Package: GPlinksR (via r-universe)

June 23, 2026

Type Package

Title Building Gene-Peak Network for ATAC-RNA Integration

Version 0.99.0

Description GPlinksR constructs gene-peak regulatory networks for ATAC-RNA integration by combining enhancer-based, promoter-based, and proximity (closest-gene) mappings. The package accepts direct peak and gene vectors as well as container-based inputs through a wrapper for common Bioconductor object classes. Enhancer-gene links are obtained from the PEREGRINE enhancer-gene datasets provided by AnnoQ, while promoter and gene coordinates are retrieved from EnsDb.Hsapiens.v86.

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URL https://github.com/Corawang123/GPlinksR

BugReports https://github.com/Corawang123/GPlinksR/issues

Encoding UTF-8

Depends R (>= 4.4.0)

Imports BiocFileCache, data.table, GenomicRanges, GenomeInfoDb, methods, MultiAssayExperiment, S4Vectors, EnsDb.Hsapiens.v86, ensembldb, biomaRt, dplyr, SingleCellExperiment, SummarizedExperiment

biocViews GeneExpression, Network, Sequencing, Transcriptomics

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Suggests BiocStyle, IRanges, knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs
make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository https://biocstaging.r-universe.dev

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Contents

`build_gp_links` *Build Gene-Peak Network (Enhancer, Promoter, Closest)*

Description

Build Gene-Peak Network (Enhancer, Promoter, Closest)

Usage

```
build_gp_links(pk, gn, ver = 19, enh_file = NULL)
```

Arguments

`pk`	Either: (1) A character vector of genomic coordinates ("chr1:1000-1200"), or (2) A data.frame containing peak coordinates with columns "chr","start","end" or a "PeakRegion" column ("chr1:1000-1200" style).
`gn`	Character vector of gene symbols (HGNC official symbols, e.g. "TP53", "FMNL2").
`ver`	Integer (17, 18, or 19) - PANTHER enhancer-gene link version.
`enh_file`	Optional local path to enhancer-gene link file (.tsv).

Value

A data.frame with columns: Peak, Gene, Src. Closest-gene mappings are based on distance from each peak to gene TSS.

Examples

```
data("gp_example_inputs", package = "GPlinksR")
data("gp_example_links", package = "GPlinksR")
pk <- gp_example_inputs$pk[seq_len(3)]
gn <- gp_example_inputs$gn[seq_len(4)]

head(gp_example_links)

if (interactive()) {
    gp <- build_gp_links(pk, gn)
    head(gp)
}
```

`build_gp_links_wrapper`

Build Gene-Peak Links from MAE or SCE Input

Description

Wrapper around `build_gp_links()` that extracts peak coordinates and gene symbols from a `MultiAssayExperiment` or `SingleCellExperiment`, then runs the standard GPlinksR workflow.

Usage

```
build_gp_links_wrapper(
    x,
    peak_experiment = NULL,
    gene_experiment = NULL,
    peak_col = NULL,
    gene_col = NULL,
    ver = 19,
    enh_file = NULL
)
```

Arguments

`x`	A `MultiAssayExperiment`, `SingleCellExperiment`, `SummarizedExperiment`, or `RangedSummarizedExperiment`.
`peak_experiment`	For `MultiAssayExperiment`, the experiment name holding peak features. For `SingleCellExperiment`, the `altExp()` name holding peak features.
`gene_experiment`	For `MultiAssayExperiment`, the experiment name holding gene features. Ignored for `SingleCellExperiment`, where the main experiment is used for genes.
`peak_col`	Optional `rowData()` column containing peak coordinates in `"chr:start-end"` format.
`gene_col`	Optional `rowData()` column containing gene symbols.

`ver`	Integer (17, 18, or 19). PEREGRINE enhancer-gene link version.
`enh_file`	Optional local path to enhancer-gene link file (`.tsv`).

Details

Peak features are extracted from `rowRanges()`, `rowData()`, or row names. Gene symbols are extracted from `rowData()` or row names.

Value

A data.frame with columns returned by `build_gp_links()`.

Examples

```
if (requireNamespace("SingleCellExperiment", quietly = TRUE) &&
    requireNamespace("SummarizedExperiment", quietly = TRUE)) {
    sce <- SingleCellExperiment::SingleCellExperiment(
        assays = list(counts = matrix(seq_len(12), nrow = 3)),
        rowData = S4Vectors::DataFrame(symbol = c("TP53", "GATA1", "SPI1"))
    )

    SingleCellExperiment::altExp(sce, "ATAC") <-
        SummarizedExperiment::SummarizedExperiment(
            assays = list(counts = matrix(seq_len(12), nrow = 3)),
            rowData = S4Vectors::DataFrame(
                PeakRegion = c(
                    "chr1:1000-1200",
                    "chr1:5000-5200",
                    "chr2:9000-9300"
                )
            )
        )

    sce
    # Example wrapper call:
    # build_gp_links_wrapper(
    #     x = sce, peak_experiment = "ATAC", gene_col = "symbol"
    # )
}
```

`get_peregrine_file` *Download Enhancer-Gene Link File from PANTHER Peregrine Database*

Description

Download Enhancer-Gene Link File from PANTHER Peregrine Database

Usage

```
get_peregrine_file(version = 19)
```

Arguments

`version`	Integer (17, 18, or 19). Which PANTHER enhancer-gene link version to download.

Value

The full path to the downloaded `.tsv` file stored in the `BiocFileCache`.

Examples

```
if (interactive()) {
    f <- get_peregrine_file(19)
    f
    readLines(f, n = 3)
}
```

`gp_example_inputs` *Example Gene and Peak Inputs for GPlinksR*

Description

A small example dataset for demonstrating `GPlinksR` workflows. The object contains 300 peak coordinates and 100 gene symbols suitable for examples and vignettes. The first few entries are curated so that the vignette examples produce enhancer-, promoter-, and closest-based links from the packaged data.

Usage

```
data(gp_example_inputs)
```

Format

A list with two elements:

`pk`	A character vector of 300 peak coordinates in `"chr:start-end"` format.
`gn`	A character vector of 100 gene symbols.

Examples

```
data(gp_example_inputs)
length(gp_example_inputs$pk)
length(gp_example_inputs$gn)
```

`gp_example_links` *Example Link Table for the Packaged GPlinksR Demo Subset*

Description

A precomputed example gene-peak link table corresponding to the curated leading entries in `gp_example_inputs`. The table includes enhancer-, promoter-, and closest-based links and is used in the vignette to display representative output without rerunning external downloads.

Usage

```
data(gp_example_links)
```

Format

A data.frame with 7 rows and 3 columns:

`Peak`	Peak coordinate in `"chr:start-end"` format.
`Gene`	Gene symbol linked to the peak.
`Src`	Link source, one of `"enh"`, `"prom"`, or `"clo"`.

Examples

```
data(gp_example_links)
head(gp_example_links)
table(gp_example_links$Src)
```

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