

# Package ‘fourDNData’

April 2, 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

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**Repository** Bioconductor 3.22

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## 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`
```

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fourDNDataCache	<i>Manage cache / download files from the 4DN data portal</i>
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**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)
```

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