flakes
            21.00000                  11.00000                  18.66667
 Frosted Mini-Wheats             Fruitful Bran    Just Right Fruit & Nut
            17.50000                  20.89552                  26.66667
Mueslix Crispy Blend          Nut&Honey Crunch Nutri-Grain Almond-Raisin
            25.37313                  22.38806                  31.34328
          Product 19               Raisin Bran            Raisin Squares
            20.00000                  18.66667                  30.00000
       Rice Krispies                    Smacks                 Special K
            22.00000                  12.00000                  16.00000

> dotchart(Kel.carbs)
```



```
> dotchart(sort(Kel.carbs))
```

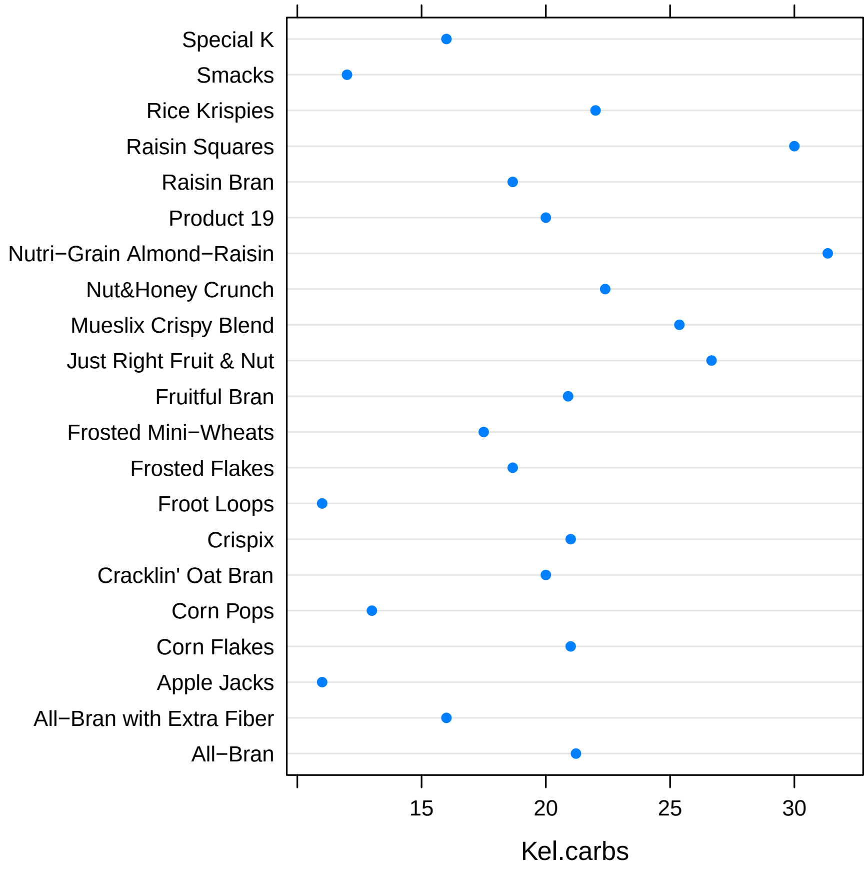


```
> dotchart(sort(Kel.carbs), xlim = c(10, 35),
+   xlab = "g carbohydrates per 1 cup serving")
```

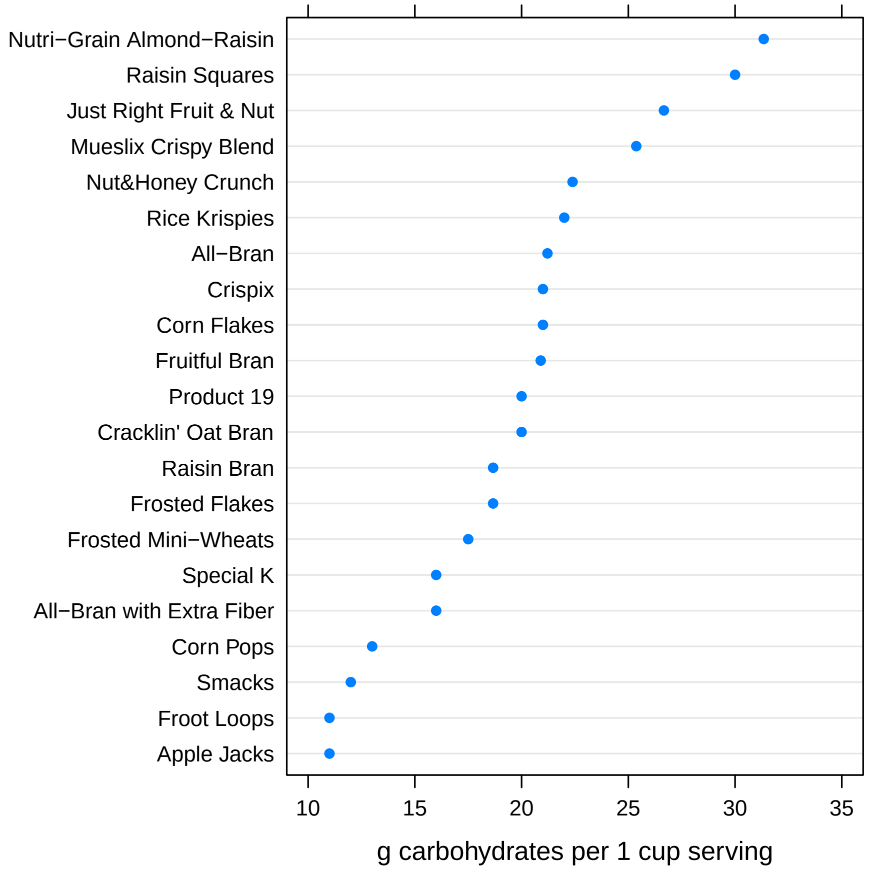


Now, use the lattice package to produce similar graphs:

```
> library(lattice)
> dotplot(Kel.carbs)  # from lattice library
```



```
> dotplot(sort(Kel.carbs), xlim = c(9, 36),
+   xlab = "g carbohydrates per 1 cup serving")
```



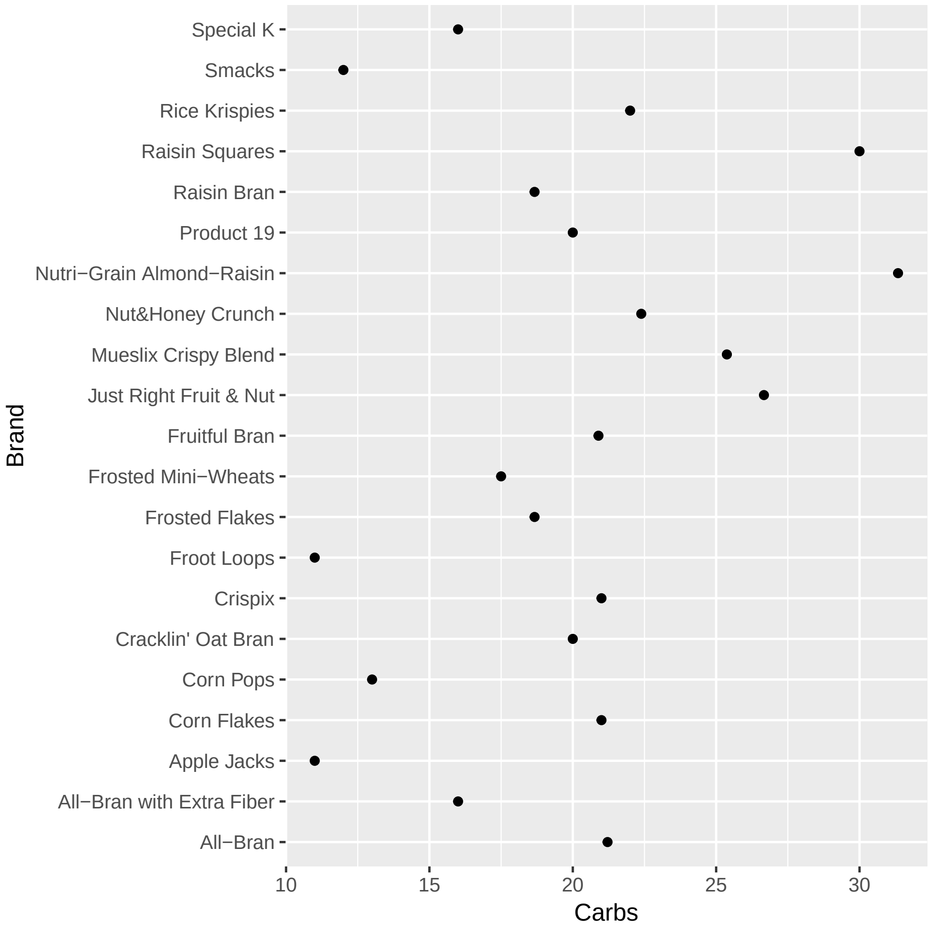
Finally, use ggplot2 to produce similar graphs:

```
> library(ggplot2)
> Kel.carbsdf <- data.frame(Brand = as.factor(names(Kel.carbs)), Carbs = Kel.carbs)
> Kel.carbsdf
```

```
                                              Brand    Carbs
All-Bran                                   All-Bran 21.21212
All-Bran with Extra Fiber All-Bran with Extra Fiber 16.00000
Apple Jacks                             Apple Jacks 11.00000
Corn Flakes                             Corn Flakes 21.00000
Corn Pops                                 Corn Pops 13.00000
Cracklin' Oat Bran               Cracklin' Oat Bran 20.00000
Crispix                                     Crispix 21.00000
Froot Loops                             Froot Loops 11.00000
```

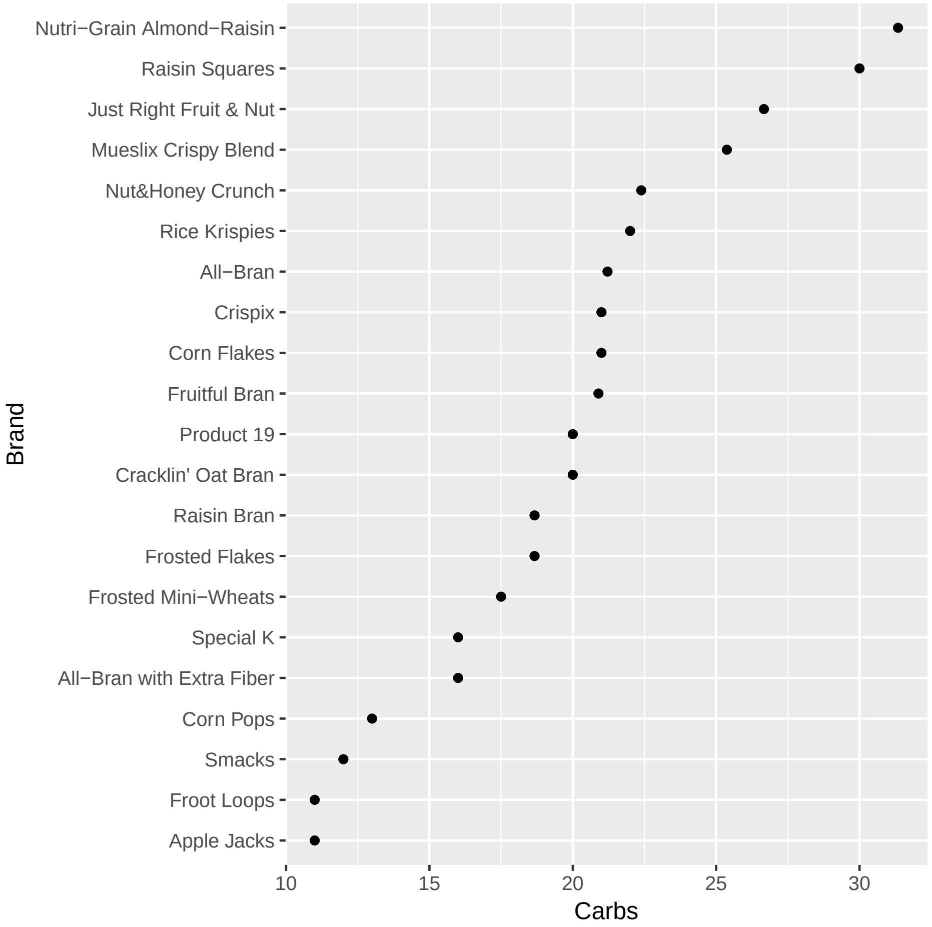
```
Frosted Flakes                       Frosted Flakes 18.66667
Frosted Mini-Wheats             Frosted Mini-Wheats 17.50000
Fruitful Bran                         Fruitful Bran 20.89552
Just Right Fruit & Nut       Just Right Fruit & Nut 26.66667
Mueslix Crispy Blend           Mueslix Crispy Blend 25.37313
Nut&Honey Crunch                   Nut&Honey Crunch 22.38806
Nutri-Grain Almond-Raisin Nutri-Grain Almond-Raisin 31.34328
Product 19                               Product 19 20.00000
Raisin Bran                             Raisin Bran 18.66667
Raisin Squares                       Raisin Squares 30.00000
Rice Krispies                         Rice Krispies 22.00000
Smacks                                       Smacks 12.00000
Special K                                 Special K 16.00000
```

```
> ggplot(Kel.carbsdf, aes(x = Carbs, y = Brand)) +
+   geom_point()
```



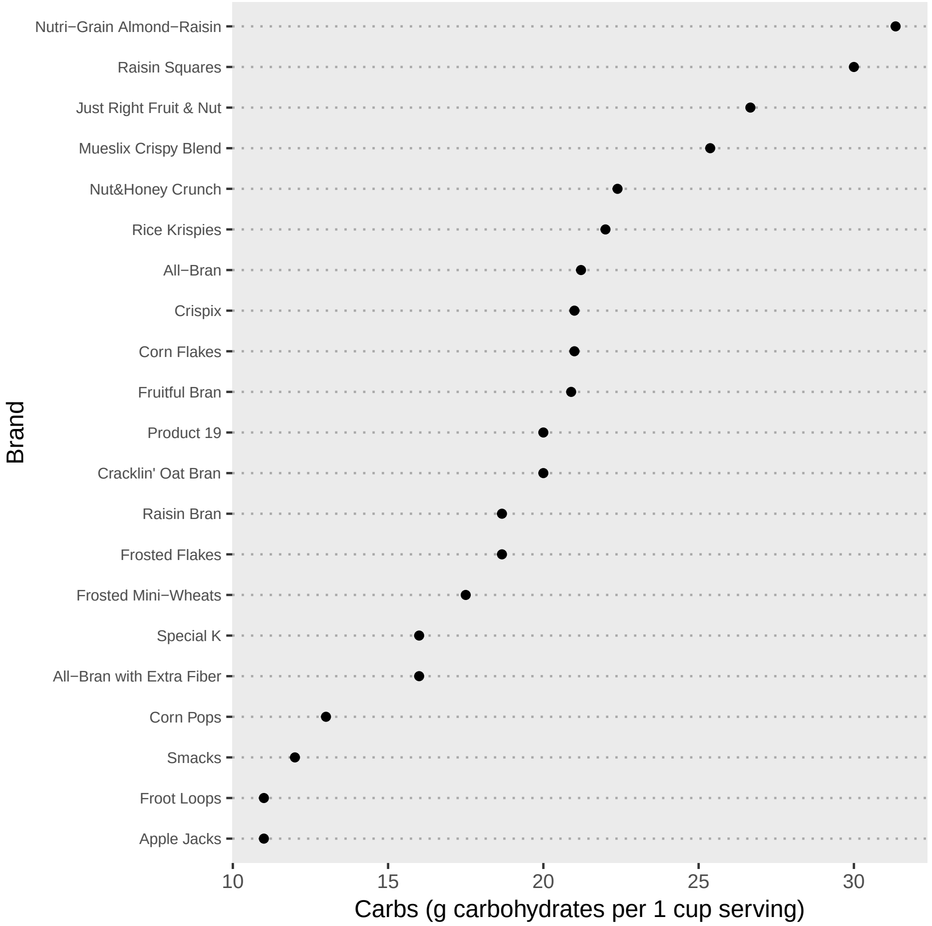
```
> # reorder by carbs
> Kel.carbsdf$Brand <- factor(Kel.carbsdf$Brand,
+                              levels = Kel.carbsdf$Brand[order(Kel.carbsdf$Carbs)])
> Kel.carbsdf$Brand

 [1] All-Bran                  All-Bran with Extra Fiber
 [3] Apple Jacks               Corn Flakes
 [5] Corn Pops                 Cracklin' Oat Bran
 [7] Crispix                   Froot Loops
 [9] Frosted Flakes            Frosted Mini-Wheats
[11] Fruitful Bran             Just Right Fruit & Nut
[13] Mueslix Crispy Blend      Nut&Honey Crunch
[15] Nutri-Grain Almond-Raisin Product 19
[17] Raisin Bran               Raisin Squares
[19] Rice Krispies             Smacks
```

```
[21] Special K
21 Levels: Apple Jacks Froot Loops Smacks ... Nutri-Grain Almond-Raisin

> ggplot(Kel.carbsdf, aes(x = Carbs, y = Brand)) +
+   geom_point()
```



The web site at `https://www.r-bloggers.com/revisiting-clevelands-the-elements-of-graphing-d` provides some useful suggestions how to further improve the appearance of these graphs:

```
> # make some further adjustments to the appearance of the grid
> ggplot(Kel.carbsdf, aes(x = Carbs, y = Brand)) +
+   geom_point() +
+   theme(
+     # remove the vertical grid lines
+     panel.grid.major.x = element_blank(),
+     panel.grid.minor.x = element_blank(),
+     # explicitly set the horizontal grid lines
+     panel.grid.major.y = element_line(linetype = 3, color = "darkgray"),
+     axis.text.y = element_text(size = rel(0.8))) +
+   xlab("Carbs (g carbohydrates per 1 cup serving)")
> # ineractive version
> library(plotly)
> ggplotly()
```



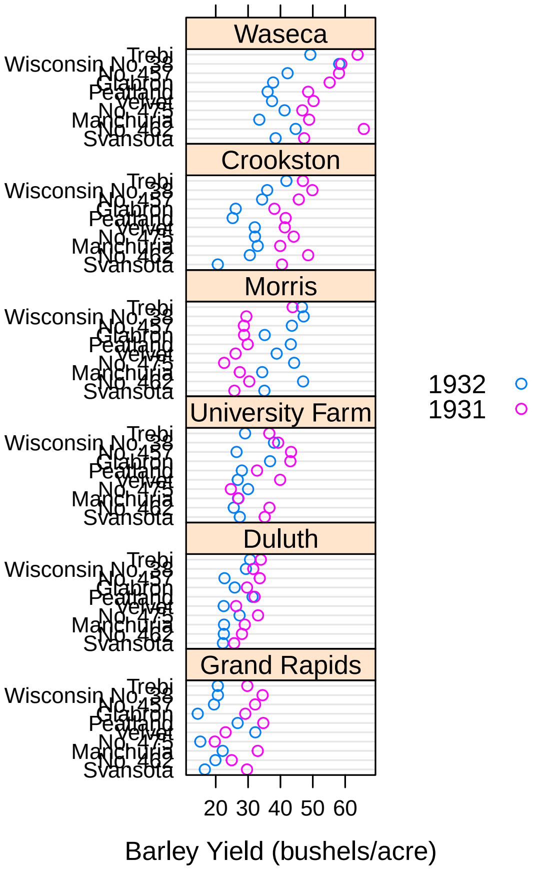
The R help page for barley in the lattice package indicates:

> “**Yield data from a Minnesota barley trial:**
>
> Total yield in bushels per acre for 10 varieties at 6 sites in each of two years.”

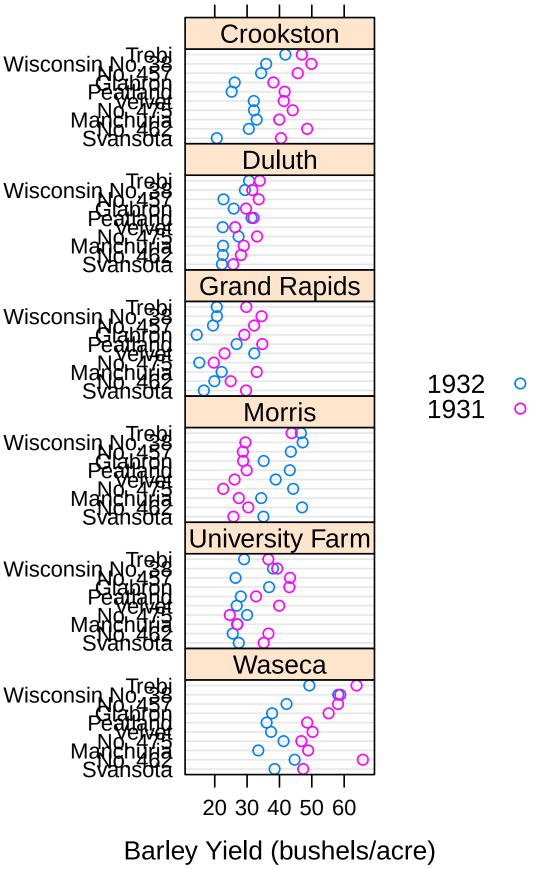
```
> library(lattice)  # for barley data
> data(barley)
> head(barley)
```

```
     yield   variety year            site
1 27.00000 Manchuria 1931 University Farm
2 48.86667 Manchuria 1931          Waseca
3 27.43334 Manchuria 1931          Morris
4 39.93333 Manchuria 1931       Crookston
5 32.96667 Manchuria 1931    Grand Rapids
6 28.96667 Manchuria 1931          Duluth
```

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



```
> levels(barley$site)

[1] "Grand Rapids"    "Duluth"          "University Farm" "Morris"
[5] "Crookston"       "Waseca"

> # alphabetical sorting of sites (top to bottom)
> dotplot(variety ~ yield | site, data = barley, groups = year,
+   key = simpleKey(levels(barley$year), space = "right"),
+   xlab = "Barley Yield (bushels/acre)",
+   aspect = 0.5, layout = c(1, 6), ylab = NULL,
+   index.cond = list(c(6, 3, 4, 1, 2, 5)))
```



Question:

What is the most striking (unusual) feature in these plots? Look carefully!

1.8 Kernel Density Plots for Univariate Data (with Rug Plot)

The R help page for density indicates:

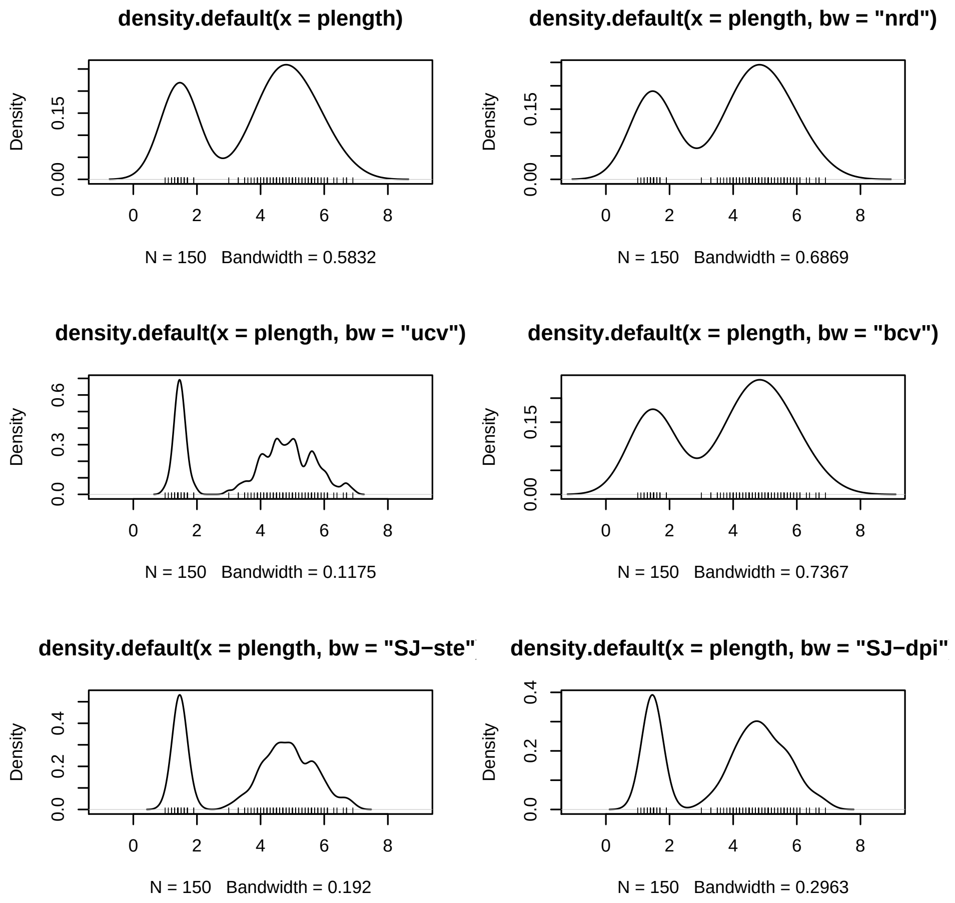
> "**Kernel Density Estimation:**
>
> The (S3) generic function density computes kernel density estimates. Its default method does so with the given kernel and bandwidth for univariate observations. [...]
> bw: the smoothing bandwidth to be used. The kernels are scaled such that this is the standard deviation of the smoothing kernel. (Note this differs from the reference books cited below, and from S–PLUS.)
> bw can also be a character string giving a rule to choose the bandwidth. See bw.nrd.
> The specified (or computed) value of bw is multiplied by adjust."

The R help page for rug indicates:

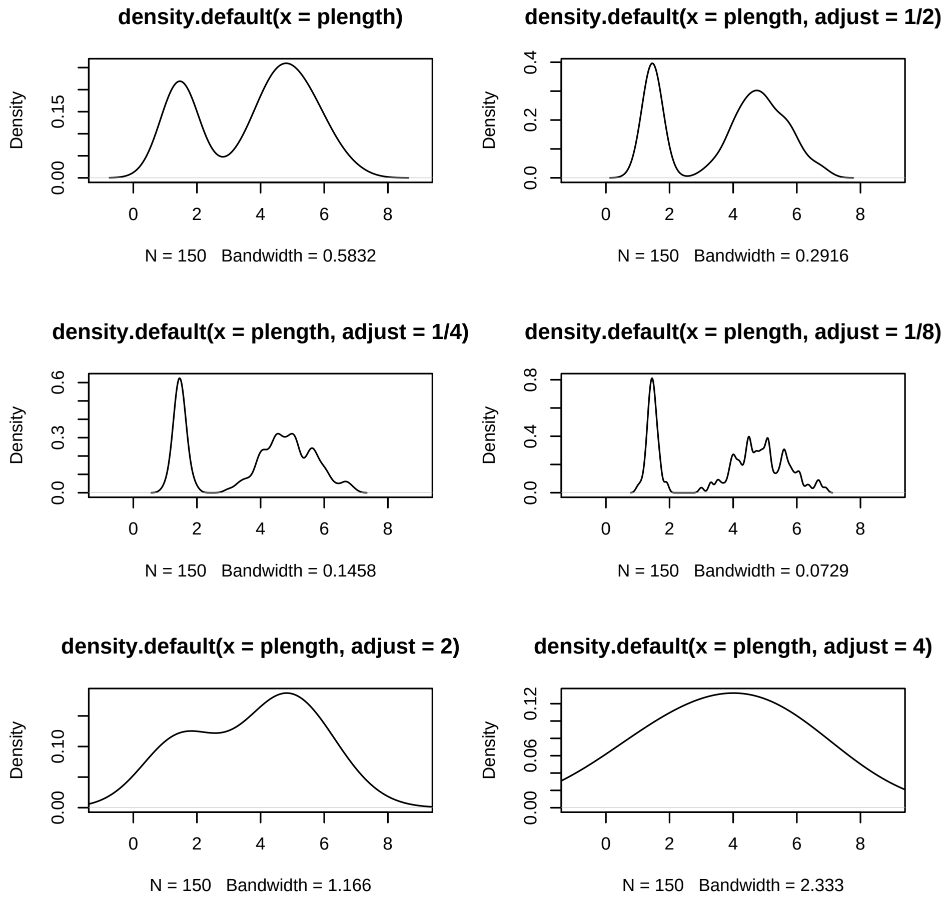
> "Adds a rug representation (1-d plot) of the data to the plot."

?, p. 548, further specify: *"rug: [...] a univariate histogram or rugplot is displayed along the base of each plot, showing the occurrence of each x–value; ties are broken by jittering."*

```
> par(mfrow = c(3, 2))
> plot(density(plength), xlim = c(-1, 9))                # default nrd0 bw
> rug(plength, ticksize = 0.05)
> plot(density(plength, bw = "nrd"), xlim = c(-1, 9))    # normal reference rule bw
> rug(plength, ticksize = 0.05)
> plot(density(plength, bw = "ucv"), xlim = c(-1, 9))
>                                    # unbiased cross-validation rule bw
> rug(plength, ticksize = 0.05)
> plot(density(plength, bw = "bcv"), xlim = c(-1, 9))
>                                    # biased cross-validation rule bw
> rug(plength, ticksize = 0.05)
> plot(density(plength, bw = "SJ-ste"), xlim = c(-1, 9))
>                                    # Sheather-Jones ("solve-the-equation") bw
> rug(plength, ticksize = 0.05)
> plot(density(plength, bw = "SJ-dpi"), xlim = c(-1, 9))
>                                    # Sheather-Jones ("direct plug-in") bw
> rug(plength, ticksize = 0.05)
```

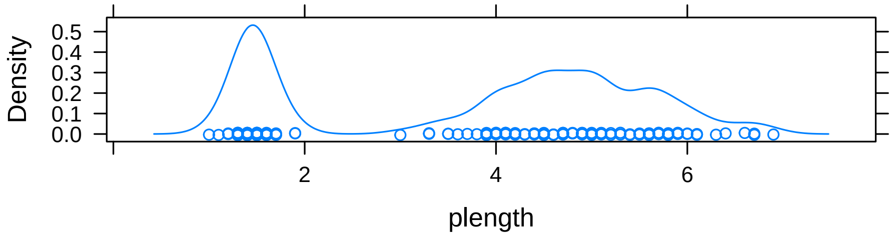


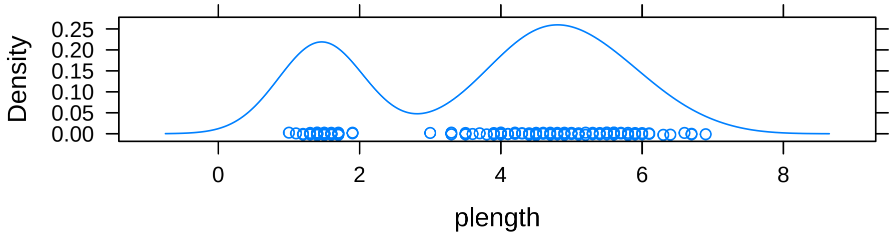
```
> par(mfrow = c(3, 2))
> plot(density(plength), xlim = c(-1, 9))
> plot(density(plength, adjust = 1/2), xlim = c(-1, 9))  #adjust default bandwidth
> plot(density(plength, adjust = 1/4), xlim = c(-1, 9))
> plot(density(plength, adjust = 1/8), xlim = c(-1, 9))
> plot(density(plength, adjust = 2), xlim = c(-1, 9))
> plot(density(plength, adjust = 4), xlim = c(-1, 9))
```

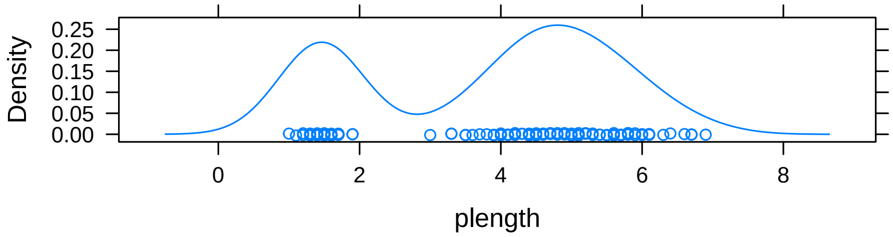


Now, use the lattice package and produce similar graphics:

```
> library(lattice)
> dp1 <- densityplot(plength)  # lattice, takes all parameters from density (above)
> dp2 <- densityplot(plength, n = 512)
> dp3 <- densityplot(plength, n = 512, bw = "SJ")
> # arrange the three plots vertically
> print(dp1, position = c(0, 0, 1, 0.33), more = TRUE)
> print(dp2, position = c(0, 0.33, 1, 0.66), more = TRUE)
> print(dp3, position = c(0, 0.66, 1, 0.99))
```



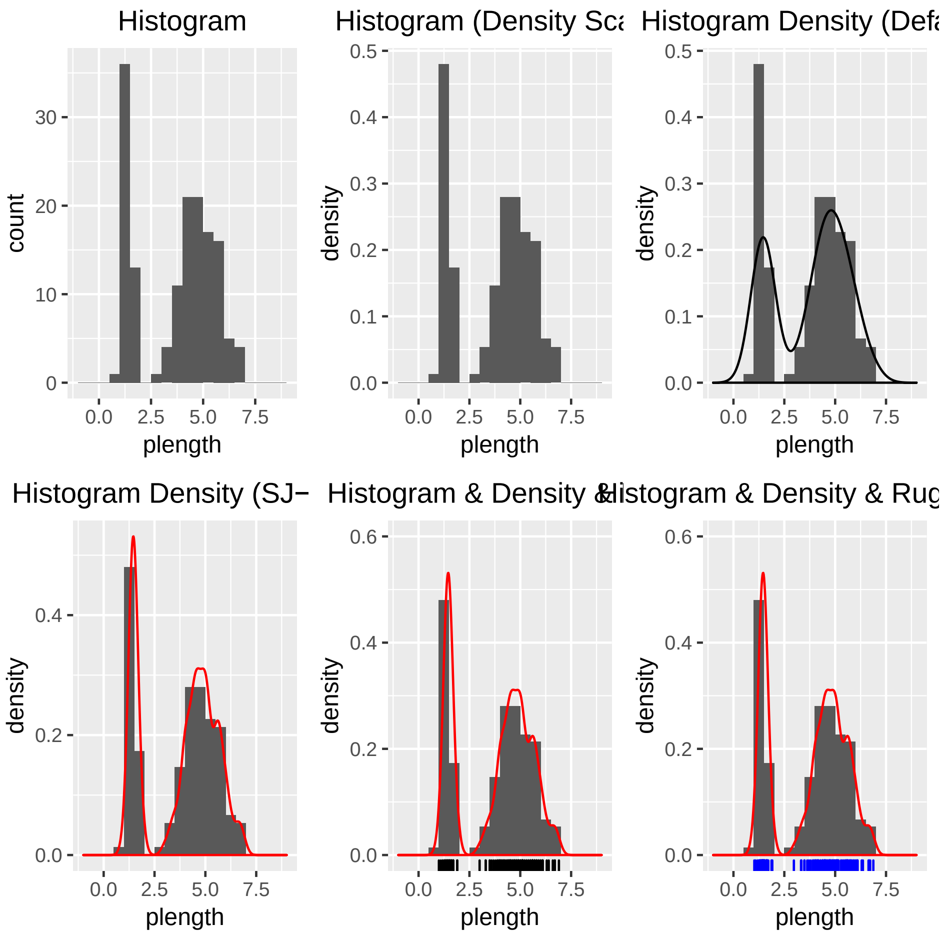




In *densityplot*, n is the "number of points at which density is to be evaluated" and the default is 50.

Now in ggplot2. The web page `https://stackoverflow.com/questions/32468772/histogram-with-a-jittery-rug` provided some suggestions how to add the jittered rug.

```
> library(ggplot2)
> library(gridExtra)
> h1 <- ggplot(iris, aes(x = plength)) +
+   xlim(-1, 9) +
+   geom_histogram(binwidth = 0.5, center = 0.25) +
+   ggtitle("Histogram") +
+   theme(plot.title = element_text(hjust = 0.5))
> h2 <- ggplot(iris, aes(x = plength)) +
+   xlim(-1, 9) +
+   geom_histogram(aes(y = ..density..), binwidth = 0.5, center = 0.25) +
+   ggtitle("Histogram (Density Scale)") +
+   theme(plot.title = element_text(hjust = 0.5))
> h3 <- ggplot(iris, aes(x = plength)) +
+   xlim(-1, 9) +
+   geom_histogram(aes(y = ..density..), binwidth = 0.5, center = 0.25) +
+   ggtitle("Histogram Density (Default)") +
+   theme(plot.title = element_text(hjust = 0.5)) +
+   geom_density()
> h4 <- ggplot(iris, aes(x = plength)) +
+   xlim(-1, 9) +
+   geom_histogram(aes(y = ..density..), binwidth = 0.5, center = 0.25) +
+   ggtitle("Histogram Density (SJ-ste)") +
+   theme(plot.title = element_text(hjust = 0.5)) +
+   geom_density(bw = "SJ-ste", col = "red")
> h5 <- ggplot(iris, aes(x = plength)) +
+   xlim(-1, 9) +
+   ylim(0, 0.6) +
+   geom_histogram(aes(y = ..density..), binwidth = 0.5, center = 0.25) +
+   ggtitle("Histogram & Density & Rug") +
+   theme(plot.title = element_text(hjust = 0.5)) +
+   geom_density(bw = "SJ-ste", col = "red") +
+   geom_rug()
> h6 <- ggplot(iris, aes(x = plength)) +
+   xlim(-1, 9) +
+   ylim(0, 0.6) +
+   geom_histogram(aes(y = ..density..), binwidth = 0.5, center = 0.25) +
+   ggtitle("Histogram & Density & Rug (Final)") +
+   theme(plot.title = element_text(hjust = 0.5)) +
+   geom_density(bw = "SJ-ste", col = "red") +
+   geom_rug(sides = "b", aes(y = 0.4), position = "jitter", col = "blue")
> grid.arrange(h1, h2, h3, h4, h5, h6, nrow = 2)
```


Histogram
count
0
10
20
30
0.0
2.5
5.0
7.5
plength
Histogram (Density Sca
density
0.0
0.1
0.2
0.3
0.4
0.5
plength
Histogram Density (Defa
density
plength
Histogram Density (SJ−
density
0.0
0.2
0.4
plength
Histogram & Density &
density
0.6
plength
Histogram & Density & Rug
density
plength

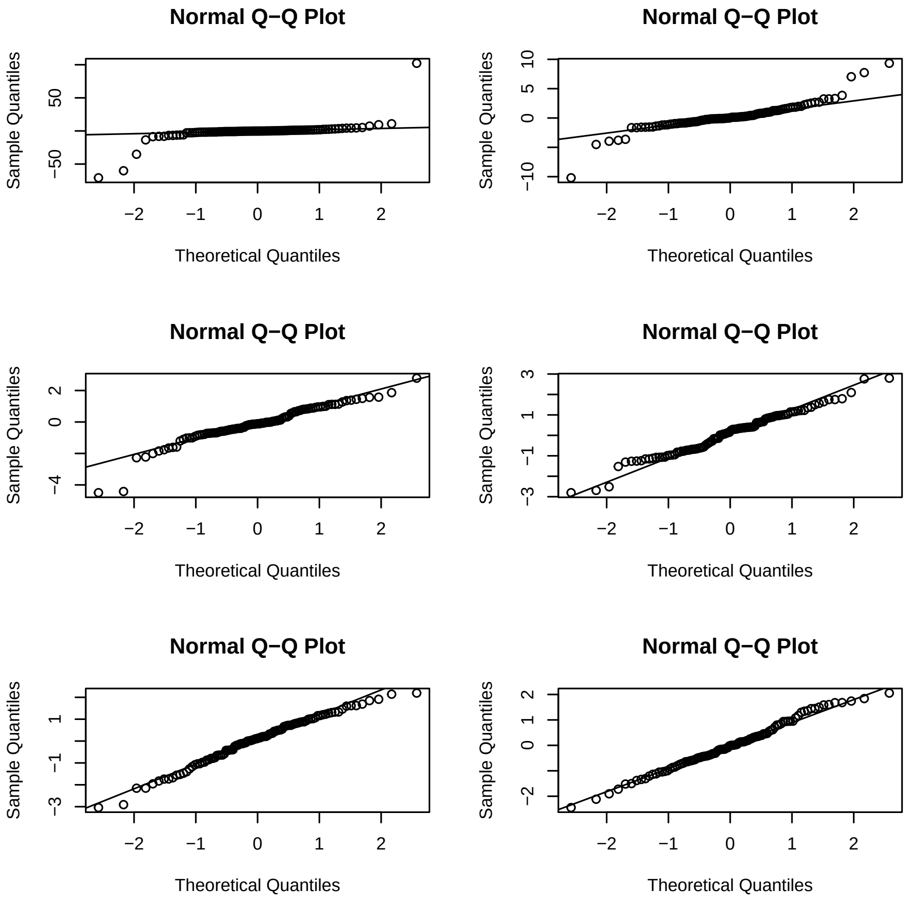
1.9 Quantile–Quantile Plots (Q–Q Plots)

One of the best ways to compare the distribution of a sample $\underline{x}$ of size n with an assumed theoretical distribution F is to use a Quantile–Quantile Plot (Q–Q Plot). In such a plot, we plot the pairs of points

$$\left(F^{-1}\left(\frac{i-0.5}{n}\right), x_{(i)}\right), \quad i = 1, \ldots, n.$$

Example 1:
Convergence of a t distribution with *df* degrees of freedom towards a normal distribution.

```
> # set seed of random number generator to be able to reproduce results
> set.seed(2)
> par(mfrow = c(3, 2))
> tdf1 <- rt(100, df = 1)
> qqnorm(tdf1)
> qqline(tdf1)
> tdf2 <- rt(100, df = 2)
> qqnorm(tdf2)
> qqline(tdf2)
> tdf5 <- rt(100, df = 5)
> qqnorm(tdf5)
> qqline(tdf5)
> tdf10 <- rt(100, df = 10)
> qqnorm(tdf10)
> qqline(tdf10)
> tdf20 <- rt(100, df = 20)
> qqnorm(tdf20)
> qqline(tdf20)
> tdf30 <- rt(100, df = 30)
> qqnorm(tdf30)
> qqline(tdf30)
```



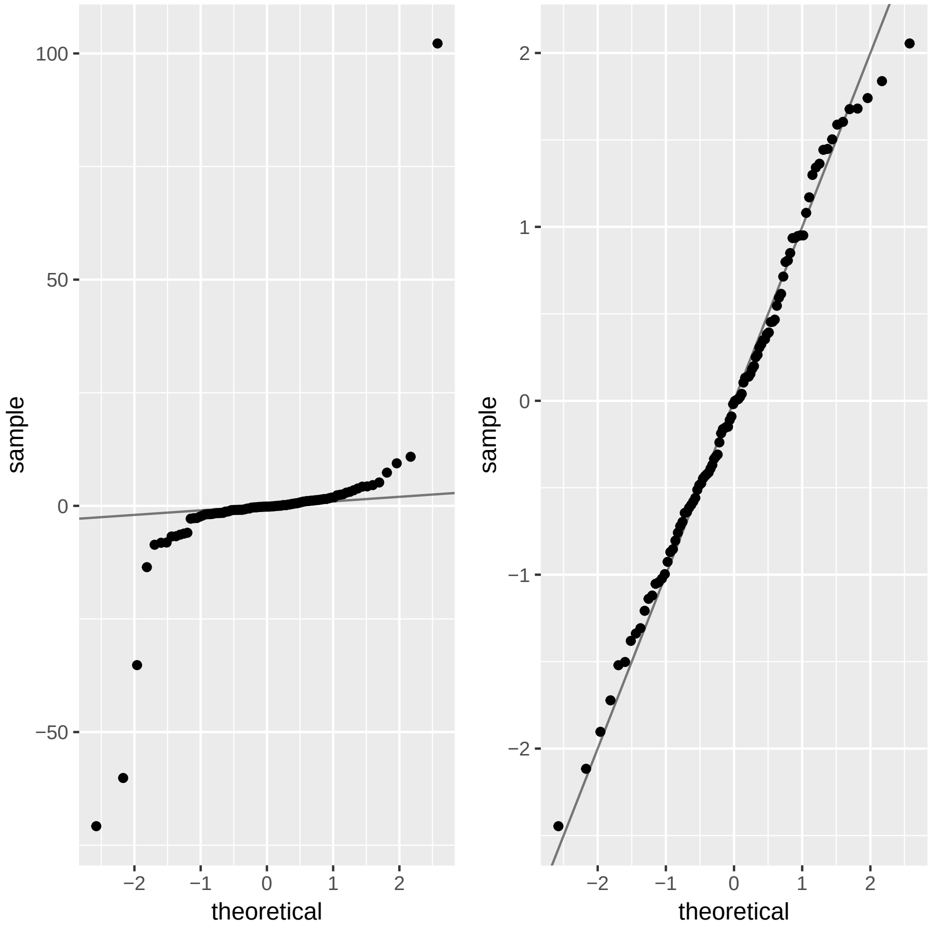
Note:

The closer the points from the sample fall to a straight line, the closer the sample distribution and the theoretical distribution are related. However, here, the greater spread of the extreme quantiles for the sample (for $df = 1, 2, 5, 10, 20$) is an indicator of a long–tailed distribution.

A quick glance at Q–Q–plots via ggplot2, with additional suggestions from `http://ggplot2.tidyverse.org/reference/geom_qq.html` and `https://gist.github.com/slowkow/9041570`.

```
> library(ggplot2)
> library(gridExtra)
> tdf1df <- data.frame(y = tdf1)
> q1 <- ggplot(tdf1df, aes(sample = y)) +
+   stat_qq() +
+   geom_abline(intercept = 0, slope = 1, alpha = 0.5)
```

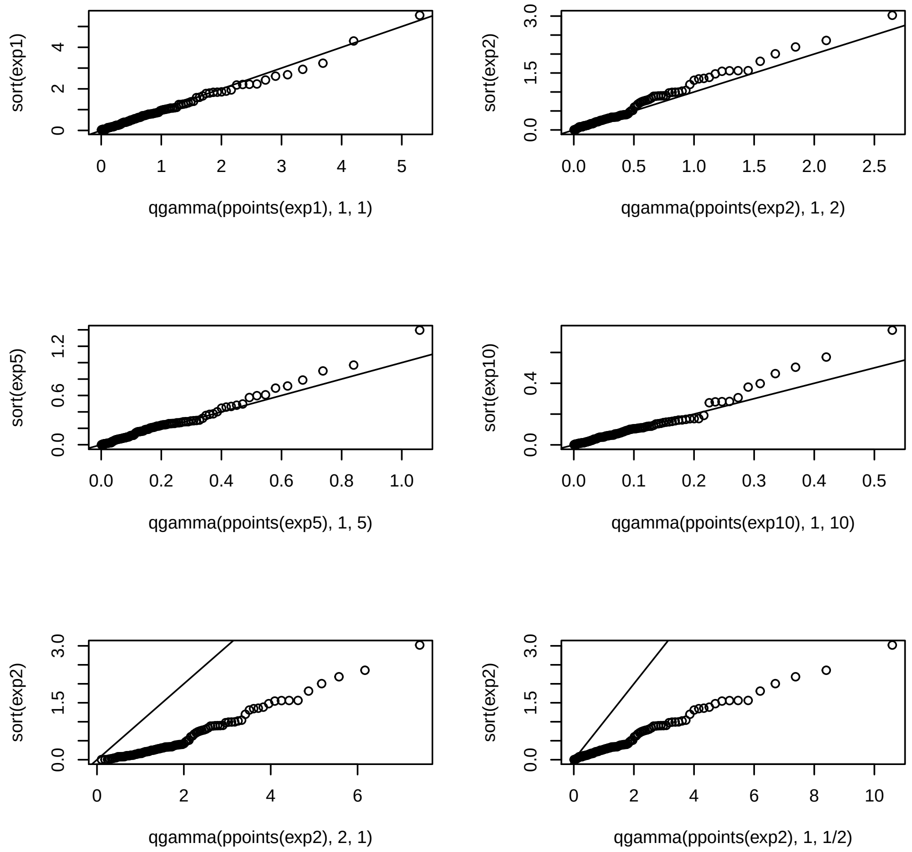
```
> tdf30df <- data.frame(y = tdf30)
> q30 <- ggplot(tdf30df, aes(sample = y)) +
+   stat_qq() +
+   geom_abline(intercept = 0, slope = 1, alpha = 0.5)
> grid.arrange(q1, q30, nrow = 1)
```



Example 2:

Recall: What is the relationship between exponential distributions and Gamma distributions? Verify this graphically!

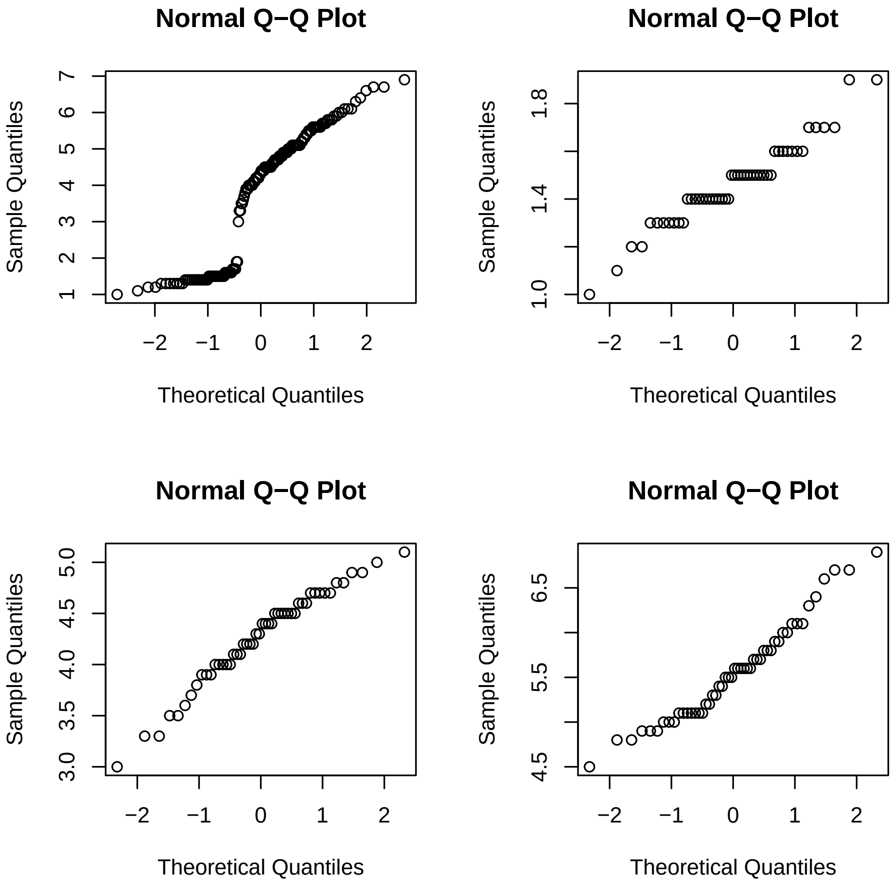
```
> par(mfrow = c(3, 2))
> set.seed(4)
> exp1 <- rexp(100, rate = 1)
> plot(qgamma(ppoints(exp1), 1, 1), sort(exp1))
> abline(0, 1)
> exp2 <- rexp(100, rate = 2)
> plot(qgamma(ppoints(exp2), 1, 2), sort(exp2))
> abline(0, 1)
> exp5 <- rexp(100, rate = 5)
> plot(qgamma(ppoints(exp5), 1, 5), sort(exp5))
> abline(0, 1)
> exp10 <- rexp(100, rate = 10)
> plot(qgamma(ppoints(exp10), 1, 10), sort(exp10))
> abline(0, 1)
> # Some major misspecifications
>
> # a) Swapping shape and rate parameters
> plot(qgamma(ppoints(exp2), 2, 1), sort(exp2))
> abline(0, 1)
> # b) Using 1/rate instead
> plot(qgamma(ppoints(exp2), 1, 1/2), sort(exp2))
> abline(0, 1)
```



Example 3:

Compare iris plength sample data with an underlying assumed normal distribution. For which of the species is the assumption of normality justified?

```
> par(mfrow = c(2, 2))
> qqnorm(plength)
> qqnorm(plength[1:50])
> qqnorm(plength[51:100])
> qqnorm(plength[101:150])
```


Normal Q−Q Plot
Sample Quantiles
1
2
3
4
5
6
7
−2
−1
0
1
2
Theoretical Quantiles
Normal Q−Q Plot
Sample Quantiles
1.0
1.4
1.8
−2
−1
0
1
2
Theoretical Quantiles
Normal Q−Q Plot
Sample Quantiles
3.0
3.5
4.0
4.5
5.0
−2
−1
0
1
2
Theoretical Quantiles
Normal Q−Q Plot
Sample Quantiles
4.5
5.5
6.5
−2
−1
0
1
2
Theoretical Quantiles

1.10 Empirical Cumulative Distribution Functions (ECDFs)

Recall from Stat 6720:

Definition 7.1.3:
Let $X_1, \ldots, X_n$ be a sample of size n from a population with distribution F. The function

$$\hat{F_n}(x) = \frac{1}{n} \sum_{i=1}^{n} I_{(-\infty, x]}(X_i)$$

is called **empirical cumulative distribution function** (**empirical cdf, ECDF**). ■

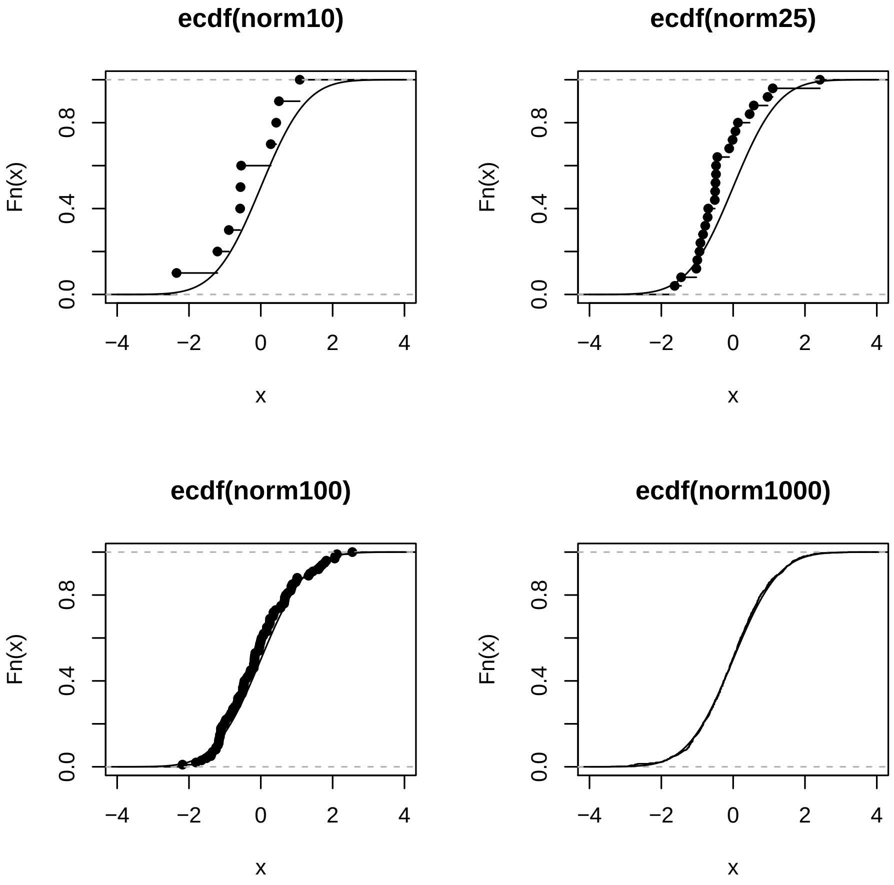
Theorem 7.1.7: **Glivenko–Cantelli Theorem**
$\hat{F_n}(x)$ converges uniformly to $F(x)$, i.e., it holds for all $\epsilon > 0$ that

$$\lim_{n \to \infty} P(\sup_{-\infty < x < \infty} \mid \hat{F_n}(x) - F(x) \mid > \epsilon) = 0.$$

■

Verify this theorem for samples from a normal distribution:

```
> par(mfrow = c(2, 2))
> set.seed(1234)
> xvals <- seq(-4, 4, 0.01)
> norm10 <- rnorm(10)
> plot(ecdf(norm10), xlim = c(-4, 4))
> lines(xvals, pnorm(xvals))
> norm25 <- rnorm(25)
> plot(ecdf(norm25), xlim = c(-4, 4))
> lines(xvals, pnorm(xvals))
> norm100 <- rnorm(100)
> plot(ecdf(norm100), xlim = c(-4, 4))
> lines(xvals, pnorm(xvals))
> norm1000 <- rnorm(1000)
> plot(ecdf(norm1000), xlim = c(-4, 4))
> lines(xvals, pnorm(xvals))
```

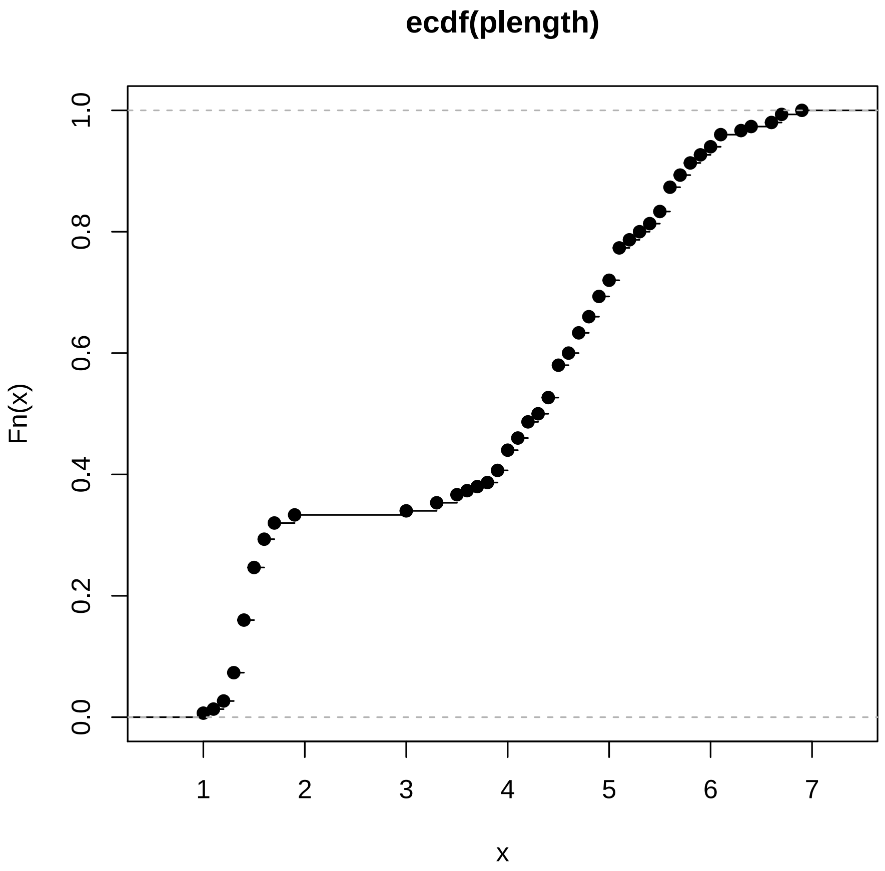


```
> # Animation
> par(mfrow = c(1, 1))
> xvals <- seq(-4, 4, 0.01)
> pnormxvals <- pnorm(xvals)
> normgrow <- NULL
> for (i in 1:150) {
+   normgrow <- c(normgrow, rnorm(1))
+   plot(ecdf(normgrow), xlim = c(-4, 4), main = length(normgrow))
+   lines(xvals, pnormxvals, col = "red")
+   Sys.sleep(0.1)
+ }
```

Example:

And here the ECDF for iris plength.

```
> plot(ecdf(plength))
```



1.11 Graphics and Small Sample Sizes

Worksheet

Your Name: ____________________

Question:

The data shown in these four histograms originate from which distribution?

The corresponding distributions are:

Upper left: ______________

Upper right: ______________

Lower left: ______________

Lower right: ______________

Worksheet

Your Name: ____________________

Question:

Do the data shown in these four qqplots follow a normal distribution?

So, does a particular qqplot suggest that the data originate from a normal distribution? Circle your answer:

Upper left: **yes** / **no**

Upper right: **yes** / **no**

Lower left: **yes** / **no**

Lower right: **yes** / **no**

Answers:

The following R code was used to create the figures shown on the previous two pages:

```
> set.seed(1234)
> jpeg("Chapter5_unknown_hist.jpg")
> par(mfrow = c(2, 2))
> xvect1 <- NULL
> for (i in 1:4) {
+   x <- rnorm(10)
+   xvect1 <- c(xvect1, x)
+   hist(x, main = "Unknown Distribution",
+     xlab = "x-values")
+ }
> dev.off()
```

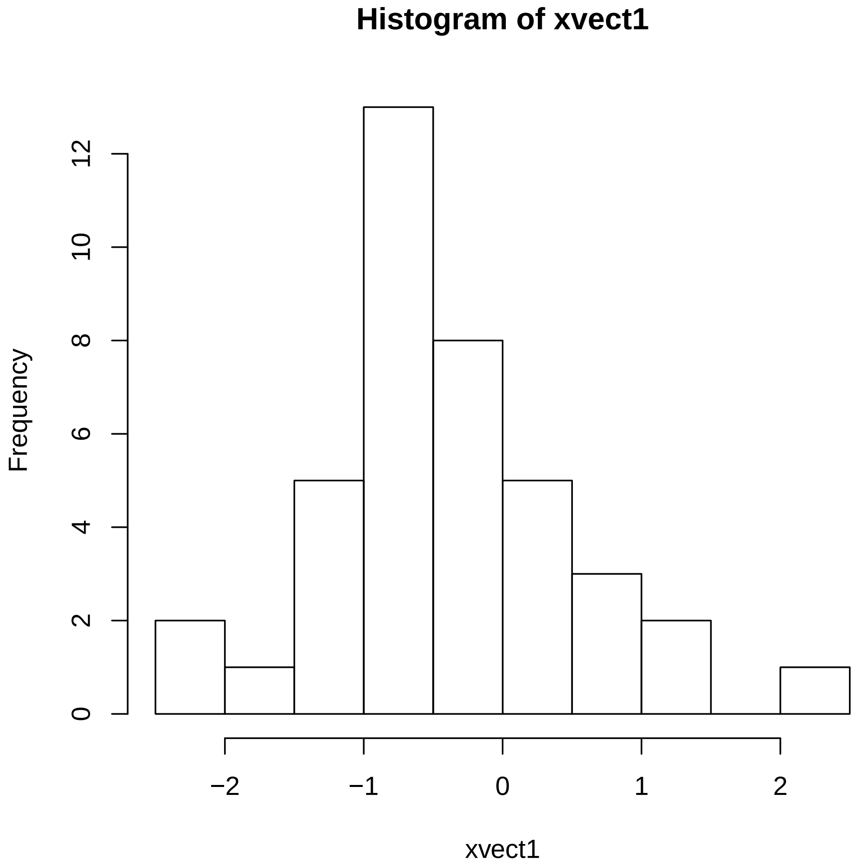
```
pdf
  2
```

```
> set.seed(1234)
> jpeg("Chapter5_unknown_qqplot.jpg")
> par(mfrow = c(2, 2))
> xvect2 <- NULL
> for (i in 1:4) {
+   x <- rnorm(10)
+   xvect2 <- c(xvect2, x)
+   qqnorm(x, main = "Unknown Distribution",
+     xlab = "Normal Quantiles")
+ }
> dev.off()
```

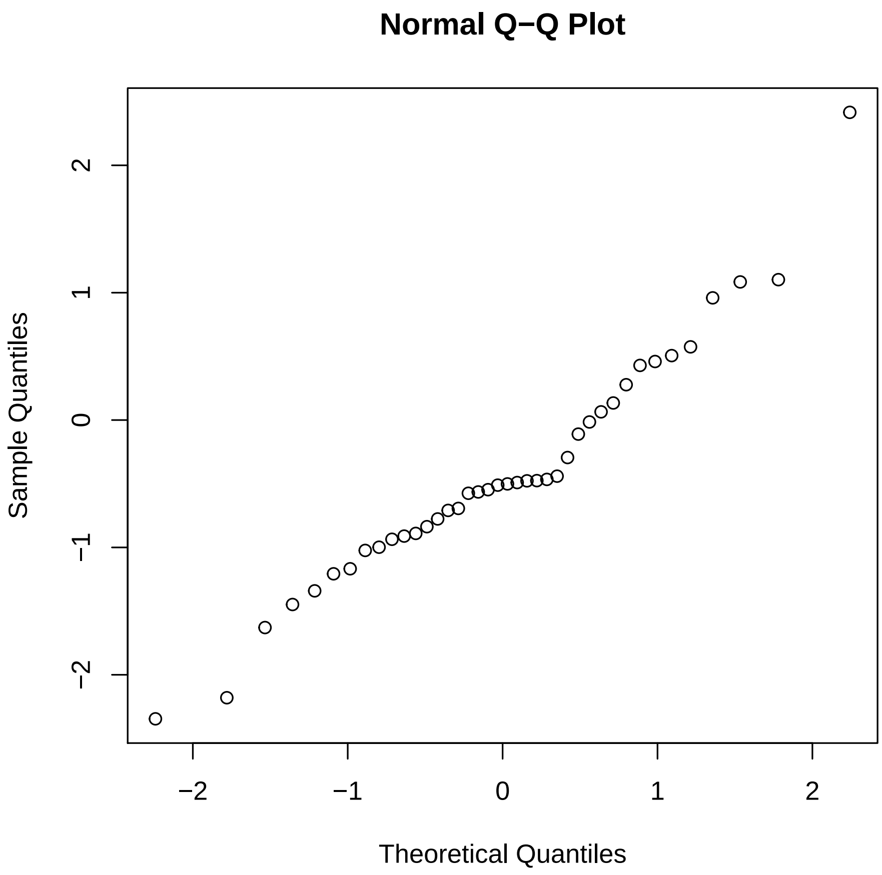
```
pdf
  2
```

When we jointly plot all 40 observations, we start to see that the underlying distribution indeed is a normal distribution. In fact, all eight plots on the previous two pages show 10 samples each drawn from the standard normal distribution!

```
> # Plot all data combined
>
> par(mfrow = c(1, 1))
> hist(xvect1)
```



```
> par(mfrow = c(1, 1))
> qqnorm(xvect2)
```


Normal Q−Q Plot
Sample Quantiles
Theoretical Quantiles
−2
−1
0
1
2
−2
−1
0
1
2

1.12 Further Reading

Additional sources for Trellis Graphics are:

- Trellis dipsplays at Bell Labs (in S/S–Plus; needs some updates for modern R): http://ect.bell-labs.com/sl/project/trellis/
- **?**, Chapter 4: https://www.stat.auckland.ac.nz/~paul/RGraphics/chapter4.pdf
- William G. Jacoby's web page on dot plots: http://polisci.msu.edu/jacoby/research/statgrph/tpm/sdlist.html

— **THE END** —