




# RSeqAn: Headers and wrappers for the SeqAn library in R

August Guang<sup>1,2</sup>

**1** Center for Computation and Visualization, Brown University, Providence, Rhode Island, United States of America **2** Center for Computational Biology of Human Disease, Brown University, Providence, Rhode Island, United States of America

DOI: [10.21105/joss.01160](https://doi.org/10.21105/joss.01160)

## Software

- [Review](#) 
- [Repository](#) 
- [Archive](#) 

**Submitted:** 17 December 2018

**Published:** 11 February 2019

## License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC-BY](#)).

## Summary

R is used heavily in the bioinformatics community for processing, analyzing, and visualizing biological sequence data due to the strong support for data exploration and analysis. One common complaint about R is its lack of speed relative to other languages, which have to do with properties of the R kernel (Sridharan, 2015). A solution to this is to rewrite key functions in C++ instead, then use Rcpp (Eddelbuettel & Balamuta, 2018) to interface with R. Many packages in R are sped up with C++ code: as of [November 2018](#), out of 13525 packages on CRAN, 1493 of those use Rcpp. On Bioconductor (Huber et al., 2015), a repository specifically for bioinformatics packages, there is a similar proportion of packages using Rcpp: 150 out of 1649.

Writing certain functions in C++ also allows the researcher to take advantage of high-performance C++ libraries. One such library that has proven powerful and popular for bioinformatics applications is SeqAn (Döring, Weese, Rausch, & Reinert, 2008; Reinert et al., 2017). SeqAn is an open source C++ library of efficient algorithms and data structures for the analysis of sequences with a focus on biological data. It has been used for many popular bioinformatics tools, including Bowtie2 (Langmead & Salzberg, 2012) and Tophat (Trapnell, Pachter, & Salzberg, 2009). Its capabilities include efficient storage and I/O of sequence data, fast algorithms for pattern matching, and much more.

To date, no R package has taken advantage of SeqAn. This is due to two issues. First, R for Windows is built with the mingw compiler, which the SeqAn development team does not offer support for. Second, SeqAn implements several custom data types in order to make the library more efficient. This means that any data type in SeqAn needs to have R to C++ conversion and C++ to R conversion functions written for it before it can be used in R.

RSeqAn solves both of these problems, thus allowing any R researcher to use the capabilities of SeqAn in their own work without need for the user to install SeqAn themselves or deal with interfacing between R and C++. RSeqAn can be installed from Bioconductor, and documentation for it can be found in the package as well as [online](#).

## Benchmarked Example

As a proof of concept for its utility, we have benchmarked a function (searching for adapter contamination) from `qckitfastq`, a package that uses RSeqAn for quality control on bioinformatics data compared to `ShortRead` (Morgan et al., 2009), another package on Bioconductor serving the same function that is purely written in R (Table 1). As can be seen, computing adapter content through `qckitfastq` is much faster than `ShortRead`.

**Table 1:** Benchmark results of qckitfastq, which uses RSeqAn, and ShortRead, which does not against a test file from each package.

File	Package	replications	elapsed	user.self	sys.self
<b>E-MTAB-1147</b>	ShortRead	100	13.3	11.58	1.37
	qckitfastq	100	5.159	4.902	0.091
<b>test.fq.gz</b>	ShortRead	100	6.612	5.739	0.567
	qckitfastq	100	0.195	0.105	0.019

## Acknowledgments

Thanks to Ashok Ragavendran for the concept of using SeqAn in R packages to speed up functions. Thanks to Fernando Gelin for help with the documentation and style. This publication was supported by an Institutional Development Award (IDeA) from the National Institute of General Medical Sciences of the National Institutes of Health under grant number P20GM109035.

## References

- Döring, A., Weese, D., Rausch, T., & Reinert, K. (2008). SeqAn an efficient, generic C++ library for sequence analysis. *BMC Bioinformatics*. doi:[10.1186/1471-2105-9-11](https://doi.org/10.1186/1471-2105-9-11)
- Eddelbuettel, D., & Balamuta, J. J. (2018). Extending R with C++: A Brief Introduction to Rcpp. *American Statistician*. doi:[10.1080/00031305.2017.1375990](https://doi.org/10.1080/00031305.2017.1375990)
- Huber, W., Carey, V. J., Gentleman, R., Anders, S., Carlson, M., Carvalho, B. S., Bravo, H. C., et al. (2015). Orchestrating high-throughput genomic analysis with Bioconductor. *Nature Methods*. doi:[10.1038/nmeth.3252](https://doi.org/10.1038/nmeth.3252)
- Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. *Nature methods*. doi:[10.1038/nmeth.1923](https://doi.org/10.1038/nmeth.1923)
- Morgan, M., Anders, S., Lawrence, M., Aboyoun, P., Pagès, H., & Gentleman, R. (2009). ShortRead: A Bioconductor package for input, quality assessment and exploration of high-throughput sequence data. *Bioinformatics*, 25, 2607–2608. doi:[10.1093/bioinformatics/btp450](https://doi.org/10.1093/bioinformatics/btp450)
- Reinert, K., Dadi, T. H., Ehrhardt, M., Hauswedell, H., Mehringer, S., Rahn, R., Kim, J., et al. (2017). The SeqAn C++ template library for efficient sequence analysis: A resource for programmers. *Journal of Biotechnology*. doi:[10.1016/j.jbiotec.2017.07.017](https://doi.org/10.1016/j.jbiotec.2017.07.017)
- Sridharan, S. (2015). Profiling R on a Contemporary Processor. *Proceedings of the VLDB Endowment*. doi:[10.14778/2735471.2735478](https://doi.org/10.14778/2735471.2735478)
- Trapnell, C., Pachter, L., & Salzberg, S. L. (2009). TopHat: Discovering splice junctions with RNA-Seq. *Bioinformatics*. doi:[10.1093/bioinformatics/btp120](https://doi.org/10.1093/bioinformatics/btp120)