

Package ‘DNAZooData’

August 21, 2025

Title DNA Zoo data package

Version 1.8.0

Date 2023-02-09

Description DNAZooData is a data package giving programmatic access to genome assemblies and Hi-C contact matrices uniformly processed by the [DNA Zoo Consortium](<https://www.dnazoo.org/>). The matrices are available in the multi-resolution `.hic` format. A URL to corrected genome assemblies in `.fastq` format is also provided to the end-user.

License MIT + file LICENSE

URL <https://github.com/js2264/DNAZooData>

BugReports <https://github.com/js2264/DNAZooData/issues>

Depends R (>= 4.2), HiCExperiment

Imports BiocFileCache, S4Vectors, rjson, utils, tools

Suggests dplyr, testthat, methods, BiocStyle, knitr, rmarkdown

biocViews ExperimentData, SequencingData

Encoding UTF-8

VignetteBuilder knitr

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

git_url <https://git.bioconductor.org/packages/DNAZooData>

git_branch RELEASE_3_21

git_last_commit 8cb7246

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-08-21

Author Jacques Serizay [aut, cre]

Maintainer Jacques Serizay <jacquesserizay@gmail.com>

Contents

DNAZooData	2
DNAZooDataCache	2
Index	4

DNAZooData	<i>DNAZooData</i>
------------	-------------------

Description

Fetches files from the DNAZoo data portal and caches them using the BiocFileCache system.

Arguments

species	Any species processed by the DNA Zoo (check https://www.dnazoo.org/assemblies) for a browser-based explorer.
---------	---

Value

DNAZooData() returns a HicFile object, which can then be imported in memory using `HicExperiment::import()`. Metadata also points to a URL to directly fetch the genome assembly corrected by the DNA Zoo consortium.

Examples

```
#####
## Importing DNAZoo `.hic` files ##
#####

head(DNAZooData())
hf <- DNAZooData(species = 'Anolis_carolinensis')
hf
```

DNAZooDataCache	<i>Manage cache / download files from the DNAZoo data portal</i>
-----------------	--

Description

Managing DNAZoo data downloads via the integrated BiocFileCache system.

Usage

```
DNAZooDataCache(...)
```

Arguments

... Arguments passed to internal `.setDNAZooDataCache` function

Value

BiocFileCache object

Examples

```
bfc <- DNAZooDataCache()  
bfc  
BiocFileCache::bfcinfo(bfc)
```

Index

DNAZooData, [2](#)

DNAZooDataCache, [2](#)