

ruby-htslib

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Summary

ruby-htslib

Code : <https://github.com/kojix2/ruby-htslib>

Statement of need

Recent advances in genome research have accumulated a lot of biological information. the Ruby language is mainly used for developing web applications, but until now there has been no way to access HTS files with the Ruby language. The BioRuby (Goto et al. 2010) project does not provide access to HTS files. Ruby-htslib is an htslib (Bonfield et al. 2021) binding that provides access to HTS files from the Ruby language and provides a means to develop bioinformatics web applications.

Bio-Samtools2 (Etherington, Ramirez-Gonzalez, and MacLean 2015)

Benchmark

(Pedersen and Quinlan 2018)

Examples

Reference

- Bonfield, James K., John Marshall, Petr Danecek, Heng Li, Valeriu Ohan, Andrew Whitwham, Thomas Keane, and Robert M. Davies. 2021. “HTSlib: C Library for Reading/Writing High-Throughput Sequencing Data.” *GigaScience* 10 (2): giab007. <https://doi.org/10.1093/gigascience/giab007>.
- Etherington, Graham J., Ricardo H. Ramirez-Gonzalez, and Dan MacLean. 2015. “Bio-Samtools 2: A Package for Analysis and Visualization of Sequence and Alignment Data with SAMtools in Ruby: Fig. 1.” *Bioinformatics* 31 (15): 2565–67. <https://doi.org/10.1093/bioinformatics/btv178>.
- Goto, Naohisa, Pjotr Prins, Mitsuteru Nakao, Raoul Bonnal, Jan Aerts, and Toshiaki Katayama. 2010. “BioRuby: Bioinformatics Software for the Ruby Programming Language.” *Bioinformatics* 26 (20): 2617–19. <https://doi.org/10.1093/bioinformatics/btq475>.
- Pedersen, Brent S, and Aaron R Quinlan. 2018. “Hts-Nim: Scripting High-Performance Genomic Analyses.” Edited by Inanc Birol. *Bioinformatics* 34 (19): 3387–89. <https://doi.org/10.1093/bioinformatics/bty358>.