

# Bioconductor L<sup>A</sup>T<sub>E</sub>X Style

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## 1 Authoring Sweave / L<sup>A</sup>T<sub>E</sub>X package vignettes

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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<sup>A</sup>T<sub>E</sub>X 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<sup>A</sup>T<sub>E</sub>X 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

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*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 packages, including a link to the release version landing page, *IRanges*.
- `\Biocannopkg{org.Hs.eg.db}` for *Bioconductor* annotation packages, including a link to the release version landing page, *org.Hs.eg.db*.
- `\Biocexptpkg{parathyroidSE}` for *Bioconductor* experiment data packages, including a link to the release version landing page, *parathyroidSE*.
- `\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](mailto:user@domain.com).
- `\file{script.R}` for file names and file paths 'script.R'.

## 3 Title, running headers, and table of contents

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

```
\biocTitle[Short title for headers]{Full title for title page}
%% also: \biocTitle{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<sup>A</sup>T<sub>E</sub>X 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<sup>A</sup>T<sub>E</sub>X floats, i.e., a list containing t, b, p, or h, where letters enumerate permitted placements. If no placement specifier is given, the default `tbp` 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}{0.25\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

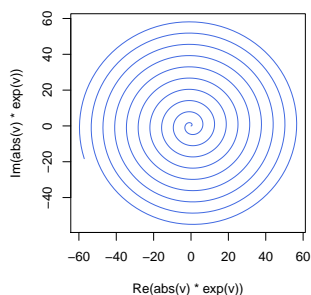


Figure 1: **A curve**. The code that creates this figure is shown in the code chunk.

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

as shown in Figure 1. When the option `short.filenames` 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 1 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.filenames=TRUE` is set, use the default 'figure/' prefix when inserting and referring to figures, e.g.:

```
\incfig{figure/figureexample-1}{0.25\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.filenames=TRUE`, figures can be referred to directly by code chunk labels, as described earlier in this section.

## 5 Bibliography

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`BiocStyle::latex()` has default argument `use.unsrtdurl=TRUE` to automatically format bibliographies using *natbib*'s `unsrtdurl` style. There is no need to explicitly include *natbib*, and it is an error to use a `\bibliographystyle` command. The *unsrtdurl.bst* format, e.g., [1, 2], supports hyperlinks to DOI and PubMed IDs but not `\citet` or `\citep`.

To use a bibliography style different from `unsrtdurl`, set `use.unsrtdurl=FALSE` and follow normal L<sup>A</sup>T<sub>E</sub>X conventions.

## 6 Session info

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

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

- R version 3.2.2 Patched (2015-10-08 r69496), x86\_64-apple-darwin10.8.0
- Locale: en\_US.UTF-8/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: BiocStyle 1.8.0
- Loaded via a namespace (and not attached): digest 0.6.8, evaluate 0.8, formatR 1.2.1, htmltools 0.2.6, knitr 1.11, magrittr 1.5, rmarkdown 0.8.1, stringi 0.5-5, stringr 1.0.0, tools 3.2.2, yaml 2.1.13

## References

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- [1] Robert C Gentleman, Vincent J Carey, Douglas M Bates, Ben Bolstad, Marcel Dettling, Sandrine Dudoit, Byron Ellis, Laurent Gautier, Yongchao Ge, Jeff Gentry, Kurt Hornik, Torsten Hothorn, Wolfgang Huber, Stefano Iacus, Rafael Irizarry, Friedrich Leisch, Cheng Li, Martin Maechler, Anthony J Rossini, Gunther Sawitzki, Colin Smith, Gordon Smyth, Luke Tierney, Jean Y H Yang, and Jianhua Zhang. Bioconductor: open software development for computational biology and bioinformatics. *Genome Biology*, 5(10):R80, 2004. [doi:10.1186/gb-2004-5-10-r80](https://doi.org/10.1186/gb-2004-5-10-r80), PMID:15461798.
- [2] Michael Lawrence, Wolfgang Huber, Hervé Pagès, Patrick Aboyoun, Marc Carlson, Robert Gentleman, Martin Morgan, and Vincent Carey. Software for computing and annotating genomic ranges. *PLoS Computational Biology*, 9, 2013. [doi:10.1371/journal.pcbi.1003118](https://doi.org/10.1371/journal.pcbi.1003118).