Introduction to R: Session 02

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Contents

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Data

Today, we will use a different examplary dataset, based on `spati2`, shipping with `lmfor`:

```
library("lmfor")
library("plyr")
data(spati2)
df <- spati2
rm(spati2)
d_breaks_cut <- quantile(df$d, probs = seq(0, 1, by = 0.05))
df$d_cut <- cut(df$d, breaks = d_breaks_cut, include.lowest = T)
dd <- ddply(df, c("d_cut"), summarise, h_mean = mean(h),
            h_q25 = quantile(h, probs = 0.25),
            h_q75 = quantile(h, probs = 0.75))
dd$d_lb <- d_breaks_cut[-length(d_breaks_cut)]
dd$d_ub <- d_breaks_cut[-1]
dd$b_mean <- apply(dd[, c("d_lb", "d_ub")], MAR = 1, FUN = mean)
```

1 Store graphics

File format:

- `pdf()`: 'portable document format'
- `jpeg()`: 'joint photographic experts group'
- `tiff()`: 'tagged image file format'
- `png()`: 'portable network graphics'
- ...

Options:

- `width`: width (for `pdf` in inches)
- `height`: height (for`pdf` in inches)
- `onefile`: logical value (should several graphics as separate pages in one file?)
- ...

Usage:

```
pdf(file='<file name>.pdf', height = 6, width = 9)
...
dev.off()
```

2 Generic plot-function `plot(x, y, type, ...)`

Das `type` Argument:

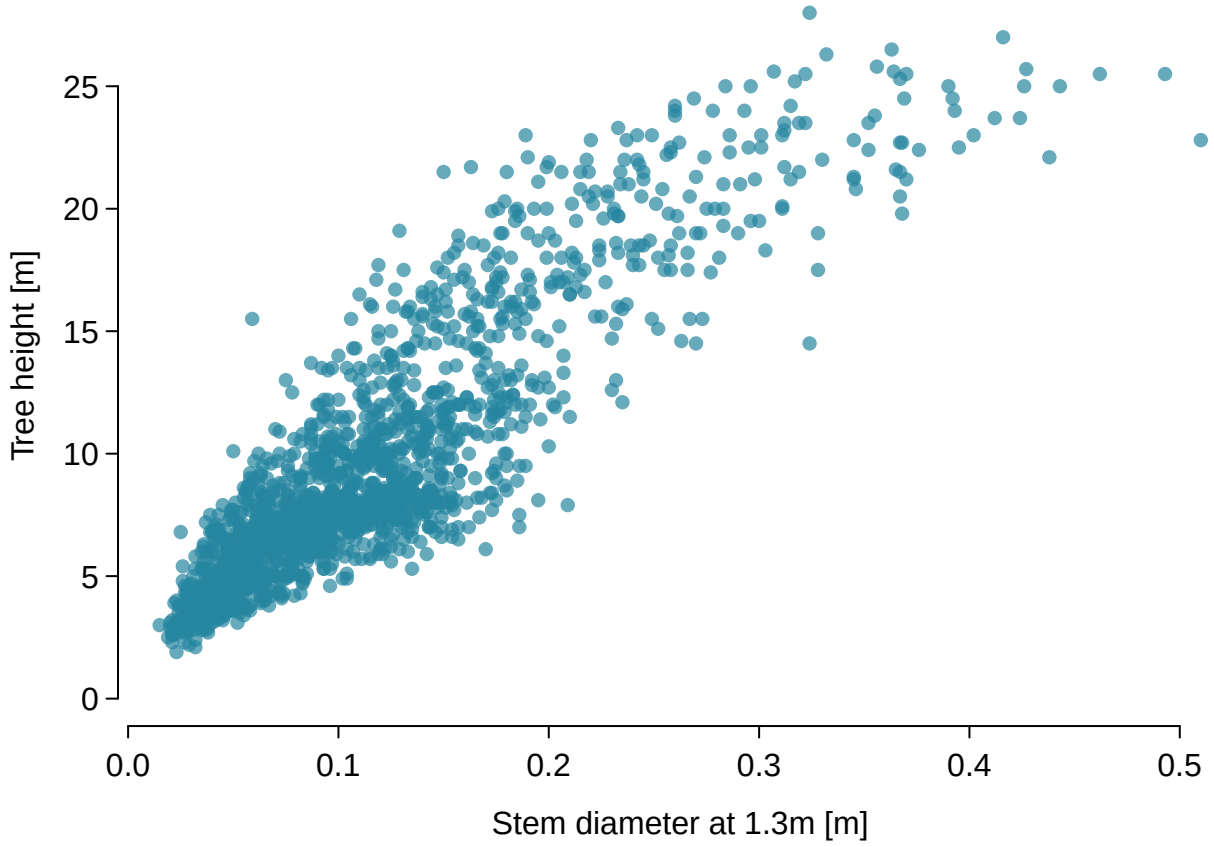
type	Plot element
`type = "p"`	**P** points (default value), scatter plot
`type = "l"`	Connecting **l**ine
`type = "b"`	**B**oth (dots and connecting lines), but not on top of each other
`type = "o"`	On top of each other (**O**verplotted): Points with connecting lines
`type = "n"`	**N**othing, e.g. if you first create a grid with `grid()`
`type = "s"`	**S**tep function
...	See also `?plot`

2.1 Frequently used arguments with `plot()`

Argument	Plot element
`axes`	Should axes be drawn?
`las = 1`	All tick labels horizontal?
`xlim, ylim`	Limit of the axes
`xlab, ylab`	Labeling of the axes
`bty`	Type of box around the plot window
`cex`	Size factor of the plot symbols
`cex.axis,cex.lab, cex.main`	Size factor of some parts of the plot
`col`	Color of the displayed data (see section on colors)
`lty`	Line style (integer)
`lwd`	Line width (real value, $ geq 0 $)
`main`	Main heading
`pch`	Symbol for points (integer)

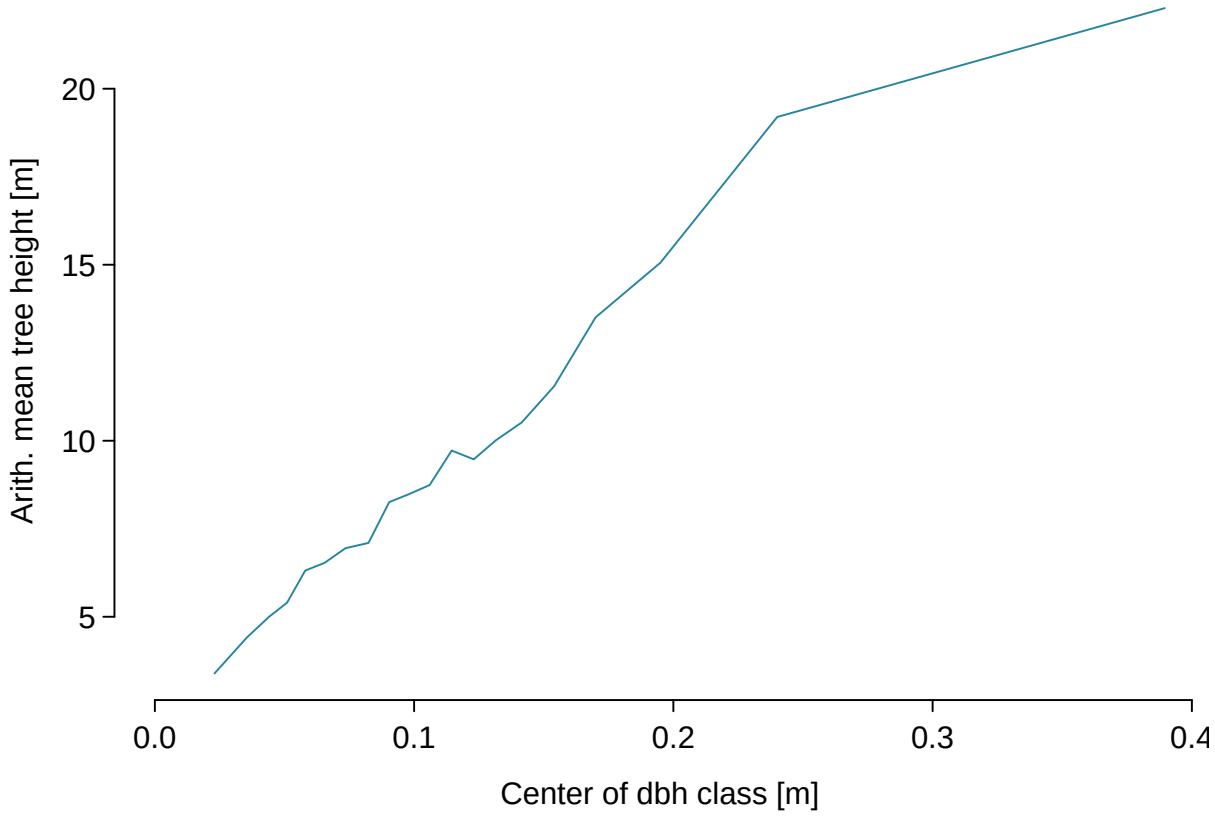
2.2 Example `plot()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .7)[3]
plot(df$d/100, df$h, xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]",
     pch = 16, col = paint, # rgb(red = 0, green = 0.38, blue = 0.27, alpha = 0.8),
     las = 1, bty = "n", ylim = c(0, max(df$h)))
```



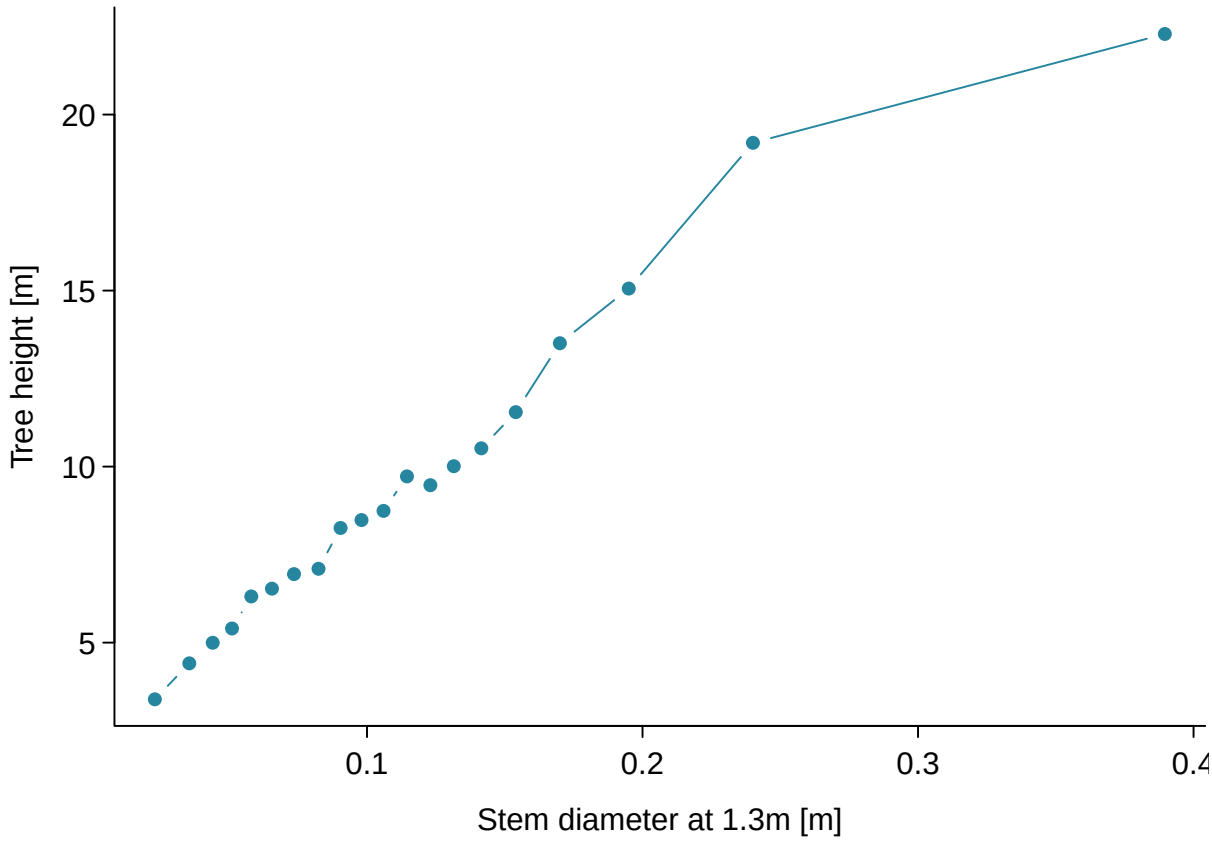
2.3 Example `plot(..., type = "l")`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
plot(dd$b_mean/100, dd$h_mean, type = "l", col = paint, # rgb(0, 0.38, 0.27),
     bty = "n", las = 1, xlab = "Center of dbh class [m]",
     ylab = "Arith. mean tree height [m]", xlim = c(0, max(dd$b_mean/100)))
```



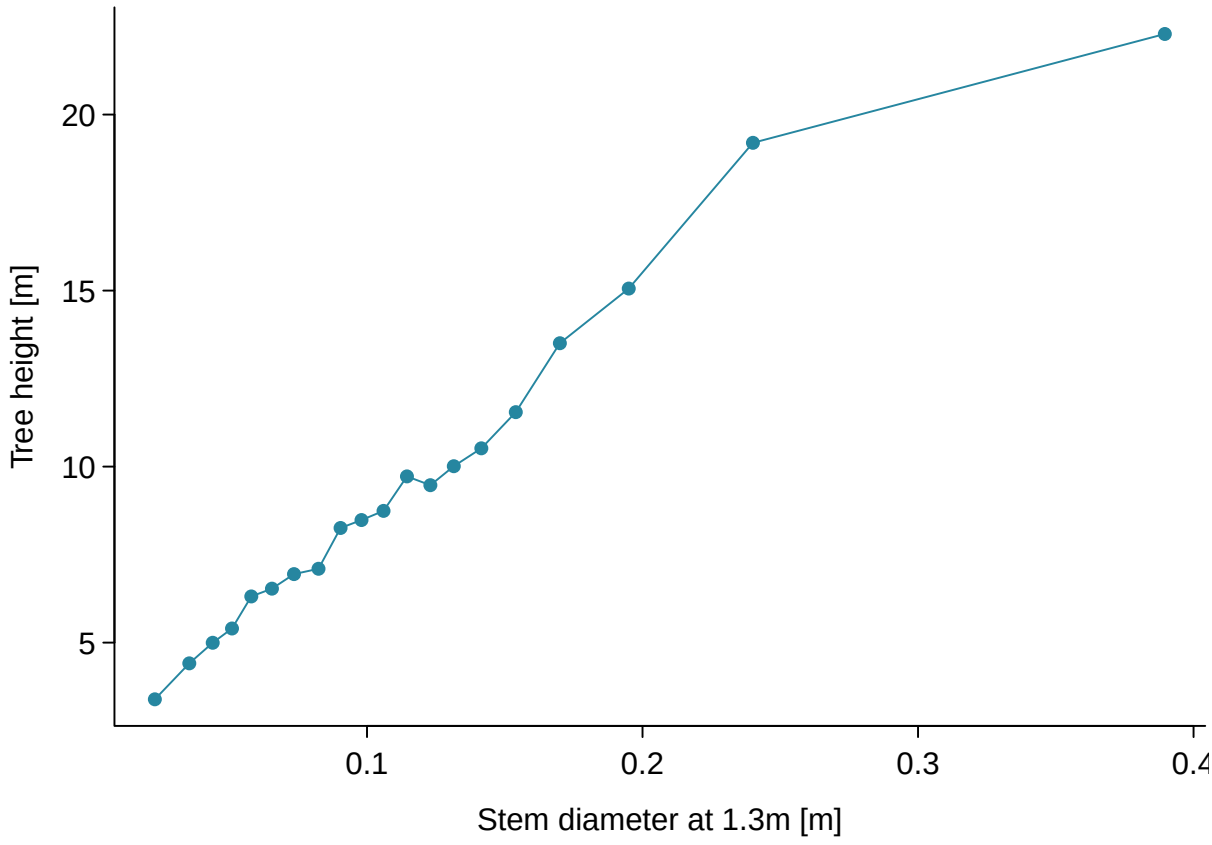
2.4 Example `plot(..., type = "b")`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
plot(dd$b_mean/100, dd$h_mean, type = "b", pch = 16, col = paint,
     bty = "l", las = 1, xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]")
```



2.5 Example `plot(..., type = "o")`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
plot(dd$b_mean/100, dd$h_mean, type = "o", pch = 16, col = paint,
     bty = "l", las = 1, xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]")
```



3 Graphic-'modules'

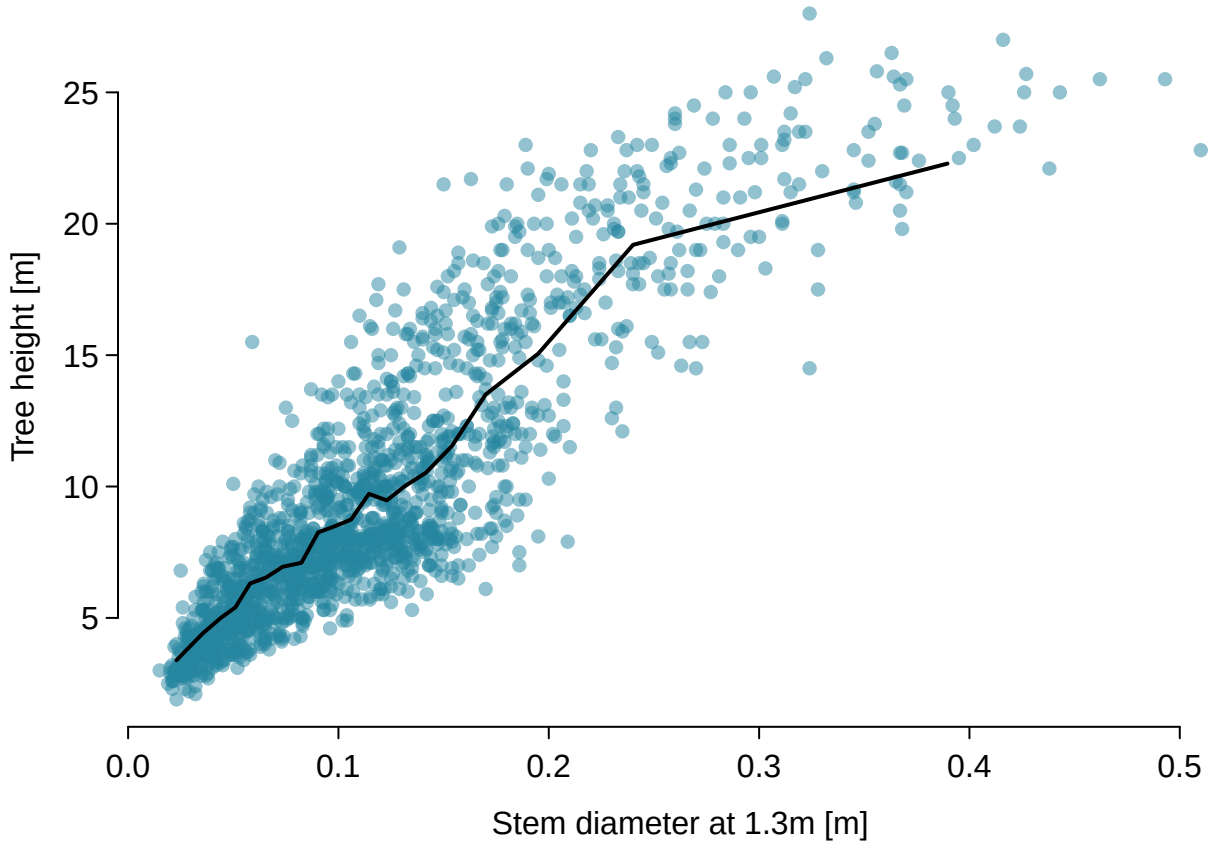
The remaining examples for `type = "n"` and `type = "s"` follow in next examples ...

First: **Functions that help us add something to a graphic**

Function	Plot element
`axis ()`	Adds an axis
`lines ()`	Adds a line between points
`points ()`	Adds points
`curve ()`	Connects points with a smooth curve
`abline ()`	Adds a straight line (horizontal, vertical, slope and y-intercept)
`grid ()`	Adds a grid (defined by tickmarks)
`legend ()`	Adds a legend (example on the next slide)
`polygon ()`	Adds a filled polygon
`text ()`	Adds text
`mtext ()`	Adds text in the plot margins

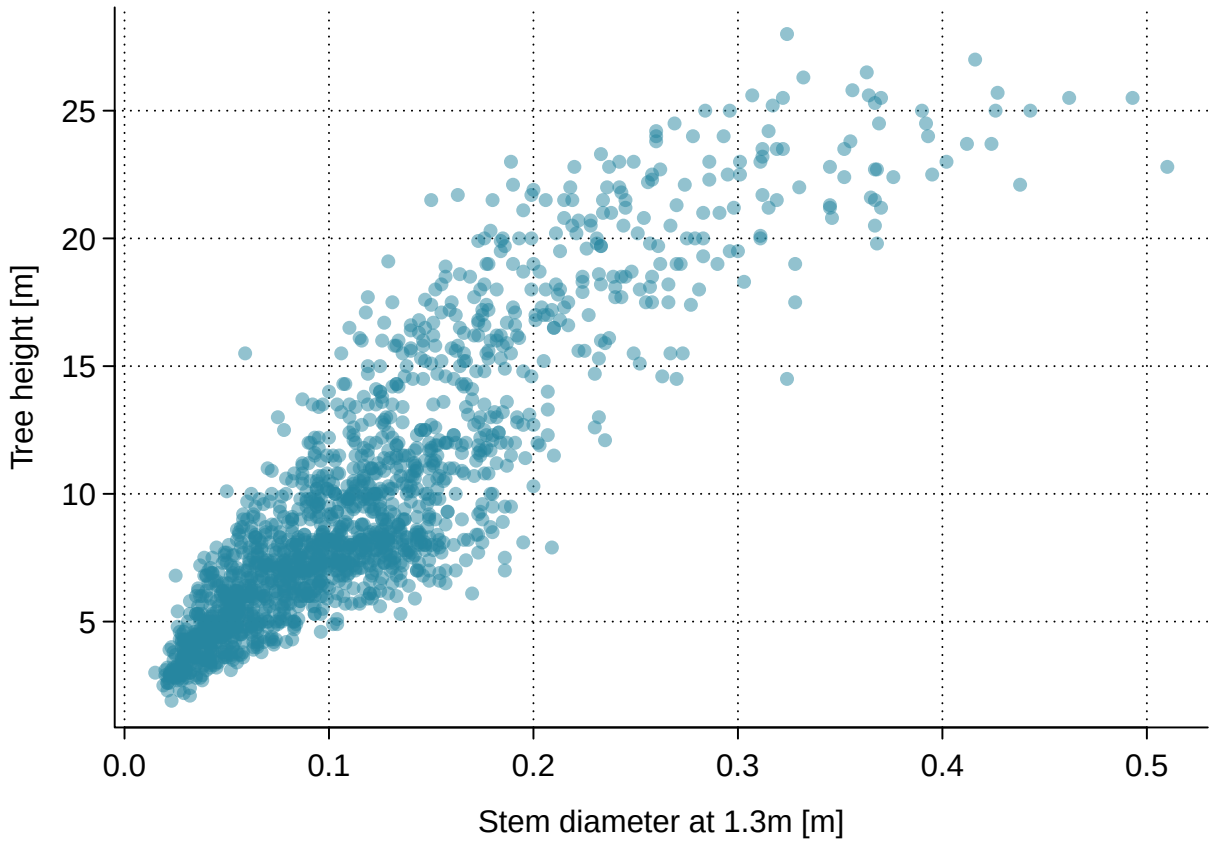
3.1 Example `lines()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
plot(df$d/100, df$h, type = "p", pch = 16, col = paint,
     bty = "n", las = 1, xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]")
lines(dd$b_mean/100, dd$h_mean, lwd = 2)
```



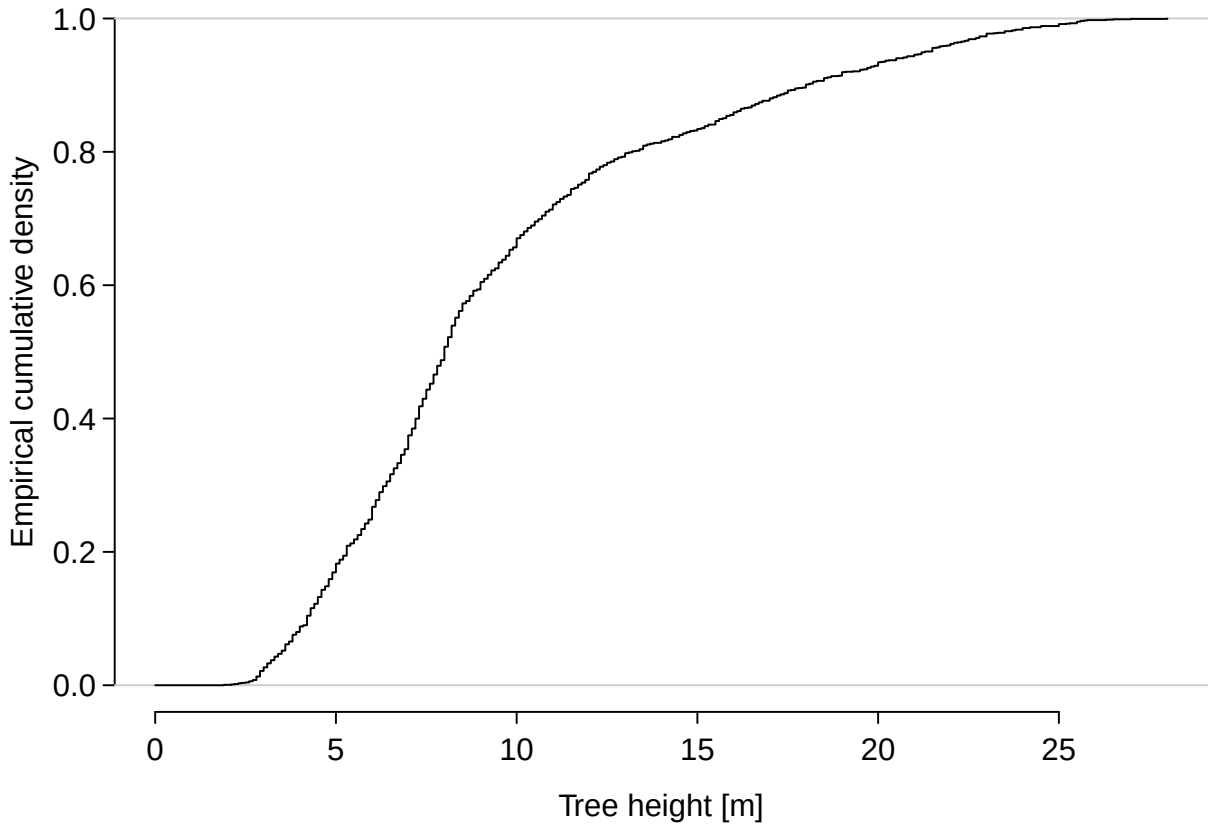
3.2 Example `plot(..., type = "n")`, `grid()` and `points()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
plot(df$d/100, df$h, type = "n", bty = "l", las = 1,
     xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]")
grid(col = 1)
points(df$d/100, df$h, pch = 16, col = paint)
```



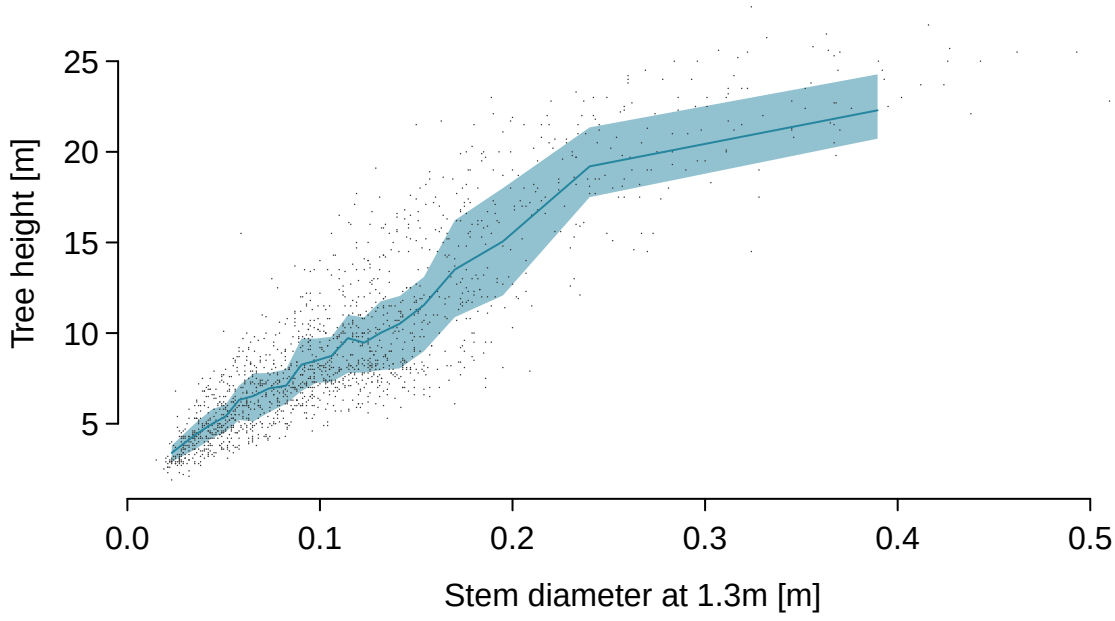
3.3 Example `lines()`, `abline()` and `lines(..., type = "s")`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
tmp <- table(df$h)
tmp1 <- as.numeric(names(tmp))
tmp2 <- as.numeric(tmp)
plot(c(0, tmp1), c(0, cumsum(tmp2)/length(df$h)), type = "n", las = 1, bty = "n",
     ylab = "Empirical cumulative density", xlab = "Tree height [m]", col = paint)
abline(h = c(0, 1), col = rgb(0.8, 0.8, 0.8))
lines(c(0, tmp1), c(0, cumsum(tmp2)/length(df$h)), type = "s")
```



3.4 Example `polygon()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
paint_a <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
plot(df$d/100, df$h, type = "n", bty = "n", las = 1, xlab = "Stem diameter at 1.3m [m]",
     ylab = "Tree height [m]")
polygon(c(dd$b_mean/100, rev(dd$b_mean/100)), c(dd$h_q25, rev(dd$h_q75)),
        col = paint_a, border = NA)
points(df$d/100, df$h, pch = 16, cex = 0.1, col = rgb(0.2, 0.2, 0.2))
lines(dd$b_mean/100, dd$h_mean, col = paint, lwd = 1)
```

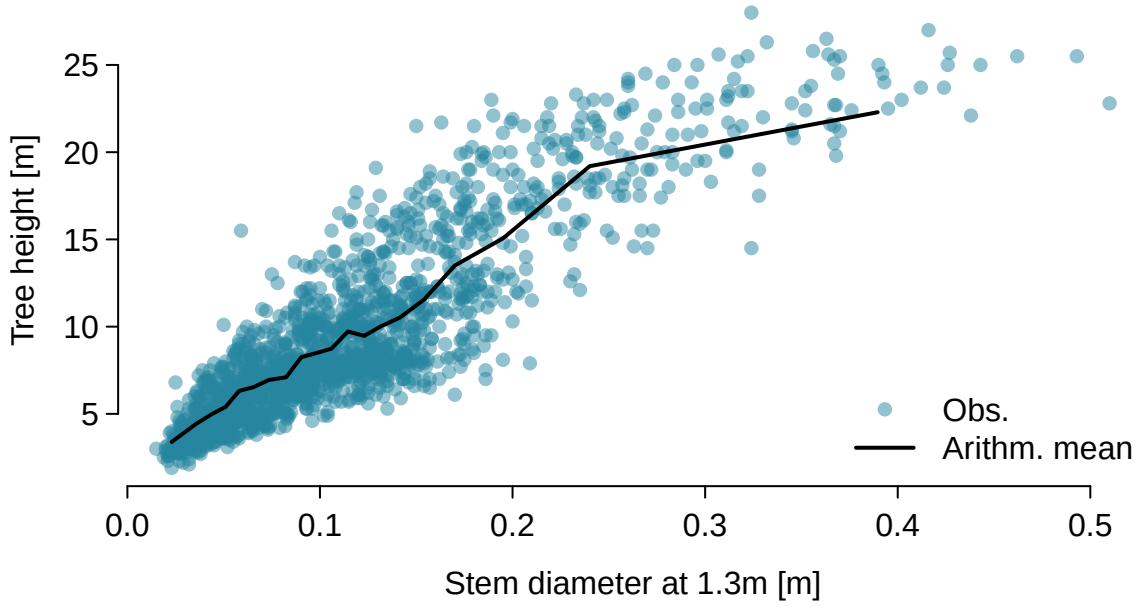


4 `legend()`

- Adds explanation for plot elements.
- Position either by `x`- and `y`-coordinates, or by specifying `"topleft"`, `"bottomleft"`, `"topright"` or `"bottomright"`
- Optional with boundary box.
- Argument `legend`: vector with explanations.
- Further arguments define colors, plot symbols, line widths, ...

4.1 Example `legend()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
plot(df$d/100, df$h, pch = 16, bty = "n", las = 1, ylab = "Tree height [m]",
     col = paint, xlab = "Stem diameter at 1.3m [m]")
lines(dd$b_mean/100, dd$h_mean, col = 1, lwd = 2)
legend("bottomright", lwd = 2, lty = c(NA, 1), pch = c(16, NA), bty = "n",
       col = c(paint, rgb(0, 0, 0)),
       c("Obs.", "Arithm. mean"))
```



5 Further plot types

5.1 `boxplot()`

A **box plot** shows:

- The median as a thick horizontal line,
- the first (Q_1) and third quartile (Q_3) as upper and lower box limits,
- 'fences' calculated by:

  $$\text{upper fence limit} = \min\left(\max(x), Q_3 + 1.5 \cdot \text{IQA}\right),$$

  other

  $$\text{lower fence edge} = \max\left(\min(x), Q_1 - 1.5 \cdot \text{IQA}\right),$$

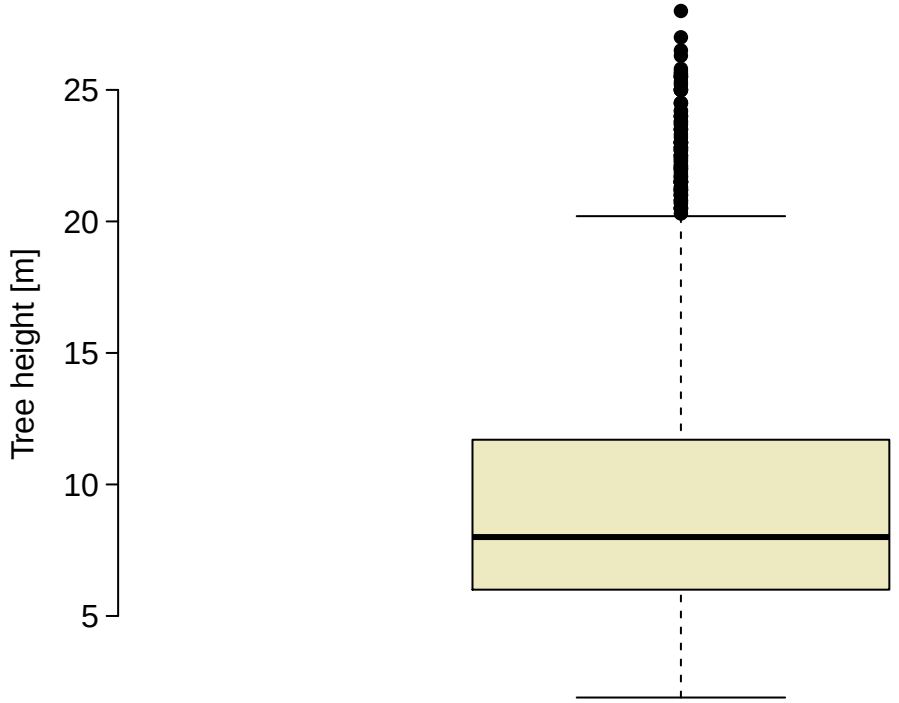
  with interquartile range $\text{IQA} = |Q_3 - Q_1|$, as well as
- Points outside the fences.

Use with argument `x` as a variable or formula:

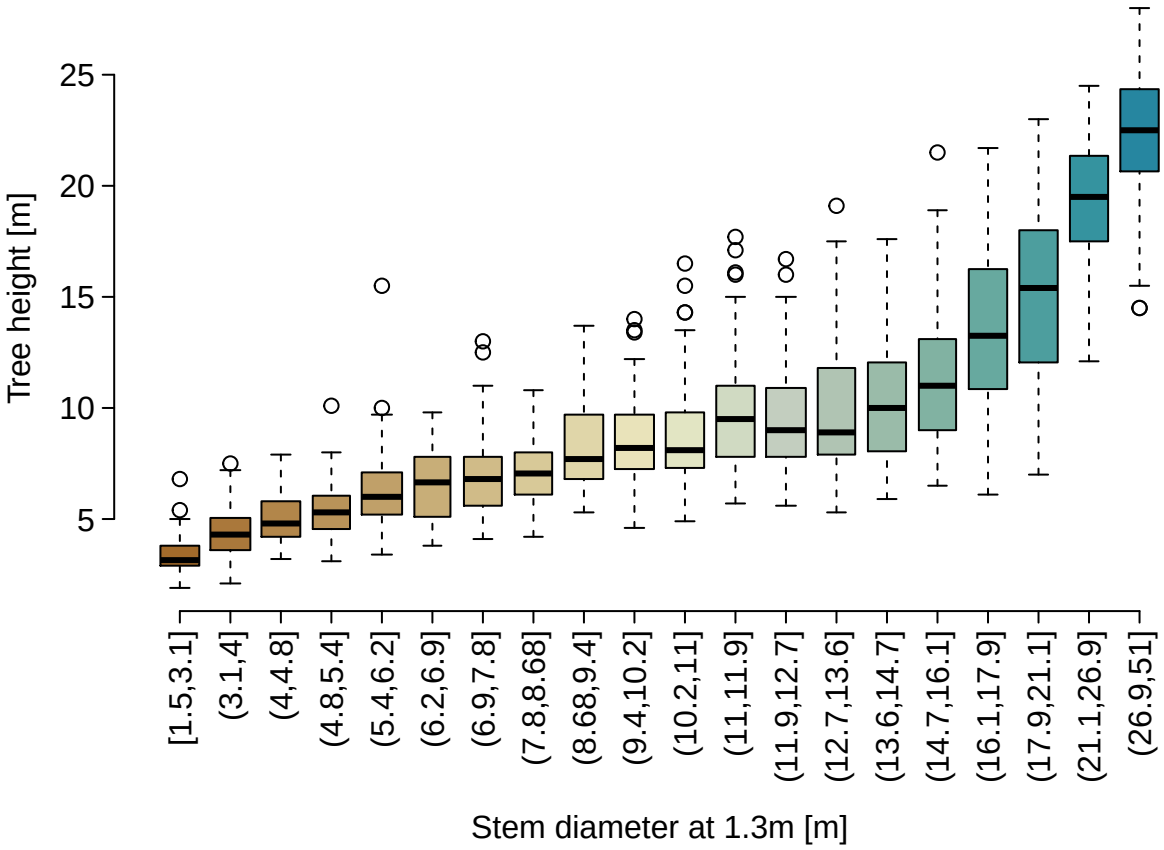
```
boxplot(x, ..., varwidth = F, names, border = par("fg"), col = NULL, log = "",
        horizontal = F, add = F)
```

5.1.1 Examples

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[2]
boxplot(df$h, ylab = "Tree height [m]", pch = 16, frame = F, las = 1,
        col = paint)
```




```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = length(levels(df$d_cut)), pal = "Earth")
tmp <- levels(df$d_cut)
par(mar = c(6.2, 4.1, 0, 0))
boxplot(h ~ d_cut, data = df, varwidth = T, names = tmp, frame = F, las = 2,
        ylab = "Tree height [m]", xlab = "",
        col = paint)## rgb(0, 0.38, 0.27, alpha = 0.5))
mtext(1, text = "Stem diameter at 1.3m [m]", line = 5.1)
```



5.2 `stripchart()`

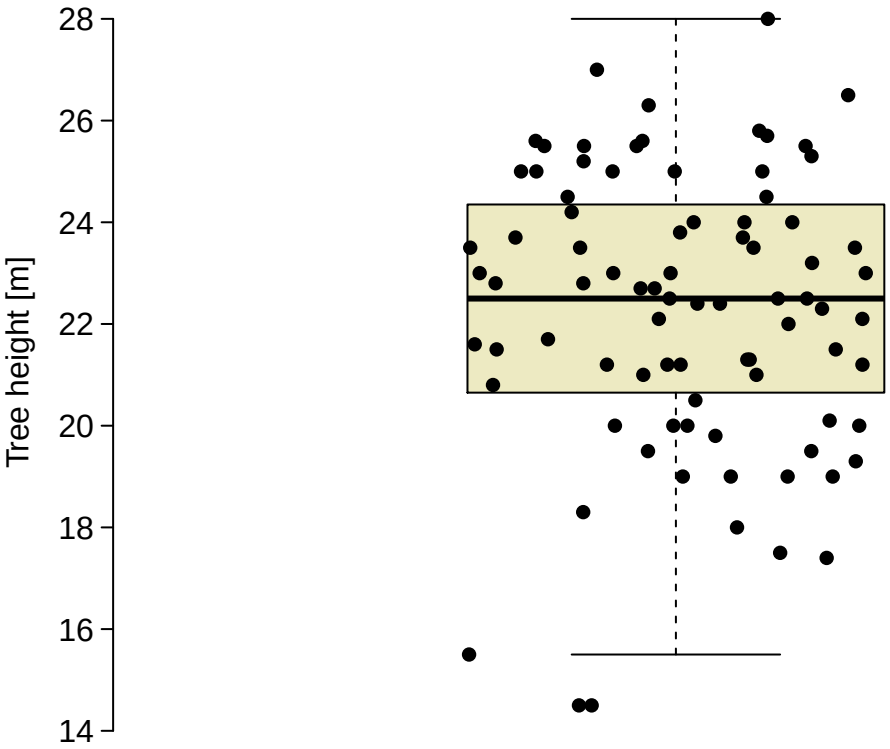
`stripcharts` can be helpful additions to box plots, especially with small samples:

"`stripchart` produces one dimensional scatter plots [...] of the given data. These plots are a good alternative to boxplots when sample sizes are small." (Quote taken from `?stripchart`)

- The argument `method` specifies by which method superimposed points should be made distinguishable, in particular `method = "jitter"` or `method = "stack"`.

5.2.1 Example

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[2]
tmp <- levels(df$d_cut)
sdf <- subset(df, d_cut == "(26.9,51]")
boxplot(sdf$h, ylab = "Tree height [m]", cex = 0, frame = F, las = 1,
        col = paint)
stripchart(sdf$h, add = T, vertical = T, pch = 16, method = "jitter",
           jitter = 0.2)
```



5.3 `hist()`

A histogram divides the value range of the sample into (preset equidistant) intervals and then shows the absolute frequency of the observations within these intervals through the heights of areas. The histogram thus provides a rough estimate for the probability density function.

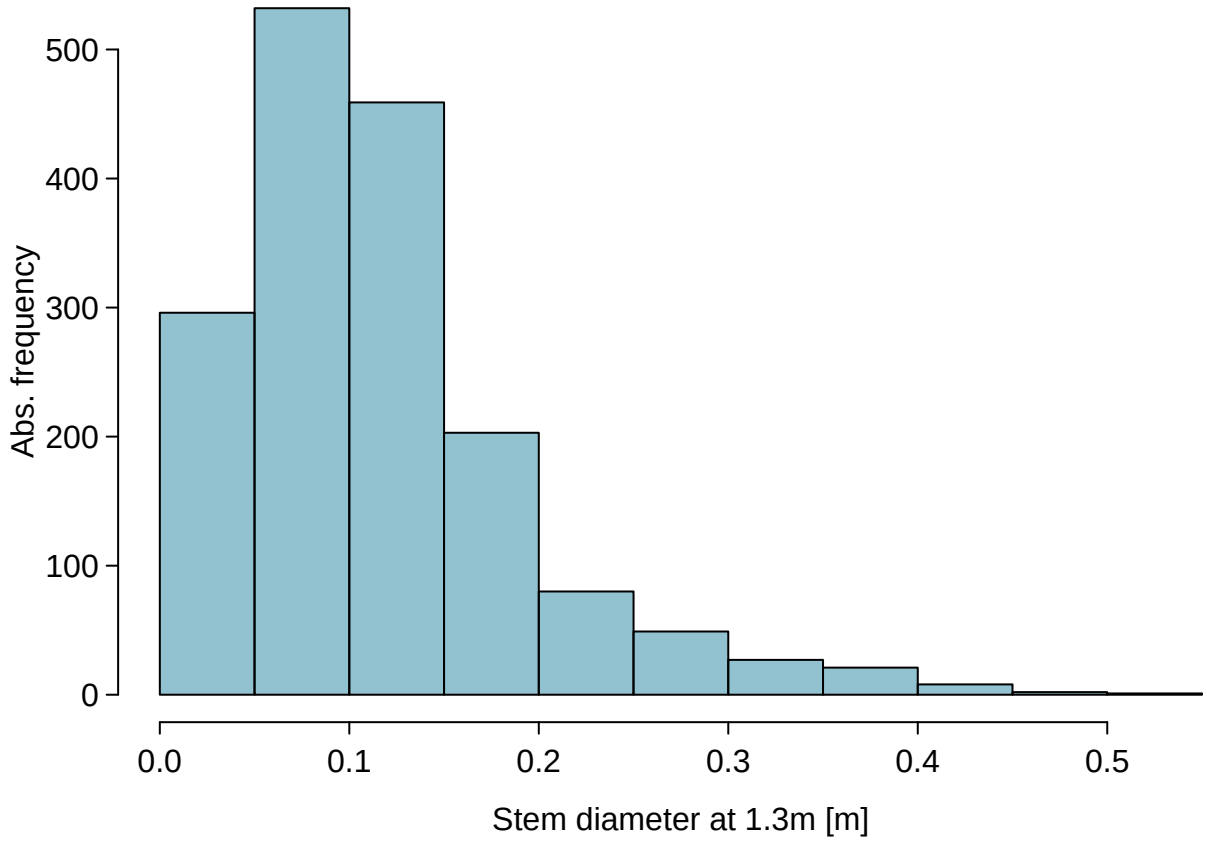
- The argument `breaks` defines the values of the interval limits or the number of intervals.

Usage:

```
hist(x, ..., breaks, freq = NULL, main, xlim, xlab, ylab, axes = TRUE, bty, col)
```

5.3.1 Example

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
hist(df$d/100, main = "", las = 1, col = paint,
     xlab = "Stem diameter at 1.3m [m]", ylab = "Abs. frequency")
```



5.4 `density()`

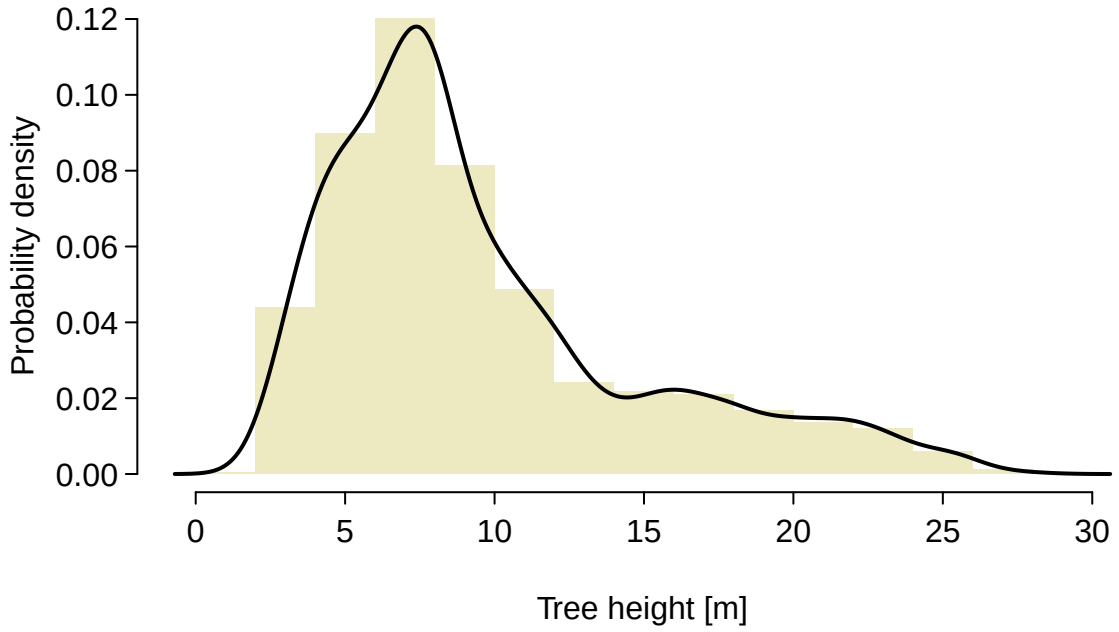
- `density ()` provides a continuous estimate of the probability density function.
- A kernel function is defined at each observation point, the weights of these functions are estimated, and the sum of the kernel functions multiplied by the weights is then returned at each point as an estimator.
- Overlapping a kernel function with areas for which the underlying size is not defined, positive density estimates can arise as artifacts that would be correctly equal to 0.
- `density ()` only returns information about the calculated estimate, the plot then works separately.
- A kernel density estimate is a statistical model with a few assumptions, but pretends to be just a simple descriptive graphic.

Usage:

```
obj <- density(x, ..., n, from, to, na.rm)
plot(obj)
```

5.4.1 Example `hist()` and `density()`

```
par(mar = c(3.5, 3.5, 0, 0) + .1, mgp = c(2.5, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[2]
tmp1 <- density(df$h); tmp2 <- hist(df$h, plot = F)
x_lim <- range(c(df$h, tmp1$x)); y_lim <- range(c(tmp1$y, tmp2$density))
hist(df$h, main = "", las = 1, freq = F, xlim = x_lim, ylim = y_lim,
     xlab = "Tree height [m]", ylab = "Probability density",
     col = paint, border = NA)
lines(tmp1$x, tmp1$y, lwd = 2)
```



5.5 `contour()` und `filled.contour()`

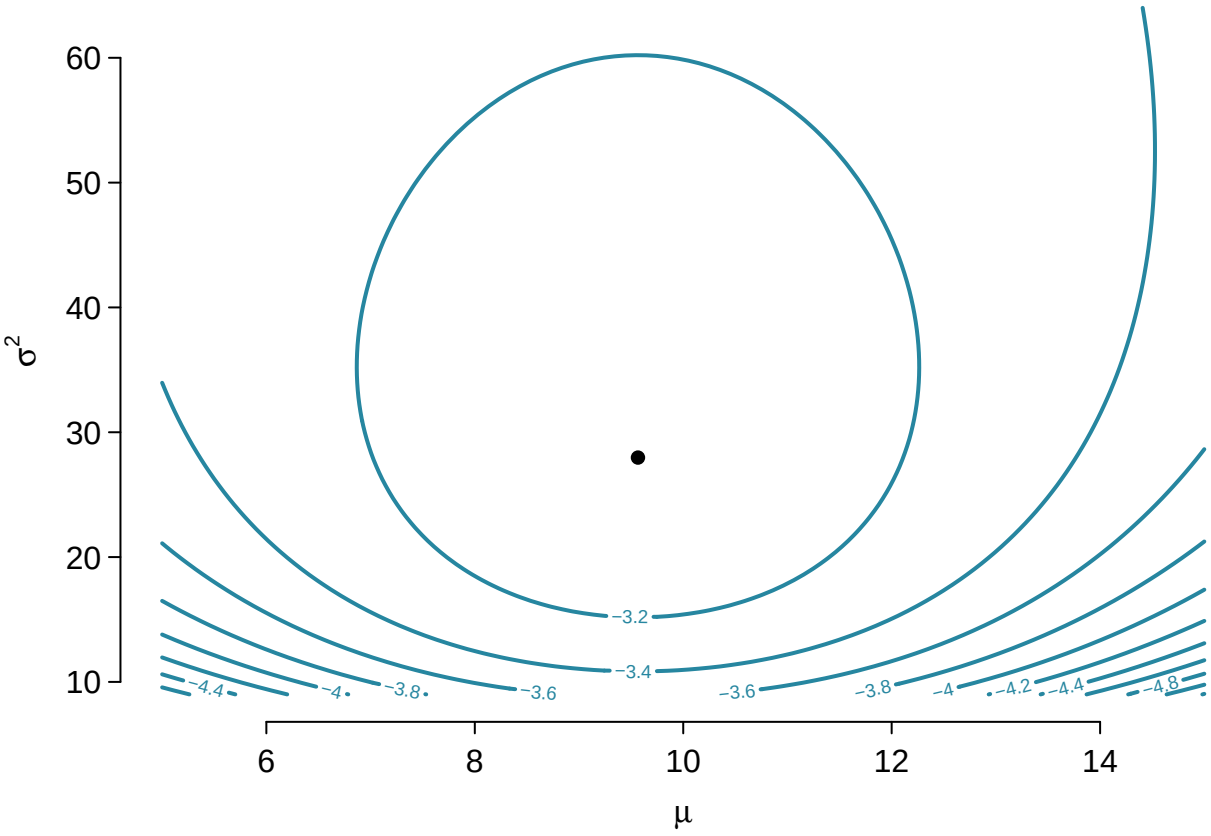
Three-dimensional information can be represented by contour lines with `contour()`.

Some preliminary work for the examples on the next two slides:

```
mu_seq <- seq(5, 15, length = 100)
sd_seq <- seq(3, 8, length = 100)
gr <- expand.grid(mu_seq, sd_seq)
z <- apply(gr, MAR = 1,
           FUN = function(x, y){
             mean(dnorm(x = y, mean = x[1], sd = x[2], log = T))},
           y = df$h)
z <- matrix(nrow = length(mu_seq), ncol = length(sd_seq), z)
# library("RColorBrewer")
# library("scales")
# nwfva_palette_1 <- gradient_n_pal(c("#7C4113","#90BD88","#004E92"))(seq(0, 1,le = 50))
```

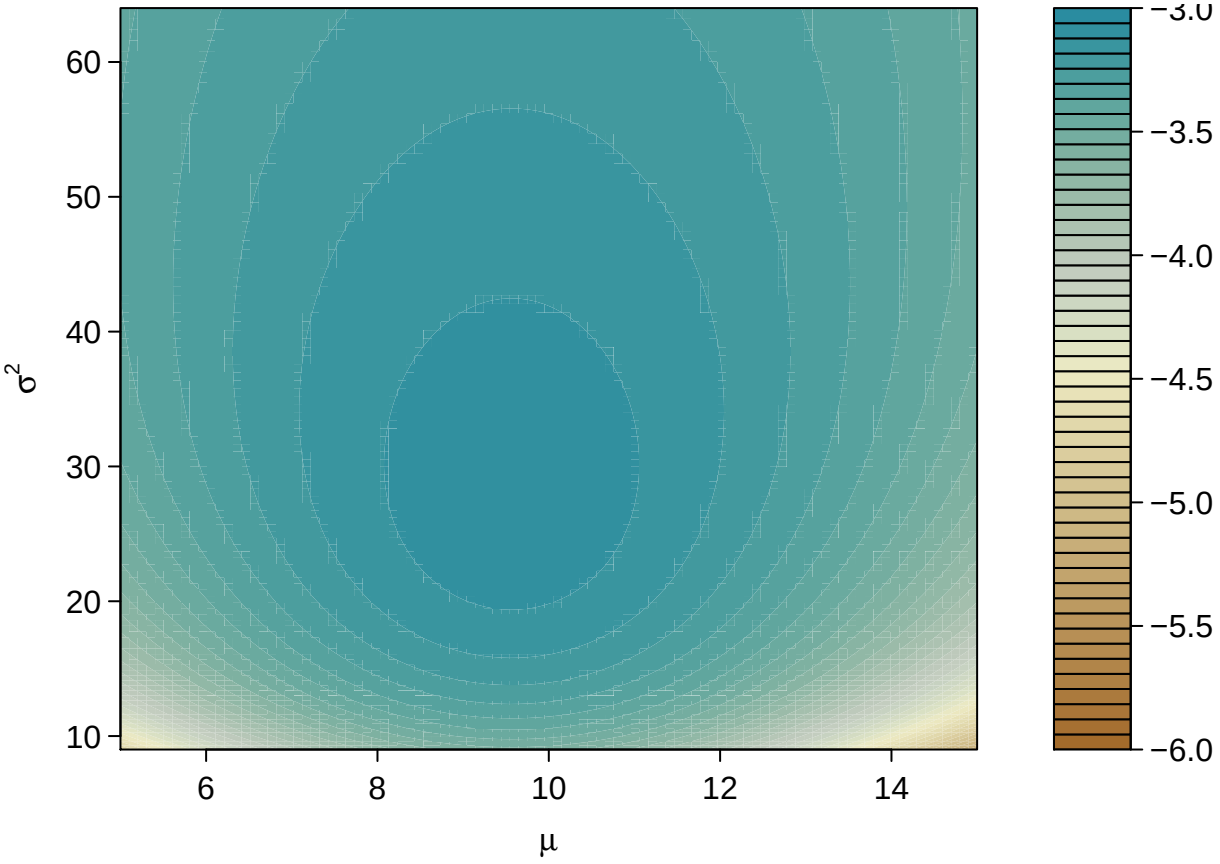
5.5.1 Example `contour()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
contour(x = mu_seq, y = sd_seq^2, z = z, las = 1, bty = "n",
        xlab = expression(paste(mu)), ylab = expression(paste(sigma^2)),
        col = paint, lwd = 2)
points(mean(df$h), var(df$h), pch = 16)
```



5.5.2 Example `filled.contour()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 50, pal = "Earth")
filled.contour(x = mu_seq, y = sd_seq^2, z = z, col = paint,
               levels = seq(floor(min(z)), ceiling(max(z)), length = 50), las = 1,
               xlab = expression(paste(mu)), ylab = expression(paste(sigma^2)))
```



5.6 `mosaicplot()`

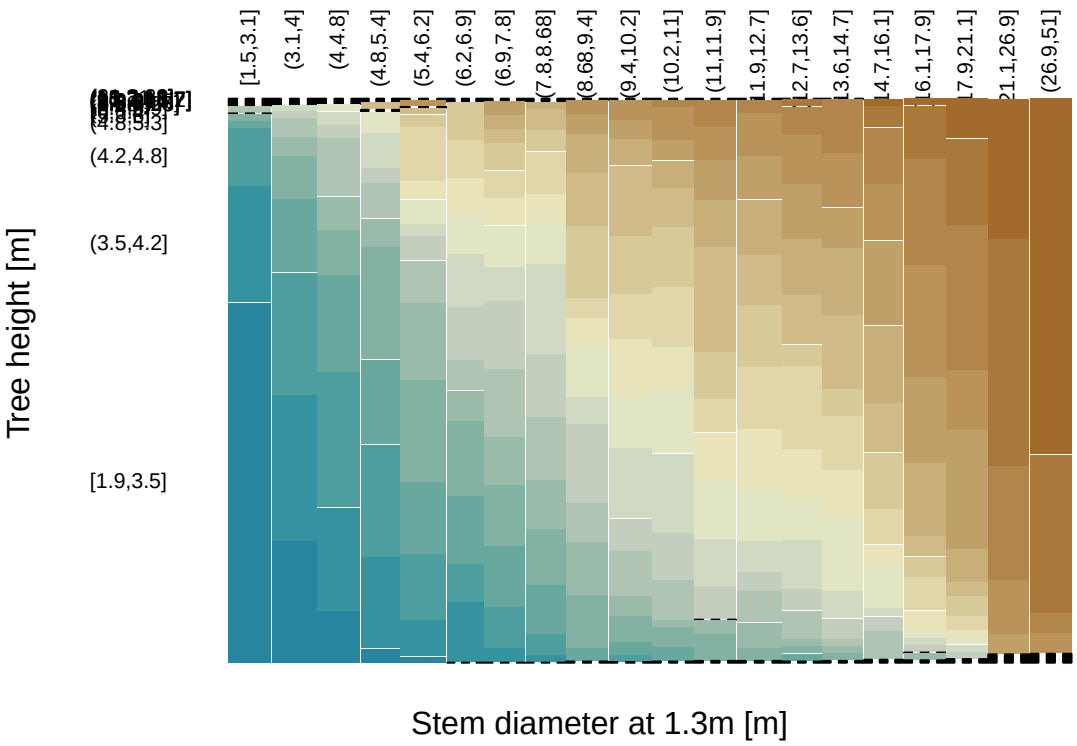
Two-dimensional frequency tables can be displayed with `mosaicplot()`.

Some preliminary work for the following example:

```
df$h_cut <- cut(df$h, breaks = quantile(df$h, probs = seq(0, 1, by = 0.05)),
                include.lowest = T)
df$h_cut <- factor(df$h_cut, levels = rev(levels(df$h_cut)))
tab <- table(df$d_cut, df$h_cut)
```

5.6.1 Example

```
par(mar = c(5, 5, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = length(levels(df$h_cut)), pal = "Earth")
mosaicplot(tab, xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]", main = "",
           las = 2, col = paint, off = 2, border = NA)
```



5.7 Quantile-quantile plot

- Compares two samples (one sample and one distribution) by their quantiles.
- Each observation defines a quantile.
- Similar distributions should result in straight diagonal.

```
qqnorm(y, ylim, main = "Normal Q-Q Plot",
       xlab = "Theoretical Quantiles", ylab = "Sample Quantiles",
       plot.it = TRUE, datax = FALSE, ...)
qqline(y, datax = FALSE, ...)
qqplot(x, y, plot.it = TRUE, xlab = deparse(substitute(x)),
       ylab = deparse(substitute(y)), ...)
```

5.7.1 Examples

```
x <- rnorm(100)
boxplot(x, horizontal = T)
hist(x)
d <- density(x)
plot(d)
d3 <- density(x, kernel = "tri", bw = 1)
lines(d3, col = "blue")
```

6 Organization of the graphics window with `par ()` and `layout ()`

- The function `par()` holds – based on a list – all relevant parameters for the graphics window.
- Overview through `?par`
- `dev.off()` restores the original values.

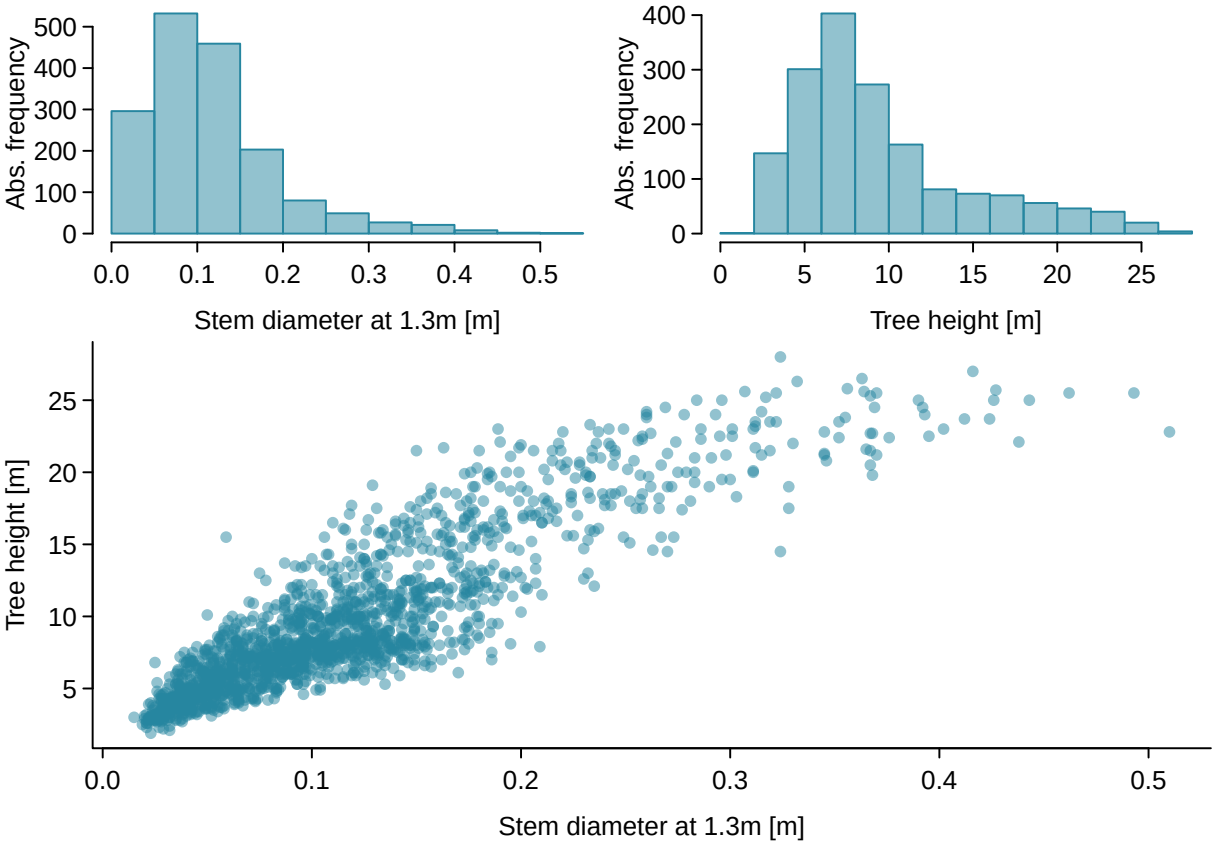
The following combination ('multiple frames' and changing the 'margin specifications') is often used:

```
par(mar = c(4.1, 4.1, 1, 1), mfrow = c(1, 2))
```

`layout()` is a further helpful too in order to organise severel graphics in one device.

6.1 Example `layout()`

```
par(mar = c(3, 3, 0, 0) + .1, mgp = c(2, .5, 0), tcl = -.3, las = 1)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
paint_a <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
#par(mar = c(4.1, 4.1, 0.5, 1.1))
layout(matrix(nrow = 2, ncol = 2, c(1, 3, 2, 3)), heights = c(0.4, 0.6))
hist(df$d/100, main = "", xlab = "Stem diameter at 1.3m [m]", ylab = "Abs. frequency",
     col = paint_a, border = paint)
hist(df$h, xlab = "Tree height [m]", main = "", ylab = "Abs. frequency",
     col = paint_a, border = paint)
plot(df$d/100, df$h, pch = 16, bty = "l", col = paint_a,
     xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]")
```

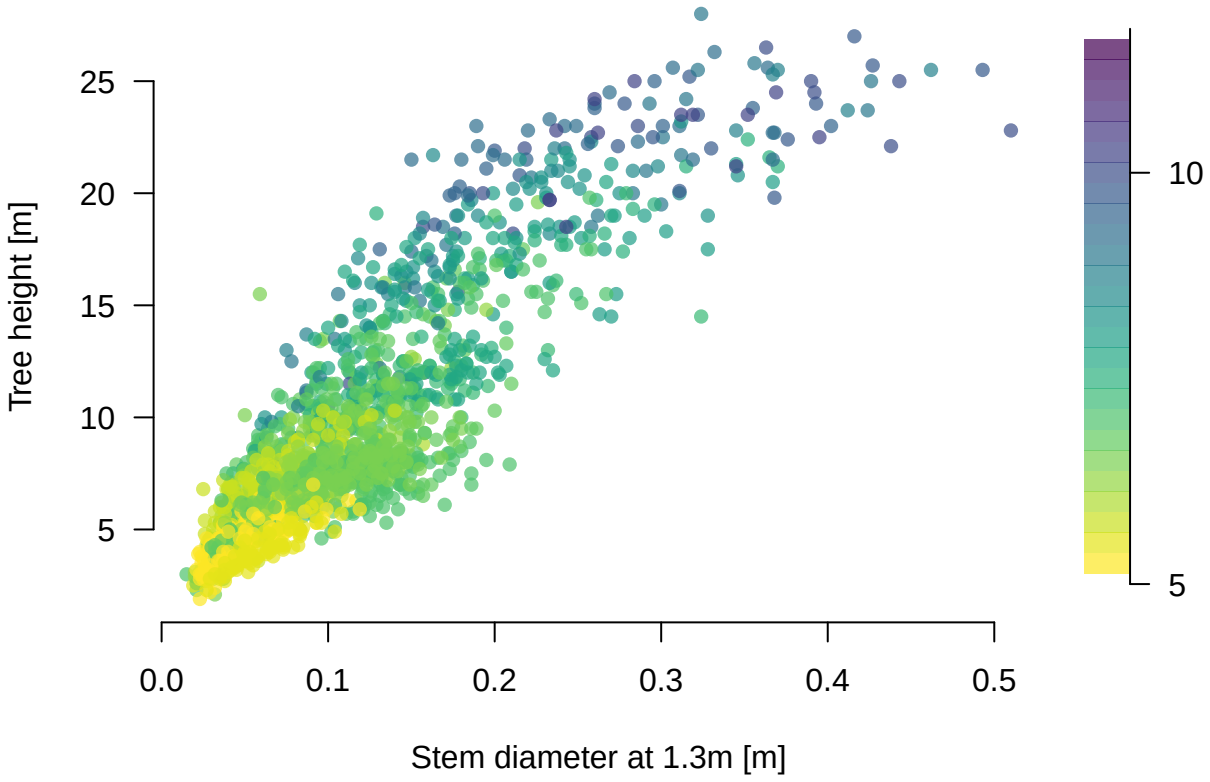


7 Colours

- Colors are changed by the argument `col = "name"`.
- The function `colors ()` contains already defined standard colors.
- The function `palette ()` contains the color palette that is used when `col` is specified by a numeric value.
- `rgb` generates colors by mixing red, green and blue components (with the possibility of **alpha** shading} through the argument `alpha`).
- In this course I mostly use the (very rich) package `colorspace` ([JSS article] (https://www.jstatsoft.org/index.php/jss/article/view/v096i01/1395)).
- Alternatively, package `viridis` supports the search for optimal colors in terms of taking into account most types of color blindness, as well as the maximum contrast in gray-scale printing of colored graphics.

7.1 Example `viridis()`

```
library("viridis")
df$dmean_rounded <- round(df$dmean)
cols <- viridis(n = 1 + max(df$dmean_rounded) - min(df$dmean_rounded), alpha = 0.7)
cols <- rev(cols)
layout(widths = c(0.9, 0.1), mat = matrix(nrow = 1, ncol = 2, 1:2))
par(mar = c(5, 5, 1, 1))
plot(df$d/100, df$h, pch = 16, bty = "n", las = 1,
     xlab = "Stem diameter at 1.3m [m]", ylab = "Tree height [m]",
     col = cols[as.numeric(as.factor(df$dmean_rounded))])
par(mar = c(6, 0, 2, 2))
plot(rep(0, length(cols)), 1:length(cols), type = "n", main = "",
     bty = "n", xlab = "", ylab = "", yaxt = "n", xaxt = "n")
axis(4, las = 2, at = c(0, 20, 40, 60, 80, 100),
     seq(min(df$dmean_rounded), max(df$dmean_rounded), length = 6))
for (i in 1:length(cols)) {
  polygon(c(-1, -1, 1, 1), i + c(-0.5, 0.5, 0.5, -0.5), border = NA,
          col = cols[i])
}
```



8 Mathematical notation in graphics

- R offers limited possibilities for mathematical notation in graphics.
- Syntax similar to LaTeX
- The formulation is passed as an argument to the `expression()` function.
- For an overview of the (im) possibilities see `?plotmath`

Command	Meaning
`frac(a,b)`	Fraction
`[i]`	Subscript
`alpha, beta`	Greek letters

Command	Meaning
`sqrt(a)`	Squarerootfunction
...	See `?plotmath`

8.1 Example

```
plot(1, 1, type = "n", bty = "n", axes = F, xlab = "", ylab = "")
txt1 <- expression(paste("Stand density: ", frac("No. individuals",
                         "Stand area"), "   [", N %.% ha^-1, "]"))
txt2 <- expression(paste("Quadratic mean Stem diameter: ", sqrt(frac(
                         sum(d[i]^2, i == 1, n),n)), "   [", cm^2, "]"))
text(1, 1.2, txt1); text(1, 0.9, txt2)
```

$$\text{Stand density: } \frac{\text{No. individuals}}{\text{Stand area}} \quad [\text{N} \cdot \text{ha}^{-1}]$$

$$\text{Quadratic mean Stem diameter: } \sqrt{\frac{\sum_{i=1}^{n} d_i^2}{n}} \quad [\text{cm}^2]$$

9 `lattice` Graphics for grouped / clustered data

- `library("lattice")`
- Conveniently plot grouped data into a graph
- 'Lattice structure' offers better division compared to `par(mfrow = c(i, j))`

Function	Graphic type
`xyplot`	Scatter plot
`bwplot`	Box plot
`barchart`	Bar plot
`contourplot`	Contour lines ('3D')
`levelplot`	Filled contour lines
`histogram`	Histogram
`densityplot`	kernel density estimation

Usage:

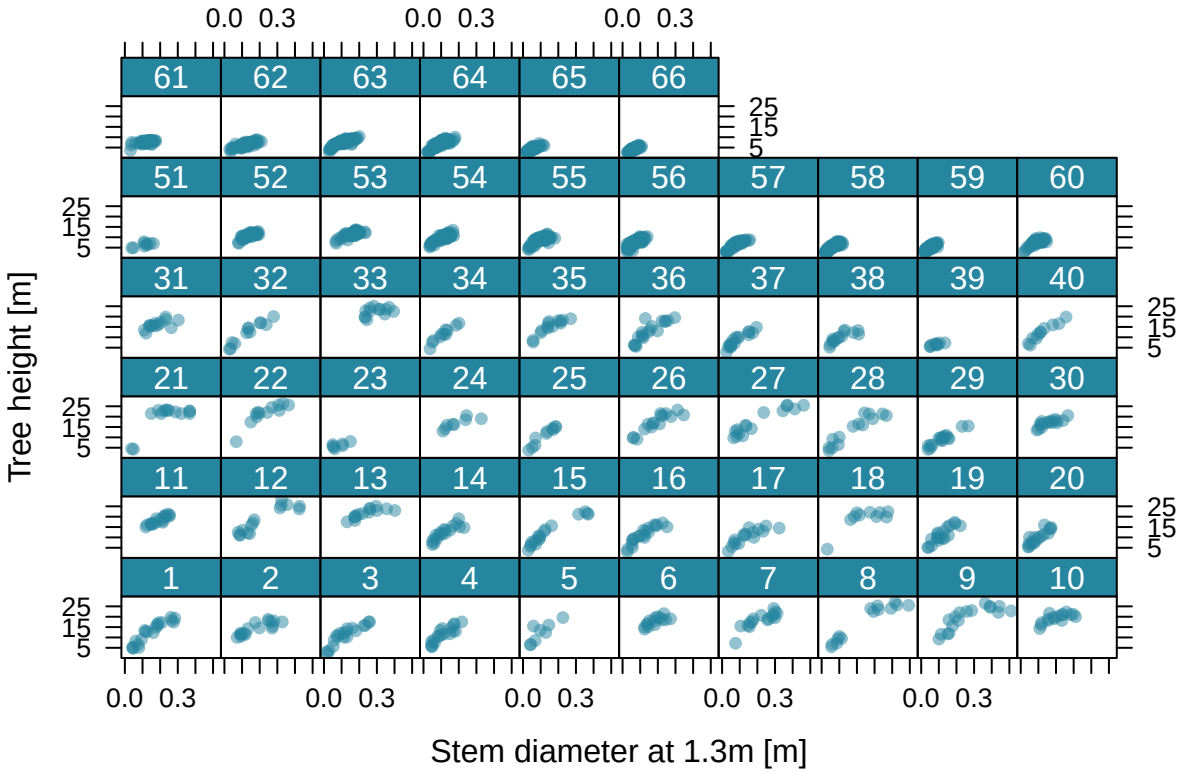
`function(y ~ x | g, data, parameters,...)`

- Plot of `x` againsty,
- Grouped (individual plot windows) by `g`,
- Returns `trellis` object (nobase plot),
- no 'target variable' `y` for`densityplot`, `bwplot` and`histogram`.

9.1 Example:

```
library("lattice")
df$plot <- factor(df$plot)
paint <- colorspace::divergingx_hcl(n = 3, pal = "Earth")[3]
paint_a <- colorspace::divergingx_hcl(n = 3, pal = "Earth", alpha = .5)[3]
xyplot(h ~ d/100 | plot, data = df, pch = 16, xlab = "Stem diameter at 1.3m [m]",
       ylab = "Tree height [m]", col = paint_a,
```

```
par.strip.text = list(col = "white"),
par.settings = list(strip.background = list(col = paint)))
```



10 ggplot

The basics to Grammar of Graphics in Session 05.