Applied Econometrics with 

Chapter 2

Basics

Basics

Overview

Basics

R at various levels:

- Standard arithmetic: R can be used as a (sophisticated) calculator.
- Graphical system: R can create graphics on many devices.
- Full-featured programming language.
- R connects to other languages, programs, and data bases, and also to the operating system.

In this chapter:

- Illustration of a few typical uses of R.
- Sophisticated shortcuts are avoided here.
- Often solutions are not unique.
  $\rightarrow$ Explore alternative solutions by reusing ideas.

Basics

R as a Calculator

R as a calculator

Standard arithmetic operators: `+`, `-`, `*`, `/`, and `^` are available, where `x^y` yields x^y.

```
R> 1 + 1
[1] 2
R> 2^3
[1] 8
```

Details: In the output, `[1]` indicates the position of the first element of the vector returned by R. (Not surprising here, where all vectors are of length `1`, but will be useful later.)

Mathematical functions: R has `log()`, `exp()`, `sin()`, `asin()`, `cos()`, `acos()`, `tan()`, `atan()`, `sign()`, `sqrt()`, `abs()`, `min()`, `max()`, `...`.

R as a calculator

```
R> log(exp(sin(pi/4)^2) * exp(cos(pi/4)^2))
[1] 1
```

Details:

- `log(x, base = a)` returns the logarithm of `x` to base `a`.
- `a` defaults to `exp(1)`.
- Convenience functions: `log10()` and `log2()`.
- See `?log` for a full list of all options and related functions.

Further functions: `gamma()`, `beta()`, and their logarithms and derivatives, are often useful in statistics and econometrics. See `?gamma` for further information.

Vector arithmetic

Basic unit: Vector. All functions above operate directly on vectors.

Generation of vectors: e.g., via `c()`, where `c` stands for "combine" or "concatenate".

```
R> x <- c(1.8, 3.14, 4, 88.169, 13)
R> length(x)
```

```
[1] 5
```

Case-sensitivity: `x` and `X` are distinct.

Assignment operators:

- `<-` (mimicking a single arrow symbol).
- `=` may also be used at the user level, but `<-` is preferred for programming.

Vector arithmetic

Use `x` in subsequent calculations:

```
R> 2 * x + 3
[1]   6.60   9.28  11.00 179.34  29.00
R> 5:1 * x + 1:5
[1]  10.00  14.56  15.00 180.34  18.00
R> log(x)
[1] 0.5878 1.1442 1.3863 4.4793 2.5649
```

Details:

- First statement: scalars 2 and 3 are recycled to the length of `x`.
- Second statement: `x` is multiplied element-wise by the vector `1:5` (the integers from 1 through 5; see below) and then the vector `5:1` is added element-wise.
- Third statement: Application of mathematical functions.

Subsetting vectors

Subsets of vectors: Operator `[` can be used in several ways.

```
R> x[c(1, 4)]
[1]  1.80 88.17
R> x[-c(2, 3, 5)]
[1]  1.80 88.17
```

Details:

- Extract elements by their index.
- Exclude elements with negative index.
- Further specifications are explained later in this chapter.

Patterned vectors

Vectors with special patterns are needed in statistics and econometrics. R provides several useful functions for this, including

```
R> ones <- rep(1, 10)
R> ones

 [1] 1 1 1 1 1 1 1 1 1 1

R> even <- seq(from = 2, to = 20, by = 2)
R> even

 [1]  2  4  6  8 10 12 14 16 18 20

R> c(ones, even)

 [1]  1  1  1  1  1  1  1  1  1  1  2  4  6  8 10 12 14 16 18 20

R> trend <- 1981:2005
R> trend

 [1] 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992
[13] 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004
[25] 2005
```

Basics

Matrix Operations

Matrix operations

Creation: A 2×3 matrix containing the elements `1:6`, by column, is generated via

```
R> A <- matrix(1:6, nrow = 2)
R> A
```

```
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
```

Alternatively: Use `nrow` instead of `ncol`.

```
R> matrix(1:6, ncol = 3)
```

```
     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6
```

Basic matrix algebra

Transpose $A^\top$ of A via

```
R> t(A)
```

```
     [,1] [,2]
[1,]    1    2
[2,]    3    4
[3,]    5    6
```

Dimensions: Access via `dim()`, `nrow()`, and `ncol()`.

```
R> dim(A)
```

```
[1] 2 3
```

```
R> nrow(A)
```

```
[1] 2
```

```
R> ncol(A)
```

```
[1] 3
```

Basic matrix algebra

Internally: Matrices are vectors with an additional dimension attribute enabling row/column-type indexing.

Indexing:

- `A[i,j]` extracts element a_{ij} of matrix A.
- `A[i,]` extracts ith row.
- `A[,j]` extracts jth column.
- Results of these operations are *vectors*, i.e., dimension attribute is dropped (by default).
- `A[i, j, drop = FALSE]` avoids dropping and returns a matrix.

Basic matrix algebra

Illustration:

```
R> A1 <- A[1:2, c(1, 3)]
R> A1
```

```
     [,1] [,2]
[1,]    1    5
[2,]    2    6
```

Equivalently:

```
R> A[, -2]
```

```
     [,1] [,2]
[1,]    1    5
[2,]    2    6
```

Basic matrix algebra

Nonsingularity: Check determinant or eigenvalues.

```
R> det(A1)

[1] -4

R> eigen(A1)

$values
[1]  7.5311 -0.5311

$vectors
        [,1]    [,2]
[1,] -0.6079 -0.9562
[2,] -0.7940  0.2928
```

Inverse: `solve()` (if direct computation cannot be avoided).

```
R> solve(A1)

     [,1]  [,2]
[1,] -1.5  1.25
[2,]  0.5 -0.25
```

Basic matrix algebra

Check: Using operator for matrix multiplication %*%.

```
R> A1 %*% solve(A1)
```

```
     [,1] [,2]
[1,]    1    0
[2,]    0    1
```

Further functionality:

- Adding and subtracting for conformable matrices via + and −.
- Recycling for non-conformable matrices proceeds along columns.
- Operator * returns the element-wise product.
- `kronecker()`: Kronecker product.
- `crossprod()`: Cross product $A^\top B$.
- `svd()`: Singular-value decomposition.
- `qr()`: QR decomposition.
- `chol()`: Cholesky decomposition.

Patterned matrices

Useful functions:

- `diag()`: Create diagonal matrix, or extract diagonal from matrix.
- `upper.tri()` and `lower.tri()`: query the positions of upper or lower triangular elements. Result is matrix of logicals.

```
R> diag(4)
     [,1] [,2] [,3] [,4]
[1,]    1    0    0    0
[2,]    0    1    0    0
[3,]    0    0    1    0
[4,]    0    0    0    1
R> diag(1:3)
     [,1] [,2] [,3]
[1,]    1    0    0
[2,]    0    2    0
[3,]    0    0    3
R> diag(A1)
[1] 1 6
```

Combining matrices

Combination: `cbind()` and `rbind()` combine matrices by columns or rows. If necessary, arguments are suitably recycled.

```
R> cbind(1, A1)
```

```
     [,1] [,2] [,3]
[1,]    1    1    5
[2,]    1    2    6
```

```
R> rbind(A1, diag(4, 2))
```

```
     [,1] [,2]
[1,]    1    5
[2,]    2    6
[3,]    4    0
[4,]    0    4
```

Basics

R as a Programming Language

R as a programming language

R:

- Full-featured, interpreted, object-oriented programming language.
- Designed for “programming with data” (Chambers 1998).
- In-depth treatment of programming in S/R: Venables and Ripley (2000).
- German introduction to programming with R: Ligges (2007).
- More technical: “Writing R Extensions” and “R Language Definition” manuals.

The mode of a vector

Basic data structure: Vector.

Mode: All elements of a vector must be of the same type; technically, they must be of the same "mode".

Examples: "`numeric`", "`logical`", and "`character`" (there are others).

```
R> x <- c(1.8, 3.14, 4, 88.169, 13)
R> mode(x)
```

```
[1] "numeric"
```

Logical vectors

Logical vectors: Contain the logical constants `TRUE` and `FALSE`.

Aliases: In a fresh session, the aliases `T` and `F` are available for compatibility with S (which uses these as the logical constants).

Recommendation: Always use `TRUE` and `FALSE` (because `T` and `F` can be changed and might have other values – e.g., sample size or F statistic).

Example: Result of comparisons.

```
R> x
[1]  1.80  3.14  4.00 88.17 13.00
R> x > 3.5
[1] FALSE FALSE  TRUE  TRUE  TRUE
```

Character vectors

Character vectors: For storing strings.

Typical basic usage: Assign labels or names to vectors, matrices, etc.

```
R> names(x) <- c("a", "b", "c", "d", "e")
R> x
```

```
    a     b     c     d     e
 1.80  3.14  4.00 88.17 13.00
```

Advanced character processing: Not much used here, but R has powerful character-manipulation facilities, e.g., for computations on text documents or command strings.

More on subsetting

Up to now: Only numeric indices have been introduced.

Character subsetting: Can be used if there is a `names` attribute.

Logical subsetting: Selects elements corresponding to `TRUE`.

```
R> x[3:5]

    c     d     e
 4.00 88.17 13.00

R> x[c("c", "d", "e")]

    c     d     e
 4.00 88.17 13.00

R> x[x > 3.5]

    c     d     e
 4.00 88.17 13.00
```

Subsetting of matrices and data frames etc. works similarly.

Lists

So far: We have only used plain vectors. Lists are related but more flexible data structures.

Lists: *Generic vectors*. Each element can be virtually any type of object.

- Vector (of arbitrary mode).
- Matrix.
- Full data frame.
- Function.
- List (again).
- ...

Due to this flexibility, lists are the basis for most complex objects in R; e.g., for data frames or fitted regression models (both described later).

Lists

Illustration: Using `list()`, create description of a sample from a standard normal distribution (generated with `rnorm()`; see below).

```
R> mylist <- list(sample = rnorm(5),
+    family = "normal distribution",
+    parameters = list(mean = 0, sd = 1))
R> mylist

$sample
[1]  0.3771 -0.9346  2.4302  1.3195  0.4503

$family
[1] "normal distribution"

$parameters
$parameters$mean
[1] 0

$parameters$sd
[1] 1
```

Lists

Select elements: Operators `$` or `[[` can be used. `[[` is similar to `[`, but can only select a single element.

```
R> mylist[[1]]
[1]  0.3771 -0.9346  2.4302  1.3195  0.4503
R> mylist[["sample"]]
[1]  0.3771 -0.9346  2.4302  1.3195  0.4503
R> mylist$sample
[1]  0.3771 -0.9346  2.4302  1.3195  0.4503
```

Combination of element selection:

```
R> mylist[[3]]$sd
[1] 1
```

Logical comparisons

Logical operators: <, <=, >, >=, == (for exact equality) and != (for "not equal").

If `expr1` and `expr2` are logical expressions,

- `expr1 & expr2` is their intersection (logical "and"),
- `expr1 | expr2` is their union (logical "or"), and
- `!expr1` is the negation of `expr1`.

```
R> x <- c(1.8, 3.14, 4, 88.169, 13)
R> x > 3 & x <= 4
```

```
[1] FALSE  TRUE  TRUE FALSE FALSE
```

Assess which elements are `TRUE`:

```
R> which(x > 3 & x <= 4)
```

```
[1] 2 3
```

Specialized functions `which.min()` and `which.max()` for computing the position of the minimum and the maximum.

Logical comparisons

In addition to `&` and `|`: `all()` and `any()` check whether all or at least some entries of a vector are `TRUE`:

```
R> all(x > 3)

[1] FALSE

R> any(x > 3)

[1] TRUE
```

Due to coercion (more later!), it is also possible to compute directly on logical vectors using ordinary arithmetic. When coerced to numeric, `FALSE` becomes `0` and `TRUE` becomes `1`, as in

```
R> 7 + TRUE

[1] 8
```

Logical comparisons

Caution: Floating-point arithmetic has to be used when assessing exact equality of numerical arguments with ==.

```
R> (1.5 - 0.5) == 1
```

```
[1] TRUE
```

```
R> (1.9 - 0.9) == 1
```

```
[1] FALSE
```

Use `all.equal()` instead:

```
R> all.equal(1.9 - 0.9, 1)
```

```
[1] TRUE
```

Furthermore, the function `identical()` checks whether two (possibly complex) R objects are exactly identical.

Coercion

Coercion functions: Can convert an object from one type or class to a different one.

Convention: If *foo* is the type/class of interest, `as.`*foo*`()` coerces to *foo* and `is.`*foo*`()` checks if an object is *foo*, e.g., `numeric`, `character`, `matrix`, `data.frame`, ...

```
R> is.numeric(x)
[1] TRUE
R> is.character(x)
[1] FALSE
R> as.character(x)
[1] "1.8"    "3.14"   "4"      "88.169" "13"
```

Coercion is enforced automatically in certain situations, e.g.,

```
R> c(1, "a")
[1] "1" "a"
```

Random number generation

Random number generators (RNGs): Vital for statistical/econometric programming environments for performing Monte Carlo studies.

In R: Several algorithms available, see `?RNG`.

Random seed: `set.seed()`. Basis for the generation of pseudo-random numbers and making simulations exactly reproducible.

```
R> set.seed(123)
R> rnorm(2)

[1] -0.5605 -0.2302

R> rnorm(2)

[1] 1.55871 0.07051

R> set.seed(123)
R> rnorm(2)

[1] -0.5605 -0.2302
```

Random number generation

Drawing samples: Sampling with or without replacement from a finite set of values, is available in `sample()`.

Default: Draw, without replacement, a vector of the same size as its input argument (i.e., to compute a permutation).

```
R> sample(1:5)

[1] 5 1 2 3 4

R> sample(c("male", "female"), size = 5, replace = TRUE,
+    prob = c(0.2, 0.8))

[1] "female" "male"   "female" "female" "female"
```

The second command draws a sample of size 5, with replacement, from the values `"male"` and `"female"`, which are drawn with probabilities 0.2 and 0.8, respectively.

Random number generation

Distributions:

- Random numbers from specific distributions are typically available in functions of type `r`*dist*`()`.
- Examples for *dist* include `norm`, `unif`, `binom`, `pois`, `t`, `f`, `chisq`.
- Functions take sample size `n` as their first argument. Further arguments control parameters of the respective distribution.

  Example: `rnorm()` takes `mean` and `sd` as further arguments, defaulting to `0` and `1`.
- Further functions for distributions: `d`*dist*`()`, `p`*dist*`()`, and `q`*dist*`()` implementing density, cumulative probability distribution function, and quantile function (inverse distribution function).

Flow control

Standard control structures: Control when a certain expression `expr` is evaluated. (See `?Control` for details.)

- `if`/`else` statements.
- `for` loops.
- `while` loops.

An `if`/`else` statement is of the form

```
if(cond) {
  expr1
} else {
  expr2
}
```

where `expr1` is evaluated if `cond` is `TRUE` and `expr2` otherwise. The `else` branch may be omitted if empty.

Flow control

Illustration: Toy example.

```
R> x <- c(1.8, 3.14, 4, 88.169, 13)
R> if(rnorm(1) > 0) sum(x) else mean(x)
```

```
[1] 22.02
```

The condition `cond` can only be of length 1. For vectorized evaluation, use `ifelse()`.

```
R> ifelse(x > 4, sqrt(x), x^2)
```

```
[1]  3.240  9.860 16.000  9.390  3.606
```

This computes the square root for those values in `x` that are greater than 4 and the square for the remaining ones.

Flow control

`for` **loop:** Similar, but the main argument to `for()` is of type `variable in sequence`.

Illustration: Recursively compute first differences in the vector `x`.

```
R> for(i in 2:5) {
+    x[i] <- x[i] - x[i-1]
+  }
R> x[-1]
```

```
[1]   1.34   2.66  85.51 -72.51
```

`while` **loop:** Similar, but the argument to `while()` is a condition that may change in every run of the loop so that it finally can become `FALSE`.

```
R> while(sum(x) < 100) {
+    x <- 2 * x
+  }
R> x
```

```
[1]   14.40   10.72   21.28  684.07 -580.07
```

Writing functions

Feature of S/R: Users naturally become developers. Repeated commands can easily be wrapped into functions.

Simple example: Deliberately awkward function computing column means in a matrix `X` using nested `for` loops.

```
R> cmeans <- function(X) {
+     rval <- rep(0, ncol(X))
+     for(j in 1:ncol(X)) {
+       mysum <- 0
+       for(i in 1:nrow(X)) mysum <- mysum + X[i,j]
+       rval[j] <- mysum/nrow(X)
+     }
+     return(rval)
+   }
```

```
R> X <- matrix(1:20, ncol = 2)
R> cmeans(X)
```

```
[1]  5.5 15.5
```

Writing functions

Built-in function `colMeans()`

```
R> colMeans(X)

[1]  5.5 15.5
```

is clearly preferable.

```
R> X <- matrix(rnorm(2*10^6), ncol = 2)
R> system.time(colMeans(X))

   user  system elapsed
  0.004   0.000   0.004

R> system.time(cmeans(X))

   user  system elapsed
  3.092   0.012   3.110
```

`cmeans()` takes only a single argument `X` wiht no default. If defaults should be defined, use `name = expr` pairs.

Vectorized calculations

Vectorized arithmetic: Can be used to avoid loops.

Example: Avoid one `for` loop by using the vectorized function `mean()`.

```
R> cmeans2 <- function(X) {
+    rval <- rep(0, ncol(X))
+    for(j in 1:ncol(X)) rval[j] <- mean(X[,j])
+    return(rval)
+  }
R> system.time(cmeans2(X))
```

```
   user  system elapsed
  0.052   0.008   0.063
```

More compactly: `apply(X, 2, mean)`. Looks less cumbersome than `for` loop (but often performs similarly). `apply()` applies functions along margins (here, columns, the second margin) of an array.

```
R> system.time(apply(X, 2, mean))
```

```
   user  system elapsed
  0.204   0.016   0.220
```

Vectorized calculations

Summary:

1. Element-wise computations should be avoided if vectorized computations are available.
2. Optimized solutions (if available) typically perform better than generic `for` or `apply()` solutions.
3. Loops can be written more compactly using `apply()`.

Several variants:

- `lapply()`: returns a list.
- `tapply()`: returns a table.
- `sapply()`: tries to simplify the result to a vector or matrix where possible.

Reserved words

Reserved words: Basic grammatical constructs of the language that cannot be used in other meanings.

In R: `if`, `else`, `for`, `in`, `while`, `repeat`, `break`, `next`, `function`, `TRUE`, `FALSE`, `NA`, `NULL`, `Inf`, `NaN`, `...`).

See `?Reserved` for a complete list.

Basics

Formulas

Formulas

Symbolic descriptions: Relationships among variables can be specified. The ~ operator is basic to formulas in R.

```
R> f <- y ~ x
R> class(f)
```

```
[1] "formula"
```

Meaning: Depends on the context, i.e., the function that evaluates the formula.

Most commonly: `y ~ x` means "`y` is explained by `x`".

Usage: Specification of plots, models, etc.

Formulas

Illustration: Artificial data.

```
R> x <- seq(from = 0, to = 10, by = 0.5)
R> y <- 2 + 3 * x + rnorm(21)
```

Use the same formula for plotting and linear regression.

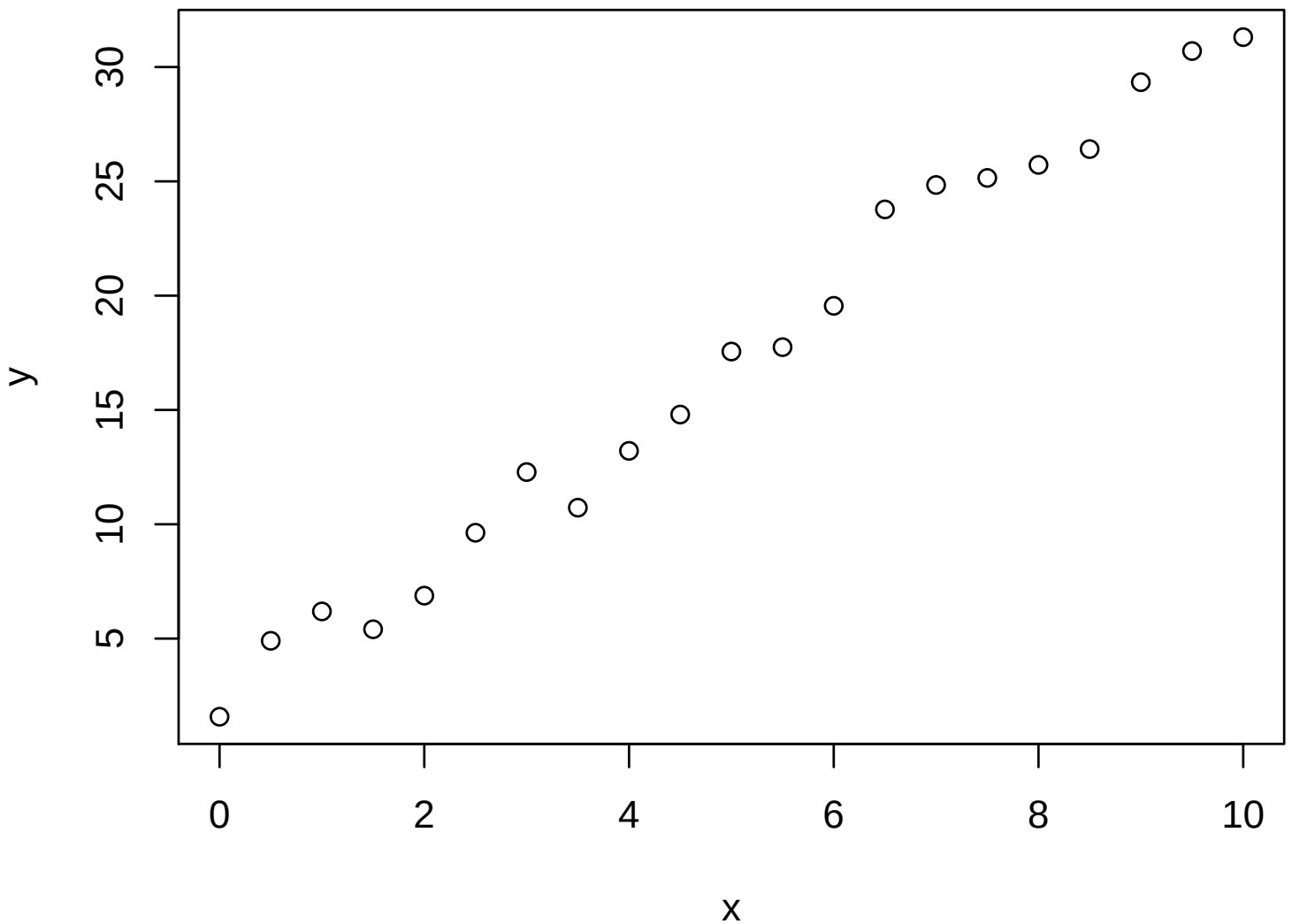
```
R> plot(y ~ x)
R> lm(y ~ x)
```

```
Call:
lm(formula = y ~ x)

Coefficients:
(Intercept)            x
       2.00         3.01
```

R formula language is much more powerful, especially for specifying (generalized) linear models (see Chapter 3).

Formulas



Basics

Data Management in R

Creation from scratch

Data frames: Basic data structure in R. (In other programs such structures are often called data matrix or data set.)

Typically: An array consisting of a list of vectors and/or factors of identical length, i.e., a rectangular format where columns correspond to variables and rows to observations.

Example: Artificial data with variables named `"one"`, `"two"`, `"three"`.

```
R> mydata <- data.frame(one = 1:10, two = 11:20, three = 21:30)
```

Alternatively:

```
R> mydata <- as.data.frame(matrix(1:30, ncol = 3))
R> names(mydata) <- c("one", "two", "three")
```

Technically: This data frame is internally represented as a list of vectors (not a matrix).

Subset selection

Select columns: Subsets of variables can be selected via `[` or `$` (for a single variable).

```
R> mydata$two

 [1] 11 12 13 14 15 16 17 18 19 20

R> mydata[, "two"]

 [1] 11 12 13 14 15 16 17 18 19 20

R> mydata[, 2]

 [1] 11 12 13 14 15 16 17 18 19 20
```

In all cases: The data frame attributes are dropped (by default).

Subset selection

Accessing variables: Variables can be `attach()`ed. (Technically, this means that the attached data set is added to the `search()` path.)

```
R> mean(two)

Error in mean(two) : Object "two" not found

R> attach(mydata)
R> mean(two)

[1] 15.5

R> detach(mydata)
```

Note: Attaching data frames can lead to confusion when there are variables with the same name in several data frames or the global environment.

For a single command:

```
R> with(mydata, mean(two))

[1] 15.5
```

Subset selection

Select rows: Subsets of observations (and variables) can be selected again via `[` or (more conveniently) via `subset()`.

```
R> subset(mydata, two <= 16, select = -two)
```

```
  one three
1   1    21
2   2    22
3   3    23
4   4    24
5   5    25
6   6    26
```

Import and export

Export as plain text: `write.table()`.

```
R> write.table(mydata, file = "mydata.txt", col.names = TRUE)
```

This creates a text file `mydata.txt` in the current working directory. To read again, use:

```
R> newdata <- read.table("mydata.txt", header = TRUE)
```

Details:

- `read.table()` returns a "`data.frame`" object
- By setting `col.names = TRUE`, `mydata.txt` contains variable names in the first row. Hence, it should be read with `header = TRUE`.
- `write.table()` allows specification of: separation symbol, decimal separator, quotes, and many more. Thus, it can create tab- or comma-separated values etc.

Import and export

CSV: Comma-separated values.

- Convenience interfaces `read.csv()` and `write.csv()` are available.
- CSV is useful format for exchanging data between R and Microsoft Excel.
- On systems with comma (and not the period) as the decimal separator, Excel uses semicolon-separated values (but still calls them CSV).
- These can be read/written with `read.csv2()` and `write.csv2()`.
- More elementary: `scan()` is useful for reading more complex structures.
- See the manual pages and the "R Data Import/Export" manual for further details.

Import and export

Binary format: To write/read R's internal binary format (by convention with extension `.RData` or `.rda`) the commands `load()` and `save()` are available.

```
R> save(mydata, file = "mydata.rda")
R> load("mydata.rda")
```

Details:

- Binary files can contain multiple arbitrary objects (not just a single data frame or matrix).
- Upon `load()` all objects are made available in the current environment (by default).

Import and export

Data in packages:

- All data sets in the package **AER** are supplied in this binary format.
- Go to the folder `~/AER/data` in your R library to check.
- As they are part of a package, they are made accessible more easily using `data()` (which in this case sets up the appropriate call for `load()`).
- Hence,
  `data("Journals", package = "AER")`
  loads the `Journals` data frame from the **AER** package, stored in the file `~/AER/data/Journals.rda`.
- If the `package` argument is omitted, all packages currently in the search path are checked whether they provide a file `Journals`.

Reading and writing foreign binary formats

Package foreign: R can also read and write a number of proprietary binary formats, including S-PLUS, SPSS, SAS, Stata, Minitab, Systat, and dBase files.

Example: Stata files.

Export:

```
R> library("foreign")
R> write.dta(mydata, file = "mydata.dta")
```

Import:

```
R> mydata <- read.dta("mydata.dta")
```

Reading and writing Excel spreadsheets

Excel spreadsheets: `.xls` and `.xlsx` files.

- Not directly supported by base R distribution $\rightarrow$ exchange via CSV files recommended.
- Several CRAN packages also offer support for reading/writing Excel spreadsheets directly.
- **gdata**: `read.xls()` for simple (and quick) reading of spreadsheets. Requires Perl installation.
- **xlsx**: `read.xlsx()` and `write.xlsx()` for simple (but not quite as quick) reading and writing of spreadsheets. Requires Java installation.
- **XLConnect**: Functionality for querying and manipulating (including reading/writing) spreadsheets. Requires Java installation.

Interaction with the file system and string manipulations

Rich functionality: Interaction with external files and communication with the operating system.

A few pointers:

- Query files available in a directory or folder: `dir()`.
- Copying and deleting files: `file.copy()`) and `file.remove()`.
- These commands are independent of the operating system.
- Potentially system-dependent commands can be issued as strings using `system()`.

Illustration: Delete the Stata file created before.

```
R> file.remove("mydata.dta")
```

Interaction with the file system and string manipulations

Save commands or their output to text files:

- One possibility: `sink()` can direct output to a `file()` connection.
- Strings can be written with `cat()` to a connection.
- In some situations `writeLines()` is more convenient for this.
- Furthermore: `dump()` can create text representations of R objects and write them to a `file()` connection.

Manipulate strings before creating output:

- `strsplit()`: splitting strings.
- `paste()`: paste strings together.
- `grep()` and `gsub()`: pattern matching and replacing.
- `sprintf()`: combining text and variable values.

Factors

Categorical information: Stored in *factors*, an extension of vectors.

Typical econometric examples: gender, union membership, or ethnicity.

In many software packages: Stored using a numerical encoding (e.g., 0 for males and 1 for females). Especially in regression settings, a single categorical variable with more than two categories is often stored in several such dummy variables.

In R:

```
R> g <- rep(0:1, c(2, 4))
R> g <- factor(g, levels = 0:1, labels = c("male", "female"))
R> g
```

```
[1] male   male   female female female female
Levels: male female
```

Factors

Details:

- Here, a `factor()` is created from a dummy-coded vector.
- Internally: stored as the integers `1` to `k` (= number of levels) plus a character vector of labels, here `"male"` and `"female"`.
- `factor()` can create the same information from numerical, character or logical vectors.
- For ordinal information, set the argument `ordered = TRUE`.

Advantage: R knows that a certain variable is categorical and can choose appropriate methods automatically.

- Labels can be used in printed output.
- Different summary and plotting methods can be chosen.
- Contrast codings (e.g., dummy variables) can be computed in linear regressions.

Missing values

In R: Missing values are coded as `NA` (for "not available"). All standard computations on `NA` become `NA`.

Caution: Data sets may have missing values with a different encoding.

Example: Sometimes `-99` or `-999` is used in flat text files. These can be converted appropriately via:

```
R> newdata <- read.table("mydata.txt", na.strings = "-999")
```

Query `NA`s: `is.na()`.

Basics

Object Orientation

Object orientation:

Object-oriented programming (OOP): Paradigm of programming where users/developers can create objects of a certain "class" (that are required to have a certain structure) and then apply "methods" for certain "generic functions" to these objects.

Simple example: `summary()` is a generic function choosing different methods based on the class of its argument

```
R> x <- c(1.8, 3.14, 4, 88.169, 13)
R> g <- factor(rep(c(0, 1), c(2, 4)), levels = c(0, 1),
+    labels = c("male", "female"))
R> summary(x)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.80    3.14    4.00   22.00   13.00   88.20

R> summary(g)

  male female
     2      4
```

Object orientation:

Several paradigms: In fact, R has several OOP systems. The base installation already has two, usually called S3 and S4.

S3: Much simpler, using a dispatch mechanism based on a naming convention for methods.

S4: More sophisticated and closer to other OOP concepts used in computer science.

For most tasks: S3 is sufficient and hence briefly discussed here.

S3 generics: Functions with a certain list of arguments and then a `UseMethod()` call with the name of the generic function.

```
R> summary
```

```
function (object, ...)
UseMethod("summary")
<bytecode: 0x2b621c8>
<environment: namespace:base>
```

Object orientation:

Details:

- Arguments: `object` (required) plus an arbitrary number of optional arguments passed through `...` to its methods.
- When applied to an object of class "`foo`": R tries to apply the function `summary.foo()` if it exists. If not, it will call `summary.default()` if such a default method exists (which it does for `summary()`).
- R objects can also have a vector of classes, e.g., `c("foo", "bar")` meaning that the object is of class "`foo`" inheriting from "`bar`").
- In this case, R first tries to apply `summary.foo()`, then (if this does not exist) `summary.bar()`, and then (if both do not exist) `summary.default()`.

Object orientation:

Using methods:

- Methods defined for a certain generic can be queried using `methods()`.
- `methods(summary)` returns a (long) list of methods including `summary.factor()` and `summary.default()` (but not `summary.numeric()`).
- As it is not recommended to call methods directly, some methods are marked as being non-visible to the user and these cannot (easily) be called directly.
- Even if visible, it is preferred to call the generic, i.e., `summary(g)` instead of `summary.factor(g)`.

Object orientation:

Illustration: Definition of a class and methods.

- Create an object of class "`normsample`" that contains a sample from a normal distribution.
- Define a `summary()` method that reports the empirical mean and standard deviation.

First, we write a simple class creator. In principle, it could have any name, but it is often called like the class itself:

```
R> normsample <- function(n, ...) {
+    rval <- rnorm(n, ...)
+    class(rval) <- "normsample"
+    return(rval)
+  }
```

Object orientation:

Details:

- It takes a required argument `n` (the sample size) and further arguments `...`, which are passed on to `rnorm()` for generating normal random numbers.
- `rnorm()` takes further arguments like the mean and the standard deviation.
- After generation of the vector of normal random numbers, it is assigned the class "`normsample`" and then returned.

```
R> set.seed(123)
R> x <- normsample(10, mean = 5)
R> class(x)
```

```
[1] "normsample"
```

Object orientation:

New `summary()` **method:** `summary.normsample()`. It conforms with the argument list of the generic (although `...` is not used) and computes sample size, empirical mean, and standard deviation.

```
R> summary.normsample <- function(object, ...) {
+    rval <- c(length(object), mean(object), sd(object))
+    names(rval) <- c("sample size","mean","standard deviation")
+    return(rval)
+  }
```

This method is found when calling:

```
R> summary(x)
```

```
       sample size                mean standard deviation
           10.0000              5.0746              0.9538
```

Typical generics: `print()`, `plot()`, and `str()`, which print, plot, and summarize the structure are available for most basic classes.

Basics

R Graphics

R graphics

Early publications on S and R already emphasized the powerful graphics:

- Beckers and Chambers (1984): “S: An Interactive Environment for Data Analysis and Graphics”.
- Ihaka and Gentleman (1996): “R: A Language for Data Analysis and Graphics”.

Here: Brief introduction to “conventional” graphics as implemented in base R.

Even more flexible: grid graphics (Murrell 2005), enabling “trellis”-type graphics (Cleveland 1993) in package **lattice**. Not discussed here.

The function `plot()`

Generic function: `plot()`. Methods for many objects, including data frames, time series, and fitted linear models.

Basic: Default `plot()` method, creates various types of scatterplots. Many of the explanations below extend to other methods and high-level plotting functions.

Scatterplot: `plot(x, y)` produces a scatterplot of `y` vs. `x`.

The function `plot()`

Illustration: Relationship between the number of subscriptions and the price per citation for economics journals.

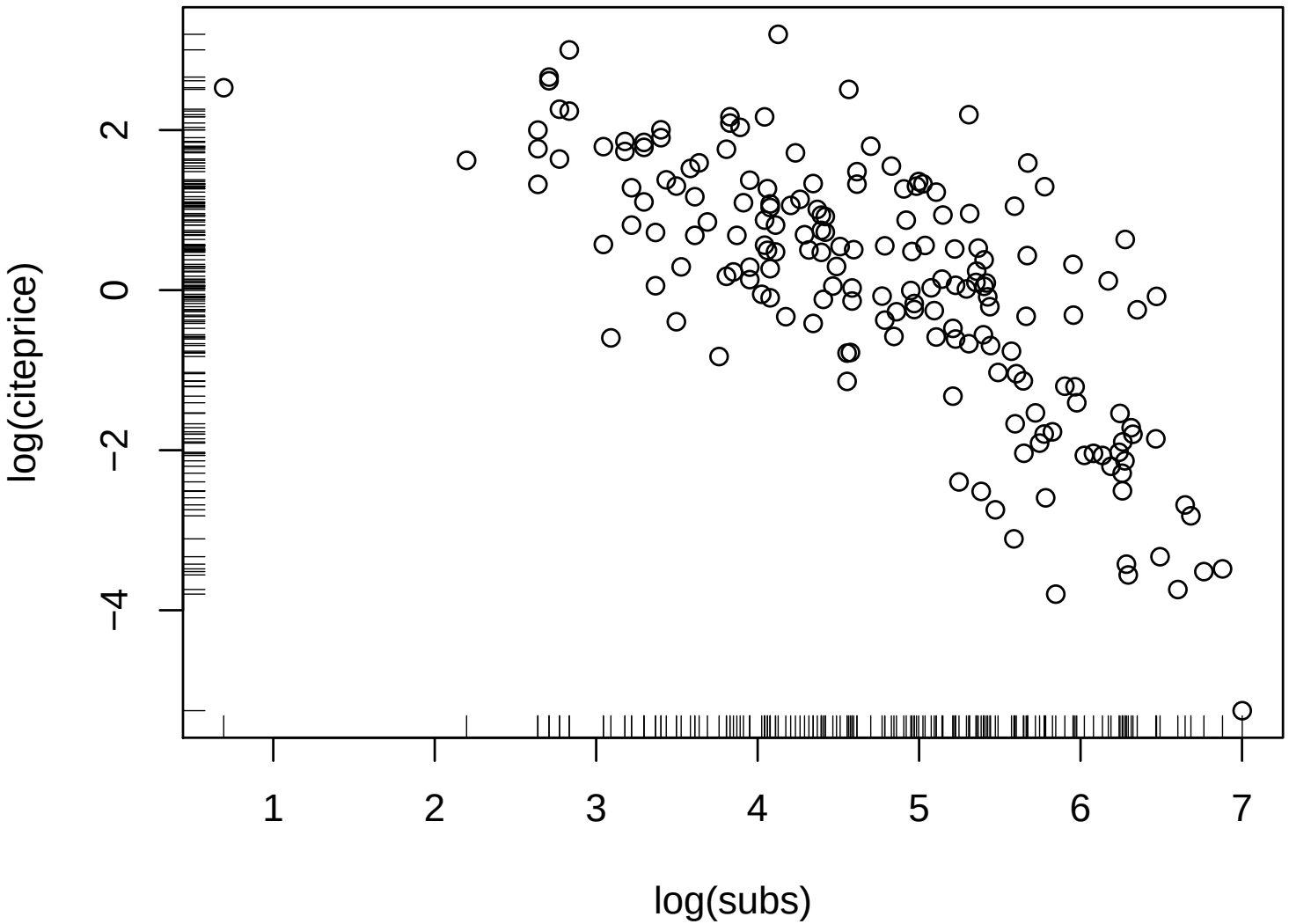
```
R> data("Journals")
R> Journals$citeprice <- Journals$price/Journals$citations
R> attach(Journals)
R> plot(log(subs), log(citeprice))
R> rug(log(subs))
R> rug(log(citeprice), side = 2)
R> detach(Journals)
```

Rug: `rug()` adds ticks, thus visualizing the marginal distributions of the variables.

Alternatively: Instead of attaching/detaching the data, one can use

```
R> plot(log(subs) ~ log(citeprice), data = Journals)
```

The function `plot()`



Graphical parameters

Modifications: `plot()` has many arguments, including

- `type`: modify plot type, e.g., points (`type = "p"`, default), lines (`type = "l"`), both (`type = "b"`), stair steps (`type = "s"`).
- `main`, `xlab`, `ylab`: modify title and axis labels.
- Further graphical parameters (see `?par`) can be passed to `plot()` or set separately via `par()`.
- `col`: set color(s).
- `xlim`, `ylim`: adjust plotting ranges.
- `pch`: modify the plotting character for points.
- `cex`: corresponding character extension.
- `lty`, `lwd`: line type and width.
- `cex.lab`, `cex.axis`, `cex.`*foo*: size of labels, axis ticks, etc.

Graphical parameters

Argument	Description
`axes`	should axes be drawn?
`bg`	background color
`cex`	size of a point or symbol
`col`	color
`las`	orientation of axis labels
`lty, lwd`	line type and line width
`main, sub`	title and subtitle
`mar`	size of margins
`mfcol, mfrow`	array defining layout for several graphs on a plot
`pch`	plotting symbol
`type`	types (see text)
`xlab, ylab`	axis labels
`xlim, ylim`	axis ranges
`xlog, ylog, log`	logarithmic scales

Graphical parameters

Example:

```
R> plot(log(subs) ~ log(citeprice), data = Journals, pch = 20,
+    col = "blue", ylim = c(0, 8), xlim = c(-7, 4),
+    main = "Library subscriptions")
```

Add further layers: `lines()`, `points()`, `text()`, `legend()`.

```
R> text(-3.798, 5.846, "Econometrica", pos = 2)
```

Straight line: `abline(a, b)` with intercept `a` and slope `b`.

Further plotting functions: `barplot()`, `pie()` (pie charts), `boxplot()`, `qqplot()` (QQ plots), `hist()` (histograms).

Instructive overview: `demo("graphics")`.

Exporting graphics

Storing graphical results: e.g., for publication in a report, journal article, or thesis.

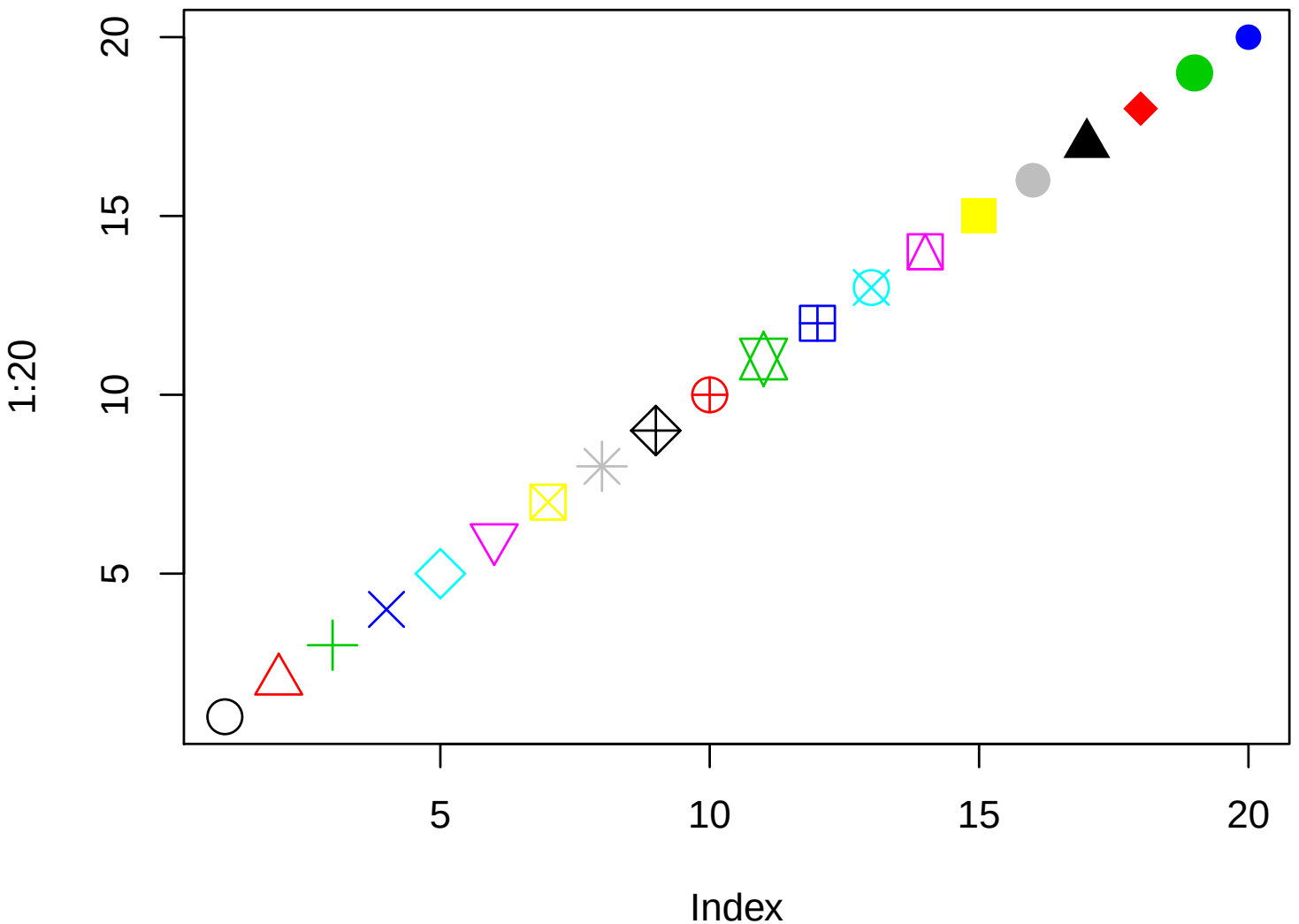
For Microsoft Windows and Microsoft Word: A simple option is to "copy and paste".

More generally: Create external files using a suitable graphics device. Devices available on all platforms include the vector formats PostScript and PDF. The bitmap formats PNG and JPEG and the vector format WMF are system-dependent. See `?Devices` for details.

Usage: First the device is opened, then the plot commands are executed, and finally the device is closed by `dev.off()`.

```
R> pdf("myfile.pdf", height = 5, width = 6)
R> plot(1:20, pch = 1:20, col = 1:20, cex = 2)
R> dev.off()
```

Exporting graphics



Exporting graphics

Details:

- Creates the PDF file `myfile.pdf` in the current working directory.
- Contains the graphic generated by the `plot()` call.
- The plot illustrates a few graphical parameters: 20 plotting symbols in double size and different colors (a basic set of colors is numbered).

Alternatively: Instead of opening, printing and closing a device, it is possible to print an existing plot in the graphics window to a device using `dev.copy()` and `dev.print()`.

Mathematical annotation of plots

Overview: `?plotmath` and `demo("plotmath")`.

Syntax: Somewhat similar to LaTeX.

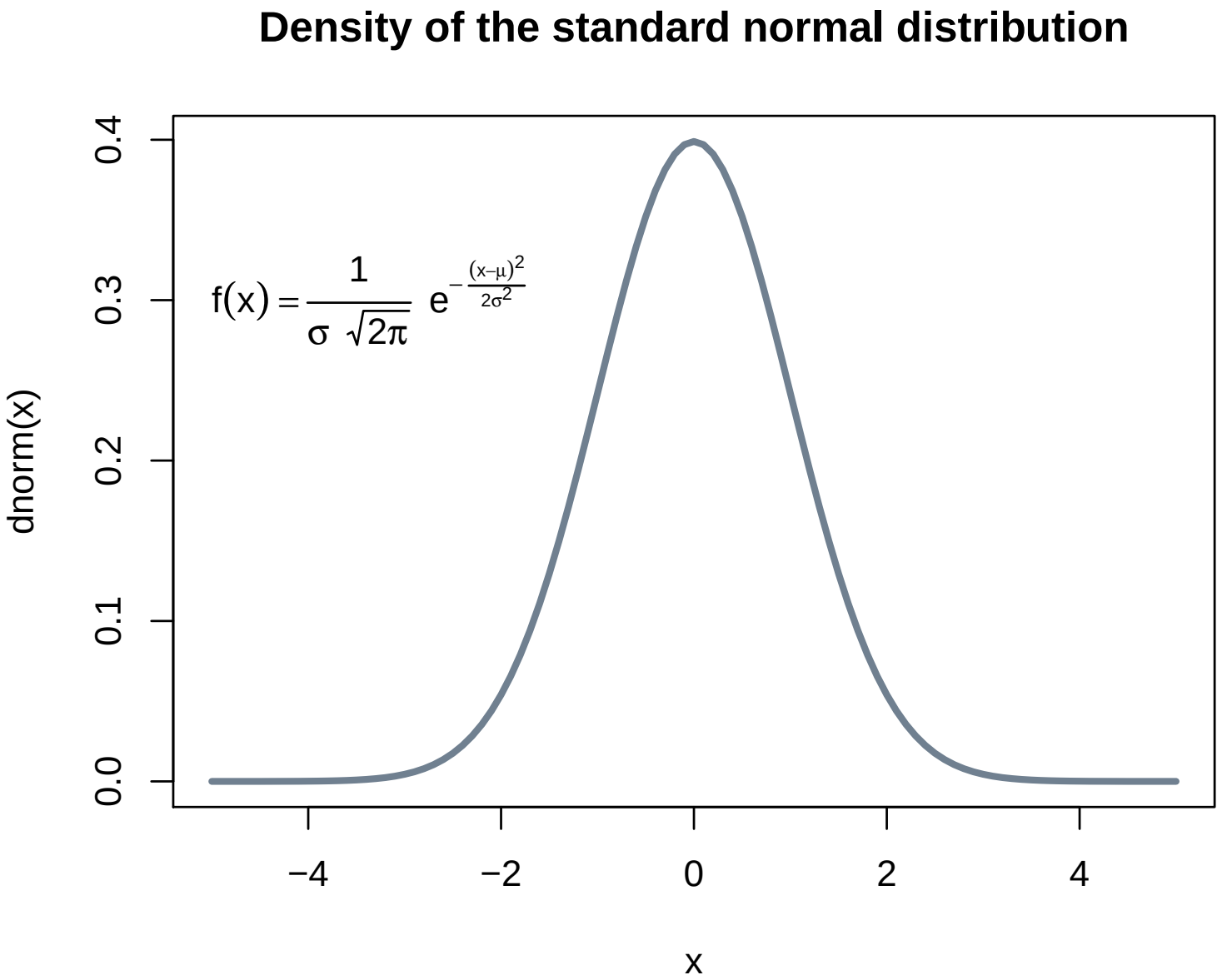
Illustration: Density of the standard normal distribution along with its mathematical definition.

$$f(x) = \frac{1}{\sigma\sqrt{2\pi}} \, e^{-\frac{(x-\mu)^2}{2\sigma^2}}.$$

In R:

```
R> curve(dnorm, from = -5, to = 5, col = "slategray", lwd = 3,
+    main = "Density of the standard normal distribution")
R> text(-5, 0.3, expression(f(x) == frac(1, sigma ~~
+    sqrt(2*pi)) ~~ e^{- ~ frac((x - mu)^2, 2*sigma^2)}), adj = 0)
```

Mathematical annotation of plots



Basics

Exploratory Data Analysis with R

Exploratory data analysis with R

Here: Brief introduction. More details in Dalgaard (2008).

Data: `CPS1985` from Berndt (1991).

```
R> data("CPS1985")
R> str(CPS1985)
```

```
'data.frame': 534 obs. of  11 variables:
 $ wage      : num  5.1 4.95 6.67 4 7.5 ...
 $ education : num  8 9 12 12 12 13 10 12 16 12 ...
 $ experience: num  21 42 1 4 17 9 27 9 11 9 ...
 $ age       : num  35 57 19 22 35 28 43 27 33 27 ...
 $ ethnicity : Factor w/ 3 levels "cauc","hispanic",..: 2 1 1 1 1..
 $ region    : Factor w/ 2 levels "south","other": 2 2 2 2 2 2 1 ..
 $ gender    : Factor w/ 2 levels "male","female": 2 2 1 1 1 1 1 ..
 $ occupation: Factor w/ 6 levels "worker","technical",..: 1 1 1 ..
 $ sector    : Factor w/ 3 levels "manufacturing",..: 1 1 1 3 3 3..
 $ union     : Factor w/ 2 levels "no","yes": 1 1 1 1 1 2 1 1 1 1..
 $ married   : Factor w/ 2 levels "no","yes": 2 2 1 1 2 1 1 1 2 1..
```

Exploratory data analysis with R

Inspect top or bottom: `head()` or `tail()`, returning (by default) the first or last 6 rows.

```
R> head(CPS1985)
```

```
      wage education experience age ethnicity region gender
1     5.10         8         21  35  hispanic  other female
1100  4.95         9         42  57      cauc  other female
2     6.67        12          1  19      cauc  other   male
3     4.00        12          4  22      cauc  other   male
4     7.50        12         17  35      cauc  other   male
5    13.07        13          9  28      cauc  other   male
     occupation        sector union married
1        worker manufacturing    no     yes
1100     worker manufacturing    no     yes
2        worker manufacturing    no      no
3        worker         other    no      no
4        worker         other    no     yes
5        worker         other   yes      no
```

Exploratory data analysis with R

Overview: Summary by variable.

```
R> summary(CPS1985)
```

```
      wage          education       experience         age       
 Min.   : 1.00   Min.   : 2   Min.   : 0.0   Min.   :18.0  
 1st Qu.: 5.25   1st Qu.:12   1st Qu.: 8.0   1st Qu.:28.0  
 Median : 7.78   Median :12   Median :15.0   Median :35.0  
 Mean   : 9.02   Mean   :13   Mean   :17.8   Mean   :36.8  
 3rd Qu.:11.25   3rd Qu.:15   3rd Qu.:26.0   3rd Qu.:44.0  
 Max.   :44.50   Max.   :18   Max.   :55.0   Max.   :64.0  
    ethnicity     region       gender          occupation  
 cauc    :440   south:156   male  :289   worker    :156  
 hispanic: 27   other:378   female:245   technical :105  
 other   : 67                           services  : 83  
                                         office    : 97  
                                         sales     : 38  
                                         management: 55  
           sector    union     married   
 manufacturing: 99   no :438   no :184  
 construction : 24   yes: 96   yes:350  
 other        :411                      
```

Exploratory data analysis with R

For compactifying input and output:

```
R> levels(CPS1985$occupation)[c(2, 6)] <- c("techn", "mgmt")
R> attach(CPS1985)
```

In the following:

- Exploratory analysis of a single numerical/categorical variable.
- Exploratory analysis of pairs of variables.

One numerical variable

Distribution of wages: Tukey's five-number summary and sample mean.

```
R> summary(wage)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
   1.00    5.25    7.78    9.02   11.20   44.50
```

Standalone functions: `mean()`, `median()`, `min()`, `max()`, `fivenum()`.

```
R> mean(wage)
```

```
[1] 9.024
```

Arbitrary quantiles: `quantile()`.
Measures of spread: variance and standard deviation.

```
R> var(wage)
```

```
[1] 26.41
```

```
R> sd(wage)
```

```
[1] 5.139
```

One numerical variable

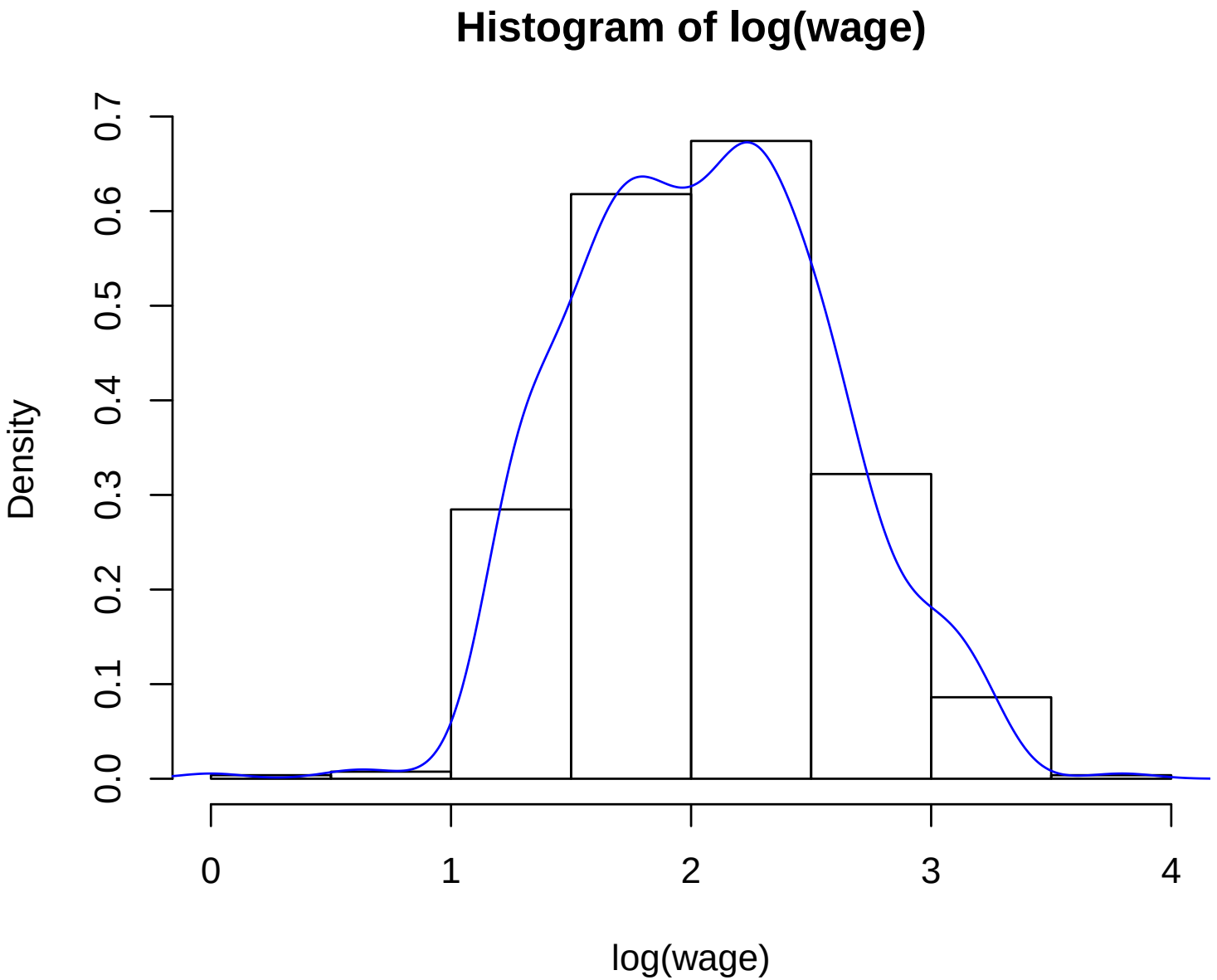
Graphical summary: Density visualizations (via histograms or kernel smoothing) and boxplots.

```
R> hist(log(wage), freq = FALSE)
R> lines(density(log(wage)), col = 4)
```

Details:

- Density of logarithm of `wage` (i.e., area under curve equals 1).
- Default: absolute frequencies, changed to density via `freq = FALSE`.
- Further fine tuning possible via selection of `breaks`.
- Added kernel density estimate.

One numerical variable



One categorical variable

Appropriate summary chosen automatically for "`factor`" variables.

```
R> summary(occupation)
```

```
  worker    techn services   office    sales     mgmt
     156      105       83       97       38       55
```

Alternatively: Use `table()` and also compute relative frequencies.

```
R> tab <- table(occupation)
R> prop.table(tab)
```

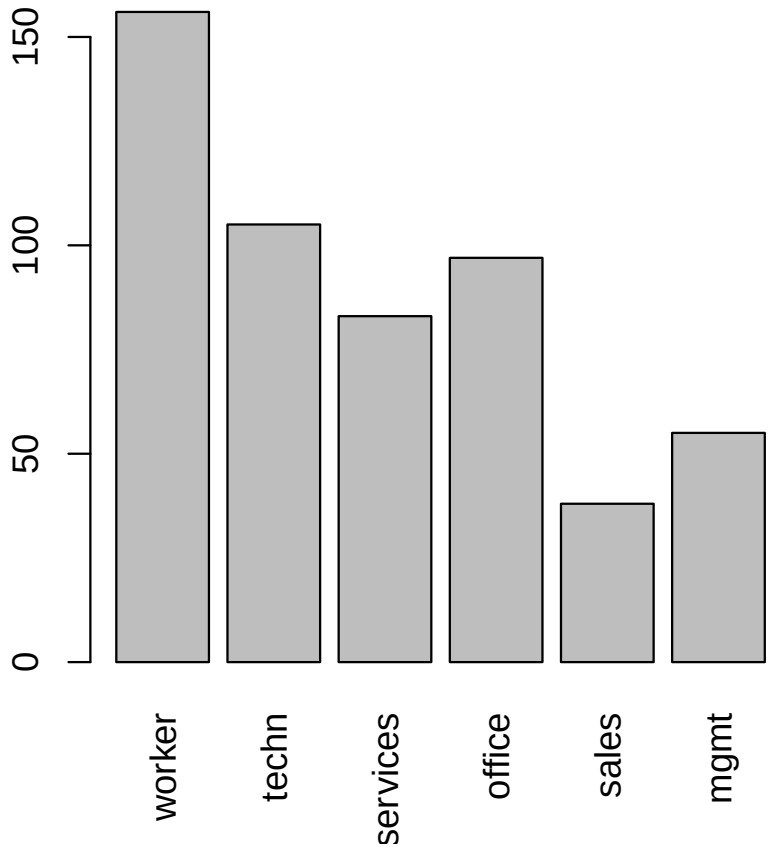
```
occupation
  worker    techn services   office    sales     mgmt
 0.29213  0.19663  0.15543  0.18165  0.07116  0.10300
```

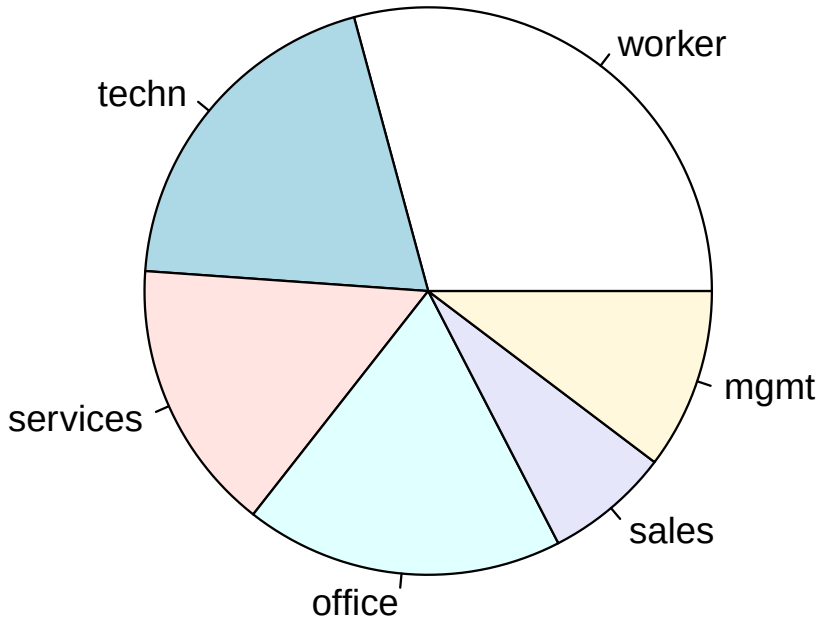
Visualization: `barplot()`. If majorities are to be brought out, `pie()` charts might be useful. Both expect tabulated frequencies as input.

```
R> barplot(tab)
R> pie(tab)
```

`plot(occupation)` is equivalent to `barplot(table(occupation))`.

One categorical variable





Two categorical variables

Relationship between two categorical variables:
Numerical summary: Contingency table(s) via `xtabs()` (with formula interface) or `table()`. Use `table(gender, occupation)` or

```
R> xtabs(~ gender + occupation, data = CPS1985)
```

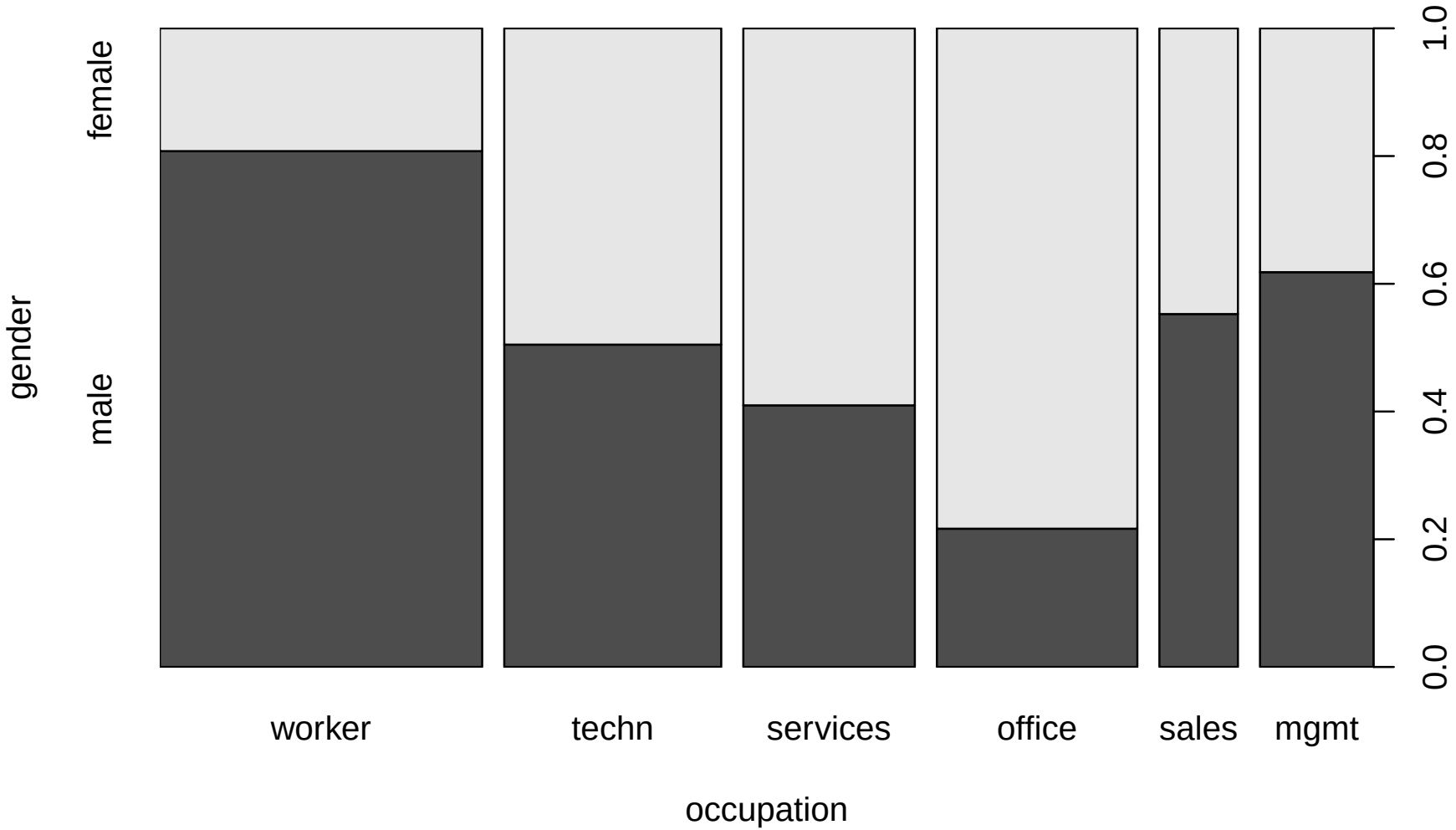
```
        occupation
gender   worker techn services office sales mgmt
  male      126    53       34     21    21   34
  female     30    52       49     76    17   21
```

Graphical summary: Mosaic plot, a generalization of stacked barplots. The following variant is also called “spine plot”:

```
R> plot(gender ~ occupation, data = CPS1985)
```

Bar heights correspond to the conditional distribution of `gender` given `occupation`. Bar widths visualize the marginal distribution of `occupation`.

Two categorical variables



Two numerical variables

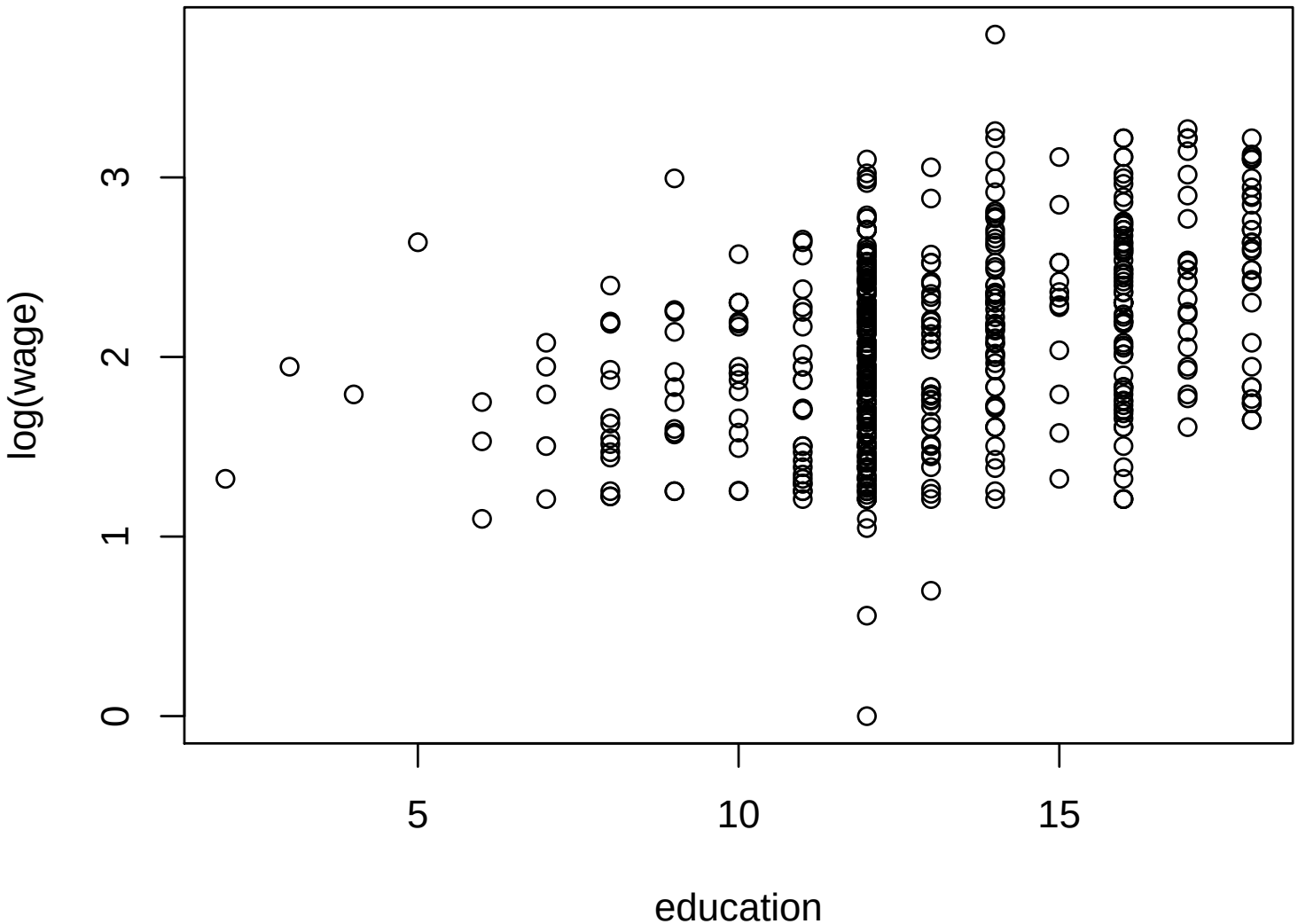
Numerical summary: Correlation coefficient(s) via `cor()`. Default is the standard Pearson correlation coefficient, alternatives include the nonparametric Spearman's ϱ.

```
R> cor(log(wage), education)
[1] 0.3804
R> cor(log(wage), education, method = "spearman")
[1] 0.3813
```

Graphical summary: Scatterplot.

```
R> plot(log(wage) ~ education)
```

Two numerical variables



One numerical and one categorical variable

Numerical summary: Grouped numerical summaries (for the numerical variable given the categorical variable).

In R: `tapply()` applies functions grouped by a (list of) categorical variable(s). Mean wages conditional on gender are available using:

```
R> tapply(log(wage), gender, mean)
```

```
  male female
 2.165  1.934
```

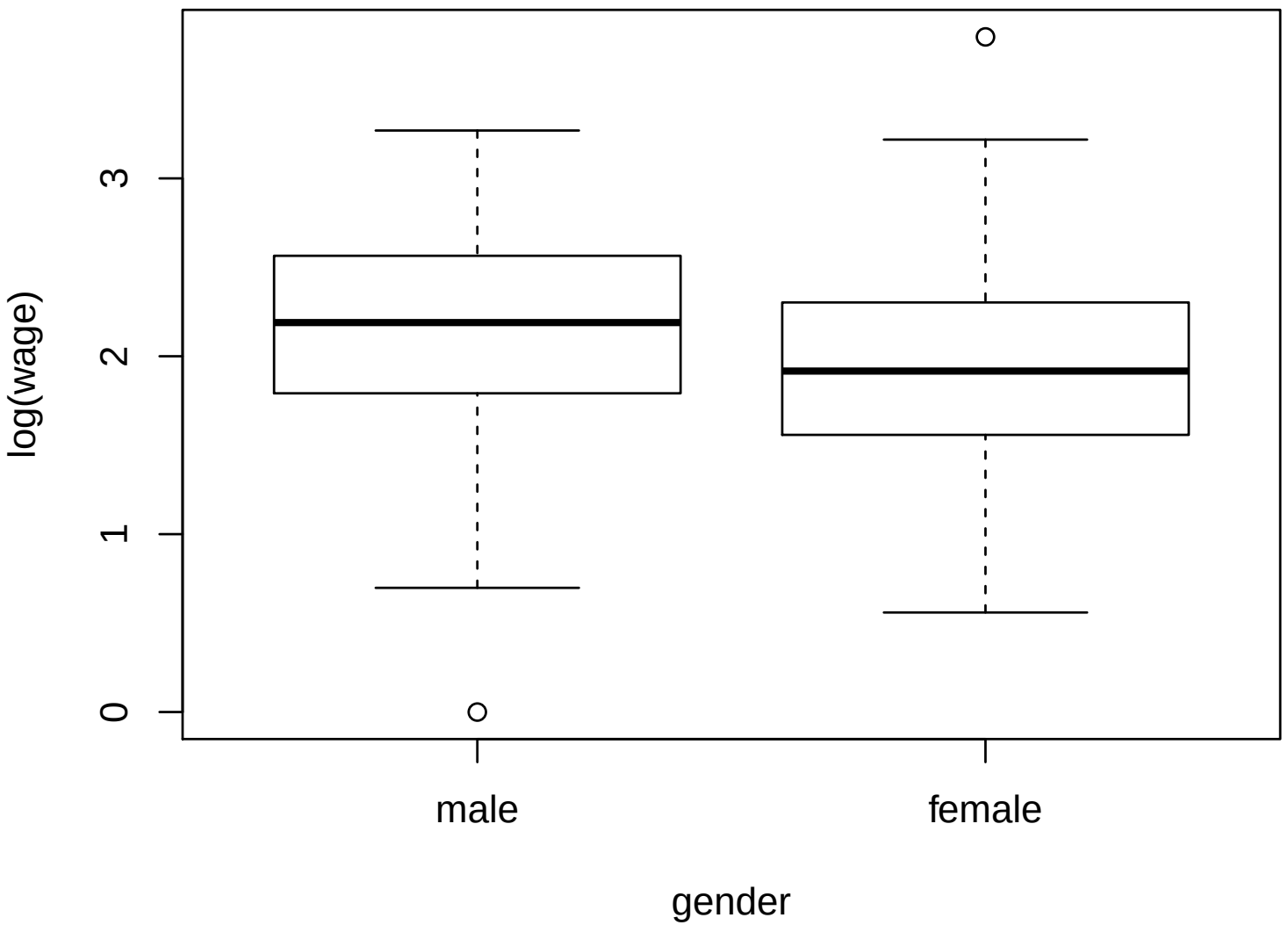
Other measures: Replace `mean` by other function, e.g., `summary`.

Graphical summary: Parallel boxplos or quantile-quantile (QQ) plots.

```
R> plot(log(wage) ~ gender)
```

The commands `plot(y ~ x)` and `boxplot(y ~ x)` both yield the same parallel boxplot if `x` is a "`factor`".

One numerical and one categorical variable



One numerical and one categorical variable

Boxplot:

- Coarse graphical summary of an empirical distribution.
- Box indicates “hinges” (approximately the lower and upper quartiles) and the median.
- “Whiskers” indicate the largest and smallest observations falling within a distance of 1.5 times the box size from the nearest hinge.
- Observations outside this range are outliers (in an approximately normal sample).

QQ plot indicates here that, for most quantiles, male wages are typically higher than female wages.

```
R> mwage <- subset(CPS1985, gender == "male")$wage
R> fwage <- subset(CPS1985, gender == "female")$wage
R> qqplot(mwage, fwage, xlim = range(wage), ylim = range(wage),
+    xaxs = "i", yaxs = "i", xlab = "male", ylab = "female")
R> abline(0, 1)
```

One numerical and one categorical variable