

# Changes in R

From version 3.2.2 to version 3.2.3

*by the R Core Team*

## CHANGES IN R 3.3.1 patched

### NEW FEATURES

- `extSoftVersion()` now reports the version (if any) of the readline library in use.
- Convenience function `hasName()` has been added; it is intended to replace the common idiom `!is.null(x$name)` without the usually unintended partial name matching.
- The version of LAPACK included in the sources has been updated to 3.6.1, a bug-fix release including a speedup for the non-symmetric case of `eigen()`.
- Use `options(deparse.max.lines)` to limit the number of lines recorded in `.Traceback` and other deparsing activities.

### INSTALLATION and INCLUDED SOFTWARE

- Versions of the readline library  $\geq 6.3$  had been changed so that terminal window resizes were not signalled to readline: code has been added using an explicit signal handler to work around that (when R is compiled against readline  $\geq 6.3$ ). ([PR#16604](#))
- `configure` works better with Oracle Developer Studio 12.5.

### UTILITIES

- `R CMD check` reports more dubious flags in files `'src/Makevars.in'`, including `'-w'` and `'-g'`.
- `R CMD check` has been set up to filter important warnings from recent versions of `gfortran` with `'-Wall -pedantic'`: this now reports non-portable GNU extensions such as out-of-order declarations.

### BUG FIXES

- The check for non-portable flags in `R CMD check` could be stymied by `'src/Makevars'` files which contained targets.
- (Windows only) When using certain desktop themes in Windows 7 or higher, `Alt-Tab` could cause `Rterm` to stop accepting input. ([PR#14406](#); patch submitted by Jan Gleixner.)
- `pretty(d, ...)` behaves better for date-time `d` ([PR#16923](#)).
- When a class name matches multiple classes in the cache, perform a dynamic search in order to obey namespace imports. This should eliminate annoying messages about multiple hits in the class cache. Also, pass along the package from the `ClassExtends` object when looking up superclasses in the cache.
- `sample(NA_real_)` now works.
- Packages using non-ASCII encodings in their code did not install data properly on systems using different encodings.

## Developer support

A very natural progression in the R and Bioconductor community is from user to package developer, transforming your knowledge and domain expertise into software that others can use. The Bioconductor web site includes [developer resources](#) to help this transition. The Bioconductor [developer mailing list](#) provides a forum dedicated to developer-related questions.

New packages are now submitted to Bioconductor using an open review model. Prospective authors develop their package and, when ready, open an issue on the public [Contributions](#) github repository. Packages are then built and checked across Linux, Mac, and Windows platforms for conformance to R (`R CMD check`) and Bioconductor (using the [BiocCheck](#) package) standards. Once the package is in good shape, a member of the Bioconductor core team performs a preview of the package. The preview identifies technical issues that are not easy to detect automatically.

A key strength of the Bioconductor project is the use of well-defined objects (especially from the [GenomicRanges](#) infrastructure) to represent data; this encourages software re-use and enables end-user interoperability between packages. For this reason, the technical review often leads to suggestions for data representations and interfaces that use Bioconductor objects rather than general-purpose containers such as a `data.frame`.

## Forthcoming activities

Forthcoming Bioconductor [events](#) include an Asian workshop [workshop](#) and [developer meeting](#) (3-4 November, Brisbane, Australia) and European [developer conference](#) (6-7 December, Basel, Switzerland) developer conferences, as well as global training opportunities.

The next Bioconductor release will occur in October, 2016.

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