Introduction to R: Session 04

Holger Sennhenn-Reulen[a], Nordwestdeutsche Forstliche Versuchsanstalt (NW-FVA)

November 02, 2021 (Version 0.2)

Contents

[a] Private webpage: uncertaintree.github.io

1 Working with 'real' data

R is a powerful tool, not only for analysis, but also for managing of data.

1.1 Reproducible data management

- Avoid any steps in spreadsheet-software as MS Excel that are done 'by hand' and are non-repdroducible.
- *Workflow A*:
  - Generate an R-Script `01_datamanagement.R` that loads your data and does all the steps and stops with an object `df` that is used for any further steps.
  - Run this file using `source(01_datamanagement.R)`.
- *Workflow B*: Generate a markdown file that not only doeas the above, but also documents all your steps (A short intro to markdown in Session 05).

1.2 Preparatory steps prior R

Data management in *R* begins with loading the data into *R*. But before we think about the technical way in which we read our data into *R*, we should first ensure that they are 'prepared' for this *R* import. If we neglect a few basic rules in this preparatory work, we actually only hold back problems (for which we then only have to find unnecessarily 'complicated' solutions in *R*).

- The first line of the dataframe is reserved for the variable names: If we set `header = TRUE` (*R* functions`read.csv ()`or`read.table ()`) the first line in the dataframe becomes for the variable names recycled.
- The first column (s) should be used to define the observation unit: Tree ID (, section, section ID, . . .). It is preferable to keep the information here separately:
- It is easier to combine several variables (in *R*) than to split one variable into several variables.

1.3 Variable names

- Avoid variable names, values, or cells with spaces. If ignored – and not adequately handled during data import – each word is treated as a (value of) a separate variable. This leads to errors that are always related to the fact that the number of elements varies between the lines (matrix 'behavior' of the dataframe).
- If several words are to be put together, ideally use underscores, eg. `Count_per_ha` (Alternatively, you can also use dots – `Count.per.ha` –, or start every single word with a capital letter – `CountPerHa`).
- **Decide on a rule and try to stick to it!**
- Functions like `tolower`,`gsub ()`and`stringsplit` are useful helpers to quickly carry out repairs in *R*.
- Make sure that all missing values – especially empty cells – are marked with *NA*.
- Delete all free text comments (this only leads to extra columns or an inflation of *NA*s).

1.4 Preparatory Work in R

Before reading in a dataframe, you have to tell R where the file can be found.

- To achieve this, it can be helpful to find out which working directory *R* is currently accessing:

```
getwd()
```

- If different from the storage location of the dataframe, we have to change this working directory:

```
setwd("<Path of the folder in which the data file is saved>")
```

By executing this function call, *R* now knows in which working directory we want to work.

For RStudio users

It is very helpful to save the current `.R` code file and the dataframe in the same directory: At the beginning of a working session, you can then click on *Session* → *Set Working Directory* → *To Source File Location* (this also facilitates collaboration).

Spreadsheet software (such as MS Excel) allows dataframes to be saved in many different file formats:

- The most popular non-standard formats (i.e. not .xls or.xlsx) to save a dataframe are .csv (for *comma-separated value*) and.txt (tab-separated text file).
- Depending on this choice, a line's contents are either separated by commas or tabs (referred to as 'separation argument').
- **Attention:** Under operating systems with German language setting, commas are the default setting for the argument to represent decimal numbers. Here it is necessary to change the default values for the arguments sep anddec to sep ="; " and dec =", " (required in read.table(), read.csv() and read.csv2(); see also the next sections).

1.5 read.table()

If the data was saved in the above-mentioned tab-separated text format .txt, the function read.table() is a simple way of importing data:

```
d <- read.table("<FileName>.txt", header = TRUE)
```

- By previously defining the working directory (setwd ()), the dataser can be imported directly by specifying the file name.
- The value of the header argument can be used to determine whether the first line of the dataframe contains the variable names (TRUE is the default value here).
- The separation argument sep is set to the value "", since the read.table command is defined for tab-separated text formats.

To specify a different separation argument, the value of the argument sep must be changed:

```
df <- read.table("<FileName>.txt", header = FALSE, sep = ";")
```

1.6 read.csv() and read.csv2()

The functions read.csv() and read.csv2() can be used to read data files in .csv (Comma Separated Values) format.

- .csv dataframes can be easily imported into *R* and are therefore a preferred format.
- read.csv() and read.csv2() use different separation arguments: for read.csv() the comma, for read.csv2() the semicolon (open your dataframe in a text editor in order to quickly find out your separation argument).
- read.csv() and read.csv2() are special cases of read.table(): This means that the arguments for read.table() can alternately also be used for read.csv() and read.csv2().
- read.csv() and read.csv2() are very similar to read.table() and differ from read.table() in only three aspects:
  - The separation argument sep,
  - he argument header is always set toTRUE, and
  - the argument fill is also TRUE, which means that if lines have unequal lengths, read.csv() and read.csv2() will always fill the short lines with empty cells.

```
d <- read.csv("data.csv", header = T, sep = ";", dec = ",", stringsAsFactor = F)
names(d)
```

1.7 Factors

Working with factors:

- Import the data with `stringsAsFactor = FALSE`
- Check the structure of the dataframe with the help of `str()`: Surprisingly, have variables been imported as strings (class `chr`)? If so, check the characteristics of these variables for incorrect values with `unique()` or `xtabs ()`.
- Also check with `unique()` or `xtabs()` the characteristics of the variables that were planned to be read in as `chr`: Typing errors can easily lurk here as well.
- Use `df$var <- as.factor(df$var)` to finally assign the `factor` class to variable `var`.

1.8 attach, subset and merge

Never say never but **never use attach()**.

... use a short name for the dataframe object (e.g. df) to keep the paperwork to a minimum!

The function merge(data_set1, data_set2, by, ...) can be used to link two dataframes using a key variable:

```
library("plyr")
dd <- ddply(drought, c("species"), summarize,
            mean_bair = mean(bair),
            sd_bair = sd(bair),
            mean_elev = mean(elev),
            sd_elev = sd(elev))
head(merge(drought, dd, by = c("species")))
```

```
##   species  bair  elev mean_bair   sd_bair mean_elev  sd_elev
## 1   Beech 0.697 475.0 0.8152727 0.2159037  804.3182 277.0922
## 2   Beech 0.606 480.0 0.8152727 0.2159037  804.3182 277.0922
## 3   Beech 0.718 507.5 0.8152727 0.2159037  804.3182 277.0922
## 4   Beech 0.480 580.0 0.8152727 0.2159037  804.3182 277.0922
## 5   Beech 0.822 750.0 0.8152727 0.2159037  804.3182 277.0922
## 6   Beech 0.944 780.0 0.8152727 0.2159037  804.3182 277.0922
```

subset can be used to split a dataframe according to the result of a logical comparison:

```
(tmp <- range(drought$elev %/% 250))
```

```
## [1] 1 6
```

```
br <- seq(tmp[1] * 250, (tmp[2] + 1) * 250, by = 250)
drought$elev_cut <- cut(drought$elev, breaks = br)
sdf <- subset(drought, elev_cut == "(500,750]" & species == "Beech")
sdf
```

```
##     bair  elev species  elev_cut
## 26 0.718 507.5   Beech (500,750]
## 27 0.480 580.0   Beech (500,750]
## 28 0.822 750.0   Beech (500,750]
```

2 Descriptive analysis for univariate samples

2.1 Continuously scaled variable

2.1.1 Location

- mean, weighted.mean
- median, quantile (calculates percentiles probs = seq(0, 1, by = .01), and quartiles for probs = c(.25, .5, .75))
- summary (returns: min, 1st quartile, median, mean, 3rd quartile, max)

```
## mean:
mean(drought$bair)
```

```
## [1] 0.7489118
```

```
## weighted mean:
tmp <- nrow(drought)/table(drought$species)
tmp <- data.frame(species = factor(levels(drought$species), levels = levels(drought$species)),
                  w = as.numeric(tmp))
tmp <- merge(drought[, c("species", "bair")], tmp, by = "species")
tmp$w <- tmp$w/sum(tmp$w)
aggregate(x = tmp[, c("w")], by = list(tmp$species), FUN = sum)
```

```
##   Group.1   x
## 1   Beech 0.5
## 2  Spruce 0.5
```

```
weighted.mean(tmp$bair, w = tmp$w)
```

```
## [1] 0.7662233
```

```
rm(tmp)
## median:
median(drought$bair)
```

```
## [1] 0.71
```

```
## quartiles:
quantile(drought$bair, probs = c(.25, .5, .75))
```

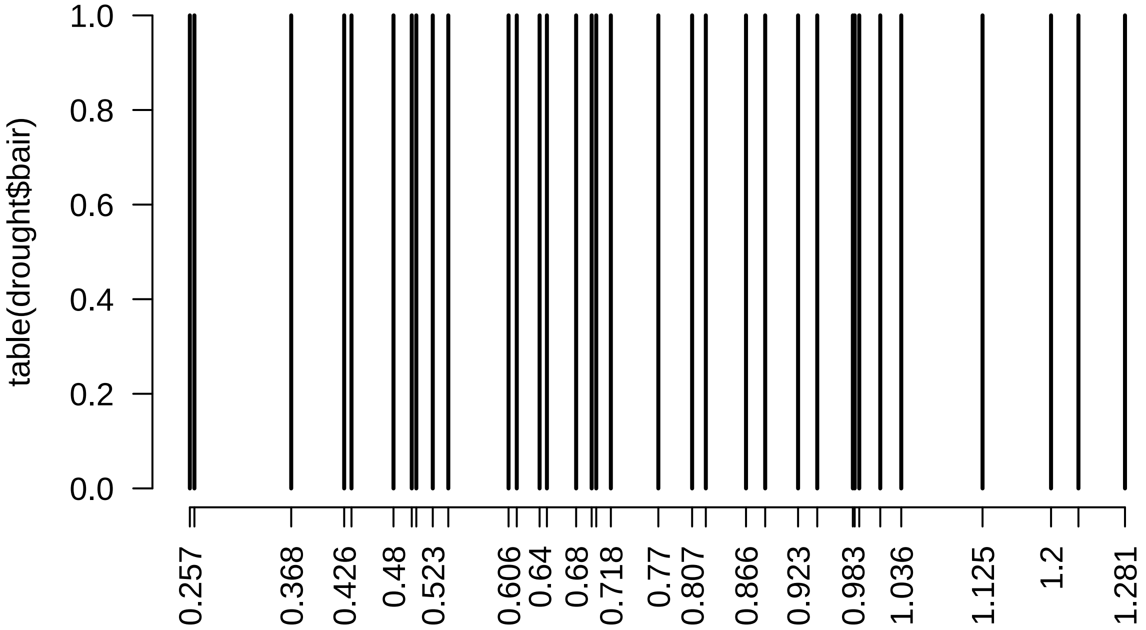
```
##     25%     50%     75% 
## 0.52725 0.71000 0.97325
```

```
## summary:
summary(drought$bair)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max. 
##  0.2570  0.5272  0.7100  0.7489  0.9732  1.2810
```

A sample of a continuously scaled variable doesn't have a mode:

```
plot(table(drought$bair), las = 2, bty = "n")
```



... but the density of such a variable might have a maximum. So we cannot **calculate** a mode, but with using techniques such as kernel density estimation – R function `density` – the location of the maximum density can be **estimated**.

```
get_mode <- function(x, ...){
  tmp <- density(x, ...)
  index <- which.max(tmp$y)
  return(tmp$x[index])
}
tmp <- density(drought$bair)
plot(tmp, las = 1, bty = "n", xlab = "BAIR",
     main = paste0("Kernel density estimation, gaussian kernel function, bandwidth: ", round(tmp$bw,
rug(drought$bair)
abline(v = print(get_mode(drought$bair)))
```

2.1.2 Scale / variation

Methods to describe the scale / variation:

- `range` (calculates `min` and `max`)
- `var` (variance)
- `sd` (standard deviation)
- `mad` ('median absolute deviation', function `mad(x)` is just a more general implementation of `median(abs(x - median(x)))`)
- `IQR` (interquartile range)

Argument `na.rm = TRUE` removes all missing values in advance!

```
x <- drought$bair
mad
```

```
## function (x, center = median(x), constant = 1.4826, na.rm = FALSE,
##     low = FALSE, high = FALSE)
## {
##     if (na.rm)
##         x <- x[!is.na(x)]
##     n <- length(x)
##     constant * if ((low || high) && n%%2 == 0) {
##         if (low && high)
##             stop("'low' and 'high' cannot be both TRUE")
##         n2 <- n%/%2 + as.integer(high)
##         sort(abs(x - center), partial = n2)[n2]
##     }
##     else median(abs(x - center))
## }
## <bytecode: 0x55d4e47c11b0>
## <environment: namespace:stats>
```

```
c(mad(x, constant = 1),
  median(abs(x - median(x))),
  sd(x),
  var(x),
  IQR(x))
```

```
## [1] 0.21150000 0.21150000 0.27400800 0.07508039 0.44600000
```

2.2 Categorically scaled variables

table as 'standard function' for absolute frequency distribution, xtabs as an alternative with formula syntax (and labeling with variable names if table is created from data set).

. . . while preparing, this section somehow got longer and longer. For a general introduction to R, at some point, when you feel like it, just move on to next section on bivariate sample.

2.2.1 One dimensional:

```
table(drought$species)
```

```
##
##  Beech Spruce
##     11     23
```

```
xtabs(~ drought$species)
```

```
## drought$species
##  Beech Spruce
##     11     23
```

```
xtabs(~ species, data = drought)
```

```
## species
##  Beech Spruce
##     11     23
```

addNA and useNA show slightly different behavior:

```
tmp <- as.factor(c(as.character(drought$species), NA))
table(tmp)
```

```
## tmp
##  Beech Spruce
##     11     23
```

```
table(drought$species, useNA = "ifany")
```

```
##
##  Beech Spruce
##     11     23
```

```
table(tmp, useNA = "ifany")
```

```
## tmp
##  Beech Spruce   <NA>
##     11     23      1
```

```
table(drought$species, useNA = "always")
```

```
##
##   Beech Spruce   <NA>
##      11     23      0
```

```
table(tmp, useNA = "always")
```

```
## tmp
##   Beech Spruce   <NA>
##      11     23      1
```

```
xtabs(~ drought$species, addNA = TRUE)
```

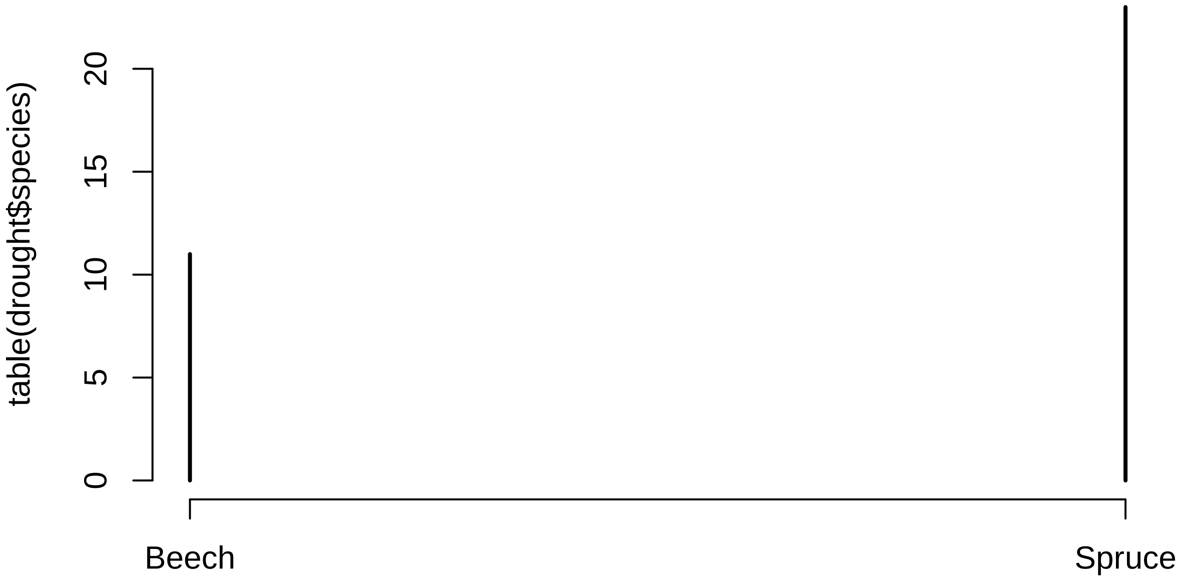
```
## drought$species
##   Beech Spruce
##      11     23
```

```
xtabs(~ tmp, addNA = T)
```

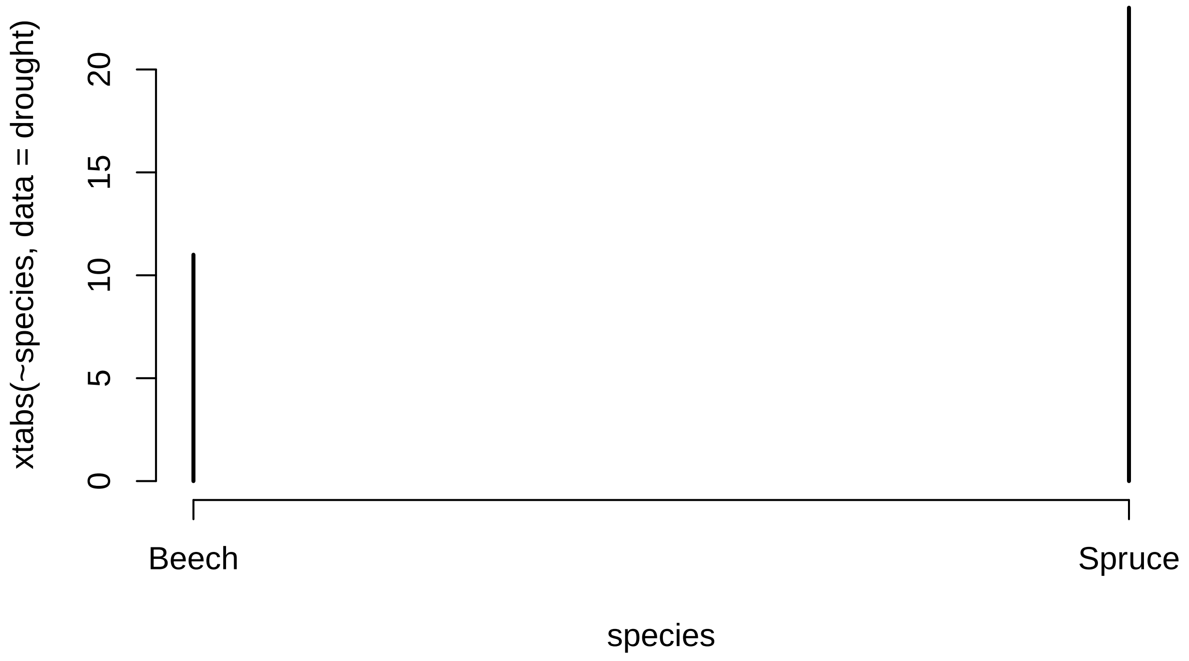
```
## tmp
##   Beech Spruce   <NA>
##      11     23      1
```

Default plot:

```
plot(table(drought$species))
```



```
plot(xtabs(~ species, data = drought))
```



2.2.2 Two dimensional

... this illustrational example shows *bad scientific practice* since we cut continuous variables into binary categories, and by this bin a lot of valuable information!

```
tmp <- data.frame(species = drought$species)
tmp$elevGreater1000 <- (drought$elev > 1000)
tmp$bairGreater1 <- (drought$bair > 1)
table(tmp$bairGreater1, tmp$elevGreater1000) ## We are lost!
```

```
##
##         FALSE TRUE
##   FALSE    19    9
##   TRUE      0    6
```

```
xtabs(~ bairGreater1 + elevGreater1000, data = tmp) ## Labels!
```

```
##             elevGreater1000
## bairGreater1 FALSE TRUE
##        FALSE    19    9
##        TRUE      0    6
```

Default plot:

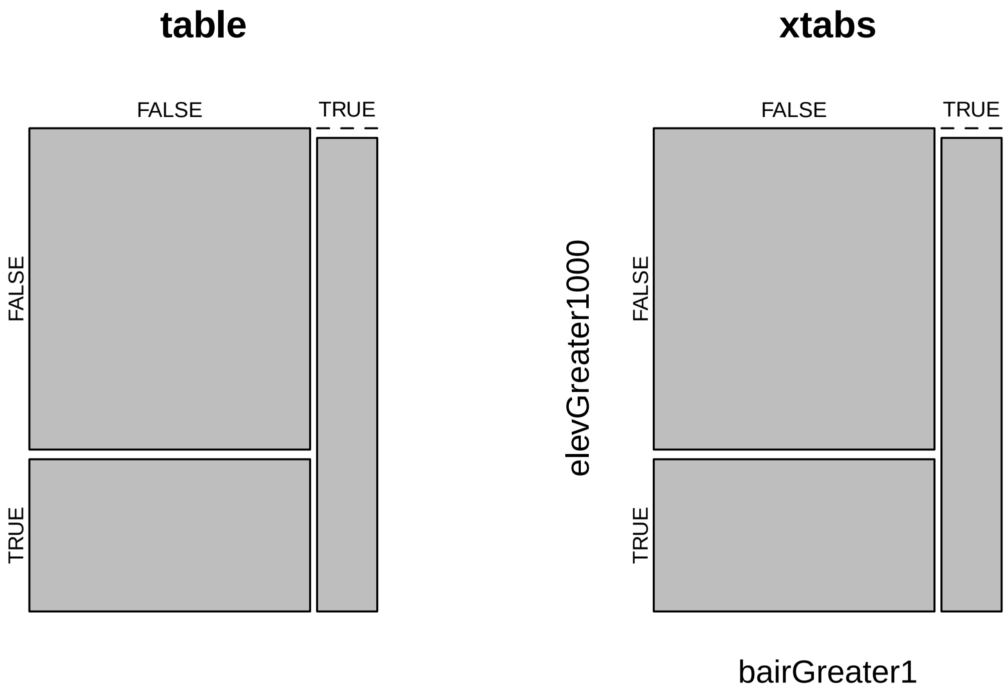
```
par(mfrow = c(1, 2))
table(tmp$bairGreater1, tmp$elevGreater1000) ## We are lost!
```

```
##
##         FALSE TRUE
##   FALSE    19    9
##   TRUE      0    6
```

```
xtabs(~ bairGreater1 + elevGreater1000, data = tmp) ## Labels!
```

```
##             elevGreater1000
## bairGreater1 FALSE TRUE
##        FALSE    19    9
##        TRUE      0    6
```

```
plot(table(tmp$bairGreater1, tmp$elevGreater1000), main = "table")
plot(xtabs(~ bairGreater1 + elevGreater1000, data = tmp), main = "xtabs")
```



2.2.3 addmargins, margin.table, and prop.table

One dimensional:

```
addmargins(table(tmp$bairGreater1))
```

```
##
## FALSE  TRUE   Sum
##    28     6    34
```

```
margin.table(table(tmp$bairGreater1))
```

```
## [1] 34
```

```
prop.table(table(tmp$bairGreater1))
```

```
##
##     FALSE      TRUE
## 0.8235294 0.1764706
```

```
margin.table(prop.table(tmp$table(bairGreater1)))
```

```
## Error in prop.table(tmp$table(bairGreater1)): Versuch eine Nicht-Funktion anzuwenden
```

Two dimensional:

```
addmargins(table(tmp$elevGreater1000, tmp$bairGreater1))
```

```
##
##          FALSE TRUE Sum
##   FALSE    19    0  19
##   TRUE      9    6  15
##   Sum      28    6  34
```

```
margin.table(table(tmp$elevGreater1000, tmp$bairGreater1))
```

```
## [1] 34
```

```
margin.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 1)
```

```
##
## FALSE  TRUE
##    19    15
```

```
margin.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 2)
```

```
##
## FALSE  TRUE
##    28     6
```

```
prop.table(table(tmp$elevGreater1000, tmp$bairGreater1))
```

```
##
##              FALSE      TRUE
##   FALSE 0.5588235 0.0000000
##   TRUE  0.2647059 0.1764706
```

```
prop.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 1)
```

```
##
##         FALSE TRUE
##   FALSE   1.0  0.0
##   TRUE    0.6  0.4
```

```
prop.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 2)
```

```
##
##              FALSE      TRUE
##   FALSE 0.6785714 0.0000000
##   TRUE  0.3214286 1.0000000
```

```
margin.table(prop.table(table(tmp$elevGreater1000, tmp$bairGreater1)))
```

```
## [1] 1
```

```
addmargins(prop.table(table(tmp$elevGreater1000, tmp$bairGreater1)))
```

```
##
##              FALSE      TRUE       Sum
##   FALSE 0.5588235 0.0000000 0.5588235
##   TRUE  0.2647059 0.1764706 0.4411765
##   Sum   0.8235294 0.1764706 1.0000000
```

```
addmargins(prop.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 1))
```

```
##
##         FALSE TRUE Sum
##   FALSE   1.0  0.0 1.0
##   TRUE    0.6  0.4 1.0
##   Sum     1.6  0.4 2.0
```

```
addmargins(prop.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 2))
```

```
##
##              FALSE      TRUE       Sum
##   FALSE 0.6785714 0.0000000 0.6785714
##   TRUE  0.3214286 1.0000000 1.3214286
##   Sum   1.0000000 1.0000000 2.0000000
```

```
addmargins(prop.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 1), margin = 2)
```

```
##
##         FALSE TRUE Sum
##   FALSE   1.0  0.0 1.0
##   TRUE    0.6  0.4 1.0
```

```
addmargins(prop.table(table(tmp$elevGreater1000, tmp$bairGreater1), margin = 2), margin = 1)
```

```
##
##              FALSE      TRUE
##   FALSE 0.6785714 0.0000000
##   TRUE  0.3214286 1.0000000
##   Sum   1.0000000 1.0000000
```

2.2.4 Applied example

```
## Session 03:
overlap_seq <- function(x, delta) {
  tmp <- x %/% delta
  tmp2 <- x %% delta
  if (tmp2[which.max(x)] == 0) {
    result <- delta * (min(tmp, na.rm = T):max(tmp, na.rm = T))
  } else {
    result <- delta * (min(tmp, na.rm = T):(max(tmp, na.rm = T) + 1))
  }
  return(result)
}
tmp$elevCut <- cut(drought$elev, breaks = overlap_seq(x = drought$elev, delta = 250), dig.lab = 4)
tmp$bairCut <- cut(drought$bair, breaks = overlap_seq(x = drought$bair, delta = .25))
(xtab <- xtabs(~ elevCut + bairCut + species, data = tmp))
```

```
## , , species = Beech
##
##              bairCut
## elevCut       (0.25,0.5] (0.5,0.75] (0.75,1] (1,1.25] (1.25,1.5]
##   (250,500]            0          2        0        0          0
##   (500,750]            1          1        1        0          0
##   (750,1000]           0          0        2        0          0
##   (1000,1250]          0          1        1        2          0
##   (1250,1500]          0          0        0        0          0
##   (1500,1750]          0          0        0        0          0
##
## , , species = Spruce
##
##              bairCut
## elevCut       (0.25,0.5] (0.5,0.75] (0.75,1] (1,1.25] (1.25,1.5]
##   (250,500]            0          3        0        0          0
##   (500,750]            4          1        1        0          0
##   (750,1000]           1          1        1        0          0
##   (1000,1250]          1          2        2        1          1
##   (1250,1500]          0          0        1        2          0
##   (1500,1750]          0          0        1        0          0
```

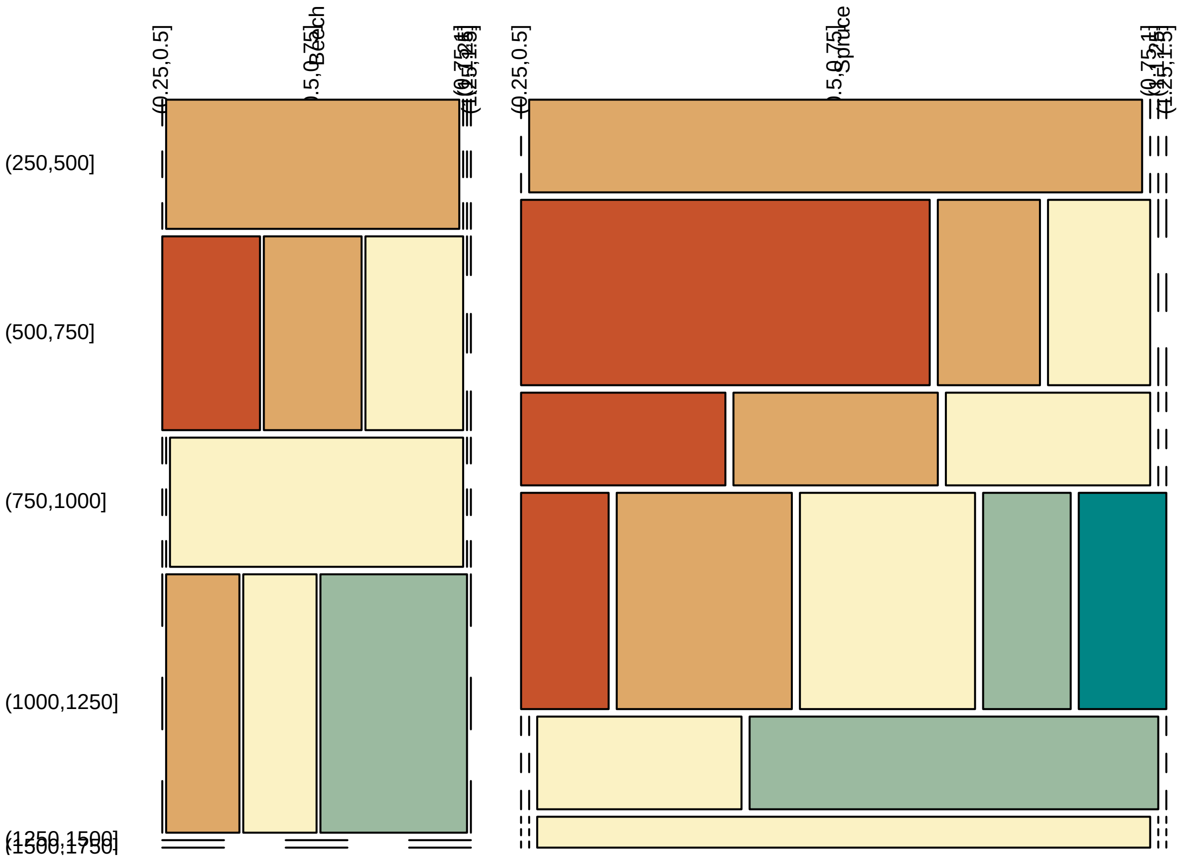
```
round(100 * addmargins(prop.table(xtab, margin = c(1, 3))), 2)[, , "Beech"]
```

```
##              bairCut
## elevCut       (0.25,0.5] (0.5,0.75] (0.75,1] (1,1.25] (1.25,1.5]    Sum
##   (250,500]         0.00     100.00     0.00     0.00       0.00 100.00
##   (500,750]        33.33      33.33    33.33     0.00       0.00 100.00
##   (750,1000]        0.00       0.00   100.00     0.00       0.00 100.00
##   (1000,1250]       0.00      25.00    25.00    50.00       0.00 100.00
##   (1250,1500]
##   (1500,1750]
##   Sum
```

```
round(100 * addmargins(prop.table(xtab, margin = c(1, 3))), 2)[, , "Spruce"]
```

```
##              bairCut
## elevCut       (0.25,0.5] (0.5,0.75] (0.75,1] (1,1.25] (1.25,1.5]    Sum
##   (250,500]         0.00     100.00     0.00     0.00       0.00 100.00
##   (500,750]        66.67      16.67    16.67     0.00       0.00 100.00
##   (750,1000]       33.33      33.33    33.33     0.00       0.00 100.00
##   (1000,1250]      14.29      28.57    28.57    14.29      14.29 100.00
##   (1250,1500]       0.00       0.00    33.33    66.67       0.00 100.00
##   (1500,1750]       0.00       0.00   100.00     0.00       0.00 100.00
##   Sum             114.29     178.57   211.90    80.95      14.29 600.00
```

```
par(mfrow = c(1, 1), mar = c(0, 0, 0, 0) + .1)
plot(xtabs(~ species + elevCut + bairCut, data = tmp), las = 2, off = 5, main = "",
     col = colorspace::divergingx_hcl(n = length(levels(tmp$bairCut)), rev = T))
```



2.2.5 Mode

```
(xtab <- xtabs(~ species + elevCut + bairCut, data = tmp))
sort(xtab, decreasing = TRUE)[1]
which(xtab == max(xtab), arr.ind = TRUE)
xtab[2, 2, 1]
```

3 Bivariate samples

A bivariate sample is a set of observation units, for which each has two characteristics that have been measured.

```
A <- matrix(nrow = 5, ncol = 5, data = runif(25))
A[, 1:2]
```

```
##              [,1]      [,2]
## [1,] 0.1396081 0.3325211
## [2,] 0.3202437 0.4279907
## [3,] 0.0514994 0.7383844
## [4,] 0.4064086 0.4589070
## [5,] 0.7010141 0.5211673
```

```
pmax(A[, 1], A[, 2])
```

```
## [1] 0.3325211 0.4279907 0.7383844 0.4589070 0.7010141
```

- cor for correlation coefficient,
- cov for (variance) covariance (matrix).

```
x <- drought$bair
y <- drought$elev/1000
cor(x, y, method = "pearson")
```

```
## [1] 0.6174439
```

```
cov(cbind(x, y))
```

```
##            x          y
## x 0.07508039 0.05579038
## y 0.05579038 0.10874194
```

```
c(cov(x, y), var(x), var(y))
```

```
## [1] 0.05579038 0.07508039 0.10874194
```

4 Probability distribution models

4.1 Definitions for continuous random variables:

- Random variable $X \in \mathbf{R}$ follows distribution F with density $f(x) \geq 0 \forall x \in \mathbf{R}$
- Cumulative density function $F(x) = \int\limits_{-\infty}^{x} f(z)\mathrm{d}z$, with $F(-\infty) = 0$ and $F(\infty) = 1$.
- Quantile function $Q(x) = F^{-1}(x)$

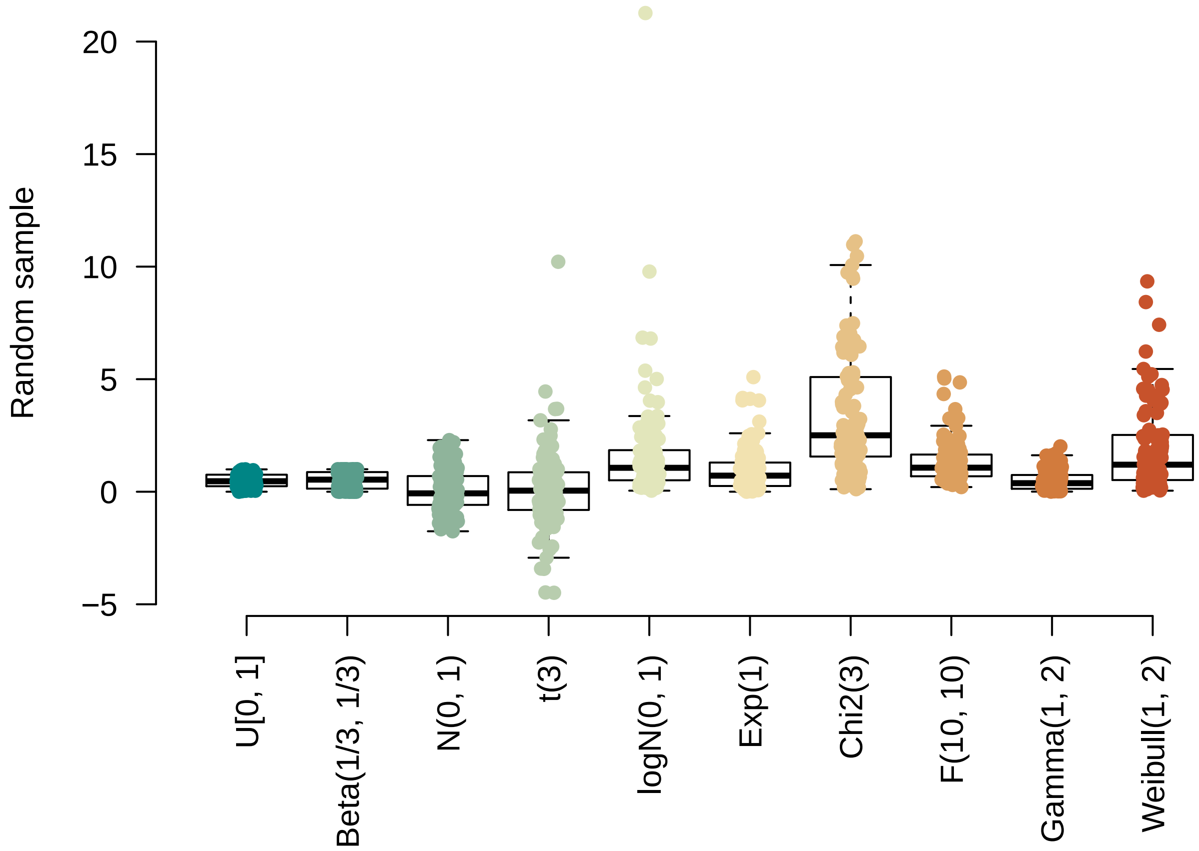
Implementation in R: code + distribution abbreviation

Code	meaning
d	density
p	cdf (probability)
q	quantile
r	random number generation

4.2 Distribution models for continuous random variables:

Distribution	Abbreviation	Parameter	Wiki
Continuous uniform	unif	min, max	Link
Normal (aka. Gaussian)	norm	mean, sd	Link
Lognormal	lnorm	meanlog, sdlog	Link
Exponential	exp	rate	Link
Beta	beta	shape1, shape2	Link
Chi-squared	chisq	df, ncp	Link
F	f	df1, df2, ncp	Link
Student-t	t	df, ncp	Link
Gamma	gamma	shape, rate, scale = 1/rate	Link
Weibull	weibull	shape, scale	Link

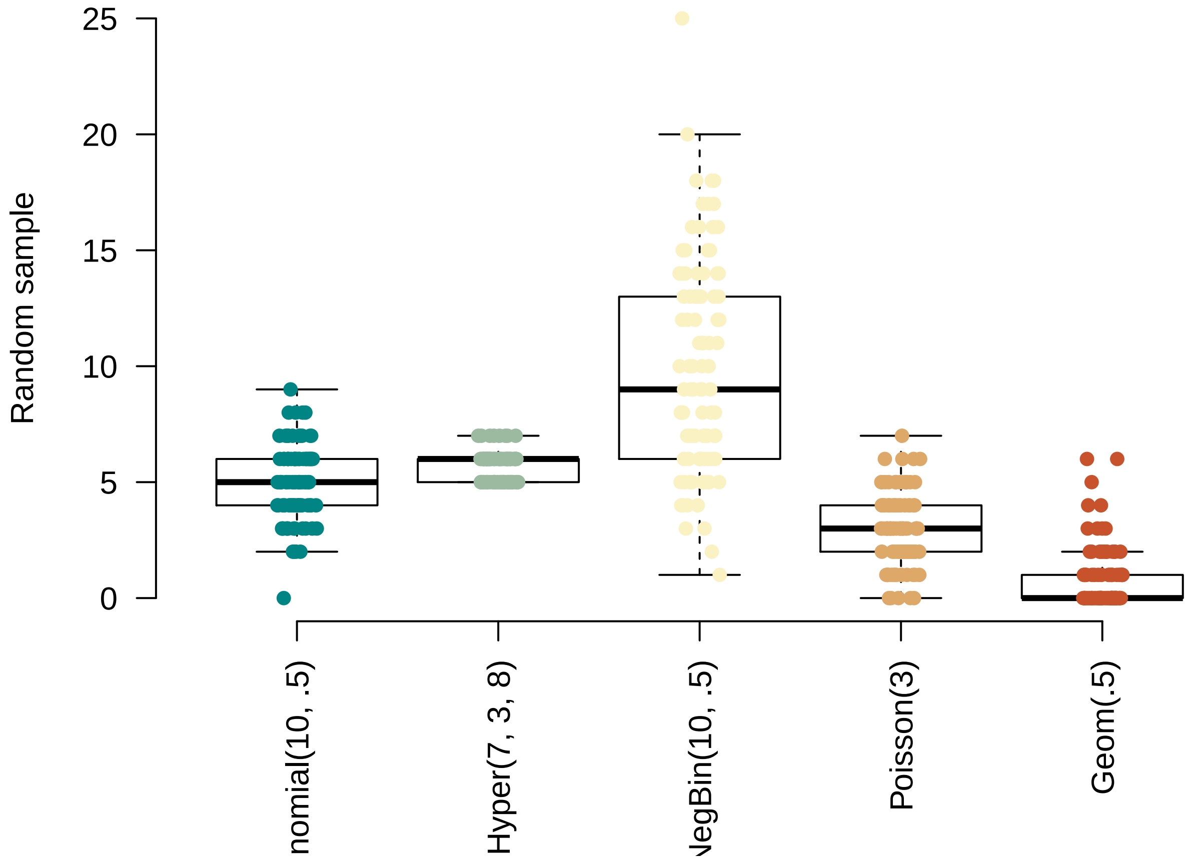
```
N <- 100
set.seed(123)
A <- cbind("U[0, 1]" = runif(n = N, min = 0, max = 1),
           "Beta(1/3, 1/3)" = rbeta(n = N, shape1 = 1/3, shape2 = 1/3),
           "N(0, 1)" = rnorm(n = N, mean = 0, sd = 1),
           "t(3)" = rt(n = N, df = 3, ncp = 0),
           "logN(0, 1)" = rlnorm(n = N, meanlog = 0, sdlog = 1),
           "Exp(1)" = rexp(n = N, rate = 1),
           "Chi2(3)" = rchisq(n = N, df = 3, ncp = 0),
           "F(10, 10)" = rf(n = N, df1 = 10, df2 = 10, ncp = 0),
           "Gamma(1, 2)" = rgamma(n = N, shape = 1, rate = 2),
           "Weibull(1, 2)" = rweibull(n = N, shape = 1, scale = 2))
par(mar = c(6, 4, 0, 0) + .1)
boxplot(A, las = 2, frame = F, pch = NA, ylab = "Random sample")
stripchart(as.data.frame(A), add = T, method = "jitter", vertical = T, pch = 16,
           col = colorspace::divergingx_hcl(n = ncol(A)))
```



4.3 Distribution models for discrete random variables:

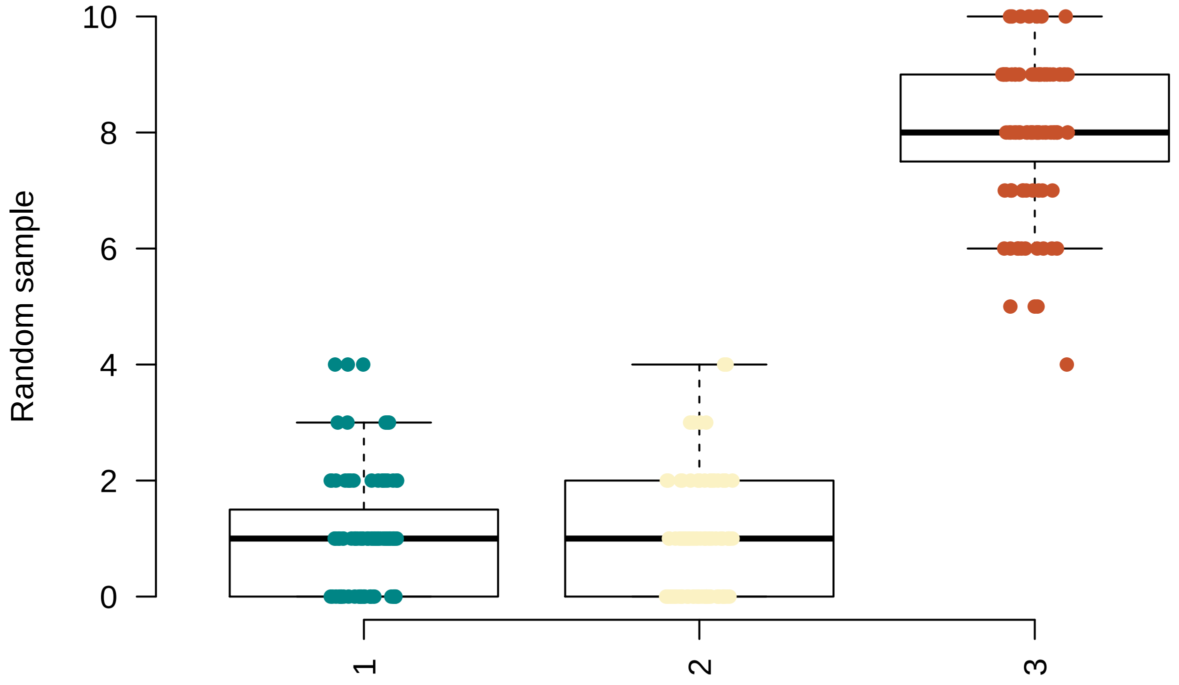
Distribution	Abbreviation	Parameters	Wiki
Binomial	binom	size, prob	Link
Hypergeometric	hyper	m, n,k	Link
Negative binomial	nbinom	size, prob,mu	Link
Poisson	pois	lambda	Link
Geometric	geom	prob	Link
Multinomial	multinom	size, prob	Link

```
N <- 100
set.seed(123)
A <- cbind("Binomial(10, .5)" = rbinom(n = N, size = 10, prob = .5),
           "Hyper(7, 3, 8)" = rhyper(nn = N, m = 7, n = 3, k = 8),
           "NegBin(10, .5)" = rnbinom(n = N, size = 10, prob = .5),
           "Poisson(3)" = rpois(n = N, lambda = 3),
           "Geom(.5)" = rgeom(n = N, prob = .5))
par(mar = c(6, 4, 0, 0) + .1)
boxplot(A, las = 2, frame = F, pch = NA, ylab = "Random sample")
stripchart(as.data.frame(A), add = T, method = "jitter", vertical = T, pch = 16,
           col = colorspace::divergingx_hcl(n = ncol(A)))
```



Multinomial:

```
A <- rmultinom(n = N, size = 10, prob = c(.1, .1, .8))
par(mar = c(6, 4, 0, 0) + .1)
boxplot(t(A), las = 2, frame = F, pch = NA, ylab = "Random sample")
stripchart(as.data.frame(t(A)), add = T, method = "jitter", vertical = T, pch = 16,
        col = colorspace::divergingx_hcl(n = ncol(t(A))))
```



5 Generating 'random' numbers

- Random numbers are generated in R by an algorithm, they are not real random – whatever this is . . .
- Before a new random number is generated, this algorithm is in a certain state.
- The (next) random number depends on this state, drawing this new number alters the state.
- `RNGkind()` lists three character strings for three tasks:
  - `kind` is for draws from the continuous uniform distribution.
  - `normal.kind` is for draws from the normal distribution (I don't know why there's this specific kind for the normal, I suppose as the normal distribution is historically so important, there have been algorithms specifically designed for drawing from this distribution . . .).
  - `sample.kind` for drawing from the diccrete uniform distribution.
- Why we won't have a look on the other algorithms, seeing the idea behind `Inversion` sampling is really helpful in order to see why being able to generate draws from continuous uniform distribution is already sufficient in order to sample from any other distribution.
- Reproducibility is often an important property!
  - The state of the random number generating algorithm is initialized by a seed.
  - Seeds are generated by system time and session ID (`?RNG`)

```
Sys.getpid()
```

```
## [1] 12066
```

```
(t1 <- Sys.time())
```

```
## [1] "2021-11-02 12:36:44 CET"
```

```
(t2 <- Sys.time())
```

```
## [1] "2021-11-02 12:36:44 CET"
```

```
t2 - t1
```

```
## Time difference of 0.00297308 secs
```

- We can overwrite thus seed generating by using `set.seed()`:

```
runif(5)
```

```
## [1] 0.6229466 0.2511743 0.4641535 0.1655092 0.8578065
```

```
set.seed(123)
runif(5)
```

```
## [1] 0.2875775 0.7883051 0.4089769 0.8830174 0.9404673
```

```
runif(5)
```

```
## [1] 0.0455565 0.5281055 0.8924190 0.5514350 0.4566147
```

```
set.seed(123)
runif(5)
```

```
## [1] 0.2875775 0.7883051 0.4089769 0.8830174 0.9404673
```

- Generate random numbers using `r` + distribution abbreviation (uses inversion - sampling)
- Random numbers from sets with `sample (c (), size, replace = TRUE)`.

```
RNGkind()
```

```
## [1] "Mersenne-Twister" "Inversion"        "Rejection"
```

```
set.seed(1604)
rbinom(5,1,0.5)
```

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

```
rbinom(5,1,0.5)
```

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

```
set.seed(1604)
rbinom(5,1,0.5)
```

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

```
sample(1:10, 5)
```

```
## [1] 5 4 1 6 2
```

```
sample(1:10, 5, replace = TRUE)
```

```
## [1] 10  5  4  5  4
```

5.1 Inversion-sampling

Inversion sampling is a rather simple application of a mathemcatical thing – the inverse of the cumulative distribution function – that one easily brands as 'interesting only in mathematical theory', but which has an incredibly applied value!

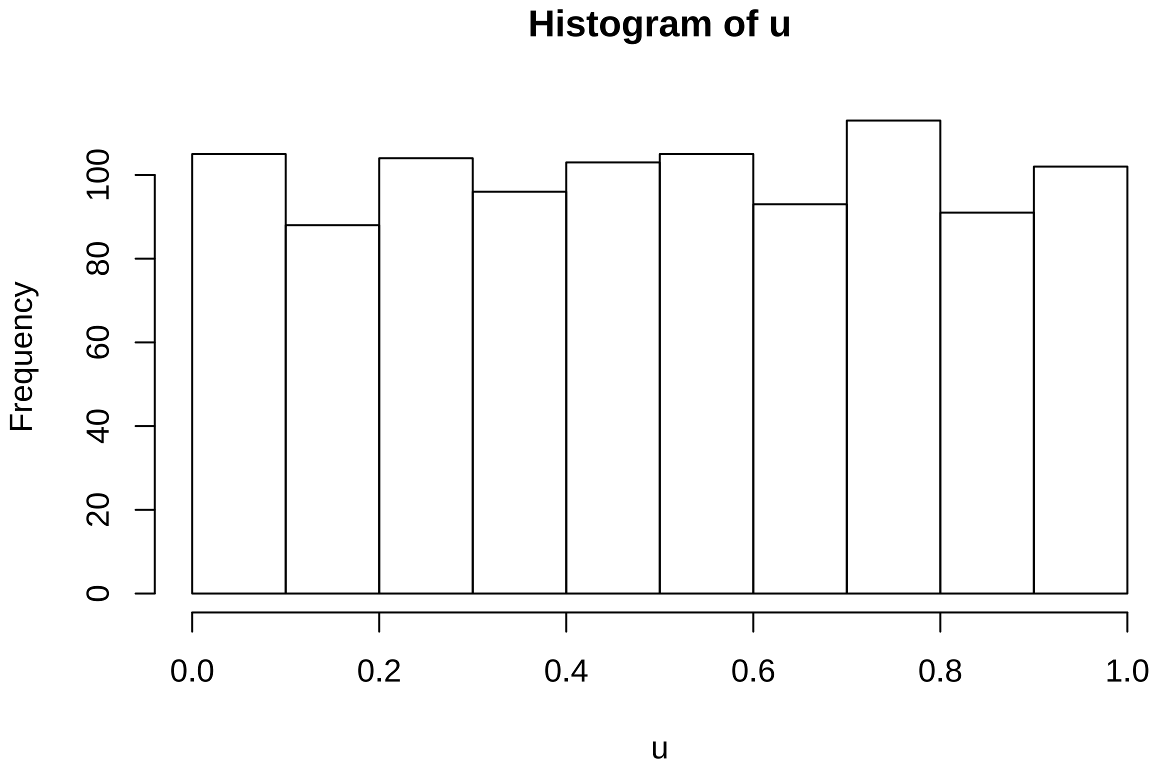
Let random variable X have cumulative distribution function F.

Let's assume for the moment we can draw random numbers from this distribution, eg. from the standard normal:

```
x <- rnorm(1000)
```

If we plug these into the cumulative distribution function

```
u <- pnorm(x)
hist(u)
```



we obviously get random draws from the continuous uniform distribution $U[0,1]$, ie. $F(X) \sim \mathrm{U}(0,1)$.

Now all we need to do is to solve this equation:

$$F(X) = Z, Z \sim U[0,1]$$

with respect to X:

$$X = F^{-1}(Z), Z \sim U[0,1]$$

For application this means that as long as we can draw from a continuous uniform distribution, and as long as we can write down F^{-1}, we can generate random draws for X.

Inversion sampling:

- generate numbers $u_1, \dots, u_n$ from the continuous uniform distribution $U[0, 1]$
- transform $x_k = F^{-1}(u_k)$

In R, $F^{-1}(u_k)$ is given as q....

```
u <- runif(5)
qnorm(p = u)
```

```
## [1] -1.9728444 -1.2169369 -2.2157531 -0.8150545  2.4262442
```

```
qweibull(p = u, shape = 1, scale = 1)
```

```
## [1] 0.02455568 0.11857422 0.01344418 0.23258871 4.87592939
```

```
qbinom(p = u, size = 10, prob = .5)
```

```
## [1] 2 3 2 4 9
```

6 Case study

6.1 Let's invent a data generating machanism

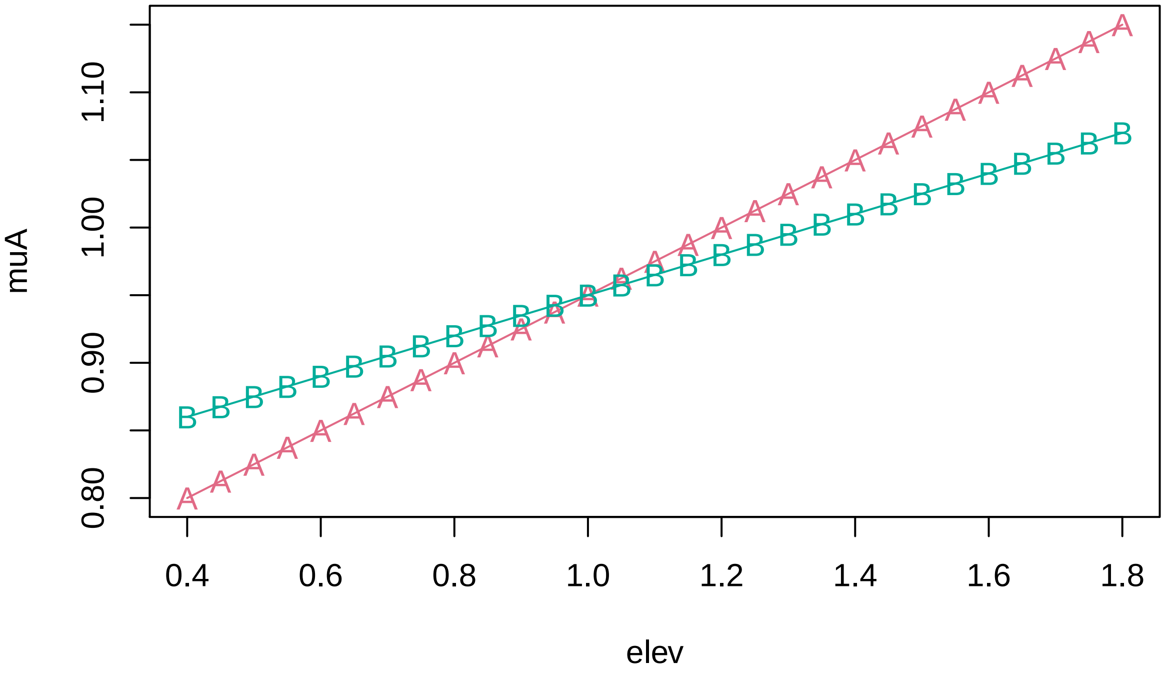
Because of a drought in one year, trees grow less in this year in comparison to the preceding year. However, by differences in the availability to growth-ressources by different elevations at the same mountain range, this reduction is reversed above a certain elevation threshold.

```
(elev <- seq(400, 1800, by = 50) / 1000)
```

```
##  [1] 0.40 0.45 0.50 0.55 0.60 0.65 0.70 0.75 0.80 0.85 0.90 0.95 1.00 1.05 1.10
## [16] 1.15 1.20 1.25 1.30 1.35 1.40 1.45 1.50 1.55 1.60 1.65 1.70 1.75 1.80
```

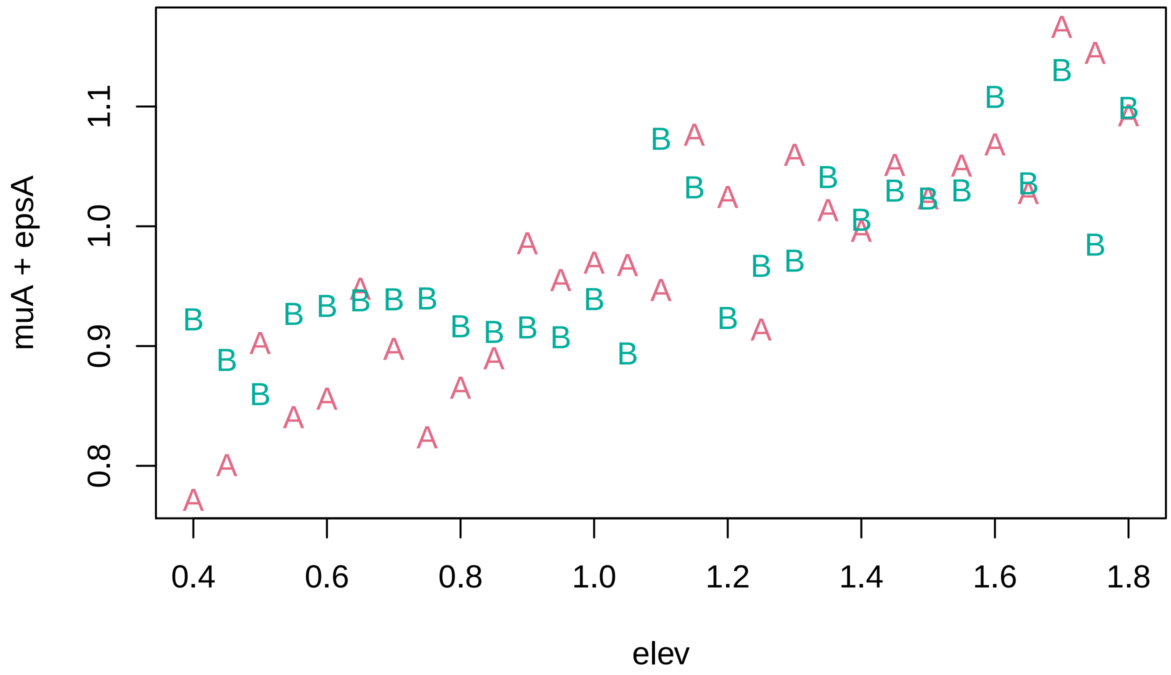
For species A and B:

```
muA <- .7 + .25 * elev
muB <- .8 + .15 * elev
paint <- colorspace::qualitative_hcl(n = 2)
plot(elev, muA, type = "o", pch = "A", col = paint[1])
lines(elev, muB, type = "o", pch = "B", col = paint[2])
```



Random variation in site-specific availability to growth-ressources:

```
set.seed(123)
epsA <- rnorm(length(muA), sd = .05)
epsB <- rnorm(length(muB), sd = .05)
plot(elev, muA + epsA, pch = "A", col = paint[1])
points(elev, muB + epsB, pch = "B", col = paint[2])
```



Compose outcome measurements y:

```
yA <- muA + epsA
yB <- muB + epsB
```

6.2 Introducing formula

formula notation for the data generating mechanism:

```
frmlaA <- as.formula(yA ~ elev)
str(frmlaA)
```

```
## Class 'formula'  language yA ~ elev
##   ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
```

```
summary(frmlaA)
```

```
##  Length   Class    Mode
##       3 formula    call
```

```
frmlaA[1]
```

```
## `~`()
```

```
frmlaA[2]
```

```
## yA()
```

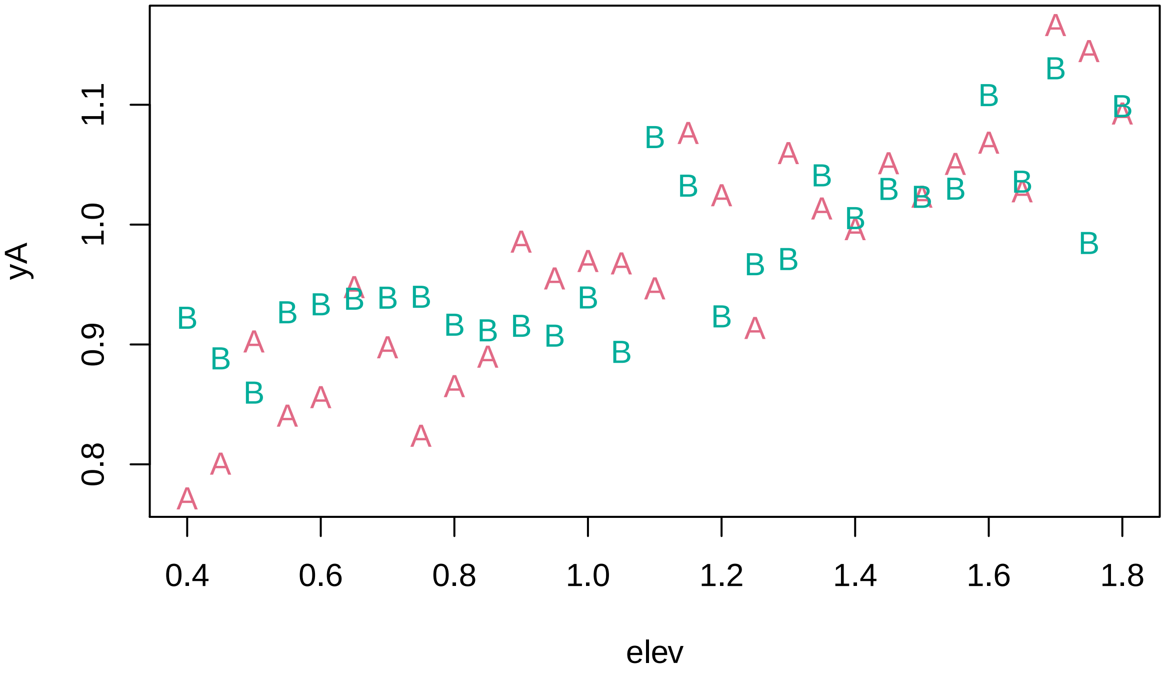
```
frmlaA[3]
```

```
## elev()
```

- yA and yB are measured outcomes, written on the left hand side of the formula
- The left hand side is separated from the right hand side by ~
- The right hand side expresses the explanatory variables that are either experimentally controlled, or – similar to the outcome – observed / measured. In our formula examples, elev is the only explanatory variable.
- The parameters used for generating the outcome, .7, .25 and .05 for A, and .8, .15 and .05 for B, are not stated in the formula. Why? . . . because in real world applications, we don't artificially invent, but rather want to estimate their plausible values based on our data.
- Let's assume it comes to our mind that a normal distribution is a statistical model that is quite useful to express the effects of variation in site-specific availability to growth-ressources on the outcome. Then:

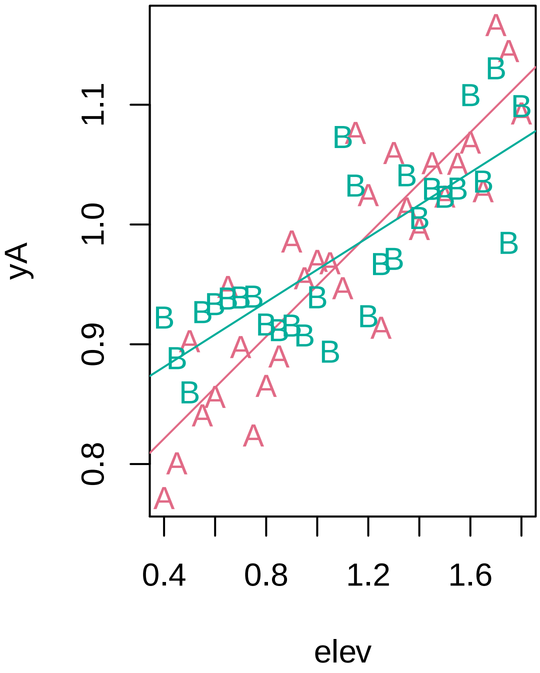
We can use a formula directly for plot:

```
frmlaB <- as.formula(yB ~ elev)
plot(frmlaA, pch = "A", col = paint[1])
points(frmlaB, pch = "B", col = paint[2])
```



6.2.1 Using formula inside lm

```
mA <- lm(frmlaA)
mB <- lm(frmlaB)
par(mfrow = c(1, 2))
plot(frmlaA, pch = "A", col = paint[1])
abline(mA, col = paint[1])
points(frmlaB, pch = "B", col = paint[2])
abline(mB, col = paint[2])
```



The data-generating mechanisms varied for varying species A, and B. Can we unify this into one description of a data-generating mechanism?

$yA = 0.7 + 0.25 \cdot \text{elev} + \texttt{rnorm(n=1, mu = 0, sd = .05)} yB = 0.8 + 0.15 \cdot \text{elev} + \texttt{rnorm(n=1, mu = 0, sd = .05)} \rightarrow y = 0.7$

```
dfsim <- data.frame(y = c(yA, yB),
                    elev = c(elev, elev),
                    species = rep(LETTERS[1:2], each = length(elev)))
dfsim$x <- dfsim$elev
## See: ?formula
frmla <- as.formula(y ~ x * species)
summary(frmla)
```

```
##  Length   Class    Mode
##       3 formula    call
```

```
head(model.matrix(object = frmla, data = subset(dfsim, species == "A")))
```

```
##   (Intercept)    x speciesB x:speciesB
## 1           1 0.40        0          0
## 2           1 0.45        0          0
## 3           1 0.50        0          0
## 4           1 0.55        0          0
## 5           1 0.60        0          0
## 6           1 0.65        0          0
```

```
head(model.matrix(object = frmla, data = subset(dfsim, species == "B")))
```

```
##    (Intercept)    x speciesB x:speciesB
## 30           1 0.40        1       0.40
## 31           1 0.45        1       0.45
## 32           1 0.50        1       0.50
## 33           1 0.55        1       0.55
## 34           1 0.60        1       0.60
## 35           1 0.65        1       0.65
```

```
m <- lm(frmla, data = dfsim)
coef(m)
```

```
## (Intercept)           x    speciesB  x:speciesB
##  0.73593782  0.21314912  0.09105386 -0.07786856
```

6.3 Inspection of estimated parameters

```
library("arm")
```

```
## Loading required package: MASS
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:spatstat':
##
##     area
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'
```

```
## The following object is masked from 'package:lmfor':
##
##     updown
```

```
## Loading required package: lme4
```

```
##
## Attaching package: 'lme4'
## The following object is masked from 'package:nlme':
##
##     lmList
```

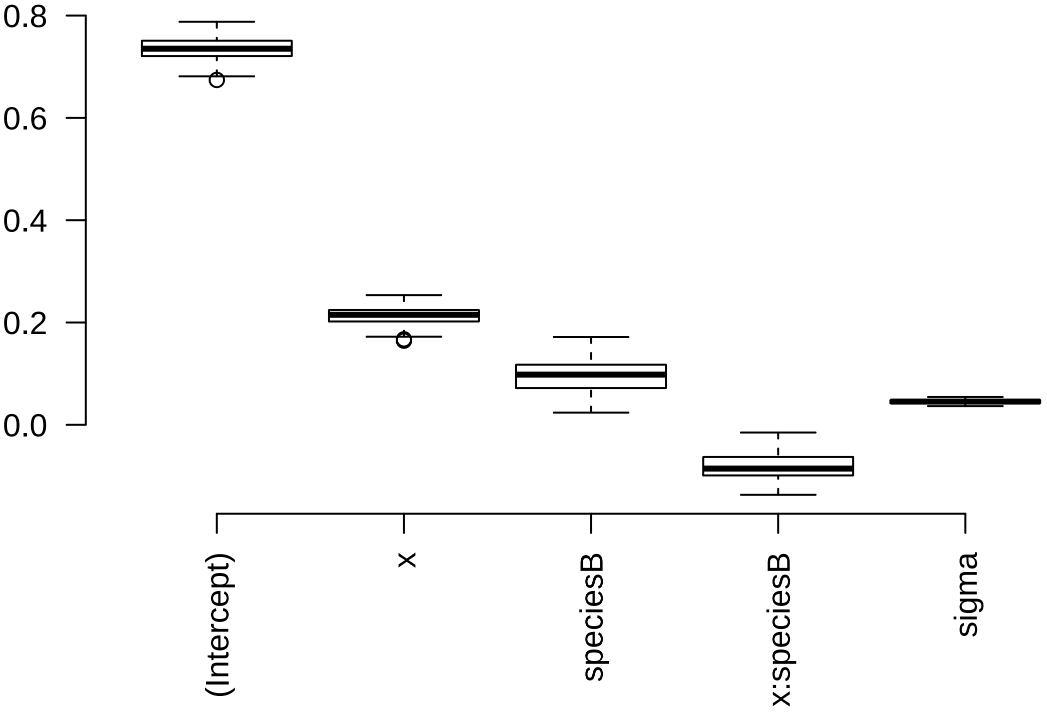
```
##
## arm (Version 1.11-1, built: 2020-4-27)
```

```
## Working directory is /home/hsennhenn/Dropbox/01_oer/00_introduction_to_R
```

```
##
## Attaching package: 'arm'
```

```
## The following object is masked from 'package:spatstat':
##
##     rescale
```

```
tmp <- sim(m)
B <- cbind(tmp@coef, tmp@sigma)
colnames(B)[ncol(B)] <- "sigma"
boxplot(B, frame = F, las = 2)
```



```
B[1, ]
```

```
## (Intercept)           x    speciesB  x:speciesB       sigma
##  0.73646218  0.21452618  0.07840359 -0.07300474  0.04516890
```

6.4 Predictive check

For only one data-point:

```
elev <- 1300 / 1000
species <- factor(c("A"), levels = levels(dfsim$species))
X <- model.matrix(frmla[-2], data = data.frame(x = elev, species = species))
X %*% B[1, -ncol(B)]
```

```
##       [,1]
## 1 1.015346
```

```
rnorm(n = 100, mean = X %*% B[1, -ncol(B)], sd = B[1, ncol(B)])
```

```
##   [1] 0.9899480 1.1019713 1.0041147 1.0777084 1.0207939 1.0035805 1.0309227
##   [8] 0.9790030 1.0654185 0.9655213 1.0515324 1.0261213 1.0216022 1.0481515
##  [15] 0.9765463 0.9598976 1.0021634 1.0701242 1.0414169 1.1183507 0.9699917
##  [22] 1.0201318 1.1534332 1.0162380 1.0556141 1.0537146 1.0881090 1.0178440
##  [29] 1.0697926 0.9364685 0.9813849 1.0188523 0.9886918 1.0254739 0.9378543
##  [36] 1.0395219 0.9930987 0.9944408 1.0085548 0.9889237 0.9373617 1.0426293
##  [43] 1.0165602 0.8777181 1.0653720 0.9841040 1.0241862 1.0285470 0.9678332
##  [50] 0.9471550 1.0845774 1.1022373 1.0423772 1.0228742 1.0215433 1.0295161
##  [57] 1.0029881 1.0627028 1.0466847 0.9884676 1.0209400 1.0170410 1.0183230
##  [64] 1.0617957 0.9920905 1.0434989 1.0232035 1.0137752 1.0596489 1.0216063
##  [71] 0.9658334 0.9573625 0.9998750 0.9829873 0.9593663 0.9856021 0.9328536
##  [78] 0.9964383 0.9988052 1.0020665 1.0143018 1.0317154 0.9942652 1.0288297
##  [85] 0.9723134 1.0454983 1.0192867 1.0104133 0.9847446 1.0920802 1.0327738
##  [92] 1.0264920 0.8984973 0.9266750 1.0125771 1.0557838 1.0140788 0.9701887
##  [99] 1.0081371 0.9915109
```

For the full data-frame:

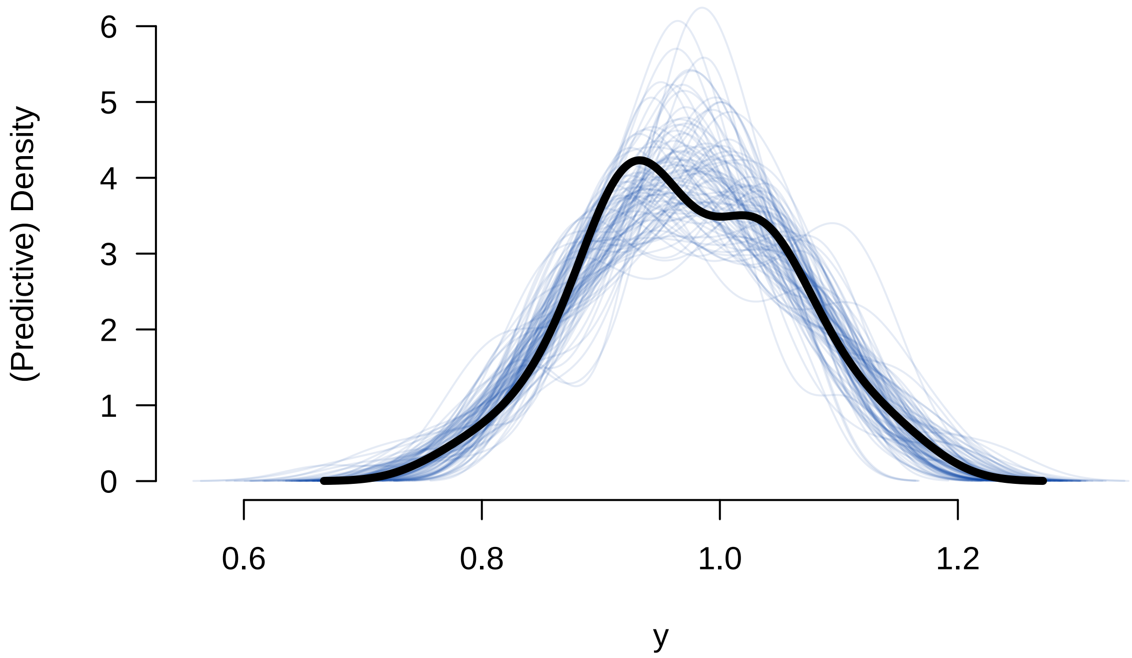
```
X <- model.matrix(frmla[-2], data = dfsim)
head(X %*% B[1, -ncol(B)])
```

```
##        [,1]
## 1 0.8222726
## 2 0.8329990
## 3 0.8437253
## 4 0.8544516
## 5 0.8651779
## 6 0.8759042
```

```
dim(X %*% B[1, -ncol(B)])
```

```
## [1] 58  1
```

```
Ytilde <- matrix(nrow = nrow(B), ncol = nrow(dfsim), NA)
for (s in 1:nrow(B)) {
  tmp <- X %*% B[s, -ncol(B)]
  for (i in 1:nrow(dfsim)) {
    Ytilde[s, i] <- rnorm(n = 1, mean = tmp[i, 1], sd = B[s, ncol(B)])
  }
}
tmp <- apply(Ytilde, MAR = 1, FUN = density)
plot(0, 0, ylim = c(0, max(sapply(tmp, FUN = function(x){return(max(x$y))}))),
     xlim = c(min(sapply(tmp, FUN = function(x){return(min(x$x))})),
              max(sapply(tmp, FUN = function(x){return(max(x$x))}))),
     type = "n", bty = "n", las = 1, xlab = "y", ylab = "(Predictive) Density")
invisible(sapply(tmp, FUN = lines, col = colorspace::sequential_hcl(n = 1, alpha = .1)))
lines(density(dfsim$y), lwd = 4)
```

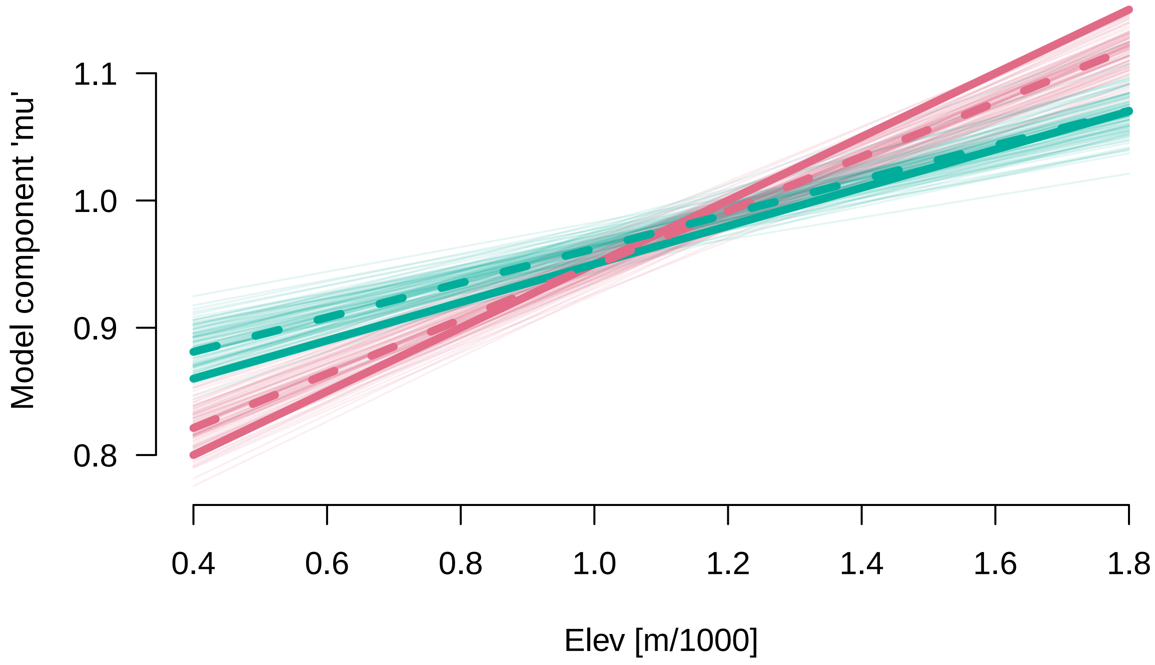


6.5 Model component mu

```
elev <- rep(c(400, 1800), 2) / 1000
species <- factor(rep(LETTERS[1:2], each = 2), levels = levels(dfsim$species))
(X <- model.matrix(frmla[-2], data = data.frame(x = elev, species = species)))
```

```
##   (Intercept)   x speciesB x:speciesB
## 1           1 0.4        0        0.0
## 2           1 1.8        0        0.0
## 3           1 0.4        1        0.4
## 4           1 1.8        1        1.8
## attr(,"assign")
## [1] 0 1 2 3
## attr(,"contrasts")
## attr(,"contrasts")$species
## [1] "contr.treatment"
```

```
Mu <- matrix(nrow = nrow(B), ncol = nrow(X), NA)
for (s in 1:nrow(B)) {
  Mu[s, ] <- X %*% B[s, -ncol(B)]
}
paint <- colorspace::qualitative_hcl(n = 2, alpha = .1)
plot(range(elev), range(Mu), type = "n", las = 1, xlab = "Elev [m/1000]",
     ylab = "Model component 'mu'", bty = "n")
for (s in 1:nrow(Mu)) {
  lines(range(elev), Mu[s, 1:2], col = paint[1])
  lines(range(elev), Mu[s, 3:4], col = paint[2])
}
lines(range(elev), .7 + .25 * range(elev), col = colorspace::qualitative_hcl(n = 2)[1], lwd = 4)
lines(range(elev), .8 + .15 * range(elev), col = colorspace::qualitative_hcl(n = 2)[2], lwd = 4)
lines(range(elev), coef(m)[1] + coef(m)[2] * range(elev), col = colorspace::qualitative_hcl(n = 2)[1
lines(range(elev), coef(m)[1] + coef(m)[3] + (coef(m)[2] + coef(m)[4]) * range(elev),
      col = colorspace::qualitative_hcl(n = 2)[2], lwd = 4, lty = 2)
```



6.6 Real data

```
drought$x <- drought$elev / 1000
drought$y <- drought$bair
m <- lm(frmla, data = drought)
tmp <- sim(m)
B <- cbind(tmp@coef, tmp@sigma)
```

6.6.1 Predictive check

```
X <- model.matrix(frmla[-2], data = drought)
head(X %*% B[1, -ncol(B)])
```

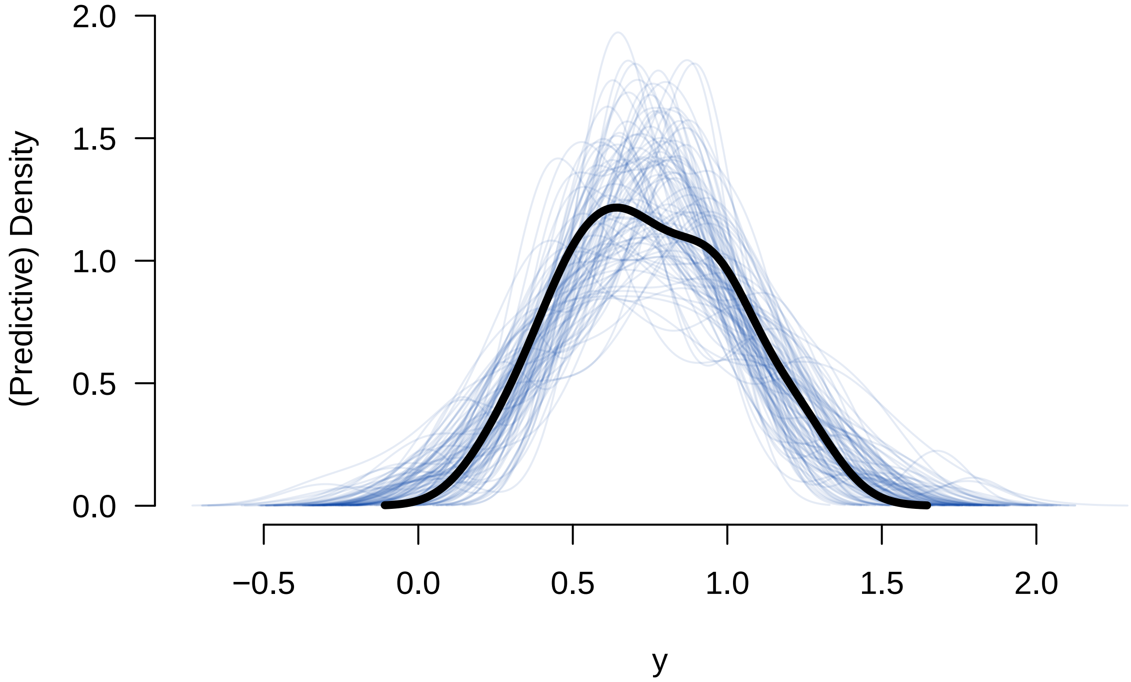
```
##        [,1]
## 1 0.3949298
## 2 0.4520939
## 3 0.4612401
## 4 0.4772460
## 5 0.4886789
## 6 0.5389832
```

```
dim(X %*% B[1, -ncol(B)])
```

```
## [1] 34  1
```

```
Ytilde <- matrix(nrow = nrow(B), ncol = nrow(drought), NA)
for (s in 1:nrow(B)) {
  tmp <- X %*% B[s, -ncol(B)]
  for (i in 1:nrow(drought)) {
    Ytilde[s, i] <- rnorm(n = 1, mean = tmp[i, 1], sd = B[s, ncol(B)])
  }
}
tmp <- apply(Ytilde, MAR = 1, FUN = density)
plot(0, 0, ylim = c(0, max(sapply(tmp, FUN = function(x){return(max(x$y))}))),
     xlim = c(min(sapply(tmp, FUN = function(x){return(min(x$x))})),
              max(sapply(tmp, FUN = function(x){return(max(x$x))}))),
     type = "n", bty = "n", las = 1, xlab = "y", ylab = "(Predictive) Density")
```

```
invisible(sapply(tmp, FUN = lines, col = colorspace::sequential_hcl(n = 1, alpha = .1)))
lines(density(drought$y), lwd = 4)
```

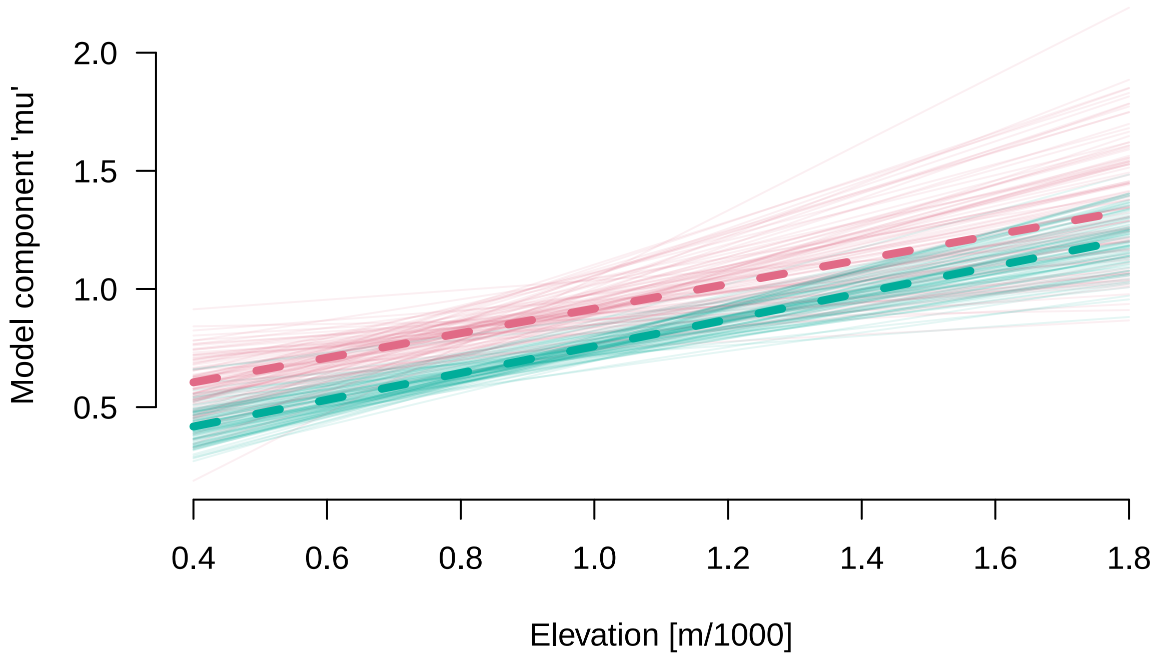


6.6.2 Model component `mu`

```
elev <- rep(c(400, 1800), 2) / 1000
species <- factor(rep(levels(drought$species), each = 2), levels = levels(drought$species))
(X <- model.matrix(frmla[-2], data = data.frame(x = elev, species = species)))
```

```
##   (Intercept)   x speciesSpruce x:speciesSpruce
## 1           1 0.4             0             0.0
## 2           1 1.8             0             0.0
## 3           1 0.4             1             0.4
## 4           1 1.8             1             1.8
## attr(,"assign")
## [1] 0 1 2 3
## attr(,"contrasts")
## attr(,"contrasts")$species
## [1] "contr.treatment"
```

```
Mu <- matrix(nrow = nrow(B), ncol = nrow(X), NA)
for (s in 1:nrow(B)) {
  Mu[s, ] <- X %*% B[s, -ncol(B)]
}
paint <- colorspace::qualitative_hcl(n = 2, alpha = .1)
plot(range(elev), range(Mu), type = "n", las = 1, xlab = "Elevation [m/1000]",
     ylab = "Model component 'mu'", bty = "n")
for (s in 1:nrow(Mu)) {
  lines(range(elev), Mu[s, 1:2], col = paint[1])
  lines(range(elev), Mu[s, 3:4], col = paint[2])
}
lines(range(elev), coef(m)[1] + coef(m)[2] * range(elev), col = colorspace::qualitative_hcl(n = 2)[1]
lines(range(elev), coef(m)[1] + coef(m)[3] + (coef(m)[2] + coef(m)[4]) * range(elev),
      col = colorspace::qualitative_hcl(n = 2)[2], lwd = 4, lty = 2)
```


Model component 'mu'
0.5
1.0
1.5
2.0
0.4
0.6
0.8
1.0
1.2
1.4
1.6
1.8
Elevation [m/1000]