

# Package ‘DNAZooData’

April 3, 2025

**Title** DNA Zoo data package

**Version** 1.7.0

**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

**git\_url** <https://git.bioconductor.org/packages/DNAZooData>

**git\_branch** devel

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## Contents

|                           |          |
|---------------------------|----------|
| DNAZooData . . . . .      | 2        |
| DNAZooDataCache . . . . . | 2        |
| <b>Index</b>              | <b>4</b> |

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| DNAZooData | <i>DNAZooData</i> |
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### 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
```

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|-----------------|--|
| DNAZooDataCache | <i>Manage cache / download files from the DNAZoo data portal</i> |
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### 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](#)