Package 'DNAZooData'

November 10, 2026

Title DNA Zoo data package

Version 1.12.0

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.

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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

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`DNAZooData` *DNAZooData*

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` *Manage cache / download files from the DNAZoo data portal*

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)
```

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