

Bioconductor L^AT_EX Style

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1 Authoring Sweave / L^AT_EX package vignettes

To use with Sweave, add the following to your package 'DESCRIPTION' file:

```
Suggests: BiocStyle
```

and add this code chunk to the preamble (between the `\documentclass{article}` and `\begin{document}` latex commands) of your .Rnw file:

```
<<style-Sweave, eval=TRUE, echo=FALSE, results=tex>>=
BiocStyle::latex()
@
```

To use with [knitr](#), add the following to the 'DESCRIPTION' file:

```
VignetteBuilder: knitr
Suggests: BiocStyle, knitr
```

this to the top of the .Rnw file:

```
%\VignetteEngine{knitr::knitr}
```

and this to the preamble:

```
<<style-knitr, eval=TRUE, echo=FALSE, results="asis">>=
BiocStyle::latex()
@
```

See `?latex` for additional options. [BiocStyle](#) automatically attaches the following L^AT_EX packages: `color`, `enumitem`, `fancyhdr`, `geometry`, `hyperref`, `parskip`, `sectsty`.

Provided the package has been installed, a convenient way to view the vignette as it is being written is with the command

```
R CMD Sweave --pdf vignette.Rnw
```

A short-cut useful for checking the L^AT_EX portion of vignettes is to toggle evaluation of code chunks to FALSE

```
SWEAVE_OPTIONS="eval=FALSE" R CMD Sweave --pdf vignette.Rnw
```

When using [knitr](#), the command to process the vignette is

```
R CMD Sweave --engine=knitr::knitr --pdf vignette.Rnw
```

By default, [knitr](#) automatically caches results of vignette chunks, greatly accelerating the turnaround time required for edits. Both the default and [knitr](#) incantations create PDF files using `texi2dvi -pdf`; many versions of this software incorrectly display non-breaking spaces as a tilde, `~`. This can be remedied (as on the *Bioconductor* build system) with a final run of

```
R CMD texi2dvi --pdf vignette.tex
R CMD pdflatex vignette.tex
```

2 Style macros

BiocStyle introduces the following additional markup styling commands useful in typical *Bioconductor* vignettes.

Software:

- `\R{}` and `\Bioconductor{}` to reference *R* software and the *Bioconductor* project.
- `\software{GATK}` to reference third-party software, e.g., *GATK*.

Packages:

- `\Biocpkg{IRanges}` for *Bioconductor* software, annotation and experiment data packages, including a link to the release landing page or if the package is only in devel, to the devel landing page. *IRanges*.
- `\CRANpkg{data.table}` for *R* packages available on CRAN, including a link to the FHCRC CRAN mirror landing page, *data.table*.
- `\Githubpkg{rstudio/rmarkdown}` for *R* packages available on GitHub, including a link to the package repository, *rmarkdown*.
- `\Rpackage{MyPkg}` for *R* packages that are *not* available on *Bioconductor* or CRAN, *MyPkg*.

Code:

- `\Rfunction{findOverlaps}` for functions *findOverlaps*.
- `\Robject{olaps}` for variables *olaps*.
- `\Rclass{GRanges}` when referring to a formal class *GRanges*.
- `\Rcode{log(x)}` for *R* code, *log(x)*.

Communication:

- `\bioccomment{additional information for the user}` communicates *comment: additional information for the user*.
- `\warning{common pitfalls}` signals *warning: common pitfalls*.
- `\fixme{incomplete functionality}` provides an indication of *fixme: incomplete functionality*.

General:

- `\email{user@domain.com}` to provide a linked email address, *user@domain.com*.
- `\file{script.R}` for file names and file paths 'script.R'.

3 Title, running headers, and table of contents

Create a title and running headers by defining the `\biocitle` and `\author` commands in the preamble

```
\biocitle[Short title for headers]{Full title for title page}
%% also: \biocitle{Title used for both header and title page}
%% or... \title{Title used for both header and title page}
\author{Iman Author\footnote{iman@author.org}}
```

Use `\maketitle` at the start of the document to create the title in the document.

Use `\tableofcontents` for a hyperlinked table of contents, `\section`, `\subsection`, `\subsubsection` for structuring your vignette.

Formatting of subsections and subsubsections are as follows.

3.1 This is a subsection

3.1.1 This is a subsubsection

4 Figures

Besides the usual L^AT_EX capabilities (figure environment and `\includegraphics` command), 'Bioconductor.sty' defines a macro `\incfig[placement]{filename}{width}{shorttitle}{extendedcaption}`, which expects four arguments:

filename The name of the figure file, also used as the label by which the float can be referred to by `\ref{}`. Some Sweave and *knitr* options place figures in a subdirectory; unless `short.fignames=TRUE` is set the full file name, including the subdirectory and any prefixes, should be provided. By default, these are '`<sweavename>-`' for Sweave and '`figure/`' for *knitr*. Please note the different naming scheme used by *knitr*: figure files are named '`<chunkname>-i`' where *i* is the number of the plot generated in the chunk.

width Figure width.

shorttitle A short description, used in the list of figures and printed in bold as the first part of the caption.

extendedcaption Continuation of the figure caption.

The optional **placement** specifier controls where the figure is placed on page and takes the usual values allowed by L^AT_EX floats, i.e., a list containing t, b, p, or h, where letters enumerate permitted placements. If no placement specifier is given, the default tpb is assumed.

For `incfig` with Sweave, use

```
<<figureexample, fig=TRUE, include=FALSE, width=4.2, height=4.6>>=
v = seq(0, 60i, length=1000)
plot(abs(v)*exp(v), type="l", col="Royalblue")
@
\incfig{LatexStyle-figureexample}{0.5\textwidth}{A curve.}
{The code that creates this figure is shown in the code chunk.}
as shown in Figure~\ref{LatexStyle-figureexample}.
```

This results in

```
> v = seq(0, 60i, length=1000)
> plot(abs(v)*exp(v), type="l", col="Royalblue")
```

as shown in Figure ???. When the option `short.fignames` is set to `TRUE`, figure names used by `\incfig` and `\ref` do not contain any prefix and are identical to the corresponding code chunk labels (plus figure number in case of *knitr*). For example, in Sweave the respective code for the above example would be `\incfig{figureexample}{...}{...}{...}` and `\ref{figureexample}`, while in *knitr* these are expected to be `\incfig{figureexample-1}{...}{...}{...}` and `\ref{figureexample-1}`.

For `\incfig` with *knitr*, use the option `fig.show='hide'` rather than `include=FALSE`. The *knitr*-equivalent code for Figure ?? is:

```
<<figureexample, fig.show='hide', fig.width=4.2, fig.height=4.6>>=
v = seq(0, 60i, length=1000)
plot(abs(v)*exp(v), type="l", col="Royalblue")
@
```

Note the difference in option names setting the figure width and height compared to Sweave. Unless `short.fignames=TRUE` is set, use the default '`figure/`' prefix when inserting and referring to figures, e.g.:

```
\incfig{figure/figureexample-1}{0.5\textwidth}{A curve.}
{The code that creates this figure is shown in the code chunk.}
```

A custom prefix for figure file names can be passed to latex using the `fig.path` option. When `short.fignames=TRUE`, figures can be referred to directly by code chunk labels, as described earlier in this section.

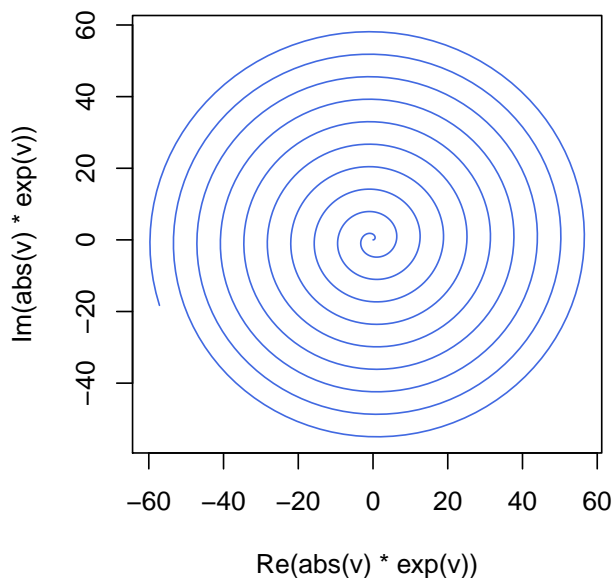


Figure 1: **A curve**. The code that creates this figure is shown in the code chunk.

5 Bibliography

`BiocStyle::latex()` has default argument `use.unsrurl=TRUE` to automatically format bibliographies using *natbib*'s `unsrurl` style. There is no need to explicitly include *natbib*, and it is an error to use a `\bibliographystyle` command. The *unsrurl.bst* format, e.g., `[?, ?]`, supports hyperlinks to DOI and PubMed IDs but not `\citet` or `\citep`.

To use a bibliography style different from `unsrurl`, set `use.unsrurl=FALSE` and follow normal L^AT_EX conventions.

6 Session info

Here is the output of `sessionInfo` on the system on which this document was compiled:

```
> toLatex(sessionInfo())
```

- R version 3.3.1 (2016-06-21), x86_64-apple-darwin13.4.0
- Locale: C/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Other packages: BiocStyle 2.0.3
- Loaded via a namespace (and not attached): Rcpp 0.12.6, digest 0.6.10, evaluate 0.9, formatR 1.4, htmltools 0.3.5, knitr 1.13, magrittr 1.5, rmarkdown 1.0, stringi 1.1.1, stringr 1.0.0, tools 3.3.1, yaml 2.1.13