

Bioconductor and R 4.0

S3 method registration!!

Many packages are currently failing because of undeclared S3 methods in the NAMESPACE. There is some background found on the [R developers blog](#).

Solution: Register the S3 method in the package NAMESPACE

```
S3method(<function>, <dispatch>)
```

Examples:

```
S3method(plot, TCC) #TCC package
```

```
S3method(transform, ProbeSet) #affy pdnn package
```

S3 method registration!!

The resulting ERROR seems to take many forms depending on package code. Some of the current ERRORS seen on the build report related to S3 method declaration:

- Cannot coerce class <structure> to a data.frame
- Cannot coerce type 'S4' to vector of type 'double'
- No applicable method for <foo> applied to an object of class <bar>
- 'X' is a list, but does not have components 'x' and 'y'

Conditional lengths > 1

R 4.0 current condition has length > 1 will produce a Warning message.

Bioconductor build systems treat this as an ERROR in R CMD check

Traditionally `if` / `while` statements could act on vectors using the first element as the conditional value. This now produces a warning as seen in this dummy example and documented on [R developer blog](#)

```
> if (c(TRUE, FALSE)) {}
```

```
NULL
```

```
Warning message:
```

```
In if (c(TRUE, FALSE)) { :
```

```
  the condition has length > 1 and only the first element will be used
```

`class(x) == "foo" vs is(x, "foo")/inherits(x, "foo")`

There isn't a change in R or Bioconductor as of yet?

There is a much better discussion and explanation on [R developer blog](#)

The sum up:

`class(x) == "foo"` should be avoided. Misleading if classes extend other class

`is / inherits` safer, cleaner, avoids assumptions

This has been encouraged as part of [Bioconductor coding best practices](#)

Partial Argument Matching

There is now a more strict check on argument matching with regards to partial argument matching.

```
setGeneric("mycoolfunction", function(object, break)
  standardGeneric("mycoolfunction")
setMethod("mycoolfunction",
  signature=c(object="GRanges", breaks="GRanges"),
  <code>)
```

Partial argument matching when invoking functions should be avoided too!

Package Dependency Issues

- CRAN binaries for 4.0 are not available yet. As binaries become available for mac and windows they will be added to the daily builder automatically. Out of our hands and we will not take extraordinary efforts to find work arounds. When they are available - they will be added.
- Packages have been removed from CRAN. If this occurs Bioconductor packages must alter their package to not utilize the code. We will only support dependencies actively maintained on CRAN or Bioconductor.
- Packages have been removed from Bioconductor. We try to be more aware of orphaned packages and packages that remain broken for extended periods of time. Package deprecation and removal occurs and packages will have to alter to not utilize code from these packages or could potential offer to take over maintenance of broken packages but that would require original maintainers permission. (SNPchip, GenomeGraphs, ...[List of Deprecated Package 3.10](#))

Deprecated Functions

Most ERROR have a message indicating what function should be used instead

- RangedData

Error : RangedData objects are defunct. Please migrate your code to use GRanges or GRangesList objects instead. See IMPORTANT NOTE in ?RangedData

- Normalize

Error: processing vignette 'using_schex.Rmd' failed with diagnostics:
'normalize' is defunct.
Use "normalize,SingleCellExperiment-method" is defunct.
Use 'logNormCounts' instead' instead.

- calculateQCMetrics

Error: processing vignette 'MAST-interopability.Rmd' failed with diagnostics:
'calculateQCMetrics' is defunct.
Use 'perCellQCMetrics' instead.

Useful Links

R developers blog:

<https://developer.r-project.org/Blog/public/>

Troubleshooting Bioconductor Documentation:

Coming soon! (Link will be updated to website once created)