Package ‘HumanRetinaLRSData’

May 7, 2026

Type Package

Title Long-read RNA-seq gene count data from human retinal organoids

Version 1.0.0

Description Dataset package containing gene and isoform count matrices, and sample metadata for long-read direct cDNA sequencing of human retinal organoids, 2D retinal ganglion cell (RGC) cultures, and flowthrough fractions from H9 and EP1 iPSC cell lines. Data were generated using Oxford Nanopore Technology (ONT) direct cDNA sequencing and mapped to the GRCh38 reference genome (GENCODE v46 annotation). The package provides accessor functions returning SummarizedExperiment objects for gene-level counts, isoform-level counts, and a matrix of allele-specific expression (ASE) gene counts. Data files are stored in flat CSV format in an Open Science Framework (OSF) repository and cached locally via BiocFileCache.

License MIT + file LICENSE

Encoding UTF-8

URL https://github.com/sparthib/HumanRetinaLrsData

BugReports https://github.com/sparthib/HumanRetinaLrsData/issues

biocViews ExperimentData, RNASeqData, ExpressionData, Homo_sapiens_Data, CellCulture

RoxygenNote 7.3.2

Depends R (>= 4.6.0), SummarizedExperiment

Imports osfr, BiocFileCache

Suggests testthat, knitr, rmarkdown, ggplot2, ggrepel

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/HumanRetinaLRSData

git_branch RELEASE_3_23

git_last_commit 028947c

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-05-07

Author Sowmya Parthiban [aut, cre]

Maintainer Sowmya Parthiban <`sparthi1@jhu.edu`>

Contents

`ASEGeneCounts` *Allele-specific expression (ASE) gene counts*

Description

Allele-specific expression (ASE) gene counts

Usage

```
ASEGeneCounts()
```

Value

A numeric matrix

Examples

```
ase_counts <- ASEGeneCounts()
head(ase_counts)
```

`clear_osf_cache` *Clear OSF cache*

Description

Clear OSF cache

Usage

```
clear_osf_cache(
  bfc = BiocFileCache::BiocFileCache(tools::R_user_dir("HumanRetinaLRSData", which =
    "cache"), ask = FALSE)
)
```

Arguments

`bfc`	BiocFileCache object

Value

NULL (invisibly). Called for side effect of clearing cache.

Examples

```
clear_osf_cache()
```

`FTRGCGeneLevelData` *Gene-level counts for flow through (FT) and retinal ganglion cell (RGC) samples*

Description

Gene-level counts for flow through (FT) and retinal ganglion cell (RGC) samples

Usage

```
FTRGCGeneLevelData()
```

Value

A SummarizedExperiment object

Examples

```
ftrgc_data <- FTRGCGeneLevelData()
ftrgc_data
```

`FTRGCIsoformLevelData` *Isoform-level counts for flow through (FT) and retinal ganglion cell (RGC) samples*

Description

Isoform-level counts for flow through (FT) and retinal ganglion cell (RGC) samples

Usage

```
FTRGCIsoformLevelData()
```

Value

A SummarizedExperiment object

Examples

```
ftrgc_iso_data <- FTRGCIsoformLevelData()
ftrgc_iso_data
```

`list_osf_files` *List available files on OSF*

Description

List available files on OSF

Usage

```
list_osf_files()
```

Value

Character vector of file names

Examples

```
list_osf_files()
```

`load_object` *Load a dataset from OSF with BiocFileCache*

Description

Validates `osf_file_name` against the bundled '`inst/extdata/metadata.csv`' (no internet connection required for validation). On first use the data files are downloaded from OSF and cached via **BiocFileCache**; subsequent calls load from the local cache.

Usage

```
load_object(
  osf_file_name,
 bfc = BiocFileCache::BiocFileCache(tools::R_user_dir("HumanRetinaLRSData", which =
    "cache"), ask = FALSE)
)
```

Arguments

`osf_file_name`	Character scalar. Dataset base name; see `list_osf_files`.
`bfc`	A `BiocFileCache` object. Defaults to a per-user package cache.

Value

A `SummarizedExperiment` or a `matrix`, depending on the dataset.

Examples

```
## Not run:
se <- load_object("ROGeneLevelData")
se

## End(Not run)
```

`ROGeneLevelData` *Gene-level counts for retinal organoid (RO) samples*

Description

Gene-level counts for retinal organoid (RO) samples

Usage

```
ROGeneLevelData()
```

Value

A SummarizedExperiment object

Examples

```
ro_data <- ROGeneLevelData()
ro_data
```

`ROIsoformLevelData` *Isoform-level counts for retinal organoid (RO) samples*

Description

Isoform-level counts for retinal organoid (RO) samples

Usage

```
ROIsoformLevelData()
```

Value

A SummarizedExperiment object

Examples

```
ro_iso_data <- ROIsoformLevelData()
ro_iso_data
```

Index