

As was already mentioned, your easiest path forward is to first ask your users to install the {BiocManager} package from CRAN, then use that to install your package.

As it is, you are already asking your end users to install {devtools} (really {remotes}) first in order to install your package anyway, ie:

Instead of asking them to do this:

```
R> install.packages("remote")
R> remotes::install_github("klausjung-hannover/bootGSEA")
```

You should instead ask them to:

```
R> install.packages("BiocManager")
R> BiocManager::install("klausjung-hannover/bootGSEA")
```

While the remotes package still works, <https://github.com/r-lib/pak> is now a better alternative. It also comes with built-in Bioconductor support:

```
pak::pkg_install("klausjung-hannover/bootGSEA")
```

Thank you,

I am still wondering why everyone on the internet mentions adding "biocView" to the DESCRIPTION-File. I couldn't find a source for that but everyone on Biostart, Stackoverflow or any other forum keeps mentioning adding biocView.

What does adding biocView do if anything? When should I add BiocView to the DESCRIPTION-File?

Sorry if this is spam, I think my last message got bounced because my mail client converted the GitHub link into a nice jpg.

As you mentioned, you can just add biocViews: Software to your DESCRIPTION: <https://github.com/r-lib/remotes/issues/477>. If you need further explanation then the code is here: <https://github.com/r-lib/remotes/blob/b9091cc471ea59471d10981330a868402e1b7bd9/install-github.R#L687-L694>

Adding the field causes remotes to add BioC to the repo list when installing dependencies. I think it's worth doing so your users can use remotes if they want and not have to install/use other installation managers.

Does it apply only to the remotes package or also to devtools::install\_git function?

Sergej

I believe that devtools just uses remotes under the hood, so it should work.