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Abstract

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Introduction

Users of the popular statistical and mathematical computing platform R (R Core Team 2014) enjoy a wealth of readily installable comparative phylogenetic methods and tools.

To make the capabilities of NeXML available to R users in an easy-to-use form, and to lower the hurdles to adoption of the standard, we present RNeXML, an R package that aims to provide easy programmatic access to reading and writing NeXML documents, tailored for the kinds of use-cases that will be common for users and developers of the wealth of evolutionary analysis methods within the R ecosystem.

The rgbif package

The `rgbif` package ...

Conclusions and future directions

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rgbif ...
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23 *Data Accessibility*

24 All software, scripts and data used in this paper can be found in the permanent data archive Zenodo
25 under the digital object identifier (DOI). This DOI corresponds to a snapshot of the GitHub repository
26 at github.com/sckott/msrgbif.

27 **References**

28 R Core Team. (2014). *R: A language and environment for statistical computing*. R Foundation for
29 Statistical Computing, Vienna, Austria. Retrieved from <http://www.R-project.org/>