Template file for the documentation of the seqinR package

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Contents

1 Introduction

This is a template file to explain how to re-use data from or to contribute to the documentation of the seqinR package.

2 Where are the files

All the files used to compile the documentation are located in the `src` folder. We are currently in the `template` folder within the `src` folder, we move one step back in the hierarchy to show the content of the `src` folder:

```
getwd()
```

```
[1] "/Users/lobry/seqinr/inst/doc/src/template"
```

```
setwd("..")
dir()
```

```
[1] "CVS"         "appendix"    "book"        "config"      "figs"
[6] "frontmatter" "mainmatter"  "misc"        "tables"      "template"
```

```
setwd("template")
```

The documentation is in fact a collection of independent LaTeX articles generated by Sweaving a `*.rnw` file. They are merged into a single multi-author document by Sweaving the file `book.rnw` in the `book` folder. The articles to be incorporated in the final documentation are located in the `frontmatter`, `mainmatter` and `appendix` folders.

2.1 Bibliography

The references are in the `book.bib` file located in the `config` folder:

```
bib <- readLines("../config/book.bib")
cat(head(bib), sep = "\n")
```

```
@incollection{seqinr,
    author = {Charif, D. and Lobry, J.R.},
    title = {Seqin{R} 1.0-2: a contributed package to the {R} project for statistical computing devoted to biolog
    booktitle = {Structural approaches to sequence evolution: Molecules, networks, populations},
    year = {2007},
    editor = {U. Bastolla, M. Porto, H.E. Roman and M. Vendruscolo},
```

New references should be included in this file. There is a line at the end of all `*.rnw` files saying `\bibliography{../config/book}` so that this file can be used by bibTeX. References are called in the text with a `\cite{}` command, for instance `\cite{seqinr}` to cite the seqinR package [1].

2.2 Tables

The LaTeX tables are all in the `tables` folder.

2.2.1 Regular LaTeX tables

For example, the file `templatetable.tex` looks like:

```
ttab <- readLines("../tables/templatetable.tex")
cat(ttab, sep = "\n")
```

```
% Example of latex table
\begin{table}[ht]
\begin{center}
\begin{tabular}{rll}
\hline
 & Type & Description \\
\hline
1 &      CDS &             .PE protein coding region \\
2 &    LOCUS &                 sequenced DNA fragment \\
3 & MISC\_RNA & .RN other structural RNA coding region \\
4 &     RRNA &             .RR mature ribosomal RNA \\
5 &    SCRNA &          .SC small cytoplasmic RNA \\
6 &    SNRNA &               .SN small nuclear RNA \\
7 &     TRNA &              .TR mature transfer RNA \\
\hline
\end{tabular}
\caption{Example of latex table (available subsequences in genbank)}
\label{templatetable}
\end{center}
\end{table}
```

This LaTeX table can be included with a `\input{../tables/templatetable.tex}` command and called in the text with a `\ref{templatetable}` command (see table 1).

	Type	Description
1	CDS	.PE protein coding region
2	LOCUS	sequenced DNA fragment
3	MISC_RNA	.RN other structural RNA coding region
4	RRNA	.RR mature ribosomal RNA
5	SCRNA	.SC small cytoplasmic RNA
6	SNRNA	.SN small nuclear RNA
7	TRNA	.TR mature transfer RNA

Table 1: Example of latex table (available subsequences in genbank)

2.2.2 Tables generated with `xtable()`

Tables can also be generated on the fly at the ® level with `xtable()`. Here is an example:

```
data(toyaa)
print(xtable(toyaa,
  digits = rep(0,4),
  caption = "Data to be loaded with \\texttt{data(toyaa).}",
  label = "toyaa"),
  file = "../tables/toyaa.tex")
```

	Ala	Val	Cys
1	130	70	0
2	60	40	0
3	60	35	5

Table 2: Data to be loaded with `data(toyaa)`.

This LATEX table is included as previously with a `\input{../tables/toyaa.tex}` command and called in the text with a `\ref{toyaa}` command (see table 2). Note the use of the double escape sequence `\\` in the caption.

2.3 Figures

All figures are in the `figs` folder in PDF format.

2.3.1 Regular LATEX figures

The file `Rlogo.pdf` contains for instance the ℝ logo. The following code includes figure 1:

```
\begin{figure}
\centering
\fbox{
\begin{minipage}{\textwidth}
\centering
\includegraphics[width=0.5\textwidth]{../figs/Rlogo}
\caption{The \Rlogo{} logo}
\label{Rlogofig}
\end{minipage}
}
\end{figure}
```
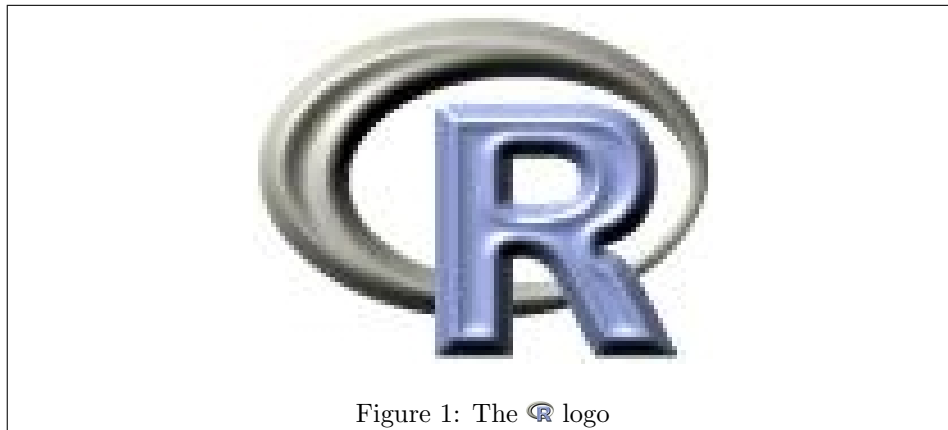
The following code include the figure in the margin:

```
\marginpar{
\includegraphics[width=\marginparwidth]{../figs/Rlogo}\\
\tiny{The \Rlogo{} logo}
}
```


The ℝ logo

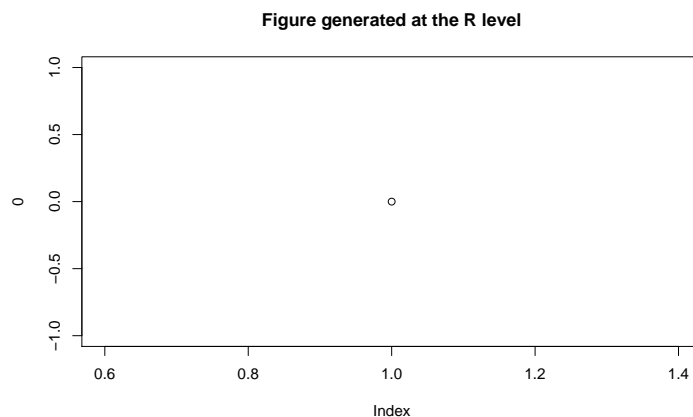### 2.3.2 Figures generated at the ℝ level

Add a `fig=T` in the header to insert a figure. The following code chunk:

```
<<tryfig, width = 8, height = 5, fig=T>>=
plot(0, main = "Figure generated at the R level")
```

Figure 1: The ℝ logo

yields:

```
plot(0, main = "Figure generated at the R level")
```


All the figures are generated in PDF format in the `figs` folder. To avoid names collisions they are prefixed with the name of the the current `*.rnw` file, that is with `template-` in this case:

```
list.files(path = "../figs/", pattern = "tryfig")
```

```
[1] "template-tryfig.pdf"
```

The default figure size in the final document can be changed. For instance after `\setkeys{Gin}{width=0.5\textwidth}` the same code chunk yields:

```
plot(0, main = "Figure generated at the R level")
```

Figure generated at the R level
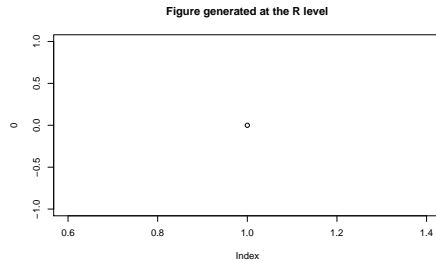
The automatic inclusion of a figure after a code chunk can be neutralized with `include=F` in the header. For example after the following code chunk the figure is generated in the `figs` folder but not included:

```
<<showinclude, width = 7, height = 7, fig=T, include=F>>=
plot(0, main = "Figure generated at the R level")
list.files(path="../figs/", pattern = "showinclude")
@
```

```
plot(0, main = "Figure generated at the R level\n (width = 7, height = 7)")
```

You can then include it with its name, here `template-showinclude`:

```
list.files(path = "../figs/", pattern = "showinclude")
```

```
[1] "template-showinclude.pdf"
```

or better use `.PrefixName` so that if you change the file name the figure will still be found. The code source of this document (`template.rnw`) shows how figure 2 was inserted.

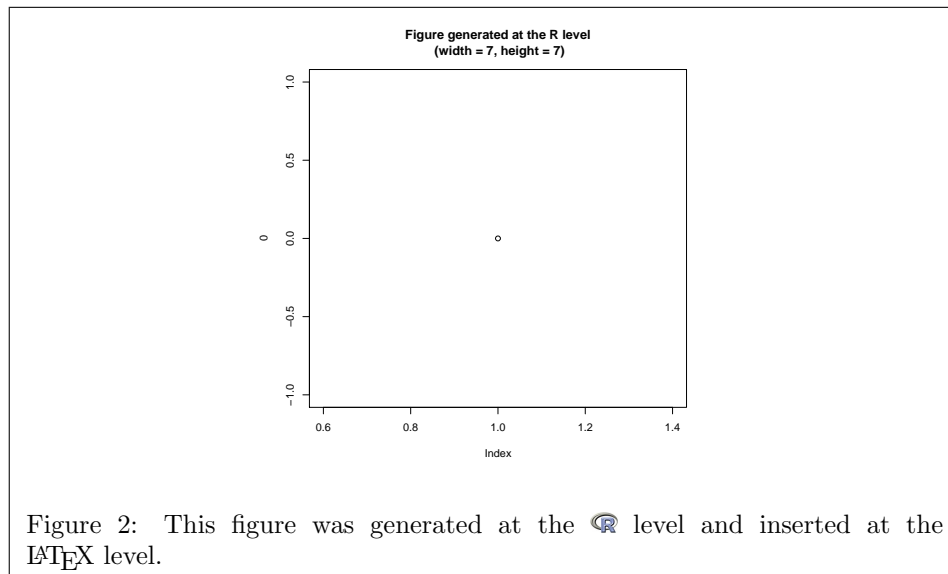# 3   Configuration files

3.1   LaTeXpackages

The second line of the `*.rnw` files contains the following LaTeX command:

```
\input{../config/commontex}
```

```
ctex <- readLines("../config/commontex.tex")
cat(ctex, sep = "\n")
```

```
\usepackage{graphicx} % Extended graphics inclusions
\usepackage{float}
\usepackage{url} % For \url{}
\usepackage{../config/atxy} % For front cover
\usepackage{amsfonts} % Needed for some fonts
\usepackage[usenames]{color} % Needed for colored R input/output
\usepackage{pdfcolmk} % Correct some problems with the color stack
```

Extra LaTeX packages should go there so that the book could be compiled.

Figure 2: This figure was generated at the Ⓡ level and inserted at the LaTeX level.

3.2 Authors

The authors should be given with `\and` as separator as in:

`\author{Lobry, J.R. \and Someone, E.L.S.E.}`

The authors of the whole document are all contributors listed in alphabetical order. This is done with the script in the file `book/book.rnw`.

3.3 Ⓡ packages

Required Ⓡ packages should be loaded in the `config/commonrnw.rnw` file which is included at the begining of the `*.rnw` files with:

`SweaveInput{../config/commonrnw.rnw}`

The current list of Ⓡ packages is as follows:

```
crnw <- readLines("../config/commonrnw.rnw")
cat(crnw[grep("library", crnw)], sep = "\n")
```

```
library(seqinr, lib = "../../../../../seqinr.Rcheck")
library(xtable)
library(ade4)
library(ape)
library(MASS)
```

Important note: if you are not working with development version of seqin**R**, then the line:

`library(seqinr, lib = "../../../../../seqinr.Rcheck")`

7

should be changed to:

```
library(seqinr)
```

3.4   Don't remove me

There is a comment line at the begining of the `*.rnw` file stating:

```
% BEGIN - DO NOT REMOVE THIS LINE
```

As suggested, do not removed it as it is used by the `book/book.rnw` script to merge the relevant parts of the individual articles into a book.

3.5   Extras in the `commonrnw.rnw` file

The LaTeX environments `Sinput` and `Soutput` are re-defined in the `commonrnw.rnw` file so that the ® inputs are in red and the ® outputs in blue:

```
getwd()
```

```
[1] "/Users/lobry/seqinr/inst/doc/src/template"
```

The ® console options `prompt` and `continue` are re-defined so that an ® input could be copy/pasted directly from the final PDF into an ® console without syntax error:

```
getOption("prompt")
```

```
[1] " "
```

```
getOption("continue")
```

```
[1] " "
```

The ® console option `width` is set to 77 characters:

```
getOption("width")
```

```
[1] 77
```

This is to fit ® code in the LaTeXpage. This works well in most cases. This may fail if you have long strings in the code. Manual editing is possible with `keep.source=T` in the header of code chunks.

Some pre-defined invisible ® constant are available:

Name	Current value
.CurFileName	template.rnw
.PrefixName	template
.RversionName	R version 2.5.1 (2007-06-27)

The CRAN repository is forced so that you can Sweave a file that need a CRAN connection without setting this manually. Default is:

```
getOption("repos")
```

```
                          CRAN
"http://cran.univ-lyon1.fr"
```

The `prefix.string` option for `Sweave()` is set so that all figures are generated in the `figs` folder with the name of the current file as a prefix.

4 Compiling this document

There are two successive compilation steps.

4.1 *.rnw → *.tex

Under ℝ with `template` as the current working directory run `Sweave()` with `template.rnw` as argument:

```
getwd()
```

```
[1] "/Users/lobry/seqinr/inst/doc/src/template"
```

```
Sweave("template.rnw")
```

The output on your ℝ console should look like:

```
Writing to file template.tex
Processing code chunks ...
 1 : term hide (label=options)
 2 : echo term verbatim (label=wherearethefiles)
 3 : echo term verbatim (label=showbookbig)
 4 : echo term verbatim (label=showtemplatetable)
[...snip...]
16 : term tex (label=sessionInfo)

You can now run LaTeX on 'template.tex'
```

4.1.1 Troubleshooting

The list of ℝ packages that must be installed is listed in the next section (Session Informations). If one package is missing you'll get an error message. It's advisable to install packages with all dependencies, for instance:

```
install.packages("ape", dependencies = TRUE)
```

If the **seqinR** package is installed but you get an error like:

```
Error in library(seqinr, lib = "../../../../../seqinr.Rcheck")
```

open the file `config/commonrnw.rnw` and change the line:

```
library(seqinr, lib = "../../../../../seqinr.Rcheck")
```

into:

```
library(seqinr)
```

4.2 *.tex → *.pdf

Use pdfLATEX to compile `template.tex` into a PDF file with something like:

```
unix$ pdflatex template.tex
unix$ bibtex template
unix$ pdflatex template.tex
```

You should obtain the PDF of the present document (`template.pdf`).

5   Session Informations

This part was compiled under the following ® environment:

- R version 2.5.1 (2007-06-27), `i386-apple-darwin8.9.1`

- Locale: `C`

- Base packages: base, datasets, grDevices, graphics, methods, stats, utils

- Other packages: MASS 7.2-34, ade4 1.4-3, ape 1.9-4, gee 4.13-12, lattice 0.15-11, nlme 3.1-83, seqinr 1.1-2, xtable 1.4-3

References

[1] D. Charif and J.R. Lobry. SeqinR 1.0-2: a contributed package to the R project for statistical computing devoted to biological sequences retrieval and analysis. In H.E. Roman U. Bastolla, M. Porto and M. Vendruscolo, editors, *Structural approaches to sequence evolution: Molecules, networks, populations*, Biological and Medical Physics, Biomedical Engineering, pages 207–232. Springer Verlag, New York, USA, 2007. ISBN 978-3-540-35305-8.