

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

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## 1 Use

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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
```

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, helvet, 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 Markup commands

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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*.
- `\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 and sectioning: this is a section

---

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.

#### 3.1 This is a subsection

Apud Helvetios longe nobilissimus fuit et ditissimus Orgetorix. Is M. Messala, M. Pisone consulibus regni cupiditate inductus coniurationem nobilitatis fecit et civitati persuasit ut de finibus suis cum omnibus copiis exirent: perfacile esse, cum virtute omnibus praestarent, totius Galliae imperio potiri.

##### 3.1.1 This is a subsubsection

His rebus fiebat ut et minus late vagarentur et minus facile finitimis bellum inferre possent; qua ex parte homines bellandi cupidi magno dolore adficiebantur. Pro multitudine autem hominum et pro gloria belli atque fortitudinis angustos se fines habere arbitrabantur, qui in longitudinem milia passuum CCXL, in latitudinem CLXXX patebant.

### 4 Bibliography

---

`BiocStyle::latex()` has default argument `use.unsrtrurl=TRUE` to automatically format bibliographies using *natbib*'s `unsrtrurl` style. There is no need to explicitly include *natbib*, and it is an error to use a `\bibliographystyle` command. The *unsrtrurl.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 `unsrtrurl`, set `use.unsrtrurl=FALSE` and follow normal L<sup>A</sup>T<sub>E</sub>X conventions.

### 5 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.filenames=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*.

**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.

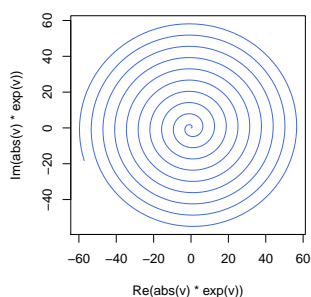


Figure 1: **A curve.** The code that creates this figure is shown in the code chunk.

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

```
> 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. For example, the respective code for the above example would be `\incfig{figureexample}{...}{...}{...}` and `\ref{figureexample}`.

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}{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 in Section 5.

## 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 3.1.0 RC (2014-04-02 r65358), i386-w64-mingw32
- Locale: LC\_COLLATE=C, LC\_CTYPE=English\_United States.1252, LC\_MONETARY=English\_United States.1252, LC\_NUMERIC=C, LC\_TIME=English\_United States.1252
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): BiocStyle 1.2.0, tools 3.1.0

## 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).