

BITS :: Call for Abstracts 2021 - Oral communication

<i>Type</i>	Oral communication
<i>Session</i>	Algorithms for Bioinformatics
<i>Title</i>	Easyreporting simplifies the implementation of ReproducibleResearch Layers in R software
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<i>Motivation</i>	<p>During last years "irreproducibility" became a general problem in omics data analysis due to the use of sophisticated and poorly described computational procedures, giving rise to the need to inspect and reproduce the entire data analysis as a unified product. Reproducible Research (RR) provides general guidelines for public access to the analytic data and related analysis code combined with natural language documentation, allowing third parties to reproduce the findings. Despite this aspect is fulfilled by standalone products such as Rmarkdown, there are no so many common solutions for facilitating the implementation of RR inside other projects.</p>
<i>Methods</i>	<p>With an eye on this need, we developed easyreporting, a novel R/Bioconductor package that helps the implementation of an RR layer inside reports/tools.</p> <p>Easyreporting is an S4 class based on the Rmarkdown language, providing easy storage and access to multiple information such as authorship, affiliation, code chunk options, bibliography and additional external resources.</p> <p>At the same time, its methods offer multiple solutions for code chunk creation, external file to source and final report compilation.</p>
<i>Results</i>	<p>During this presentation, we describe easyreporting main functionalities and how to use them in other projects to trace R functions automatically. This latter feature helps developers to implement procedures that automatically keep track of the analysis steps.</p> <p>Easyreporting can be useful in supporting the reproducibility of any data analysis project and shows great advantages for the implementation of R packages and GUIs. It turns out to be very helpful in bioinformatics, where the complexity of the analyses makes it extremely difficult to trace all the steps and parameters used in the study.</p>
<i>Info</i>	<p>https://github.com/drighelli/easyreporting_supplementary</p>
<i>Figure</i>	□
<i>Availability</i>	https://bioconductor.org/packages/easyreporting/
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