

Bedtoolsr: An R package for genomic data analysis and manipulation

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Summary

The sequencing of the human genome and subsequent advances in DNA sequencing technology have created a need for computational tools to analyze and manipulate genomic data sets. The bedtools software suite and the R programming language have emerged as indispensable tools for this purpose but have lacked integration. Here we describe `bedtoolsr`, an R package that provides simple and intuitive access to all bedtools functions from within the R programming environment. We provide several usability enhancements, support compatibility with past and future versions of bedtools, and include unit tests to ensure stability. `bedtoolsr` provides a user-focused, harmonious integration of the bedtools software suite with the R programming language that should be of great use to the genomics community.

Source Code: <https://github.com/PhanstielLab/bedtoolsr>.

Information: <http://phanstiel-lab.med.unc.edu/bedtoolsr.html>.

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Introduction

The sequencing of the human genome and subsequent advances in DNA sequencing technology have transformed modern biological research by producing data sets of ever-increasing size and complexity. While these technologies have led to breakthroughs in genetics research, the incredible throughput and breadth of the resulting data have spurred a reliance on computational tools and programming languages to interpret the results. In 2010, Quinlan et al. developed bedtools, a powerful suite of command-line tools for 'genome arithmetic' that has become one of the most widely used and indispensable tools for genomic data analysis (Quinlan & Hall, 2010). A year later, `pybedtools` extended the features of bedtools to the python programming language (Dale, Pedersen, & Quinlan, 2011). During that same time period, the use of the programming language R—with a rich trove of libraries for statistical analysis and data visualization—skyrocketed in the biological sciences (Tippmann, 2015). While several R packages have been developed for bedtools-like genome analysis, their usage and functionality differ significantly from that of bedtools (Lawrence et al., 2013; Riemyndy et al., 2017). These differences make them more difficult to use for those who are already familiar with bedtools behavior and lacks some of the capabilities of bedtools.

Here we describe `bedtoolsr`, an R package that allows seamless integration of bedtools functions into the R programming environment. `bedtoolsr` functionality, inputs, outputs,

and documentation perfectly replicate those found in the command-line version of bedtools and offer new features for improved usability within the R environment.

Methods

`bedtoolsr` is an R package that allows access to all bedtools functions from within the R environment. To support past, current, and future versions of bedtools, we wrote `bedtoolsr` using a metaprogramming approach. The `bedtoolsr` package is built by a python script that reads function names, parameters, default settings, and documentation from a local installation of bedtools and constructs a distributable R package custom-built for that bedtools version. `bedtoolsr` is version controlled and freely available on the software development platform GitHub. To ensure stability, `bedtoolsr` supports continuous integration and includes unit tests for every function. These unit tests were implemented using the R package `testthat` (Wickham, 2011) and can be run immediately after installation to ensure proper functionality. The continuous integration service Travis CI runs every time a code change is posted to GitHub to safeguard against any updates that might introduce flaws, faults, or failures.

Results

`bedtoolsr` was written with user experience in mind. To minimize the learning curve for those already familiar with bedtools we aimed to perfectly replicate the bedtools experience while adding all of the features of an R package. As such, `bedtoolsr` supports every currently available bedtools function and all function parameters. Parameters have the exact same names and documentation as those provided by bedtools with code autocompletion support from within RStudio.

`bedtoolsr` extends bedtools features for improved ease of use. Inputs for `bedtoolsr` functions can be provided either as file paths or as R objects (e.g. `data.frames`, `data.tables`, `tibbles`, etc). `bedtoolsr` automatically detects whether the input is a file path or R object and handles the data accordingly. To simplify usage, `bedtoolsr` comes preloaded with chromosome size files for commonly used genomes that are required by many bedtools functions. Results can be returned as a data frame or written directly to a file. To ensure proper installation of the package, users can run unit tests for most functions which can be executed with a single command following installation.

Discussion

`bedtoolsr` provides seamless integration of the bedtools software suite into the R programming environment. The package was designed to be as user-friendly as possible and should be intuitive for those already familiar with the bedtools command-line tool. The ability to handle multiple data types, the forward and backward compatibility, and the included unit tests ensure stability and ease of use. The harmonious combination of these two powerful analytical platforms should make `bedtoolsr` a valuable and widely used tool for genomic analysis.

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