Package: GPlinksR (via r-universe)

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Type Package

Title Building Gene-Peak Network for ATAC-RNA Integration

Version 1.0.0

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 (>= 4.5.0)

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

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`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,
  enh_coords_file = NULL,
  gene_map = NULL,
  mart = 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"). Each input peak is linked to the nearest transcript TSS among these genes.
`ver`	Integer (17, 18, or 19) - PANTHER enhancer-gene link version.
`enh_file`	Optional local path to enhancer-gene link file (.tsv).

enh_coords_file
: Optional local path to the corresponding PEREGRINE enhancer-coordinate file. The file must contain chromosome, start, end, and enhancer identifier columns without a header. If NULL, the hg38 PEREGRINE coordinate file is downloaded or retrieved from cache.

gene_map
: Optional data.frame with columns hgnc_symbol and hgnc_id. When supplied, this local mapping is used instead of querying BioMart.

mart
: Optional biomaRt::Mart object used for gene identifier mapping. If NULL, the default Ensembl human genes mart is used. Supply an object created by biomaRt::useEnsembl() to select a mirror or custom host.

Value

A data.frame with columns: Peak, Gene, Src. Closest-gene mappings assign each peak center to its single nearest transcript TSS across the genes in gn. When a peak-gene pair has multiple evidence sources, each source is returned as a separate row.

Examples

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

enh_file <- system.file(
    "extdata", "gp_example_enhancer_links.tsv",
    package = "GPlinksR", mustWork = TRUE
)
enh_coords_file <- system.file(
    "extdata", "gp_example_enhancer_coordinates.tsv",
    package = "GPlinksR", mustWork = TRUE
)
gene_map <- data.frame(
    hgnc_symbol = c("TTLL10", "SAMD11"),
    hgnc_id = c("HGNC:26693", "HGNC:28706")
)

gp <- build_gp_links(
    pk, gn,
    enh_file = enh_file,
    enh_coords_file = enh_coords_file,
    gene_map = gene_map
)
gp

if (interactive()) {
    mirror_mart <- biomaRt::useEnsembl(
        biomart = "genes",
        dataset = "hsapiens_gene_ensembl",
        mirror = "useast"
    )
    gp <- build_gp_links(pk, gn, mart = mirror_mart)
```

```
    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,
    enh_coords_file = NULL,
    gene_map = NULL,
    mart = 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`).
`enh_coords_file`	Optional local path to the corresponding PEREGRINE enhancer-coordinate file passed to `build_gp_links()`.

gene_map	Optional data.frame with columns hgnc_symbol and hgnc_id passed to build_gp_links().
mart	Optional biomaRt::Mart object passed to build_gp_links(). Supply an object created with biomaRt::useEnsembl() to use an Ensembl mirror or custom host.

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 selected from a KPMP-derived kidney single-cell analysis. The first few entries yield enhancer-, promoter-, and closest-based links in the executable examples.

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 reference gene-peak link table corresponding to the leading entries in `gp_example_inputs`. The table contains the expected enhancer-, promoter-, and closest-based links from the package's executable offline example.

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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