

Package ‘fourDNData’

January 22, 2026

Title 4DN data package

Version 1.10.0

Date 2022-08-16

Description fourDNData is a data package giving programmatic access to Hi-C contact matrices uniformly processed by the [4DN consortium](https://www.4dnucleome.org/). The matrices are available in the multi-resolution ‘.mcool’ format.

License MIT + file LICENSE

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

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

Depends R (>= 4.2)

Imports BiocFileCache, HiCExperiment, GenomicRanges, IRanges, S4Vectors, utils, tools

Suggests rtracklayer, 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/fourDNData

git_branch RELEASE_3_22

git_last_commit 77a5348

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-22

Author Jacques Serizay [aut, cre]

Maintainer Jacques Serizay <jacquesserizay@gmail.com>

Contents

fourDNData	2
fourDNDataCache	3
Index	4

fourDNData	<i>fourDNData</i>
------------	-------------------

Description

Fetches files from the 4DN data portal and caches them using the BiocFileCache system.

Arguments

experimentSetAccession	Any 4DN-provided experimentSet Accession number (check https://data.4dnucleome.org/browse/) for a browser-based explorer.
type	any of c('pairs', 'hic', 'mcool', 'boundaries', 'insulation', 'compartments')
.fetch_pairs	Whether to also download the associated pairs file

Value

fourDNData() returns the local path of the queried file cached with BiocFileCache. fourDNHiCExperiment() returns a HiCExperiment object with populated metadata and topologicalFeatures (if available).

Examples

```
#####
## Importing individual 4DN files ##
#####

head(fourDNData())
mcf <- fourDNData(experimentSetAccession = '4DNESDP9ECMN', type = 'mcool')
mcf

#####
## Importing full 4DN experiments ##
#####

id <- fourDNData() |>
  dplyr::filter(
    experimentType == 'in situ Hi-C',
    biosource == 'GM12878',
    publication == 'Sanborn AL et al. (2015)'
  ) |>
  dplyr::arrange(size) |>
  dplyr::pull(experimentSetAccession) |>
  unique()
id[1]
x <- fourDNHiCExperiment(id[1])
x
HiCExperiment::topologicalFeatures(x)
S4Vectors::metadata(x)$`4DN_info`
```

fourDNDataCache	<i>Manage cache / download files from the 4DN data portal</i>
-----------------	---

Description

Managing 4DN data downloads via the integrated BiocFileCache system.

Usage

```
fourDNDataCache(...)
```

Arguments

... Arguments passed to internal `.setFourDNDataCache` function

Value

BiocFileCache object

Examples

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

Index

fourDNData, [2](#)
fourDNDataCache, [3](#)
fourDNHiCExperiment (fourDNData), [2](#)