

Package: ace2fastq (via r-universe)

October 15, 2024

Type Package

Title ACE File to FASTQ Converter

Version 0.6.0

Description The ACE file format is used in genomics to store contigs from sequencing machines. This tools converts it into FASTQ format. Both formats contain the sequence characters and their corresponding quality information. Unlike the FASTQ file, the ace file stores the quality values numerically. The conversion algorithm uses the standard Sanger formula. The package facilitates insertion into pipelines, and content inspection.

Imports stringr

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Suggests testthat, knitr, rmarkdown, covr

VignetteBuilder knitr

URL <https://github.com/c5sire/ace2fastq>

BugReports <https://github.com/c5sire/ace2fastq/issues>

Repository <https://c5sire.r-universe.dev>

RemoteUrl <https://github.com/c5sire/ace2fastq>

RemoteRef HEAD

RemoteSha 8d247f421101a07fbee63b63a1d74ac75cceb87b

Contents

ace2fastq	2
ace_to_fastq	2
print.ace2fastq	3

Index	4
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ace2fastq	<i>ace2fastq</i>
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Description

The package provides a function that converts ".ace" files (ABI Sanger capillary sequence assembly files) to standard ".fastq" files. The file format is currently used in genomics to store contigs. To the best of our knowledge, no R function is available to convert this format into the more popular fastq file format. The development was motivated in the context of the analysis of 16S metagenomic data by the need to convert the .ace files for further analysis.

ace2fastq functionality

See: [ace_to_fastq](#)

ace_to_fastq	<i>ace_to_fastq</i>
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Description

Converts one or more contig sequences in .ace file format to .fastq format. The parameter target_dir has a special value 'stdout' which will just return the contigs as a list.

Usage

```
ace_to_fastq(filename, target_dir = dirname(filename), name2id = TRUE)
```

Arguments

filename	.ace file
target_dir	target directory or stdout
name2id	use the file name as primary id or not. Default is TRUE.

Value

list

Author(s)

Reinhard Simon

Examples

```
library(ace2fastq)
filename <- system.file("sampledat/1.seq.ace", package = "ace2fastq")

fileout <- ace_to_fastq(filename, target_dir = tempdir())
```

`print.ace2fastq` *print.ace2fastq*

Description

print method for an object of class `ace2fastq`

Usage

```
## S3 method for class 'ace2fastq'  
print(x, ...)
```

Arguments

<code>x</code>	an <code>ace2fastq</code> object
<code>...</code>	other print parameters

Author(s)

Reinhard Simon

Index

* **ace2fq_utils**

print.ace2fastq, 3

ace2fastq, 2

ace_to_fastq, 2, 2

print.ace2fastq, 3