*R Programming for Demographers*

# Writing your own functions

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## Contents

## 1 Introduction

One of the biggest advantages of `R` is its immense flexibility: if you are unhappy with a way something is implemented or if you think something is missing, you can simply define your own function. Many functions in `R` have also been programmed that way. For example, the standard deviation, `sd`:

```
sd

## function (x, na.rm = FALSE)
## sqrt(var(if (is.vector(x) || is.factor(x)) x else as.double(x),
##     na.rm = na.rm))
## <bytecode: 0x1caa8d0>
## <environment: namespace:stats>
```

Although you can write programs in `R` without defining your own functions, we would recommend that you do it anyway because it allows you to be lazy (you don't have to write the same thing over and over again), your programs become more readable, and, most importantly: it is easier to maintain your programs. If you have made a mistake (which will happen for sure, we promise!), it is easier to correct the function definition than going through the whole program and try to correct every occurrence of a specific calculation.

## 2 The basic structure (with simple examples)

Functions are always built in the same way. The syntax is:

```
nameoffunction <- function(argument1, argument2, ...) {
  function-body using argument1, argument2, ...   and producing myresult
  return(myresult)
}
```

A very simple example is to write a function that calculates the square of a given input (which could be a scalar or a vector).

```
mysquare <- function(x) {
  myresult <- x * x
  return(myresult)
}
mysquare(4)

## [1] 16

mysquare(1:12)

##  [1]   1   4   9  16  25  36  49  64  81 100 121 144
```

## 3 The individual parts of a function definition

`nameoffunction` : In `R` , you can give functions you define yourself any kind of name. There is no restriction on the length of the name. As far as we know, any kind of object in `R` (data, functions, ...) has to start with an alphabetic letter and contains afterward also numbers. We would suggest that you use a name which makes it clear what is being done. Better make sure that you do not overwrite an internally defined function with your newly defined function. Examples for legal function names are:

```
myfunction
my.function
GC.function
DoomsdayFunction
...
```

`<- function` : then you tell `R` that the object you create is a function.

`argument1, argument2, ...` : after the `function`-keyword, you can give `arguments` that make up the *input* for your function. The minimum number of `arguments` is zero:

```
hello <- function(){
  print("Hello my friends")
}
```

But this is rather the exception. Usually, the function should perform different things according to the input. Let's define, for example, a power function which takes as input a scalar or a vector $x$ and an exponent $y$. The function should return $x^y$.

```
mypower <- function(x, y) {
  result <- x^y
  return(result)
}
mypower(2, 3)

## [1] 8
```

To be more precise, we recommend to give the names of the arguments:

```
mypower(y = 3, x = 2)

## [1] 8
```

If you want to give some default values for some arguments you can do this as in the following example where we assume that the most often used power-function is to square the base.

```
mypower <- function(x, y = 2) {
  result <- x^y
  return(result)
}
mypower(2,3)

## [1] 8

mypower(2,2)

## [1] 4

mypower(2)

## [1] 4
```

`function-body` : In the `function-body` you write all the statements and operations that you want to perform on the given arguments. This is the area where typically the data transformation/manipulation takes place with all the `if`, `for`, ... statements. Although this is the shortest part of the function description here, this is the most difficult to write. Here you can put in your creativity, effort, mistakes, ....

`return` : With the `return` statement you specify what the output of the function is. You can only return one object - but this object can be anything: a number, a matrix, a data.frame, nothing at all, a list, .... The return statement is actually not mandatory. If you omit it, the last evaluated term will be returned. Experience shows however, that it can get very difficult to spot this term in moderately complex programs. That is why we suggest using it explicitly.

## 4 A statistical example: computing the Pearson correlation coefficient

To demonstrate how you can write a function, let's provide here a slightly larger example to "walk through" line by line. Specifically, we aim to write a function to compute the Pearson correlation coefficient, $r$. Given two vectors $x$ and $y$, we want to apply the following formula (Agresti and Finlay, 1997, p. 354):

$$r = \frac{\sum(X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{\sum(X_i - \bar{X})^2 \sum(Y_i - \bar{Y})^2}}$$

Here what we can write in `R` :

```
Pea.corr <- function(x,y) {
   # "Handmade" Pearson correlation, normally denoted by "r"
   # see Agresti, 1997, p. 354

   # calculate the means
   xmean <- mean(x)
   ymean <- mean(y)
```

```
  # numerator & denominator
  numerator   <- sum((x - xmean) * (y - ymean))
  denominator <- sqrt(sum((x - xmean)^2) * sum((y-ymean)^2))

  # compute the actual correlation
  r <- numerator / denominator

  return(r)
}
```

**Line 1** : Here you see the beginning of the function definition. It tells us that the new function has the name `Pea.corr` and that it takes two arguments, `x` and `y`.

**Line 2-3** : It has become good practice in many programming languages that you write a short documentation string in the second line of a function definition. With a short phrase you say what the function should do.

**Lines 5–7** : following the formula above, first calculate the means of `x` and `y`.

**Lines 09–11** : In these lines we calculate the numerator and the denominator separately.

**Line 13-14** : To obtain $r$, divide the numerator by the denominator.

**Line 16** : And finally we state that `r` is the object which should be returned from our "blackbox" `Pea.corr`.

Empty lines in between the operations and indentation are not necessary, but useful to increase code legibility. Let's use our function `Pea.corr` on random numbers:

```
myx <- rnorm(100)
myy <- rnorm(100)
Pea.corr(x=myx, y=myy)

## [1] 0.06268953
```

Of course in this case, we expect a rather low correlation: both `myx` and `myy` are independently randomized. Note that the object-names within the function can be completely different from the actual object we aim to use. Indeed we suggest using names for your in-script objects that are different from the argument-names in the function. This helps keep things clean and separate.

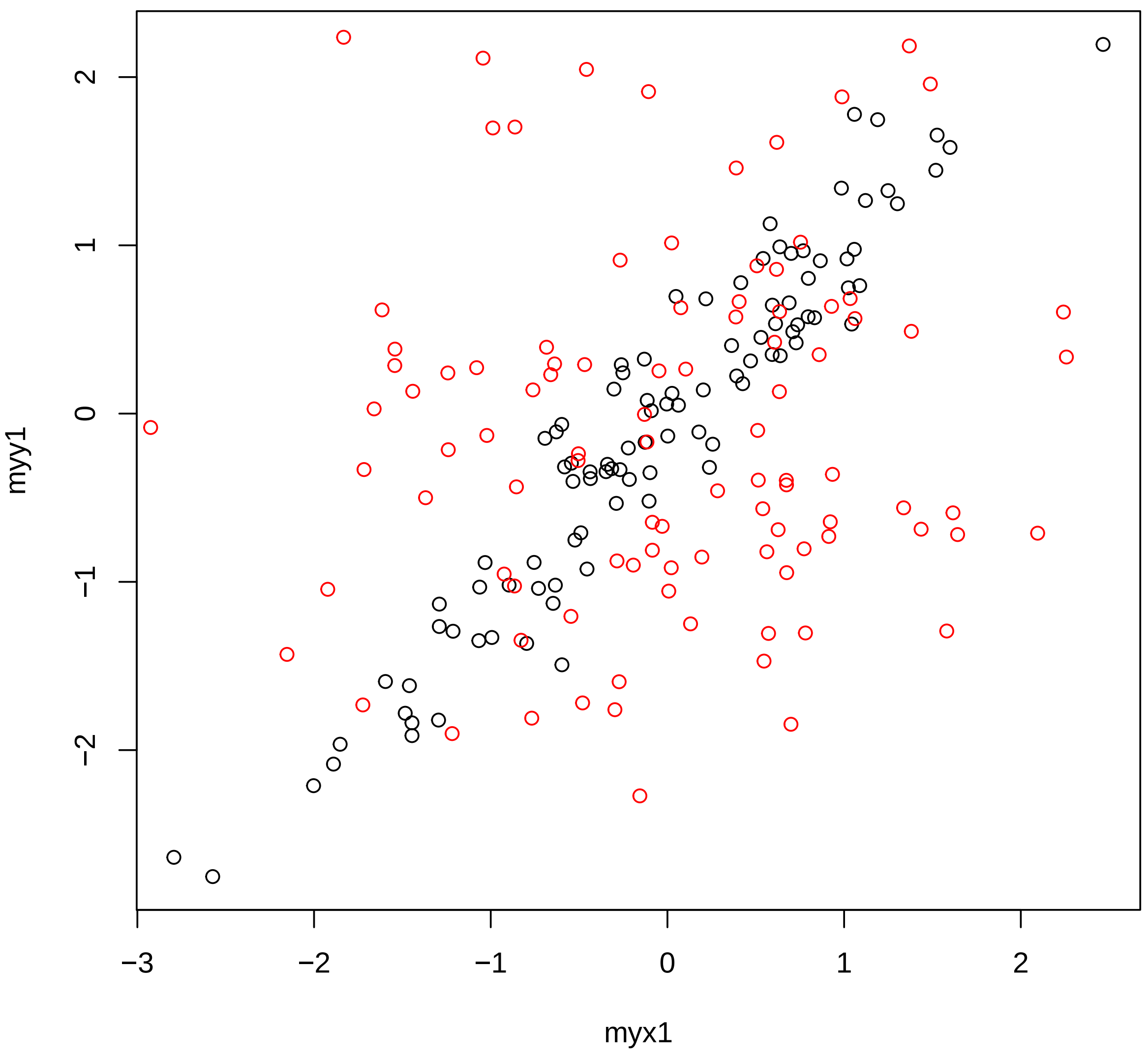
Let's simulate some data in which we ensure high correlation:

```
myx1 <- rnorm(100)
myy1 <- myx1 + rnorm(100, sd = 0.3)
Pea.corr(x = myx1, y = myy1)

## [1] 0.9557307
```

To check the correlation graphically you can plot `x` against `y` for both cases:

```
plot(myx1, myy1)
points(myx, myy, col = 2)
```



More information about plotting features in R will be given in a later module.

## 5 A demographic example: Age-standardization and decomposition

As those of your with a background in demography may know, sometimes the difference in age structures between two populations has a major influence on the crude death rates that distorts comparisons. Age-standardization is a tool for overcoming this issue(**?**, pp. 24–28).

Moreover it would be nice to quantify the difference between deaths rates in two population attributable to differences in their age distribution. In this case a decomposition of differences between rates helps (**?**, pp. 28–30).

In formulas the age-standardization:

$$\begin{aligned} ASCDR^A &= \sum_{i=1}^{\infty} M_i^A \cdot C_i^{ave} \\ ASCDR^B &= \sum_{i=1}^{\infty} M_i^B \cdot C_i^{ave} \end{aligned}$$

where $M_i^A = \frac{D_i^A}{N_i^A}$ and $M_i^B = \frac{D_i^B}{N_i^B}$ are the death rate in the $i$th interval for population $A$ and $B$, respectively.

The average age distribution is given by

$$C_i^{ave} = \left( \frac{C_i^A + C_i^B}{2} \right) .$$

We can summarize in formulas the decomposition of differences between rates such as (Kitagawa, 1955):

$$\begin{aligned} \Delta &= CDR^A - CDR^B = \\ &= \sum_i (C_i^A - C_i^B) \cdot \left[ \frac{M_i^A + M_i^B}{2} \right] + \\ &\quad + \sum_i (M_i^A - M_i^B) \cdot \left[ \frac{C_i^A + C_i^B}{2} \right] = \\ &= \text{contribution of differences in age} + \\ &\quad \text{contribution of differences in rates} \end{aligned}$$

The inputs for a function which computes those values are:

- Population by age in country $A$: `P.A`
- Deaths by age in country $A$: `D.A`
- Population by age in country $B$: `P.B`
- Deaths by age in country $B$: `D.B`

A desirable output should contain:

- Age standardized crude death rate for country $A$: `ASCDR.A`
- Age standardized crude death rate for country $B$: `ASCDR.B`
- Contribution of age compositional differences: `comp.diff`
- Contribution of age-specific rate differences: `ASR.diff`

With some comments, using the procedures in **?** and following what we have written in Section 4, we write our function:

```
stand.decom <- function(P.A, D.A, P.B, D.B){
    # CRUDE RATES
    A.crude     <- sum(D.A) / sum(P.A)
    B.crude     <- sum(D.B) / sum(P.B)
    Diff.crude  <- A.crude - B.crude

    # age distribution of country A and B
    C.A         <- P.A / sum(P.A)
    C.B         <- P.B / sum(P.B)

    # age-specific death rate in country A and B
    M.A         <- D.A / P.A
    M.B         <- D.B / P.B

    #### AGE-STANDARDIZATION
    # average age distribution
    C.ave       <- (C.A + C.B)/2

    # age-standardized crude death rate for country A and B
    ASCDR.A     <- sum(M.A * C.ave)
    ASCDR.B     <- sum(M.B * C.ave)
    #### DECOMPOSITION OF DIFFERENCES BETWEEN RATES
    comp.diff   <- sum((C.A - C.B) * ((M.A + M.B)/2))
    ASR.diff    <- sum((M.A - M.B) * C.ave)

    # preparing the outcomes
    outcome     <- c(Astand = ASCDR.A,
                     Bstand = ASCDR.B,
                     A.crude = A.crude,
                     B.crude = B.crude,
                     Diff.crude = Diff.crude,
                     Diff.comp = comp.diff,
                     Diff.rates = ASR.diff)
    # giving the outcomes
    return(outcome)
}
```

Let's use this function with the raw data which are used in Box 2.1 (**?**) on Sweden ($A$) and Kazakhstan ($B$):

```
ourdata <- read.table("swed_kaza.txt", header=TRUE)
head(ourdata)

##   pop.swe dea.swe pop.kaz dea.kaz
## 1   59727     279  174078    3720
## 2  229775      42  754758    1220
## 3  245172      31  879129     396
## 4  240110      33  808510     298
## 5  264957      61  720161     561
## 6  287176      87  622988     673

stand.decom(P.A = ourdata$pop.swe,
            D.A = ourdata$dea.swe,
            P.B = ourdata$pop.kaz,
            D.B = ourdata$dea.kaz)

##       Astand       Bstand      A.crude      B.crude   Diff.crude
##  0.007374094  0.011881997  0.010547561  0.007423042  0.003124519
##    Diff.comp   Diff.rates
##  0.007632422 -0.004507903
```

## 6 A second demographic example: Identifying the Intrinsic Growth Rate

In this section we show how to write a function for estimating the intrinsic growth rate in a stable population. Instead of following the approach proposed by Coale (1957) and described in Box 7.1 of **?**, we estimate this demographic value using Newton's method for root-finding. In this way we also introduce a popular numerical method, which might be useful in other situations.

Without going into details, we present the framework before carrying out the analysis in R . If age specific mortality and fertility rates are constant over time and net migration rates are zero at all ages, then Lotka (1939) showed that a stable population will emerge: A population with an invariable age structure and a fixed rate of natural increase.

Specifically he showed that, in such situation, a continuous model of population dynamics is described by the following equation:

$$1 = \int_{\alpha}^{\beta} e^{-ra}\, p(a)\, m(a)\, da\,,$$

where the survival and maternity (female-female) schedules over ages $a$ are represented by $p(a)$ and $m(a)$, respectively. The integral is computed between the minimum and the maximum age at childbearing: $\alpha$ and $\beta$. The intrinsic growth rate in the stable population will growth is denoted by $r$. Among many other consequences, this equation allows for an estimation of how a population igrows once stability is reached. In order to be operative we will first present its version in a discrete time for single-age intervals:

$$1 = \sum_{a=\alpha}^{\beta} e^{-ra} \, L_a \, m_a \; = y(r)$$

which we write also as a function that depends only on $r$: age, mortality and fertility schedules are given. Specifically, $L_a$ is the vector of lifetable exposure from a female period life table with $l_0 = 1$, and $m_a$ is the vector with the rate of bearing female children.

In order to search for the intrinsic growth rate that satisfies the previous equation, we have to find where the following function is equal to zero, i.e. find its root:

$$r : f(r) = y(r) - 1 = 0 \, .$$

A method for finding the roots (or zeroes) of a real-valued function is given by Newton's method. In general if we aim to

$$x : f(x) = 0 \, .$$

Starting from the Taylor-expansion of $f(x)$, this approach finds $x$ iteratively by computing the following equation:

$$x_{n+1} = x_n - \frac{f(x_n)}{f'(x_n)} \, ,$$

starting from an $x_0$ which is sufficiently close to the solution.

More details can be found under `en.wikipedia.org/wiki/Newton's_method`.

In the case of the intrinsic growth rate, the unknown is $r$ and the first derivative with respect to $r$ of $f(r)$ is given by:

$$f'(r) = y'(r) = -\sum_{a=\alpha}^{\beta} a \, e^{-ra} \, L_a \, m_a \, .$$

By dividing and multiplying $f'(r)$ by $y(r)$ we obtain:

$$f'(r) = y'(r) \cdot \frac{y(r)}{y(r)} = -\sum_{a=\alpha}^{\beta} a \, e^{-ra} \, L_a \, m_a \cdot \frac{\sum_{a=\alpha}^{\beta} e^{-ra} \, L_a \, m_a}{\sum_{a=\alpha}^{\beta} e^{-ra} \, L_a \, m_a} = -\, y(r) \, A_B$$

where $A_B = \frac{\sum_{a=\alpha}^{\beta} a \, e^{-ra} \, L_a \, m_a}{\sum_{a=\alpha}^{\beta} e^{-ra} \, L_a \, m_a}$ is the mean age at childbearing in the stable population.

We now have all the ingredients for estimating $r$ using Newton's method. This can be expressed in the following the steps:

1. set as starting value $r_0 = \frac{\ln(NRR)}{A_{B,0}}$ where the Net Reproduction Rate is computed as $NRR = \sum L_a m_a$ and $A_{B,0}$ is a starting value for the mean age at childbearing. Commonly it is assumed equal to 27, though one could also take the stationary $A_{B,0}$ (the weighted average of $a$, where $L_a * m_a$ are the weights). Reasons for such choices can be found in **?**, pp. 150-155.
2. compute $y(r_0)$ and $A_B$
3. compute $f(r)$ and $f'(r)$
4. update $r_1 = r_0 - \frac{f(r)}{f'(r)}$
5. iterate 2., 3. and 4. until convergence: $y(r)$ close to one or equivalently $f(r)$ close to zero

The inputs for our function are:

- a: the vector of ages (or mid-point of age-intervals)
- L: survival schedule. Practically, the female lifetable $L_a$ divided by its radix, $l_0$

- `m`: maternity schedule, rate of bearing female children.

These inputs need to be vectors of the same length. Moreover we can include complementary arguments such as

- `st.Ab=27`: a user-defined starting value for the mean age at childbearing. By default we set it equal to 27
- `MON=FALSE`: a logical value that tells the function whether to trace information on the progress of estimation. By default we could decide to avoid this trace.

Aside from the estimated intrinsic growth rate, we could ask the function to produce the following outcomes:

- `data`: the input information in a dataframe
- `yr`: the solution of Lotka's integral at the last iteration
- `Ab`: the internally computed mean age at childbearing, which depends on $r$
- `NRR`: the internally computed Net Reproduction Rate

Let's write down the function `IntGroRat`:

```r
IntGroRat <- function(a,
                      L,
                      m,
                      st.Ab = 27,
                      MON = FALSE){
  ## function estimating intrinsic growth rate
  ## and other demographic values
  ## by Newton's method

  ## Net Reproduction Rates
  NRR    <- sum(L * m)
  ## starting r
  r      <- log(NRR) / st.Ab
  ## iteration
  for(i in 1:20){
    ## y(r)
    yr   <- sum(exp(-r * a) * L * m)
    ## Ab
    Ab   <- sum(a * exp(-r * a) * L * m) / yr
    ## f(r)
    fr   <- yr -1
    ## f'(r)
    f1r  <- - yr * Ab
    ## updating r
    r    <- r - fr / f1r
    ## printing iteration, Lokta's equation and r
    if(MON) {
      cat(i, yr, r, fill = TRUE)
    }
    ## check convergence: fr close to zero which
    ## is equivalent to yr close to 1
    if(abs(fr) < 10^-6) {
      break
    }
  }
  # one final update to Ab (which depends on r)
  Ab   <- sum(a * exp(-r * a) * L * m) / yr
  ## outputs
  out  <- list(data = data.frame(ages = a, mort = L, fert = m),
              yr = yr,
              Ab = Ab,
              NRR = NRR,
              r = r)
  return(out)
}
```

A difference with respect to the previously coded functions is that we set up a `for`-loop within it, and we thus incorporate a conditional execution for stopping the iterations at the convergence level. Moreover we include a user-defined conditional execution for eventually tracing the estimation procedure, and the printing is done by the command `cat()` (see Module 3). Though Net Reproduction Rate (NRR) and mean age of childbearing ($A_B$) are only by-products of the main procedure, they can also be included in the final output.

Finally we compose all the results into a list: This is because they have different structures. Note that the function does not depend on the length of the age, mortality, and maternity schedules, as long they have same length. We could thus apply our function to one-year-wide age interval, grouped ages as well as to data with different number of available ages.

In order to test `IntGroRat()` we apply it to two datasets: Egypt in 1997 and USA in 1991. Both datasets are taken from **?**, pp. 149-150.

First we load the datasets and quickly look at them:

```
egy <- read.table("FunEgypt1997.txt", header=TRUE)
egy

##      a       L       m
## 1 17.5 4.66740 0.00567
## 2 22.5 4.63097 0.06627
## 3 27.5 4.58518 0.11204
## 4 32.5 4.53206 0.07889
## 5 37.5 4.46912 0.05075
## 6 42.5 4.39135 0.01590
## 7 47.5 4.28969 0.00610

usa <- read.table("FunUSA1991.txt", header=TRUE)
usa

##      a       L      m
## 1 12.5 4.94603 0.0007
## 2 17.5 4.93804 0.0303
## 3 22.5 4.92552 0.0566
## 4 27.5 4.91138 0.0578
## 5 32.5 4.89356 0.0388
## 6 37.5 4.86941 0.0157
## 7 42.5 4.83577 0.0027
## 8 47.5 4.78475 0.0001
```

They have the same column structure:

- `a`: mid-point in the 5-year age intervals
- `L`: person-years from female life-table divided by the radix
- `m`: rate of bearing female children

While Egyptian data start from age 17.5 (interval 15-19), USA data present also information about age 12.5 (interval 10-14).

Now we can apply our function to both cases:

```
fitEgy <- IntGroRat(a = egy$a, L = egy$L, m = egy$m)
fitEgy

## $data
##   ages    mort    fert
## 1 17.5 4.66740 0.00567
## 2 22.5 4.63097 0.06627
## 3 27.5 4.58518 0.11204
## 4 32.5 4.53206 0.07889
## 5 37.5 4.46912 0.05075
## 6 42.5 4.39135 0.01590
## 7 47.5 4.28969 0.00610
##
## $yr
## [1] 1
##
## $Ab
## [1] 29.47247
##
## $NRR
## [1] 1.527414
##
## $r
## [1] 0.01424406

fitUsa <- IntGroRat(a = usa$a, L = usa$L, m = usa$m,
                    st.Ab = 28, MON = TRUE)

## 1 0.9997601 -0.0001664836
## 2 1 -0.0001664824

fitUsa$r

## [1] -0.0001664824
```

In the first case we use the default values for `st.Ab` and `MON`, and then we print the whole output. For the USA data, we change the starting value for the mean age at childbearing, we trace the iterations, and we extract from the list-object `fitUSA` only the value for the intrinsic growth rate, $r$.[1]

## 7 Exercises

### 7.1 Exercise 1

Create a function for computing square roots of any number using successive approximations. Hint: have a look and solve first exercise 2 presented in Module 3, where the approach is introduced.

Your function could start as follows:

```
forsqrt <- function(x, init.guess=1, max.it=10){
#[...]
}
```

where `x` is the number you aim to compute the square root, `init.guess` is the starting value from where you begin the iteration and by default you could set up to 1, `max.it` is the maximum number of iteration of your internal `for`-loop which is set to 10 by default.

You could also add into the function a warning that inform the user when the maximum number of iteration is reached, and therefore recommend to manually increase `max.it` to reach a good approximation of the square root (given the starting value).

Finally test your function for different values of $x$, including big numbers such as $10^7$.

[1]Note that our estimated $r$ for USA in 1991 is different from the one presented in **?**, p. 150 likely due to a typo in the book.

### 7.2 Exercise 2

Write a function that, given a set of inputs, computes several fertility indicators following the ideas presented by **?** in Boxes 5.1 and 5.5.

Your function could start as follows:

```r
FertFun <- function(W, B, Bf = rep(NA, length(B)), L,
                    srb = 1.05, n = 5, l0 = 10^5){
#[...]
}
```

Here you can see the inputs, which are:

- mid-year population of women: `W`
- number of total births during the year: `B`
- number of female births during the year: `Bf`. In this case, the default is a series of `NA` values of suitable length, assuming the absence of this information.
- lifetable exposure ($L_x$) for females: `L`
- sex ratio at birth: `srb`. By default equal to 1.05 for all ages. This would be useful to internally compute the number of female births when this information is not available
- the width of age-intervals: `n`. By default 5-year-wide age intervals
- the radix of the life table used: `l0`. By default equal to $10^5$ value.

Internally this function should compute:

- age-specific fertility rates: $F_x = \frac{B_x}{W_x}$
- total fertility rate: $TFR = n \cdot \sum F_x$, where $n$ is the length of the interval
- age-specific maternity rate: $F_x^F = \frac{B_x^F}{W_x}$.
- gross reproduction rate: $GRR = n \cdot \sum F_x^F$
- net reproduction rate: $GRR = \frac{1}{l_0} \cdot \sum F_x^F \cdot L_x$

Hint: you could test the availability of information on the fraction/number of female births with the following conditional execution: `if(is.na(Bf[1]))`

Remember that sex ratio at birth for mothers of a given age, $x$, is computed as:

$$srb_x = \frac{B_x^M}{B_x},$$

where $B_x^M$ are the number of male births to females age $x$. And that, in this exercise, you are only asked to assume the same *srb* for all ages.

Test your function with the following datasets: `USAfert1991.txt`, `USAfert1992.txt` and `USAfert2000.txt`. These data contain ages, mid-year female population for USA in 1991, 1992, and 2000, as well as the number of total births during the year. Moreover information about $L_x$ from the life table for females is given. Only for 1991 is number of female births provided.

Read your data as follows:

```r
usa91 <- read.table("USAfert1991.txt", header = TRUE)
usa92 <- read.table("USAfert1992.txt", header = TRUE)
usa00 <- read.table("USAfert2000.txt", header = TRUE)
```

Assign the outcomes of the function to objects `fert91`, `fert92` and `fert00` for the 3 datasets, respectively. Check that your function produces the following results:

```
fert91
```

```
## $data
##          W       B     Bf         asfr          FxF
## 1  8620000   12014   5816 0.0013937355 0.0006747100
## 2  8371000  519577 253979 0.0620686895 0.0303403417
## 3  9419000 1089692 532712 0.1156908377 0.0565571717
## 4 10325000 1219965 596823 0.1181564165 0.0578036804
## 5 11125000  884862 431694 0.0795381573 0.0388039551
## 6 10344000  330993 162005 0.0319985499 0.0156617363
## 7  9496000   52095  25531 0.0054859941 0.0026886057
## 8  8188000    1709    829 0.0002087201 0.0001012457
##
## $TFR
## [1] 2.072706
##
## $GRR
## [1] 1.013157
##
## $NRR
## [1] 0.9952671
```

```
fert92
```

```
## $data
##          W       B          Bf         asfr          FxF
## 1  8831206   12220   5960.9756 0.0013837295 0.0006749900
## 2  8324273  505415 246543.9024 0.0607158127 0.0296174696
## 3  9344413 1070490 522190.2439 0.1145593629 0.0558826161
## 4 10047198 1179264 575250.7317 0.1173724256 0.0572548418
## 5 11165144  895271 436717.5610 0.0801844562 0.0391143689
## 6 10619275  344644 168119.0244 0.0324545696 0.0158314974
## 7  9519450   55702  27171.7073 0.0058513885 0.0028543358
## 8  7820172    2008    979.5122 0.0002567718 0.0001252546
##
## $TFR
## [1] 2.063893
##
## $GRR
## [1] 1.006777
##
## $NRR
## [1] 0.989555
```

```
fert00
```

```
## $data
##          W      B           Bf         asfr          FxF
## 1  1990582    242    118.04878 1.215725e-04 5.930366e-05
## 2  1967944   1427    696.09756 7.251222e-04 3.537182e-04
## 3  1975749   6850   3341.46341 3.467039e-03 1.691239e-03
## 4  1966356  21845  10656.09756 1.110938e-02 5.419210e-03
## 5  1937862  48581  23698.04878 2.506938e-02 1.222896e-02
## 6  1967052  86783  42333.17073 4.411830e-02 2.152112e-02
## 7  1962228 132786  64773.65854 6.767105e-02 3.301027e-02
## 8  2010232 178995  87314.63415 8.904195e-02 4.343510e-02
## 9  1989571 199510  97321.95122 1.002779e-01 4.891604e-02
## 10 1920574 202208  98638.04878 1.052852e-01 5.135862e-02
## 11 1853481 206182 100576.58537 1.112404e-01 5.426363e-02
## 12 1822935 206781 100868.78049 1.134330e-01 5.533317e-02
## 13 1784270 203125  99085.36585 1.138421e-01 5.553272e-02
## 14 1819779 208150 101536.58537 1.143820e-01 5.579609e-02
## 15 1809080 207956 101441.95122 1.149513e-01 5.607378e-02
## 16 1860643 214286 104529.75610 1.151677e-01 5.617937e-02
## 17 1947274 222130 108356.09756 1.140723e-01 5.564500e-02
## 18 2090972 235025 114646.34146 1.123999e-01 5.482921e-02
## 19 2074953 225938 110213.65854 1.088882e-01 5.311622e-02
## 20 2050623 206367 100666.82927 1.006362e-01 4.909084e-02
## 21 1979918 184174  89840.97561 9.302102e-02 4.537611e-02
## 22 2019283 165473  80718.53659 8.194642e-02 3.997386e-02
## 23 2074019 147326  71866.34146 7.103406e-02 3.465076e-02
## 24 2193370 131256  64027.31707 5.984216e-02 2.919130e-02
## 25 2267229 111446  54363.90244 4.915515e-02 2.397812e-02
## 26 2288339  88672  43254.63415 3.874950e-02 1.890220e-02
## 27 2271275  68721  33522.43902 3.025657e-02 1.475930e-02
## 28 2337368  51962  25347.31707 2.223098e-02 1.084438e-02
## 29 2311220  37255  18173.17073 1.611920e-02 7.863022e-03
## 30 2313002  24465  11934.14634 1.057716e-02 5.159593e-03
## 31 2271413  14852   7244.87805 6.538662e-03 3.189591e-03
## 32 2251570   8745   4265.85366 3.883956e-03 1.894613e-03
## 33 2198987   4696   2290.73171 2.135529e-03 1.041721e-03
## 34 2162568   2281   1112.68293 1.054764e-03 5.145192e-04
## 35 2118296   1135    553.65854 5.358080e-04 2.613697e-04
## 36 2054474    527    257.07317 2.565133e-04 1.251284e-04
## 37 1965555    250    121.95122 1.271906e-04 6.204418e-05
## 38 1950309    156     76.09756 7.998733e-05 3.901821e-05
##
## $TFR
## [1] 2.053445
##
## $GRR
## [1] 1.00168
##
## $NRR
## [1] 0.986658
```

## References

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Kitagawa, E. M. (1955). Components of a difference between two rates*. *Journal of the American Statistical Association 50*(272), 1168–1194.

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