

Bioconductor L^AT_EX Style

Martin Morgan, Andrzej Oleś, Wolfgang Huber

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1 Use

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

```
Suggests: BiocStyle
```

and add this code chunk to your .Rnw file:

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

To use with *knitr*, add the following to the 'DESCRIPTION' file:

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

and this to your .Rnw file:

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

See `?latex` for additional options. Page headers contain the title of the vignette as defined by `\title`, override it by adding the following line to the preamble of your vignette:

```
\renewcommand{\thetitle}{Short header title}
```

BiocStyle automatically attaches the following L^AT_EX packages: `color`, `fancyhdr`, `geometry`, `helvet`, `hyperref`, `sectsty`, `Sweave` and `titling`.

2 Markup commands

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:

- `\comment{comment to the user}` communicates a *comment to 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 Sectioning: this is a section

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

3.1 This is a subsection

Lorem ipsum dolor sit amet, consectetur adipisicing elit, sed do eiusmod tempor incididunt ut labore et dolore magna aliqua. Ut enim ad minim veniam, quis nostrud exercitation ullamco laboris nisi ut aliquip ex ea commodo consequat.

3.1.1 This is a subsubsection

Duis aute irure dolor in reprehenderit in voluptate velit esse cillum dolore eu fugiat nulla pariatur. Excepteur sint occaecat cupidatat non proident, sunt in culpa qui officia deserunt mollit anim id est laborum.

4 Including 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:

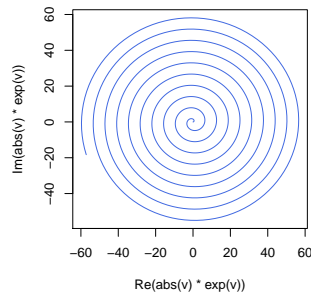


Figure 1: **A curve**. The code that creates this figure is shown in the code chunk.

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.

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 `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 4.

5 Session info

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

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

- R version 3.0.2 (2013-09-25), x86_64-unknown-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- Loaded via a namespace (and not attached): BiocStyle 1.0.0, tools 3.0.2