

# Package ‘SpliceImpactR’

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**Type** Package

**Title** An R package to identify functional impacts due to alternative RNA processing events

**Version** 0.99.4

**Description** Works by taking in processed data from the HIT Index and/or rMATS and identifying how differentially used alternative RNA processing events lead to changes in protein function through various means. Primarily this is done through protein similarity, functional protein domain analysis, and domain-domain interaction changes. Notably, we both identify alternative RNA processing event 'swaps' across condition and are able to perform holistic analyses regarding the impact of different RNA processing events.

**License** GPL-3

**Encoding** UTF-8

**Imports** data.table, BiocFileCache, BiocParallel, Biostrings, GenomicRanges, SummarizedExperiment, biomaRt, IRanges, PFAM.db, dplyr, ggplot2, ggpubr, patchwork, pwalgn, rtracklayer, scales, stats, tidyr, tools, utils, magrittr, methods, S4Vectors

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---

`.coords_to_string_1b` *Combine start/end coordinates into "start-end" strings (1-based).*

---

**Description**

Combine start/end coordinates into "start-end" strings (1-based).

**Usage**

```
.coords_to_string_1b(start, end)
```

**Arguments**

`start, end` Integer vectors of equal length.

**Value**

Character vector of "start-end" strings (NA for invalid pairs).

---

`.db_remove_domain` *Removes the part of a domain identifier after the first semicolon.*

---

**Description**

Removes the part of a domain identifier after the first semicolon.

**Usage**

```
.db_remove_domain(id)
```

**Arguments**

`id` Character vector of domain identifiers (e.g. "Pfam;Kinase").

**Value**

Character vector containing only the database name (e.g. "Pfam").

---

`.domain_remove_db`      *Removes the database portion from a semicolon-delimited domain ID.*

---

**Description**

Removes the database portion from a semicolon-delimited domain ID.

**Usage**

```
.domain_remove_db(id)
```

**Arguments**

`id`                      Character vector of domain identifiers (e.g. "Pfam;Kinase").

**Value**

Character vector of domain names (e.g. "Kinase").

---

`.find_hitindex_files`      *Locate HIT index PSI files within a directory or return the file if directly provided.*

---

**Description**

Locate HIT index PSI files within a directory or return the file if directly provided.

**Usage**

```
.find_hitindex_files(p)
```

**Arguments**

`p`                          Directory path or file path.

**Value**

Character vector of full paths to matching files.

---

<code>.getHITindex</code>	<i>Read HIT index exon tables for all samples</i>
---------------------------	---

---

### Description

Internal helper that loads exon-level HIT index tables for each sample and appends corresponding 'sample\_name' and 'condition' metadata.

### Usage

```
.getHITindex(sample_df)
```

### Arguments

<code>sample_df</code>	'data.frame' or 'data.table' containing at least: <ul style="list-style-type: none"><li>• 'path' directory path for each sample</li><li>• 'sample_name' unique sample identifier</li><li>• 'condition' experimental group</li></ul>
------------------------	---

### Value

A 'data.table' with columns: 'gene', 'exon', 'HITindex', 'sample', and 'condition'.

---

<code>.get_size_factors_from_exons</code>	<i>Compute size factors directly from exon count files</i>
---	--

---

### Description

Wrapper around 'getSizedFactors()' that can either compute normalization factors from raw exon count files ('exon\_files') or use user-provided values ('user\_given').

### Usage

```
.get_size_factors_from_exons(sample_df, method = c("exon_files", "user_given"))
```

### Arguments

<code>sample_df</code>	'data.frame' containing sample metadata with columns 'sample_name', 'path', and optionally 'condition'.
<code>method</code>	Either 'exon_files' (compute) or 'user_given' (join).

**Details**

- If `method = 'exon_files'`, the function loads exon-level count tables using `read_exon_files()` and computes per-sample size factors. - If `method = 'user_given'`, it merges the user-supplied `size_factors` data frame into `sample_df`.

Size factors are normalized to have a geometric mean of 1 (DESeq2-style).

**Value**

A `data.frame` equal to `sample_df` with an appended numeric column `sizeFactor`.

**See Also**

[`getSizeFactors()`]

---

`.needs_upstream_check` *Check for upstream frame shift*

---

**Description**

`.needs_upstream_check()` indicates whether a given alternative splicing event type should undergo upstream frame-shift evaluation via `.incoming_upstream_shift()`.

**Usage**

```
.needs_upstream_check(event_type)
```

**Arguments**

`event_type` Character scalar or vector. Event class label(s) such as `"A5SS"`, `"A3SS"`, `"RI"`, `"SE"`, `"MXE"`, etc.

**Value**

Logical vector of same length as input. `TRUE` for event types where an upstream frame-shift scan is relevant.

---

.parse\_exon\_coords      *Parse exon coordinate strings of form "chr:start-end" into components.*

---

**Description**

Parse exon coordinate strings of form "chr:start-end" into components.

**Usage**

```
.parse_exon_coords(exon_col)
```

**Arguments**

exon\_col              Character vector of exon coordinate strings.

**Value**

A list with elements chr, start, and end.

---

.parse\_listcol              *Internal helper that normalizes list columns or delimited strings of domain identifiers into unique trimmed character vectors.*

---

**Description**

Internal helper that normalizes list columns or delimited strings of domain identifiers into unique trimmed character vectors.

**Usage**

```
.parse_listcol(x, delim = "[,;|[:space:]]+")
```

**Arguments**

x                      List or character vector of domain entries.  
delim                  Regular expression used to split delimited strings.

**Value**

A list of character vectors, one per input element.

---

<code>.read_any</code>	<i>Read an object from a supported file format (.rds, .csv, .tsv)</i>
------------------------	---

---

**Description**

Internal helper to load serialized or tabular data in a uniform way.

**Usage**

```
.read_any(path)
```

**Arguments**

`path` Character scalar; path to a file ending in `‘.rds‘`, `‘.csv‘`, or `‘.tsv‘`.

**Value**

An R object (data.table, data.frame, or arbitrary R object from `‘.rds‘`).

---

<code>.read_exon_files</code>	<i>Read exon-level counts or annotations used in HIT index files.</i>
-------------------------------	---

---

**Description**

Read exon-level counts or annotations used in HIT index files.

**Usage**

```
.read_exon_files(path, columns = c("gene", "exon", "ID"))
```

**Arguments**

`path` Base path to HIT index outputs (excluding suffix like `"exon"`).  
`columns` Columns to select from the exon file.

**Value**

A data.table with the specified columns.

---

.read_one_hit	<i>Read and merge a single HIT index PSI file with its exon annotations.</i>
---------------	--

---

### Description

Read and merge a single HIT index PSI file with its exon annotations.

### Usage

```
.read_one_hit(f, sample, condition)
```

### Arguments

f	Path to a .AFEPSI/.ALEPSI/etc. file.
sample	Sample name.
condition	Experimental condition.

### Value

A standardized data.table with inclusion/exclusion metrics and metadata.

---

.site_glm	<i>Quasi-binomial GLM with Cook's Distance Filtering</i>
-----------	--

---

### Description

Fits a quasi-binomial GLM to estimate deltaPSI between two conditions. Outliers are removed based on Cook's distance before refitting.

### Usage

```
.site_glm(d, cooks_cutoff)
```

### Arguments

d	A 'data.frame' or 'data.table' with columns 'psi_adj', 'psi_raw', 'condition', and 'total'.
cooks_cutoff	Numeric. Cook's distance cutoff, passed to [cutoff_num()].

### Value

A 'data.table' with columns 'p.value', 'cooks\_max', 'n', 'n\_used', 'mean\_psi\_ctrl', 'mean\_psi\_case', and 'delta\_psi'.

---

*.si\_bfc*                      *Initialize BiocFileCache backend (internal)*

---

**Description**

Initialize BiocFileCache backend (internal)

**Usage**

```
.si_bfc(base_dir = NULL, pkg = "SpliceImpactR")
```

**Arguments**

<code>base_dir</code>	Optional cache root passed to <code>[.si_cache_root()]</code> .
<code>pkg</code>	Package name used for default user cache root.

**Value**

A 'BiocFileCache' object.

---

*.si\_bfc\_get\_rds*                      *Load cached local RDS from BiocFileCache (internal)*

---

**Description**

Load cached local RDS from BiocFileCache (internal)

**Usage**

```
.si_bfc_get_rds(bfc, rname)
```

**Arguments**

<code>bfc</code>	A 'BiocFileCache' object.
<code>rname</code>	Cache key name.

**Value**

Cached R object or 'NULL' if not present.

---

.si\_bfc\_get\_web      *Fetch a web resource through BiocFileCache (internal)*

---

**Description**

Fetch a web resource through BiocFileCache (internal)

**Usage**

```
.si_bfc_get_web(bfc, rname, url, progress = TRUE)
```

**Arguments**

bfc	A 'BiocFileCache' object.
rname	Cache key name.
url	URL to fetch.
progress	Logical passed to BiocFileCache download methods.

**Value**

Local cached file path.

---

.si\_bfc\_put\_rds      *Store R object in BiocFileCache as local RDS (internal)*

---

**Description**

Store R object in BiocFileCache as local RDS (internal)

**Usage**

```
.si_bfc_put_rds(bfc, rname, obj)
```

**Arguments**

bfc	A 'BiocFileCache' object.
rname	Cache key name.
obj	R object to serialize.

**Value**

Invisible cached file path.

---

`.si_cache_root`      *Resolve persistent cache root for SpliceImpactR (internal)*

---

**Description**

Resolve persistent cache root for SpliceImpactR (internal)

**Usage**

```
.si_cache_root(base_dir = NULL, pkg = "SpliceImpactR")
```

**Arguments**

`base_dir`      Optional directory root for cache data. If ‘NULL’, defaults to ‘tools::R\_user\_dir("SpliceImpactR", "cache")’.

`pkg`            Package name used by ‘tools::R\_user\_dir()’.

**Value**

Normalized cache root directory path.

---

`.si_gencode_urls`      *Build GENCODE download URLs (internal helper)*

---

**Description**

Internal function to construct URLs for downloading GENCODE annotation and sequence files for either human or mouse. This is used by higher-level SpliceImpactR functions.

**Usage**

```
.si_gencode_urls(species = c("human", "mouse"), release)
```

**Arguments**

`species`      Character string, either “human” or “mouse”.

`release`      Integer or string specifying the GENCODE release number.

**Value**

A named list containing URLs and the release tag.

---

.si\_get\_annotation\_mode\_guide

*Build short get\_annotation mode/use-case guide (internal)*

---

### **Description**

Build short get\_annotation mode/use-case guide (internal)

### **Usage**

.si\_get\_annotation\_mode\_guide()

### **Value**

Character scalar suitable for appending to error messages.

---

.si\_link\_asset\_path     *Resolve optional link-mode asset override (internal)*

---

### **Description**

Resolve optional link-mode asset override (internal)

### **Usage**

.si\_link\_asset\_path(bfc, provided, fallback\_path, role)

### **Arguments**

bfc	A 'BiocFileCache' object.
provided	User-supplied override value.
fallback_path	Default downloaded asset path.
role	Label used in warnings and cache key names.

### **Value**

A valid local file path.

---

<code>.si_md5_text</code>	<i>Compute an MD5 hash for a text payload (internal)</i>
---------------------------	--

---

**Description**

Compute an MD5 hash for a text payload (internal)

**Usage**

```
.si_md5_text(txt)
```

**Arguments**

<code>txt</code>	Character scalar payload.
------------------	---------------------------

**Value**

Character scalar MD5 hash.

---

<code>.si_pf_cache_key</code>	<i>Build BiocFileCache key for get_protein_features() outputs (internal)</i>
-------------------------------	--

---

**Description**

Build BiocFileCache key for get\_protein\_features() outputs (internal)

**Usage**

```
.si_pf_cache_key(
  biomaRt_databases,
  gtf_df,
  sequences,
  species,
  release,
  combine_overlaps
)
```

**Arguments**

<code>biomaRt_databases</code>	Character vector of requested databases.
<code>gtf_df</code>	Annotation table.
<code>sequences</code>	Optional sequences table.
<code>species</code>	Character species dataset string.
<code>release</code>	Ensembl release.
<code>combine_overlaps</code>	Logical merge behavior.

**Value**

Character cache key.

---

.si\_pf\_fingerprint\_gtf

*Build a stable GTF fingerprint for protein-feature caching (internal)*

---

**Description**

Build a stable GTF fingerprint for protein-feature caching (internal)

**Usage**

.si\_pf\_fingerprint\_gtf(gtf\_df)

**Arguments**

gtf\_df            Annotation table used by [get\_protein\_features()].

**Value**

Character scalar fingerprint hash.

---

.si\_pf\_fingerprint\_sequences

*Build a stable sequence fingerprint for ELM-dependent caching (internal)*

---

**Description**

Build a stable sequence fingerprint for ELM-dependent caching (internal)

**Usage**

.si\_pf\_fingerprint\_sequences(sequences)

**Arguments**

sequences        Sequence table from [get\_annotation()].

**Value**

Character scalar fingerprint hash.

---

*.si\_prepare\_assets*      *Prepare GENCODE annotation and sequence assets (internal helper)*

---

### Description

Internal function to acquire GENCODE annotation and sequence files (GTF, transcript FASTA, protein FASTA) using a package-specific ‘BiocFileCache’.

### Usage

```
.si_prepare_assets(
  base_dir,
  species = c("human", "mouse"),
  release,
  mode = c("download", "import_then_cache"),
  use_rds_cache = TRUE
)
```

### Arguments

<code>base_dir</code>	Character string giving the base directory where cache data should be stored. If ‘NULL’, uses package user cache.
<code>species</code>	Character string, either “human” or “mouse”.
<code>release</code>	Integer or string specifying the GENCODE release number (e.g., ‘45’ for human or “M35” for mouse).
<code>mode</code>	Character string, one of “download” or “import_then_cache”. The latter may parse/cache the GTF R object.
<code>use_rds_cache</code>	Logical; if ‘TRUE’, loads cached ‘.rds’ GTF file if available.

### Value

A list containing:

- ‘**paths**’ Local file paths to cached assets.
- ‘**gtf\_df**’ Imported GTF data frame if loaded or created.
- ‘**meta**’ Metadata list with species, release, and tag.
- ‘**bfc**’ ‘BiocFileCache’ instance used for retrieval.
- ‘**cache\_dir**’ Resolved cache root directory.

---

`.si_use_ensembl_mart` *Create a biomaRt Ensembl connection with explicit mirror fallback (internal)*

---

### Description

Create a biomaRt Ensembl connection with explicit mirror fallback (internal)

### Usage

```
.si_use_ensembl_mart(  
  dataset,  
  version,  
  biomaRt = "genes",  
  ensembl_mirror = NULL,  
  verbose = FALSE  
)
```

### Arguments

<code>dataset</code>	Ensembl dataset (e.g. <code>"hsapiens_gene_ensembl"</code> ).
<code>version</code>	Ensembl release version.
<code>biomaRt</code>	Biomart name, default <code>"genes"</code> .
<code>ensembl_mirror</code>	Optional mirror ( <code>"www"</code> , <code>"useast"</code> , <code>"asia"</code> ).
<code>verbose</code>	Logical passed to <code>biomaRt::useEnsembl()</code> .

### Value

A `'Mart'` object.

---

`.split_coord` *Split genomic coordinate strings into integer ranges*

---

### Description

Internal helper that converts a string like `"12345-12456"` into an integer vector `c(12345, 12456)`.

### Usage

```
.split_coord(coord)
```

### Arguments

<code>coord</code>	Character scalar of the form <code>"start-end"</code> .
--------------------	---

**Value**

Integer vector of length two ('start', 'end').

---

<code>.tail_coords_1based</code>	<i>Compute 1-based coordinates for the tail segment when one interval fully overlaps another but differs at exactly one boundary (start or end).</i>
----------------------------------	--

---

**Description**

Compute 1-based coordinates for the tail segment when one interval fully overlaps another but differs at exactly one boundary (start or end).

**Usage**

```
.tail_coords_1based(longS, longE, shortS, shortE)
```

**Arguments**

<code>longS</code>	Integer vector of start coordinates for the longer interval.
<code>longE</code>	Integer vector of end coordinates for the longer interval.
<code>shortS</code>	Integer vector of start coordinates for the shorter interval.
<code>shortE</code>	Integer vector of end coordinates for the shorter interval.

**Details**

For intervals sharing either their start or end but not both, returns the coordinates of the extra tail portion on the longer interval. Invalid or negative-length intervals are returned as 'NA'.

**Value**

A list with integer vectors:

<code>start</code>	1-based start positions of the tail region.
<code>end</code>	1-based end positions of the tail region.

---

.write\_any                      *Write an object to a supported file format (.rds, .csv, .tsv)*

---

### Description

Internal helper to save serialized or tabular data in a uniform way.

### Usage

```
.write_any(dt, path)
```

### Arguments

dt                      Object to save (typically a `data.frame` or `data.table`).

path                    Character scalar; output file path ending in `'rds'`, `'csv'`, or `'tsv'`.

### Value

Invisibly returns the output file path.

---

add\_exon\_coding\_information  
*Add per-exon coding and feature coordinates (internal)*

---

### Description

Internal helper to annotate each exon in a `GTF data.table` with strand-aware coding information. For every exon, the function records whether it overlaps coding sequence (CDS), untranslated region (UTR), start codon, or stop codon, together with absolute, genomic, and transcript-relative coordinates.

### Usage

```
add_exon_coding_information(gtf_df)
```

### Arguments

gtf\_df                      A `data.frame` or `data.table` containing GTF annotations, typically produced by `[load_gtf_long()]`. Must include columns `type`, `start`, `end`, `strand`, `transcript_id`, `exon_id`, and a unique `row_uid`.

**Details**

The function:

1. Orders exons per transcript, respecting strand.
2. Computes exon-wise coordinates for CDS, UTR, start/stop codons.
3. Merges these annotations back into the exon-level GTF table.

It relies on **data.table** joins and by-group operations for speed.

**Value**

A `data.table` identical to the input `gtf_df` but with additional per-exon fields:

- `cds_has`, `utr_has`, etc logical indicators
- Absolute (within-exon) start/stop coordinates (`_abs_*`)
- Genomic coordinates (`_gen_*`)
- Transcript-relative coordinates (`_rel_*`)
- Feature lengths (`_len`)

---

`add_exon_count_per_transcript`

*Add exon count per transcript (internal)*

---

**Description**

Internal helper that computes the number of exon entries per transcript in a GTF table and attaches it as a new column.

**Usage**

```
add_exon_count_per_transcript(gtf_df, col = "n_exons")
```

**Arguments**

<code>gtf_df</code>	A <code>data.frame</code> or <code>data.table</code> containing at least <code>type == "exon"</code> and <code>transcript_id</code> columns.
<code>col</code>	Character string giving the name of the output column for the exon count (default <code>"n_exons"</code> ).

**Value**

A `data.table` identical to `gtf_df` but with one additional column containing the number of exons per transcript.

---

add_exon_frames	<i>Add frames to exons dependent on cds location</i>
-----------------	--

---

**Description**

Internal helper

**Usage**

```
add_exon_frames(gtf_df)
```

**Arguments**

gtf_df	A data.frame or data.table containing GTF annotation data, typically from [load_gtf_long()].
--------	--

**Value**

A data.table with added start\_frame and stop\_frame

---

add_exon_order_information	<i>Add exon order and positional classification (internal)</i>
----------------------------	--

---

**Description**

Internal helper that annotates exon rows within a GTF table with strand-aware order and coding position information. Adds both absolute (by transcript) and coding-region-specific ordering, along with classification labels such as "first", "internal", "last", or "single\_exon".

**Usage**

```
add_exon_order_information(gtf_df)
```

**Arguments**

gtf_df	A data.frame or data.table containing GTF annotations (usually from [add_exon_coding_information]). Must include columns type, start, end, strand, transcript_id, exon_number, cds_has, and cds_rel_start.
--------	--

**Details**

Exons are ordered by genomic position within each transcript, taking strand into account. If exon\_number is provided, it is used to set the absolute order; otherwise order is inferred from coordinates.

**Value**

A data.table identical to gtf\_df but with added columns:

- absolute\_exon\_position exon index by transcript
- coding\_exon\_position exon index among coding exons
- absolute\_exon\_class positional label for all exons
- coding\_exon\_class positional label for coding exons

---

add\_feature\_length      *Add feature length column (internal)*

---

**Description**

Internal helper that computes the genomic length of each feature in a GTF table and appends it as feature\_length.

**Usage**

```
add_feature_length(gtf_df)
```

**Arguments**

gtf\_df                  A data.frame or data.table containing start and end columns.

**Value**

A data.table identical to the input but with an added feature\_length column (end - start + 1).

---

add\_splice\_part          *Add one part to an existing SpliceImpactResult*

---

**Description**

Add one part to an existing SpliceImpactResult

**Usage**

```
add_splice_part(
  obj,
  data = NULL,
  res = NULL,
  res_di = NULL,
  matched = NULL,
  sample_frame = NULL,
  hits_final = NULL
)
```

**Arguments**

obj	‘SpliceImpactResult‘
data	Optional raw sample-level table.
res	Optional differential result table.
res_di	Optional threshold-filtered differential table.
matched	Optional annotation-matched table.
sample_frame	Optional sample manifest table.
hits_final	Optional paired/final hits table.

**Value**

Updated ‘SpliceImpactResult‘

**Examples**

```
obj <- as_splice_impact_result()
res <- data.table::data.table(
  event_id = c("E1", "E1"),
  form = c("inc", "exc"),
  inc = c("100-110", "120-130"),
  exc = c("120-130", "100-110"),
  chr = c("chr1", "chr1"),
  strand = c("+", "+"),
  gene_id = c("ENSG000001", "ENSG000001"),
  padj = c(0.01, 0.01),
  delta_psi = c(0.25, -0.25)
)
obj <- add_splice_part(obj, res = res)
print(as_dt_from_s4(obj, "di_events"))
```

---

add\_user\_features      *Standardize user-supplied protein feature annotations*

---

**Description**

Internal helper that converts a user-provided feature table into the standardized long-format schema used throughout SpliceImpactR. Ensures consistent column names, data types, and coordinate logic.

**Usage**

```
add_user_features(x, default_database = "user")
```

**Arguments**

- `x` A `data.frame` or `data.table` supplied by the user containing at least `name`, `start`, and `stop`, and optionally one or both of `ensembl_transcript_id` or `ensembl_peptide_id`.
- `default_database` Character scalar giving the default value for the database column when none is provided (default "user").

**Details**

The function verifies the presence of required coordinate columns and at least one Ensembl identifier, fills in any missing optional columns with default values, coerces all types to their expected formats, removes invalid coordinates (`stop < start`), and reorders columns into the canonical schema used by `[to_long_features()]`.

**Value**

A `data.table` with standardized columns: `ensembl_transcript_id`, `ensembl_peptide_id`, `database`, `feature_id`, `name`, `alt_name`, `start`, `stop`, and `method = "manual"`.

---

as\_dt\_from\_s4

---

*Convert S4 slots back to data.table*


---

**Description**

Convert S4 slots back to `data.table`

**Usage**

```
as_dt_from_s4(
  x,
  slot = c("raw_events", "di_events", "res_di", "matched", "sample_frame",
           "hits_sequences", "paired_hits"),
  keep_internal_keys = FALSE
)
```

**Arguments**

- `x` `'SpliceImpactResult'`
- `slot` One of `'raw_events'`, `'di_events'`, `'res_di'`, `'matched'`, `'sample_frame'`, `'paired_hits'`. For backward compatibility, `'hits_sequences'` is treated as `'matched'`.
- `keep_internal_keys` Keep internal key columns (`'raw_key'`, `'di_key'`, `'pair_key'`).

**Value**

`'data.table'`

**Examples**

```

res <- data.table::data.table(
  event_id = c("E1", "E1"),
  form = c("inc", "exc"),
  inc = c("100-110", "120-130"),
  exc = c("120-130", "100-110"),
  chr = c("chr1", "chr1"),
  strand = c("+", "+"),
  gene_id = c("ENSG000001", "ENSG000001"),
  padj = c(0.01, 0.01),
  delta_psi = c(0.20, -0.20)
)
obj <- as_splice_impact_result(res = res)
print(as_dt_from_s4(obj, "di_events"))

```

---

as\_granges\_hits      *Convert paired hits to GRanges*

---

**Description**

Convert paired hits to GRanges

**Usage**

```
as_granges_hits(hits_dt)
```

---

as\_granges\_res      *Convert differential table to GRanges*

---

**Description**

Convert differential table to GRanges

**Usage**

```
as_granges_res(res_dt)
```

---

as\_segments\_grl      *Convert paired hit segments to GRangesList*

---

**Description**

Convert paired hit segments to GRangesList

**Usage**

```
as_segments_grl(hits_dt)
```

---

as_se_raw_events	<i>Convert sample-level table to SummarizedExperiment</i>
------------------	---

---

**Description**

Convert sample-level table to SummarizedExperiment

**Usage**

```
as_se_raw_events(data_dt)
```

---

as_splice_impact_result	<i>Build S4 SpliceImpact container</i>
-------------------------	--

---

**Description**

Accepts any subset of 'data', 'res', and 'hits\_final'. Missing pieces are stored as empty valid slots and can be added later with [add\_splice\_part()].

**Usage**

```
as_splice_impact_result(
  data = NULL,
  res = NULL,
  res_di = NULL,
  matched = NULL,
  sample_frame = NULL,
  hits_final = NULL,
  metadata = list()
)
```

**Arguments**

data	Optional sample-level input table.
res	Optional differential inclusion result table.
res_di	Optional threshold-filtered differential inclusion table.
matched	Optional annotation-matched DI table.
sample_frame	Optional sample manifest table.
hits_final	Optional paired/final hit table.
metadata	Optional list.

**Value**

‘SpliceImpactResult‘

**Examples**

```

raw <- data.table::data.table(
  event_id = c("E1", "E1"),
  form = c("inc", "exc"),
  sample = c("S1", "S1"),
  chr = c("chr1", "chr1"),
  strand = c("+", "+"),
  inc = c("100-110", "120-130"),
  exc = c("120-130", "100-110"),
  psi = c(0.70, 0.30),
  inclusion_reads = c(70, 30),
  exclusion_reads = c(30, 70)
)
res <- data.table::data.table(
  event_id = c("E1", "E1"),
  form = c("inc", "exc"),
  inc = c("100-110", "120-130"),
  exc = c("120-130", "100-110"),
  chr = c("chr1", "chr1"),
  strand = c("+", "+"),
  gene_id = c("ENSG000001", "ENSG000001"),
  padj = c(0.01, 0.01),
  delta_psi = c(0.20, -0.20)
)
hits <- data.table::data.table(
  event_id = "E1",
  event_type = "SE",
  gene_id = "ENSG000001",
  chr = "chr1",
  strand = "+",
  transcript_id_control = "TX1",
  transcript_id_case = "TX2",
  inc_control = "100-110",
  inc_case = "100-115",
  exc_control = "120-130",
  exc_case = "121-130",
  n_ppi = 1L,
  diff_n = 1L
)
obj <- as_splice_impact_result(data = raw, res = res, hits_final = hits)
obj

```

**Description**

Merges sequence data (transcript and protein sequences) onto an input table of splicing events or transcript annotations, by matching on `transcript_id`. When multiple sequences share the same `transcript_id`, the function keeps the entry with a non-missing `protein_id` and the longest `protein_seq`.

**Usage**

```
attach_sequences(x, sequences, return_class = c("auto", "data.table", "S4"))
```

**Arguments**

<code>x</code>	A <code>data.frame</code> or <code>data.table</code> containing a <code>transcript_id</code> column.
<code>sequences</code>	A <code>data.frame</code> or <code>data.table</code> with at least the columns: <code>transcript_id</code> , <code>protein_id</code> , <code>transcript_seq</code> , and <code>protein_seq</code> .
<code>return_class</code>	Character. Output mode: <code>"data.table"</code> , <code>"S4"</code> , or <code>"auto"</code> (default). In <code>'auto'</code> , <code>S4</code> input returns updated <code>S4</code> output.

**Details**

The join is left-sided: all rows from `x` are preserved. Duplicate `transcript_ids` in `sequences` are resolved internally based on protein presence and sequence length.

**Value**

A `data.table` with the same rows as `x` and appended sequence columns (`transcript_seq`, `protein_seq`, etc.).

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annots <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annots$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annots$sequences)
print(x_seq)
```

---

**attr\_get**
*Extract an attribute value from GTF/GFF attribute fields (internal)*


---

**Description**

Parses a specific key-value pair from the `'attributes'` column of a GTF/GFF line, returning the value associated with the requested key.

**Usage**

```
attr_get(x, key, strip = FALSE)
```

**Arguments**

x	Character vector of attribute strings.
key	Character string naming the attribute key to extract (e.g., "gene_id" or "transcript_id").
strip	Logical; if 'TRUE', removes version suffixes using [strip_ver()].

**Value**

Character vector of extracted values, 'NA' where the key was not found.

---

bin_under_cap	<i>Bin elements under a cumulative cap (internal)</i>
---------------	---

---

**Description**

Internal helper that groups elements sequentially into bins such that the cumulative value in each bin does not exceed a specified cap. Often used to split items for batch processing or job chunking based on approximate size or cost.

**Usage**

```
bin_under_cap(df, name_col, value_col, cap = 3100)
```

**Arguments**

df	A data.frame containing at least two columns: one with element names and one with numeric values.
name_col	Character string giving the column name for element identifiers.
value_col	Character string giving the column name for numeric values used in cumulative binning.
cap	Numeric scalar giving the maximum cumulative value allowed per bin (default 3100).

**Details**

The function walks through rows in order, adding elements to the current bin until the running total exceeds cap, then starts a new bin. The algorithm is greedy: it does not reorder or rebalance after bin formation.

**Value**

A list where each element is a character vector of names that belong to one bin. The bins are created sequentially in the order of the input rows.

---

build_domain_lookup	<i>Internal helper that constructs per-exon ('Dexon') and per-transcript ('Dtx') mappings of domain identifiers from an exon-feature annotation table.</i>
---------------------	--

---

### Description

Internal helper that constructs per-exon ('Dexon') and per-transcript ('Dtx') mappings of domain identifiers from an exon-feature annotation table.

### Usage

```
build_domain_lookup(exon_features)
```

### Arguments

exon_features	'data.frame' containing exon-feature relationships with amino acid start/end positions.
---------------	---

### Value

A named 'list' with:

'Dexon' 'data.table' keyed by 'transcript\_id, exon\_id'

'Dtx' 'data.table' keyed by 'transcript\_id'

---

build_from_annotations	<i>Build exon and transcript tables from a parsed annotation</i>
------------------------	--

---

### Description

Constructs standardized exon and transcript data tables from a flattened annotation object such as one produced by [rtracklayer::import()] on a GTF file.

### Usage

```
build_from_annotations(ann)
```

### Arguments

ann	A 'data.frame' or 'data.table' containing parsed gene annotation records with at least the following columns: type, chr, start, end, strand, gene_id, gene_name, transcript_id, transcript_name, transcript_type, protein_id, exon_id, and exon_number.
-----	---

**Details**

This function is used internally to prepare lightweight annotation summaries for downstream event mapping and HIT-index aggregation. It does not query external resources and assumes the input annotation already includes both exon and transcript entries.

**Value**

A named list with three components:

**‘exons’** A ‘data.table’ of exon records with added ‘classification’ (“first”, “last”, or “internal”) determined per transcript.

**‘transcripts’** A ‘data.table’ of transcript records.

**‘protein\_tx’** Character vector of transcript IDs annotated as protein-coding (non-NA ‘protein\_id’).

---

coerce_to_dt	<i>Coerce input to data.table for internal pipelines</i>
--------------	--

---

**Description**

Coerce input to data.table for internal pipelines

**Usage**

```
coerce_to_dt(
  x,
  what = c("raw_events", "di_events", "res_di", "matched", "sample_frame",
           "hits_sequences", "paired_hits")
)
```

---

collapse_domains	<i>Internal helper that collapses a character vector of domain identifiers into a single, stable \ delimited string.</i>
------------------	--

---

**Description**

Internal helper that collapses a character vector of domain identifiers into a single, stable | delimited string.

**Usage**

```
collapse_domains(v)
```

**Arguments**

v Character vector of domain identifiers.

**Value**

Single string joining unique sorted identifiers.

---

compare_frames	<i>Identify frameshifts and rescue events between transcript pairs</i>
----------------	--

---

**Description**

Function that evaluates whether inclusion and exclusion transcript isoforms for each alternative splicing event maintain the reading frame or induce a frameshift. Optionally identifies "rescue" cases where downstream coding structure re-aligns the frame.

**Usage**

```
compare_frames(hits, annotations, allow_ale_fs = FALSE)
```

**Arguments**

hits	'data.frame' or 'data.table' containing splicing event metadata, typically output from [compare_sequences_alignment()]. Must include columns such as 'event_type', 'transcript_id_case', 'transcript_id_control', 'exons_case', 'exons_control', and 'pc_class'.
annotations	from get_annotations (annotations)
allow_ale_fs	Logical (default 'FALSE'). Whether to allow ALE/HLE events to be considered frameshifting.

**Value**

A 'data.table' identical to 'hits' with four appended columns:

**frame\_call** "FrameShift" or "PartialMatch".

**rescue** Rescue classification (e.g. "noRescue" or type string).

**frame\_check\_exon1** Exon ID used for inclusion isoform comparison.

**frame\_check\_exon2** Exon ID used for exclusion isoform comparison.

**See Also**

[build\_coding\_index()], [.compare\_boundary\_start()], [.compare\_boundary\_end()], [.compare\_at\_overlap\_start()], [.compare\_at\_overlap\_end()], [.compare\_overlap\_frames()], [.find\_rescue()], [.incoming\_upstream\_shift()], [.needs\_upstream\_check()]

---

compare_hit_index	<i>Compare HIT index values between conditions</i>
-------------------	--

---

### Description

Computes per-event differences in the **HIT index** (Hybrid Intron Tolerance) between control and test conditions, performs t test, adjusts for multiple testing, and produces summary visualizations.

### Usage

```
compare_hit_index(
  sample_df,
  condition_map = c(control = "control", test = "case"),
  minimum_proportion = 0.5,
  top_n_heatmap = 5000,
  sig_delta = 0.2,
  fdr_thresh = 0.05
)
```

### Arguments

sample_df	'data.frame' or 'data.table' containing sample metadata with columns: 'path', 'sample_name', and 'condition'.
condition_map	Named character vector mapping experimental groups, e.g. 'c(control = "control", test = "case")'.
minimum_proportion	Minimum proportion of samples per group that must have valid HIT values for a test to be performed (default = 0.5).
top_n_heatmap	Integer; number of events to display in the heatmap ordered by absolute deltaHIT (default = 5000).
sig_delta	Absolute deltaHIT threshold for volcano highlighting (default = 0.2).
fdr_thresh	FDR threshold for volcano significance lines (default = 0.05).

### Details

For each exon-level HIT index event:

- Computes mean HIT per group ('control', 'test')
- Performs a t test if both groups have >50
- Adjusts p-values via Benjamini-Hochberg FDR
- Computes signed ('diff\_HIT') and absolute ('delta\_HIT') changes

The function returns both the full per-event results table and a combined 2x2 patchwork plot containing:

1. Control vs Test mean HIT scatter
2. Top |deltaHIT| heatmap (control/test columns)
3. Volcano plot of |deltaHIT| vs -log10(FDR)
4. Density of deltaHIT distribution

### Value

A named list with:

**'results'** Data.table of per-event statistics (means, p, FDR, deltaHIT)

**'plot'** Patchwork object with 4-panel summary visualization

### See Also

[.getHITindex()]

### Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_compare <- compare_hit_index(sample_frame, condition_map = c(control = "control", test = "case"))
print(hit_compare)
```

---

compare\_sequences\_alignment

*Compare isoform nucleotide and protein sequences by pairwise alignment*

---

### Description

Performs transcript- and protein-level global alignments between included and excluded isoform sequences to quantify sequence similarity, coding differences, and exon coverage differences.

### Usage

```
compare_sequences_alignment(  
  hits,  
  annotations,  
  include_sequences = FALSE,  
  verbose = TRUE  
)
```

## Arguments

hits	A <a href="#">data.table</a> or data.frame containing isoform pairs. Must include columns: transcript_seq_case, transcript_seq_control, protein_seq_case, and protein_seq_control. From prior analysis.
annotations	output from get_annotations (annotations)
include_sequences	Logical; if TRUE, retains raw sequences in the output. Defaults to FALSE.
verbose	Logical; if TRUE, prints processing messages.

## Details

This function wraps internal helpers for alignment (`.align_dna()`, `.align_aa()`), exon length summarization (`.sum_exon_lengths()`), and protein-coding classification (`.pc_class()`).

## Value

A [data.table](#) with added columns describing sequence length, coding length, and alignment similarity metrics, including:

- `pc_class`: protein-coding status ("protein\_coding", "onePC", "noPC")
- `prot_len_case/control`: protein sequence lengths
- `tx_len_case/control`: transcript sequence lengths
- `exon_cds_len_*`, `exon_len_*`: summed exon/CDS lengths
- `dna_pid`, `dna_score`, `prot_pid`, `prot_score`: alignment metrics

## Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annots <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annots$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annots$sequences)
pairs <- get_pairs(x_seq, source="multi")
aligned <- compare_sequences_alignment(pairs, annots$annotations)
print(aligned)
```

---

 compare\_sequence\_frame

*Compare frame states after sequence alignment*


---

## Description

Wrapper function that performs sequence alignment (via [compare\_sequences\_alignment()]) and frame-shift analysis (via [compare\_frames()]) for a complete set of inclusion/exclusion transcript pairs. It then summarizes each event by a high-level classification label.

## Usage

```
compare_sequence_frame(
  complete_hits,
  ann,
  return_class = c("auto", "data.table", "S4")
)
```

## Arguments

complete_hits	'data.frame', 'data.table', or 'SpliceImpactResult' containing complete event information for inclusion/exclusion transcript pairs, typically from [get_pairs()] or similar.
ann	Annotation object (output of [get_annotation()]) used for both sequence alignment and coding index construction.
return_class	Character. Output mode: "data.table", "S4", or "auto" (default). In 'auto', S4 input returns updated S4 output.

## Details

'compare\_sequence\_frame()' is a convenience function that integrates sequence and frame comparison stages in one call, producing an annotated table suitable for downstream summarization or visualization.

The summary label 'summary\_classification' follows this precedence: 1. "Match" - identical protein sequences. 2. "FrameShift" - frame disrupted. 3. "Rescue" - frame restored downstream. 4. Otherwise, inherited from 'pc\_class'.

## Value

A 'data.table' (or updated 'SpliceImpactResult' when 'return\_class' resolves to S4) containing all columns from 'complete\_hits', plus:

**frame\_call** Result from [compare\_frames()].

**rescue** Rescue classification.

**summary\_classification** One of "FrameShift", "Rescue", "Match", or the original 'pc\_class'.

**See Also**

[compare\_frames()], [compare\_sequences\_alignment()]

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annots <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annots$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annots$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annots$annotations)
print(seq_compare)
```

---

compare\_transcript\_pairs

*Compare user-selected transcript pairs*

---

**Description**

Builds a matched-like table for pairs of transcripts by extracting all coding exon coordinates from annotations.

**Usage**

```
compare_transcript_pairs(transcript_pairs, annotations)
```

**Arguments**

transcript\_pairs      data.frame with columns 'transcript1', 'transcript2'  
annotations          flattened GTF-style data.frame or data.table (from get\_annotation)

**Value**

data.table mimicking 'matched' structure, ready for downstream comparison.

**Examples**

```
annotation_df <- load_example_data("annotation_df")$annotation_df
pairs <- data.frame(
  transcript1 = c("ENST00000337907", "ENST00000426559"),
  transcript2 = c("ENST00000400908", "ENST00000399728")
)
matched <- compare_transcript_pairs(pairs, annotation_df$annotations)
print(matched)
```

---

cutoff_num	<i>Compute Cook's Distance Threshold</i>
------------	--

---

### Description

Converts a Cook's distance cutoff specification into a numeric threshold. Used internally by [`site_glm()`] and [`fit_sites_parallel()`].

### Usage

```
cutoff_num(n_rows, cooks_cutoff)
```

### Arguments

n_rows	Integer. Number of observations in the model.
cooks_cutoff	Character or numeric. One of: <b>"Inf"</b> No filtering. <b>"4/n"</b> Use the rule-of-thumb 4 / n threshold. <b>numeric</b> Explicit numeric value.

### Value

Numeric scalar cutoff value.

---

domains_on_exons	<i>Internal helper that returns all domain identifiers overlapping a given set of exons within a transcript.</i>
------------------	--

---

### Description

Internal helper that returns all domain identifiers overlapping a given set of exons within a transcript.

### Usage

```
domains_on_exons(Dexon, tx, exons_vec)
```

### Arguments

Dexon	Output of [ <code>build_domain_lookup()</code> ] ('Dexon' element).
tx	Character scalar; transcript ID.
exons_vec	Character vector of exon IDs.

### Value

Character vector of unique domain identifiers for those exons.

---

domains_on_protein	<i>Internal helper returning all domains mapped to a given transcript's protein.</i>
--------------------	--

---

**Description**

Internal helper returning all domains mapped to a given transcript's protein.

**Usage**

```
domains_on_protein(Dtx, tx)
```

**Arguments**

Dtx	Output of [build_domain_lookup()] ('Dtx' element).
tx	Character scalar; transcript ID.

**Value**

Character vector of domain identifiers.

---

enrich_by_db	<i>Run domain enrichment by database</i>
--------------	--

---

**Description**

Convenience wrapper for [enrich\_domains\_hypergeo()] that runs the enrichment test separately for each database (e.g. "Pfam", "SMART") and combines the results.

**Usage**

```
enrich_by_db(hits, background, dbs, ...)
```

**Arguments**

hits, background	See [enrich_domains_hypergeo()].
dbs	Character vector of database prefixes to test.
...	Additional arguments passed to [enrich_domains_hypergeo()].

**Value**

Combined 'data.table' with an added 'database' column.

**See Also**

[enrich\_by\_event()]

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)

enriched_domains <- enrich_by_db(hits_domain, bg, dbs = 'interpro')
print(enriched_domains)
```

---

enrich\_by\_event

*Run domain enrichment by event type*

---

**Description**

Convenience wrapper for [enrich\_domains\_hypergeo()] that runs the enrichment test separately for each event type and combines results.

**Usage**

```
enrich_by_event(hits, background, events, ...)
```

**Arguments**

hits, background

See [enrich\_domains\_hypergeo()].

events

Character vector of event types to analyze.

...

Additional arguments passed to [enrich\_domains\_hypergeo()].

**Value**

Combined 'data.table' with an added 'event\_type' column.

**See Also**

[enrich\_by\_db()]

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)

enriched_domains <- enrich_by_event(hits_domain, bg, events = 'AFE', db_filter = 'interpro')
print(enriched_domains)
```

---

enrich\_domains\_hypergeo

*Domain-level enrichment via hypergeometric test*

---

**Description**

Tests whether particular protein domains are overrepresented among inclusion/exclusion transcript pairs (foreground) relative to a matched background set, using the hypergeometric test.

**Usage**

```
enrich_domains_hypergeo(
  hits,
  background,
  domain_col_fg = "either_domains_list",
  domain_col_bg = "total_sd_domains",
  event_col = "event_type",
  event_filter = NULL,
  db_filter = NULL,
  min_fg_count = 2,
  delim = "[,;|[:space:]]+"
)
```

**Arguments**

hits	‘data.frame’ or ‘data.table’ containing the foreground transcript pairs (typically the significant inclusion/exclusion events). Must include a list column of domain IDs (default: “either_domains_list”).
background	‘data.frame’ or ‘data.table’ representing the matched background pairs. Must include a list column of domain IDs (default: “total_sd_domains”).
domain_col_fg	Name of the domain list column in ‘hits’.
domain_col_bg	Name of the domain list column in ‘background’.
event_col	Name of the column giving event type (default: “event_type”). Set ‘NULL’ to skip event filtering.
event_filter	Character vector of event types to include (e.g. “A5SS”, “A3SS”). If ‘NULL’, all events are used.
db_filter	Character vector of database prefixes to retain (e.g. “Pfam”, “SMART”). If ‘NULL’, all domains are used.
min_fg_count	Minimum number of foreground hits required to test a domain (default ‘2’).
delim	Regular expression describing the delimiters in string list columns (default ‘[,; [:space:]]+’).

**Details**

Each domain identifier is counted once per transcript pair based on its presence in a list column (e.g. ‘either\_domains\_list’). The probability of observing at least ‘k’ such pairs is computed under the hypergeometric distribution

$$P(X \geq k), \quad X \sim \text{Hypergeom}(M, B - M, K)$$

where:

- K = number of foreground pairs,
- B = number of background pairs,
- M = background count of pairs containing the domain,
- k = foreground count of pairs containing the domain.

P-values are Benjamini-Hochberg adjusted ('padj').

Optionally, analyses can be restricted by event type or database prefix (e.g. "Pfam", "SMART") and domains with fewer than 'min\_fg\_count' foreground occurrences are skipped.

### Value

A 'data.table' with one row per domain, including:

- 'domain\_id' Domain identifier (database prefix removed).
- 'db' Database prefix (e.g. "Pfam").
- 'k', 'K' Foreground domain count and total foreground pairs.
- 'M', 'B' Background domain count and total background pairs.
- 'fg\_prop', 'bg\_prop' Proportion of pairs with the domain.
- 'OR' Odds ratio (Haldane-Anscombe corrected).
- 'pval', 'padj' Raw and BH-adjusted p-values.
- 'events' Event IDs contributing to the domain count.

### See Also

\* [enrich\_by\_event()] run per event type \* [enrich\_by\_db()] run per database \* [add\_domain\_columns()] attach domain lists to hits

### Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)

enriched_domains <- enrich_domains_hypergeo(hits_domain, bg, db_filter = 'interpro')
print(enriched_domains)
```

---

explode_coords	<i>Expand semicolon-delimited coordinate strings into long-format tables</i>
----------------	--

---

### Description

Parses inclusion or exclusion coordinate strings of the form "start-end;start-end;..." into per-exon start/stop rows.

### Usage

```
explode_coords(ev, which = c("inc", "exc"))
```

### Arguments

ev	A 'data.frame' or 'data.table' containing at least 'inc', 'exc', 'event_type', 'gene_id', 'chr', 'strand', and 'form' columns.
which	Character. One of "inc" or "exc" specifying which coordinate column to explode (default "inc").

### Details

This helper is used internally to vectorize exon coordinate parsing for downstream construction of 'GRanges' or other genomic features.

### Value

A 'data.table' with one row per coordinate interval containing: 'event\_row', 'event\_type', 'gene\_id', 'chr', 'strand', 'form', 'event\_id', 'start', 'stop', and optionally 'inc\_idx' (ordinal index for inclusion parts).

---

filter\_spliceimpact\_hits

*Filter a SpliceImpactResult by arbitrary paired-hit columns*

---

### Description

Filters 'paired\_hits' using one or more logical expressions evaluated in the paired-hit table, then synchronizes all event-linked slots ('segments', 'res\_di', 'di\_events', 'matched', 'raw\_events').

### Usage

```
filter_spliceimpact_hits(obj, ..., keep_sample_frame = TRUE)
```

**Arguments**

obj                   A [SpliceImpactResult].

...                   Logical filter expressions evaluated in paired-hit context (e.g., 'event\_id == "A3SS:44"', 'n\_ppi > 0', 'frame\_call == "Match"'). Multiple expressions are combined with '&'.

keep\_sample\_frame    Logical; keep 'sample\_frame' unchanged (default 'TRUE').

**Value**

Filtered [SpliceImpactResult].

**Examples**

```
hits <- data.table::data.table(
  event_id = c("E1", "E2"),
  event_type = c("SE", "A3SS"),
  gene_id = c("ENSG000001", "ENSG000002"),
  chr = c("chr1", "chr2"),
  strand = c("+", "-"),
  transcript_id_control = c("TX1", "TX3"),
  transcript_id_case = c("TX2", "TX4"),
  inc_control = c("100-110", "200-210"),
  inc_case = c("100-115", "205-215"),
  exc_control = c("120-130", "220-230"),
  exc_case = c("121-130", "225-235"),
  n_ppi = c(1L, 0L),
  diff_n = c(1L, 0L),
  frame_call = c("Match", "Frameshift")
)
obj <- as_splice_impact_result(hits_final = hits)
obj_keep <- filter_spliceimpact_hits(obj, n_ppi > 0L)
print(as_dt_from_s4(obj_keep, "paired_hits"))
```

---

fit\_sites\_parallel      *Parallel Quasi-binomial GLM Fitting Across Sites*

---

**Description**

Fits quasi-binomial GLMs per splicing site (or event) in parallel, splitting data into chunks to limit overhead. Each site-level fit is performed by [`.site_glm()`].

**Usage**

```
fit_sites_parallel(
  x,
  chunk_size = 2000L,
  progress = TRUE,
```

```

    verbose = TRUE,
    cooks_cutoff,
    BPPARAM = BiocParallel::SerialParam()
  )

```

### Arguments

x	A 'data.frame' or 'data.table' with columns: 'site_id', 'condition', 'psi_adj', 'psi_raw', and 'total'.
chunk_size	Integer. Approximate number of sites per chunk to send to each worker (default 2000).
progress	Logical. Show progress bar (default 'TRUE').
verbose	Logical. Print progress messages (default 'TRUE').
cooks_cutoff	Numeric or character. Cook's distance cutoff, passed to [cutoff_num()].
BPPARAM	A [BiocParallel::BiocParallelParam-class] object controlling backend and worker settings. Default is [BiocParallel::SerialParam()].

### Value

A 'data.table' with one row per site and columns: 'site\_id', 'p.value', 'cooks\_max', 'n', 'n\_used', 'mean\_psi\_ctrl', 'mean\_psi\_case', and 'delta\_psi'.

---

getSizeFactors

*Compute library size factors from exon-level read counts*

---

### Description

Estimates per-sample normalization factors (size factors) using the **median-of-ratios** method based on exon-level read coverage (nUP + nDOWN). This approach provides robust depth normalization for splicing event comparisons.

### Usage

```
getSizeFactors(df)
```

### Arguments

df	'data.frame' or 'data.table' with at least columns: 'sample_name', 'exon', 'nUP', 'nDOWN'.
----	--

### Details

The function aggregates reads per exon across samples, constructs an exon x sample matrix, and computes size factors:

$$SF_j = \text{median}_i((\text{counts}_{ij} + 1)/\text{geoMean}_i)$$

where the geometric mean is computed across samples for each exon.

**Value**

A 'data.frame' identical to the input with an added 'sizeFactor' column, suitable for downstream normalization.

**See Also**

[.get\_size\_factors\_from\_exons()]

---

get_annotation	<i>Load and cache GENCODE annotations, sequences, and hybrid exon annotations</i>
----------------	---

---

**Description**

This function loads GENCODE gene models (GTF), processes exon annotations, extracts transcript and protein sequences, identifies hybrid exons, and optionally caches the processed objects for future fast access.

**Usage**

```
get_annotation(
  load = c("link", "path", "cached", "test"),
  base_dir = NULL,
  species = c("human", "mouse"),
  release = 45,
  gtf_path = NULL,
  transcript_path = NULL,
  translation_path = NULL,
  filter_tsl = c("1", "2", "3")
)
```

**Arguments**

load	Character string specifying load mode: one of "link", "path", "cached", "test".
base_dir	Optional cache root. If 'NULL' (default), uses a persistent package cache under 'tools::R_user_dir("SpliceImpactR", "cache)". A package-specific 'BiocFile-Cache' is created under this root.
species	Species label used in filenames (default "human").
release	GENCODE release version (default '45').
gtf_path	Path to a GTF file when 'load = "path"'. transcript_path
translation_path	Path to transcript FASTA (.fa/.fa.gz) when 'load = "path"'. translation_path
filter_tsl	Path to protein FASTA (.fa/.fa.gz) when 'load = "path"'. Transcript support levels to retain (default 'c("1","2","3)'). Transcripts outside this set are dropped unless the row is a gene record.

## Details

Four loading modes are supported:

- 'test'** Load small internal test data shipped with the package.
- 'cached'** Load previously processed objects from package `'BiocFileCache'`.
- 'path'** Read local GTF and FASTA files, process, then cache processed objects in package `'BiocFileCache'`.
- 'link'** Download GENCODE files from URLs, process, then cache processed objects in package `'BiocFileCache'`. Optional `'gtf_path'`, `'transcript_path'`, and `'translation_path'` are only used as overrides when they are existing local files or valid URLs; otherwise downloaded GENCODE assets are used.

Processed objects are cached in package `'BiocFileCache'` entries:

```
annotation/{species}/v{release}/tsl-.../annotations.rds
annotation/{species}/v{release}/tsl-.../sequences.rds
annotation/{species}/v{release}/tsl-.../hybrids.rds
```

## Value

A list with:

- 'annotations'** Processed long-format GTF as `'data.table'`
- 'sequences'** List with elements `'transcripts'` and `'proteins'` (or `'NULL'` if not loaded)
- 'hybrids'** Hybrid exon annotation list

## Examples

```
# Load bundled test data
ann <- load_example_data("annotation_df")$annotation_df
print(ann)

# Load from local files and cache processed objects
# ann <- get_annotation(
#   load = "path",
#   gtf_path = "/downloaded_gtf_directory/gencode.v45.annotation.gtf.gz",
#   transcript_path = "/downloaded_gtf_directory/gencode.v45.pc_transcripts.fa.gz",
#   translation_path = "/downloaded_gtf_directory/gencode.v45.pc_translations.fa.gz"
# )

# Download files, process, and cache to a custom cache root
# ann <- get_annotation(
#   load = "link",
#   base_dir = "/project/annotation_cache/"
# )

# Load from cached RDS (fast)
# ann <- get_annotation(
#   load = "cached",
#   base_dir = "/project/annotation_cache/"
```

```
# )
```

---

get_background	<i>Build a transcript-pair background with domain and length annotations</i>
----------------	--

---

### Description

Constructs a background dataset of transcript pairs suitable for domain-level or exon-level enrichment analyses. Depending on the source parameter, the function can derive the background from HIT index results, annotated transcripts, or a user-provided list of transcript IDs.

### Usage

```
get_background(
  source = c("hit_index", "annotated", "user-given"),
  input,
  annotations,
  protein_features,
  keep_annotated_first_last = TRUE,
  minOverlap = 0.8,
  BPPARAM = BiocParallel::bpparam()
)
```

### Arguments

source	Character string specifying the source of the background. One of: <ul style="list-style-type: none"> <li>• "hit_index" use HIT index output directories.</li> <li>• "annotated" use all transcripts from the annotation.</li> <li>• "user-given" use a user-supplied list of transcript IDs.</li> </ul>
input	Source-specific input: <ul style="list-style-type: none"> <li>• For "hit_index": a data.frame of paths with a path column.</li> <li>• For "annotated": ignored.</li> <li>• For "user-given": a character vector or data.frame containing transcript_id.</li> </ul>
annotations	A data.table annotations from get_annotations
protein_features	A data.frame of protein domain or motif features (e.g. InterPro, Pfam) with at least ensembl_transcript_id, ensembl_peptide_id, database, and name columns from get_comprehensive_annotations
keep_annotated_first_last	Logical; passed to read_background to control filtering of annotated first/last exons. Defaults to TRUE.
minOverlap	Numeric (0-1); minimum fraction overlap required when matching exons between HIT index data and annotations. Defaults to 0.8.
BPPARAM	A [BiocParallel::BiocParallelParam-class] object controlling parallel execution in domain background calculations. Defaults to [BiocParallel::bpparam()].

**Value**

A [data.table](#) in which each row represents a transcript pair annotated with gene ID, CDS/exon length differences, and protein domain differences. Columns include: gene\_id, transcript\_id\_1, transcript\_id\_2, prot\_aa\_1, prot\_aa\_2, domains\_1, domains\_2, and related summary metrics.

**Examples**

```

annots <- load_example_data("annotation_df")$annotation_df
interpro_features <- get_protein_features(c("interpro"), annots$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

# Build background from HIT index paths
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annots$annotations,
                    protein_features = protein_feature_total)

# Or from user-supplied transcript IDs
tx_ids <- c("ENST00000466994", "ENST00000484435")
bg_user <- get_background(source = "user-given",
                        input = tx_ids,
                        annotations = annots$annotations,
                        protein_features = protein_feature_total)

```

---

```
get_biomart_protein_features
```

*Retrieve protein feature annotations from Ensembl BioMart (internal)*

---

**Description**

Internal helper to query Ensembl BioMart for per-transcript protein feature annotations such as InterPro or Pfam domains. Designed for batched retrieval using [split\_into\_bits()] to avoid large single queries.

**Usage**

```

get_biomart_protein_features(
  protein_features = c("interpro"),
  gtf_df,
  max_accession_size = 3500,
  species_dataset = "hsapiens_gene_ensembl",
  release = 109,
  ensembl_mirror = NULL
)

```

**Arguments**

protein_features	Character vector specifying which feature types to request (e.g. "interpro", "pfam").
gtf_df	A data.frame or data.table containing GTF annotations; used to derive chromosome groups for batching.
max_accession_size	Integer specifying the maximum total number of transcripts per query batch (default 3500).
species_dataset	Character string giving the Ensembl BioMart dataset (default "hsapiens_gene_ensembl"). For mouse, use "mmusculus_gene_ensembl".
release	Release version from Ensembl associated with the GENCODE version used in [get_annotation()]. See the GENCODE human release listing to map GENCODE and Ensembl versions.

**Details**

The function queries the Ensembl BioMart service using **biomaRt::getBM()** with filters "chromosome\_name" and "transcript\_biotype", restricted to "protein\_coding" transcripts. Queries are executed in chunks per chromosome group to avoid API timeouts.

**Value**

A data.table containing protein feature annotations including transcript and peptide IDs, feature start/end positions, and database-specific identifiers (e.g., InterPro accession).

---

get\_comprehensive\_annotations

*Combine multiple sources of protein feature annotations*

---

**Description**

Aggregates all available feature tables (e.g., biomaRt + manual) into a single unified long-format annotation table.

**Usage**

```
get_comprehensive_annotations(
  protein_feature_list,
  load_path_list = NULL,
  save_path = NULL
)
```

**Arguments**

- protein\_feature\_list      List of data.table objects, typically from [get\_protein\_features()] or [get\_manual\_features()].
- load\_path\_list      Optional vector of file paths to load each feature source from disk (instead of providing in memory).
- save\_path      Optional path to cache the combined annotations.

**Value**

A combined data.table containing all unique feature rows.

**Examples**

```

annotation_df <- load_example_data("annotation_df")$annotation_df
user_df <- data.frame(
  ensembl_transcript_id = c(
    "ENST00000511072", "ENST00000374900", "ENST00000373020", "ENST00000456328",
    "ENST00000367770", "ENST00000331789", "ENST00000335137", "ENST00000361567",
    NA, "ENST00000380152"
  ),
  ensembl_peptide_id = c(
    "ENSP00000426975", NA, "ENSP00000362048", "ENSP00000407743",
    "ENSP00000356802", "ENSP00000326734", NA, "ENSP00000354587",
    "ENSP00000364035", NA
  ),
  name = c(
    "Low complexity", "Transmembrane helix", "Coiled-coil", "Signal peptide",
    "Transmembrane helix", "Low complexity", "Coiled-coil", "Transmembrane helix",
    "Signal peptide", "Low complexity"
  ),
  start = c(80L, 201L, 35L, 1L, 410L, 150L, 220L, 30L, 1L, 300L),
  stop = c(120L, 223L, 80L, 20L, 430L, 190L, 260L, 55L, 24L, 360L),
  database = c("seg", "tmhmm", "ncoils", "signalp", "tmhmm", "seg", "ncoils", "tmhmm", "signalp", NA),
  alt_name = c(NA, "TMhelix", NA, "SignalP-noTM", "TMhelix", NA, NA, "TMhelix", "SignalP-TAT", NA),
  feature_id = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA)
)
user_features <- get_manual_features(user_df, annotation_df$annotations)
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(user_features, interpro_features))
print(protein_feature_total)

```

## Description

Performs per-site differential inclusion testing from a hit-index or junction-form table. Each site is modeled with a quasi-binomial GLM ( $\psi_{adj} \sim \text{condition}$ ) to estimate deltaPSI and significance, optionally using parallel processing.

## Usage

```
get_differential_inclusion(
  DT,
  min_total_reads = 10L,
  minimum_proportion_containing_event = 0.5,
  terminal_fill = "event_max",
  cooks_cutoff = "Inf",
  adjust_method = "fdr",
  verbose = TRUE,
  parallel_glm = TRUE,
  chunk_size_glm = 1000,
  BPPARAM = BiocParallel::SerialParam(),
  return_class = c("auto", "data.table", "S4")
)
```

## Arguments

DT	A 'data.frame', 'data.table', or 'SpliceImpactResult' containing at least the columns 'event_type', 'gene_id', 'chr', 'inc', 'exclusion_reads', 'inclusion_reads', 'condition', and 'sample'.
min_total_reads	Integer. Minimum total reads per site/sample required for inclusion (default '10').
minimum_proportion_containing_event	Numeric in '[0,1]'. Minimum fraction of samples per condition that must contain the event (default '0.5').
terminal_fill	Character or numeric. Strategy for completing AFE/ALE events that are missing in a given sample. Choose one of: <b>"none"</b> Do not add missing terminal sites. <b>"gene_max"</b> Fill missing sites with zero counts and set 'total' to the maximum observed within each 'gene_id'/'sample'/'condition' group. <b>"event_max"</b> Fill missing sites with zero counts and set 'total' to the maximum observed within each 'event_id'/'sample'/'condition' group. <b>"zero"</b> Fill missing sites with zero counts and 'total = 0'. Alternatively, supply a single numeric value to use as the 'total' for all filled rows. Defaults to "gene_max".
cooks_cutoff	Character or numeric. Cook's distance cutoff: "4/n", "Inf", "none", or a numeric value.
adjust_method	Character. Multiple-testing correction method passed to [stats::p.adjust()] (default "fdr").

<code>verbose</code>	Logical. Print progress messages (default 'TRUE').
<code>parallel_glm</code>	Logical. Use parallel fitting via <code>[fit_sites_parallel()]</code> (default 'TRUE').
<code>chunk_size_glm</code>	Integer. Number of sites per parallel chunk (default '1000').
<code>BPPARAM</code>	A <code>[BiocParallel::BiocParallelParam-class]</code> object used when <code>'parallel_glm = TRUE'</code> . Default is <code>[BiocParallel::SerialParam()]</code> .
<code>return_class</code>	Character. Output mode: <code>"data.table"</code> , <code>"S4"</code> , or <code>"auto"</code> (default). In <code>'auto'</code> , S4 input returns an updated S4 object; otherwise a <code>'data.table'</code> is returned.

## Details

The function filters out low-coverage and low-presence events, optionally fills AFE/ALE sites with zero counts where necessary, and then applies site-level GLMs. Parallelization uses `[BiocParallel]` back-ends for reproducibility across platforms. To run in parallel, supply `'BPPARAM'` (for example `[BiocParallel::MulticoreParam()]` on Linux/macOS or `[BiocParallel::SnowParam()]` on Windows).

## Value

If `'return_class'` resolves to `"data.table"`, a `'data.table'` with one row per site containing:

- Metadata columns (`'site_id'`, `'event_type'`, `'event_id'`, `'gene_id'`, ...)
- Sample counts (`'n_samples'`, `'n_control'`, `'n_case'`)
- Mean PSI per group (`'mean_psi_ctrl'`, `'mean_psi_case'`)
- deltaPSI (`'delta_psi'`)
- Raw and adjusted p-values (`'p.value'`, `'padj'`)
- Maximum Cook's distance (`'cooks_max'`)

## See Also

`[fit_sites_parallel()]`, `[cutoff_num()]`, `[stats::glm()]`, `[BiocParallel::bplapply()]`

## Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
head(res)
```

---

`get_di_gene_enrichment`*Extract Differential-Inclusion Genes for Enrichment*

---

**Description**

Select genes whose splicing passes significance and effect-size thresholds.

**Usage**

```
get_di_gene_enrichment(hits, padj_threshold, delta_psi_threshold)
```

**Arguments**

`hits` Data frame output from differential inclusion testing.  
`padj_threshold` FDR cutoff (default '0.05').  
`delta_psi_threshold` Absolute deltaPSI threshold (default '0.1').

**Value**

Character vector of gene IDs.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)

annotation_df <- load_example_data("annotation_df")$annotation_df
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
enrichment <- get_enrichment(get_di_gene_enrichment(res, .05, .1), bg$gene_id, species = 'human', 'ensembl', 'MSig')
print(enrichment)
```

get\_domains

*Add protein domain annotations to splicing events***Description**

Annotates each splicing event with protein domains that are gained, lost, or uniquely present in inclusion or exclusion isoforms.

**Usage**

```
get_domains(
  hits,
  exon_features,
  show_protein_domains = FALSE,
  return_class = c("auto", "data.table", "S4")
)
```

**Arguments**

hits	'data.frame', 'data.table', or 'SpliceImpactResult' containing transcript pairs with at least 'transcript_id_case', 'transcript_id_control', 'exons_case', 'exons_control', and 'event_type'.
exon_features	'data.frame' of exon-domain annotations with columns 'ensembl_transcript_id', 'ensembl_peptide_id', 'exon_id', 'database', 'feature_id', 'name', 'overlap_aa_start', 'overlap_aa_end'.
show_protein_domains	Logical; if 'TRUE', include full protein-level domain sets ('domains_protein_case' / 'domains_protein_control').
return_class	Character. Output mode: "data.table", "S4", or "auto" (default). In 'auto', S4 input returns updated S4 output.

**Details**

Internally, this function builds a domain lookup table from an exon feature annotation (e.g. InterPro, Pfam) and extracts per-exon and per-transcript domain lists for each isoform in 'hits'. Differences between the inclusion ('\*\_case') and exclusion ('\*\_control') isoforms are then summarized as:

\* 'case\_only\_domains': domains unique to the inclusion isoform \* 'control\_only\_domains': domains unique to the exclusion isoform \* 'diff\_n': total number of non-shared domains

If 'show\_protein\_domains = TRUE', additional columns report full domain sets across the entire inclusion/exclusion proteins.

**Value**

The input 'hits' table with added columns (or updated 'SpliceImpactResult' when 'return\_class' resolves to S4):

- 'domains\_exons\_case', 'domains\_exons\_control' domains found on event exons
- 'case\_only\_domains', 'control\_only\_domains' domains unique to each isoform
- 'case\_only\_domains\_list', 'control\_only\_domains\_list', 'either\_domains\_list' list-columns
- 'case\_only\_n', 'control\_only\_n', 'diff\_n' domain counts
- optionally, 'domains\_protein\_case' / 'domains\_protein\_control'

### Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)
print(hits_domain)
```

---

```
get_domain_gene_for_enrichment
```

*Extract Domain-Altering Genes for Enrichment*

---

### Description

Return genes whose inclusion/exclusion isoforms show unique protein domain gain or loss.

### Usage

```
get_domain_gene_for_enrichment(hits)
```

### Arguments

`hits`                    Data frame with domain-annotation columns.

### Value

Character vector of gene IDs.

## Examples

```

ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
enrichment <- get_enrichment(get_domain_gene_for_enrichment(hits_domain), bg$gene_id, species = 'human', 'ensembl')
print(enrichment)

```

---

get\_enrichment

*Gene Set Enrichment for Splicing-Linked Gene Lists*

---

## Description

Perform over-representation analysis for a foreground gene set, optionally against a background universe, using GO, MSigDB, and Reactome categories.

## Usage

```

get_enrichment(
  foreground,
  background = NULL,
  species = c("human", "mouse"),
  gene_id_type = c("symbol", "ensembl"),
  sources = c("GO:BP", "GO:MF", "GO:CC", "MSigDB:H", "MSigDB:C2:CP:REACTOME"),
  min_size = 10,
  max_size = 2000,
  p_adjust_cutoff = 0.05,
  simplify_go = TRUE,
  top_n_plot = 20,
  plot_type = c("dot", "bar")
)

```

**Arguments**

foreground	Character vector of gene IDs (symbols or Ensembl IDs).
background	Optional character vector of background genes (universe). If 'NULL', all genes present in annotation collections are used.
species	Species for enrichment catalog ("human" or "mouse").
gene_id_type	Type of input gene IDs ("symbol" or "ensembl").
sources	Character vector selecting enrichment sources. Example options include: <ul style="list-style-type: none"> <li>"GO:BP", "GO:MF", "GO:CC"</li> <li>"MSigDB:H", "MSigDB:C2:CP:REACTOME"</li> </ul>
min_size	Minimum term size (default '10').
max_size	Maximum term size (default '2000').
p_adjust_cutoff	FDR cutoff for reporting significant terms.
simplify_go	Whether to apply GO term redundancy reduction.
top_n_plot	Number of terms to visualize in the quick plot.
plot_type	"dot" (default) or "bar".

**Details**

This is a convenience wrapper around 'clusterProfiler', 'msigdb', and optionally 'ReactomePA', producing a combined enrichment table and a quick visualization of top significant terms.

Input genes are internally mapped to Entrez IDs. Enrichment tests are performed using:

```
* 'clusterProfiler::enrichGO' * 'clusterProfiler::enricher' (MSigDB) * 'ReactomePA::enrichPathway' (optional)
```

**Value**

A list with:

**results\_per\_source** List of enrichment result tables per source

**results\_combined** Combined enrichment table

**results\_signif** Filtered table by FDR cutoff

**plot** A 'ggplot2' object visualizing top terms

**Note**

Requires these packages installed: 'clusterProfiler', 'msigdb', 'data.table', 'AnnotationDbi', 'ggplot2', and 'org.Hs.eg.db' or 'org.Mm.eg.db'. For Reactome analysis you must also install 'ReactomePA'.

## Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)

annotation_df <- load_example_data("annotation_df")$annotation_df
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
enrichment <- get_enrichment(res$gene_id, bg$gene_id, species = 'human', 'ensembl', 'MSigDB:H')
print(enrichment)
```

---

get\_example\_data      *Helper to fetch test files for vignettes / tests*

---

## Description

Helper to fetch test files for vignettes / tests

## Usage

```
get_example_data(filename)
```

## Arguments

filename      file to probe

## Value

proper path to example data

---

get_exon_features	<i>Map protein features to coding exons</i>
-------------------	---

---

### Description

Overlaps amino acid-based protein features (e.g., InterPro, TMHMM) with exon coding spans defined by transcript-relative CDS coordinates.

### Usage

```
get_exon_features(gtf_dt, feat, inclusive = TRUE)
```

### Arguments

gtf_dt	A <code>data.frame</code> or <code>data.table</code> containing transcript and exon annotation, including <code>type</code> , <code>transcript_id</code> , <code>cds_rel_start</code> , and <code>cds_rel_stop</code> columns (see <code>[add_exon_coding_information()]</code> ).
feat	A <code>data.frame</code> or <code>data.table</code> of long-format protein features (from <code>[get_protein_features()]</code> or <code>[get_comprehensive_annotations()]</code> ) containing columns <code>ensembl_transcript_id</code> , <code>start</code> , <code>stop</code> , <code>database</code> , <code>feature_id</code> , <code>name</code> , and <code>alt_name</code> .
inclusive	Logical; whether to round both feature and exon boundaries upward when converting from nucleotide to amino acid coordinates (default <code>TRUE</code> ). If <code>FALSE</code> , downstream exons own partial codons to avoid double counting.

### Value

A `data.table` of overlapping feature-exon pairs with amino acid coordinates (`overlap_aa_start`, `overlap_aa_end`, `overlap_aa_len`) and associated exon and feature metadata.

### Examples

```
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)
print(exon_features)
```

---

get\_gene\_enrichment     *Unified gene selector for enrichment foregrounds*

---

## Description

Selects a foreground gene vector for enrichment from DI results ('res') or hits-final-like tables ('hits') using a single wrapper.

## Usage

```
get_gene_enrichment(
  mode = c("di", "ppi", "domain"),
  x = NULL,
  res = NULL,
  hits = NULL,
  padj_threshold = 0.05,
  delta_psi_threshold = 0.1
)
```

## Arguments

mode	One of "di", "ppi", "domain".
x	Optional generic input. For 'mode="di"', this should be 'res'-like; for 'mode="ppi"/"domain"', this should be hits-final-like. If 'x' is S4, the appropriate slot is used automatically.
res	Optional DI table (or S4) used when 'mode="di"'. If provided, it is preferred over 'x'.
hits	Optional hits-final-like table (or S4) used when 'mode="ppi"/"domain"'. If provided, it is preferred over 'x'.
padj_threshold	FDR cutoff used only for 'mode="di"'. delta_psi_threshold
	Absolute delta-psi cutoff used only for 'mode="di"'. delta_psi_threshold

## Details

- 'mode = "di"' uses differential inclusion columns ('gene\_id', 'padj', 'delta\_psi') - 'mode = "ppi"' uses hits-final-like columns ('gene\_id', 'n\_ppi') - 'mode = "domain"' uses hits-final-like columns ('gene\_id', 'diff\_n')

Inputs can be a 'data.table'/ 'data.frame' or a 'SpliceImpactResult' S4 object.

## Value

Character vector of unique gene IDs.

**Examples**

```

res <- data.table::data.table(
  gene_id = c("ENSG000001", "ENSG000001", "ENSG000002"),
  padj = c(0.01, 0.20, 0.03),
  delta_psi = c(0.25, 0.05, -0.30)
)
hits <- data.table::data.table(
  gene_id = c("ENSG000001", "ENSG000002", "ENSG000003"),
  n_ppi = c(1L, 0L, 2L),
  diff_n = c(0L, 1L, 2L)
)
get_gene_enrichment(mode = "di", res = res)
get_gene_enrichment(mode = "ppi", hits = hits)
get_gene_enrichment(mode = "domain", hits = hits)

hits_s4 <- data.table::data.table(
  event_id = c("E1", "E2", "E3"),
  event_type = c("SE", "A3SS", "MXE"),
  gene_id = c("ENSG000001", "ENSG000002", "ENSG000003"),
  chr = c("chr1", "chr1", "chr2"),
  strand = c("+", "+", "-"),
  transcript_id_control = c("TX1", "TX3", "TX5"),
  transcript_id_case = c("TX2", "TX4", "TX6"),
  inc_control = c("100-110", "200-210", "300-310"),
  inc_case = c("100-115", "205-215", "305-315"),
  exc_control = c("120-130", "220-230", "320-330"),
  exc_case = c("121-130", "225-235", "325-335"),
  n_ppi = c(1L, 0L, 2L),
  diff_n = c(0L, 1L, 2L)
)
obj <- as_splice_impact_result(hits_final = hits_s4)
get_gene_enrichment(mode = "ppi", x = obj)
get_gene_enrichment(mode = "domain", x = obj)

```

---

get\_hitindex

*Load HIT index PSI files for one or more samples/conditions.*


---

**Description**

Load HIT index PSI files for one or more samples/conditions.

**Usage**

```
get_hitindex(paths_df, keep_annotated_first_last = FALSE)
```

**Arguments**

`paths_df` Data.frame with columns: path, condition, and optionally `sample_name`.  
`keep_annotated_first_last` Logical; if TRUE, retain only annotated first/last exons and normalize PSI.

**Value**

A standardized 'data.table' of HIT index PSI values with inclusion/exclusion and metadata.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame, keep_annotated_first_last = TRUE)
print(hit_index)
```

---

get\_hits\_core

*Convenience accessor for core paired-hit columns*


---

**Description**

Convenience accessor for core paired-hit columns

**Usage**

```
get_hits_core(x, drop_missing = TRUE, keep_internal_keys = FALSE)
```

**Arguments**

**x** A [SpliceImpactResult] object or a paired-hits 'data.frame'/'data.table'.

**drop\_missing** Logical; if 'TRUE', silently drops requested columns that are absent. If 'FALSE', errors on missing columns.

**keep\_internal\_keys** Passed through when 'x' is S4. Default 'FALSE'.

**Value**

'data.table' with the 'core' subset. Works for both S4 and paired-hits 'data.table' input.

**Examples**

```
hits <- data.table::data.table(
  event_id = c("E1", "E2"),
  event_type = c("SE", "A3SS"),
  gene_id = c("ENSG000001", "ENSG000002"),
  chr = c("chr1", "chr2"),
  strand = c("+", "-"),
  transcript_id_control = c("TX1", "TX3"),
  transcript_id_case = c("TX2", "TX4"),
  n_ppi = c(1L, 0L),
  diff_n = c(1L, 0L)
)
print(get_hits_core(hits))
```

---

get_hits_domain	<i>Convenience accessor for domain-focused paired-hit columns</i>
-----------------	---

---

## Description

Convenience accessor for domain-focused paired-hit columns

## Usage

```
get_hits_domain(x, drop_missing = TRUE, keep_internal_keys = FALSE)
```

## Arguments

x	A [SpliceImpactResult] object or a paired-hits 'data.frame'/'data.table'.
drop_missing	Logical; if 'TRUE', silently drops requested columns that are absent. If 'FALSE', errors on missing columns.
keep_internal_keys	Passed through when 'x' is S4. Default 'FALSE'.

## Value

'data.table' with the 'domain' subset. Works for both S4 and paired-hits 'data.table' input.

## Examples

```
hits <- data.table::data.table(  
  event_id = c("E1", "E2"),  
  event_type = c("SE", "A3SS"),  
  gene_id = c("ENSG000001", "ENSG000002"),  
  chr = c("chr1", "chr2"),  
  strand = c("+", "-"),  
  transcript_id_control = c("TX1", "TX3"),  
  transcript_id_case = c("TX2", "TX4"),  
  case_only_domains = c("IPR0001", ""),  
  control_only_domains = c("", "IPR0002"),  
  case_only_n = c(1L, 0L),  
  control_only_n = c(0L, 1L),  
  diff_n = c(1L, 1L)  
)  
print(get_hits_domain(hits))
```

---

get\_hits\_final\_view    *Access paired-hits as compact data.table subsets*

---

### Description

Extracts 'paired\_hits' columns from a [SpliceImpactResult] (or a paired-hits 'data.table') using predefined subset groups such as 'core', 'domain', 'ppi', and 'sequence'.

### Usage

```
get_hits_final_view(
  x,
  col_subset = c("core"),
  cols = NULL,
  drop_missing = TRUE,
  keep_internal_keys = FALSE
)
```

### Arguments

x	A [SpliceImpactResult] object or a paired-hits 'data.frame'/'data.table'.
col_subset	Character vector of subset names. Any of "core", "domain", "ppi", "sequence", or "all".
cols	Optional explicit column vector. If supplied, 'col_subset' is ignored.
drop_missing	Logical; if 'TRUE', silently drops requested columns that are absent. If 'FALSE', errors on missing columns.
keep_internal_keys	Passed through when 'x' is S4. Default 'FALSE'.

### Value

A 'data.table' containing the selected columns. Row count and row order are preserved from the input ('SpliceImpactResult@paired\_hits' or provided 'data.table').

### Examples

```
hits <- data.table::data.table(
  event_id = c("E1", "E2"),
  event_type = c("SE", "A3SS"),
  gene_id = c("ENSG000001", "ENSG000002"),
  chr = c("chr1", "chr2"),
  strand = c("+", "-"),
  transcript_id_control = c("TX1", "TX3"),
  transcript_id_case = c("TX2", "TX4"),
  protein_id_control = c("P1", "P3"),
  protein_id_case = c("P2", "P4"),
  inc_control = c("100-110", "200-210"),
```

```

inc_case = c("100-115", "205-215"),
exc_control = c("120-130", "220-230"),
exc_case = c("121-130", "225-235"),
case_only_domains = c("IPR0001", ""),
control_only_domains = c("", "IPR0002"),
case_only_n = c(1L, 0L),
control_only_n = c(0L, 1L),
diff_n = c(1L, 1L),
case_ppi = c("A;B", "C"),
control_ppi = c("A", "C;D"),
n_case_ppi = c(2L, 1L),
n_control_ppi = c(1L, 2L),
n_ppi = c(1L, 1L),
dna_pid = c(0.95, 0.90),
prot_pid = c(0.90, 0.85),
frame_call = c("Match", "Frameshift")
)
print(get_hits_final_view(hits, col_subset = c("core", "ppi")))

```

---

get\_hits\_ppi

*Convenience accessor for PPI-focused paired-hit columns*


---

## Description

Convenience accessor for PPI-focused paired-hit columns

## Usage

```
get_hits_ppi(x, drop_missing = TRUE, keep_internal_keys = FALSE)
```

## Arguments

**x** A [SpliceImpactResult] object or a paired-hits 'data.frame'/'data.table'.

**drop\_missing** Logical; if 'TRUE', silently drops requested columns that are absent. If 'FALSE', errors on missing columns.

**keep\_internal\_keys** Passed through when 'x' is S4. Default 'FALSE'.

## Value

'data.table' with the 'ppi' subset. Works for both S4 and paired-hits 'data.table' input.

## Examples

```

hits <- data.table::data.table(
  event_id = c("E1", "E2"),
  event_type = c("SE", "A3SS"),
  gene_id = c("ENSG000001", "ENSG000002"),
  chr = c("chr1", "chr2"),

```

```

strand = c("+", "-"),
transcript_id_control = c("TX1", "TX3"),
transcript_id_case = c("TX2", "TX4"),
case_ppi = c("A;B", "C"),
control_ppi = c("A", "C;D"),
n_case_ppi = c(2L, 1L),
n_control_ppi = c(1L, 2L),
n_ppi = c(1L, 1L)
)
print(get_hits_ppi(hits))

```

---

get\_hits\_sequence      *Convenience accessor for sequence/frame-focused paired-hit columns*

---

## Description

Convenience accessor for sequence/frame-focused paired-hit columns

## Usage

```
get_hits_sequence(x, drop_missing = TRUE, keep_internal_keys = FALSE)
```

## Arguments

**x**                    A [SpliceImpactResult] object or a paired-hits 'data.frame'/'data.table'.

**drop\_missing**      Logical; if 'TRUE', silently drops requested columns that are absent. If 'FALSE', errors on missing columns.

**keep\_internal\_keys**  
                      Passed through when 'x' is S4. Default 'FALSE'.

## Value

'data.table' with the 'sequence' subset. Works for both S4 and paired-hits 'data.table' input.

## Examples

```

hits <- data.table::data.table(
  event_id = c("E1", "E2"),
  event_type = c("SE", "A3SS"),
  gene_id = c("ENSG000001", "ENSG000002"),
  chr = c("chr1", "chr2"),
  strand = c("+", "-"),
  transcript_id_control = c("TX1", "TX3"),
  transcript_id_case = c("TX2", "TX4"),
  protein_id_control = c("P1", "P3"),
  protein_id_case = c("P2", "P4"),
  dna_pid = c(0.95, 0.90),
  prot_pid = c(0.90, 0.85),
  frame_call = c("Match", "Frameshift")
)

```

```
)
print(get_hits_sequence(hits))
```

---

get_linear_motifs	<i>Get short linear motif validated instances from ELM and convert to pf form</i>
-------------------	---

---

### Description

Get short linear motif validated instances from ELM and convert to pf form

### Usage

```
get_linear_motifs(
  gtf_df,
  protein_seqs,
  species = c("hsapiens_gene_ensembl", "mmusculus_gene_ensembl"),
  release = 109,
  ensembl_mirror = NULL
)
```

### Arguments

gtf_df	A data.frame or data.table containing GTF annotations; used to derive chromosome groups for batching.
protein_seqs	only necessary if loading SLiMs from elm get_annotation() (default "sequences") output
species	Character string giving the Ensembl BioMart dataset (default "hsapiens_gene_ensembl"). For mouse, use "mmusculus_gene_ensembl".
release	Release version from Ensembl associated with the GENCODE version used in [get_annotation()]. See the GENCODE human release listing to map GENCODE and Ensembl versions.
ensembl_mirror	Optional Ensembl mirror passed to the BioMart connector.

### Details

Here we access ELM's SLiM database to pull instances and classes and use BiomaRt to match up uniprot to ensembl + confirm with regex checks

### Value

A data.table containing protein feature annotations including transcript and peptide IDs, feature start/end positions, and database-specific identifiers (e.g., InterPro accession) for elm SLiMs

---

get\_manual\_features     *Incorporate user-supplied protein features*

---

### Description

Converts a manual feature table into the standardized long format and optionally merges it with biomaRt-derived features.

### Usage

```
get_manual_features(
  manual_features,
  gtf_df,
  biomaRt_features = NULL,
  load_path = NULL,
  save_path = NULL
)
```

### Arguments

manual_features	Data.frame or data.table with at least name, start, stop amino acid, and one of ensembl_transcript_id or ensembl_peptide_id.
gtf_df	get_annotation annotation output
biomaRt_features	Optional data.table of features from [get_protein_features()] to merge with.
load_path	Optional path to load precomputed manual features.
save_path	Optional path to save the combined feature table.

### Value

A data.table of manual (and optionally combined) protein features.

### See Also

[add\_user\_features()]

### Examples

```
annotation_df <- load_example_data("annotation_df")$annotation_df
user_df <- data.frame(
  ensembl_transcript_id = c(
    "ENST00000511072", "ENST00000374900", "ENST00000373020", "ENST00000456328",
    "ENST00000367770", "ENST00000331789", "ENST00000335137", "ENST00000361567",
    NA, "ENST00000380152"
  ),
  ensembl_peptide_id = c(
```

```

      "ENSP00000426975", NA, "ENSP00000362048", "ENSP00000407743",
      "ENSP00000356802", "ENSP00000326734", NA, "ENSP00000354587",
      "ENSP00000364035", NA
    ),
    name = c(
      "Low complexity", "Transmembrane helix", "Coiled-coil", "Signal peptide",
      "Transmembrane helix", "Low complexity", "Coiled-coil", "Transmembrane helix",
      "Signal peptide", "Low complexity"
    ),
    start = c(80L, 201L, 35L, 1L, 410L, 150L, 220L, 30L, 1L, 300L),
    stop = c(120L, 223L, 80L, 20L, 430L, 190L, 260L, 55L, 24L, 360L),
    database = c("seg", "tmhmm", "ncoils", "signalp", "tmhmm", "seg", "ncoils", "tmhmm", "signalp", NA),
    alt_name = c(NA, "TMhelix", NA, "SignalP-noTM", "TMhelix", NA, NA, "TMhelix", "SignalP-TAT", NA),
    feature_id = c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA)
  )
  user_features <- get_manual_features(user_df, annotation_df$annotations)
  print(user_features)

```

---

```
get_matched_events_chunked
```

*Match splicing events to transcript annotations in chunks*

---

## Description

This is a wrapper around `match_events_to_annotations_vec` that processes large event tables in manageable chunks to reduce memory usage. It sequentially runs matching per chunk and concatenates the results.

## Usage

```

get_matched_events_chunked(
  events,
  annotations,
  chunk_size = 50000,
  minOverlap = 0.05,
  return_class = c("auto", "data.table", "S4")
)

```

## Arguments

<code>events</code>	A data.frame or data.table of event definitions. Must include coordinates compatible with <code>match_events_to_annotations_vec</code>
<code>annotations</code>	A data.frame of transcript/exon annotation rows. Typically generated by <code>get_annotations</code>
<code>chunk_size</code>	Integer, number of event rows to process per chunk (default = 50,000).
<code>minOverlap</code>	double ranging from 0 to 1 (default 0.05), required minimum overlap to consider a match
<code>return_class</code>	Character. Output mode: "data.table", "S4", or "auto" (default). In "auto", S4 input returns updated S4 output.

**Details**

This function is intended for large-scale event matching across many splicing events, where running the full table at once may exceed memory limits. It can later be parallelized using **future.apply** or similar.

**Value**

A data.table with matched transcripts and exons for all events. The output order matches the original event order.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
print(sample_frame)

hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annots <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annots$annotations, chunk_size = 2000)
print(matched)
```

---

get\_pairs

*Pair inclusion and exclusion forms of splicing events*


---

**Description**

Builds paired tables of inclusion/exclusion forms for splicing events from rMATS-like or HITindex-like inputs. In rMATS mode, events are paired when both INC and EXC forms exist for a given event ID. In HITindex mode, all positive and negative deltaPSI rows within each event are cross-joined.

**Usage**

```
get_pairs(
  x,
  source = c("paired", "multi"),
  return_class = c("auto", "data.table", "S4")
)
```

**Arguments**

x	A data.frame, data.table, or ‘SpliceImpactResult’ containing splicing event information.
source	Character string specifying input structure: “paired” (rMATS-like) requires exactly one INC and one EXC per event ID.

"multi" (HITindex-like) pairs all positive and negative delta\_psi values within each event.

return\_class Character. Output mode: "data.table", "S4", or "auto" (default). In 'auto', S4 input returns updated S4 output.

### Details

In source="paired" mode, only events with exactly one INC and one EXC row are retained. In source="multi" mode, all positive deltaPSI rows are joined with all negative deltaPSI rows (cartesian join) within each event.

### Value

A [data.table](#) (or updated 'SpliceImpactResult' when 'return\_class' resolves to S4) where each row represents an inclusion-exclusion pair of the same event.

### Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annots <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annots$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annots$sequences)
pairs <- get_pairs(x_seq, source="multi")
print(pairs)
```

---

get\_ppi\_gene\_enrichment

*Extract Protein-Interaction-Affected Genes for Enrichment*

---

### Description

Return genes whose splicing affects known protein-protein interactions.

### Usage

```
get_ppi_gene_enrichment(hits)
```

### Arguments

hits Data frame with PPI annotation columns.

### Value

Character vector of gene IDs.

**Examples**

```

ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)
ppi <- get_ppi_interactions()
hits_final <- get_ppi_switches(hits_domain, ppi, protein_feature_total)
bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
enrichment <- get_enrichment(get_ppi_gene_enrichment(hits_final), bg$gene_id, species = 'human', 'ensembl', 'MSig')
print(enrichment)

```

---

get\_ppi\_interactions *Pull PPI from SpliceImpactR's data*

---

**Description**

Generation details in inst/scripts

**Usage**

```
get_ppi_interactions()
```

**Value**

A 'data.table' of interaction edges used by PPI switching utilities.

**Examples**

```
ppi_int <- get_ppi_interactions()
print(ppi_int)
```

---

get_ppi_switches	<i>Annotate hits_domain with PPI changes for inclusion vs exclusion forms</i>
------------------	---

---

### Description

Adds list-cols case\_ppi/control\_ppi (partner genes) plus counts. Also returns (optionally useful) per-event token sets in PFAM + ELM forms.

### Usage

```
get_ppi_switches(
  hits_domain,
  ppi,
  protein_feature_total,
  return_class = c("auto", "data.table", "S4")
)
```

### Arguments

hits_domain	data.table with gene_id and list-cols case_only_domains_list / control_only_domains_list
ppi	wide interaction table from saved data (get_ppi)
protein_feature_total	table with database/clean_name/feature_id for interpro mapping
return_class	Character. Output mode: "data.table", "S4", or "auto" (default). In 'auto', S4 input returns updated S4 output.

### Value

A 'data.table' identical to 'hits\_domain' with added columns (or updated 'SpliceImpactResult' when 'return\_class' resolves to S4):

**'case\_ppi', 'control\_ppi'** Lists of partner transcripts unique to inclusion or exclusion isoforms.

**'n\_control\_ppi', 'n\_ppi'** Counts of gained/lost interactions.

**'n\_ppi'** Total PPI changes (sum of both directions).

### Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
```

```

annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
ppi <- get_ppi_interactions()
hits_ppi <- get_ppi_switches(hits_domain, ppi, protein_feature_total)
print(hits_ppi)
hits_ppi[n_ppi > 0, .(event_id, gene_id, n_case_ppi, n_control_ppi, n_ppi, case_ppi, control_ppi)]

```

---

get\_protein\_features    *External function to fetch protein features from biomaRt*

---

## Description

Here we also remove any duplicate and overlapping domains We also add the genomic location to the name of the protein feature for downstream safeguarding and precision. This is to prevent different occurrences of the same domain being called as the same in domain identification and enrichment.

## Usage

```

get_protein_features(
  biomaRt_databases = c("interpro", "mobidblite", "seg", "ncoils", "tmhmm", "signalp",
    "elm", "gene3d", "pfam"),
  gtf_df,
  sequences = NULL,
  load_path = NULL,
  save_path = NULL,
  base_dir = NULL,
  use_cache = TRUE,
  force_refresh = FALSE,
  timeout = 600,
  ensembl_mirror = NULL,
  species = c("human", "mouse"),
  release = 109,
  test = FALSE,
  combine_overlaps = FALSE
)

```

**Arguments**

biomaRt_databases	choose what biomaRt attribute to access, defaulting to interpro, mobidblite, seg, ncoils, tmhmm, signalp
gtf_df	annotations from get_annotation()
sequences	only necessary if loading SLiMs from elm get_annotation() (default "sequences") output
load_path	path to load prior protein features from
save_path	path to save prior protein features from
base_dir	Optional cache root. If 'NULL' (default), uses package cache under 'tools::R_user_dir("SpliceImpactR", "cache")'.
use_cache	Logical; if 'TRUE' (default), cache and reuse final 'get_protein_features()' outputs through BiocFileCache.
force_refresh	Logical; if 'TRUE', recompute and overwrite any existing BiocFileCache entry for this parameter/input signature.
timeout	ability to extend timeout if biomaRt is not cooperating
ensembl_mirror	Optional Ensembl mirror to try first for BioMart connections; one of "useast", "www", or "asia". If 'NULL', mirrors are tried in fallback order when 'release = NULL'. If a specific 'release' is provided, biomaRt ignores mirror selection.
species	Character string giving the Ensembl BioMart dataset (default "human"). For mouse, use "mouse".
release	Release version from Ensembl associated with the GENCODE version used in [get_annotation()]. See the GENCODE human/mouse release listings to map GENCODE and Ensembl versions.
test	Logical; bool for whether to load from reduced test set.
combine_overlaps	simplifies protein feature output and combines protein features with the same ID and overlapping coords. Sometimes not desirable

**Value**

A 'data.table' with one row per protein feature and transcript coupling

**Examples**

```
annotation_df <- load_example_data("annotation_df")$annotation_df
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, annotation_df$sequences, timeout=10)
print(interpro_features)
```

---

`get_proximal_shift_from_hits`*Classify splicing events as proximal or distal*

---

### Description

Determines whether inclusion/exclusion events correspond to proximal or distal terminal exon usage for **AFE** (Alternative First Exon) and **ALE** (Alternative Last Exon) events, based on genomic coordinates and strand orientation.

### Usage

```
get_proximal_shift_from_hits(hits)
```

### Arguments

`hits` 'data.frame' or 'data.table' containing at least:

- 'event\_id'
- 'event\_type'
- 'strand'
- 'inc\_case', 'inc\_control'
- 'delta\_psi\_case', 'delta\_psi\_control'

### Details

The function compares the genomic coordinates of the inclusion ('inc\_case') and exclusion ('inc\_control') segments per event:

- For **AFE** events, proximal = exon with smaller start coordinate on the '+' strand (or larger end on '-' strand).
- For **ALE** events, proximal = exon with smaller start coordinate on the '+' strand (or larger end on '-' strand).

Events outside these types are labeled "nonTerminal".

If `plot = TRUE`, a summary donut chart is printed showing the proportion of proximal vs distal usage per event type.

### Value

A 'data.table' identical to 'hits' with an additional column (named 'V1') specifying "proximal", "distal", "overlap", or "nonTerminal".

### See Also

[plot\_prox\_dist()]

**Examples**

```

ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
proximal_output <- get_proximal_shift_from_hits(pairs)
print(proximal_output)

```

---

get_rmats	<i>Expand rMATS event tables into scalar exon inclusion/exclusion coordinates.</i>
-----------	--

---

**Description**

Converts rMATS "event" tables (SE, MXE, A3SS, A5SS, RI) into standardized scalar representations with explicit inclusion/exclusion segments for downstream genomic mapping.

**Usage**

```
get_rmats(DT)
```

**Arguments**

DT                    A 'data.table' or 'data.frame' of rMATS output (merged or per-sample).

**Details**

Handles all five canonical rMATS event types (SE, MXE, A3SS, A5SS, RI), applying strand-aware logic for MXE and coordinate adjustments for A3/A5. Non-standard columns (e.g. IJC\_SAMPLE\_1) are checked for presence.

**Value**

A standardized 'data.table' containing:

- event\_id unique event identifier.
- event\_type rMATS event type (SE, MXE, etc.).
- form inclusion/exclusion form.
- gene\_id, chr, strand.
- inc, exc scalar genomic segments (string: e.g. "100-200;300-400").
- inclusion\_reads, exclusion\_reads, psi - numeric metrics.
- condition, sample, source\_file - carried forward if present.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
rmats <- get_rmats(load_rmats(sample_frame, use = "JCEC", event_types = c("MXE", "SE", "A3SS", "A5SS", "RI")))
print(rmats)
```

---

get\_rmats\_hit

*Wrapper function to get both rmats and hit index cleanly*


---

**Description**

Wrapper function to get both rmats and hit index cleanly

**Usage**

```
get_rmats_hit(
  sample_frame,
  event_types = c("ALE", "AFE", "MXE", "SE", "A3SS", "A5SS", "RI"),
  use = "JCEC",
  keep_annotated_first_last = TRUE
)
```

**Arguments**

sample\_frame     Data.frame with columns: path, condition, and sample\_name.  
event\_types       event types to load from rMATS  
use                Character scalar, one of "JC" or "JCEC".  
keep\_annotated\_first\_last  
                    Logical; if TRUE, retain only annotated first/last exons and normalize PSI.

**Value**

a 'data.table' for all the event types desired from the paths supplied contains: event\_id (unique id for event), event\_type (AS event type), form (INC/EXC), gene\_id (ensembl id), strand, inc, exc (inclusion and exclusion coords) inclusion reads, exclusion reads, psi, sample, condition, source file

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
data <- get_rmats_hit(sample_frame, event_types = c("ALE", "AFE", "MXE", "SE", "A3SS", "A5SS", "RI"))
print(data)
```

---

get\_rmats\_post\_di      *Import post-differential-inclusion rMATS results*

---

### Description

This function reads post-DI rMATS results and converts them into the standardized SpliceImpactR long format with one row per event x (INC/EXC) form.

Input can be: \* a data.frame with columns 'path', 'grp1', 'grp2', 'event\_type', in which case each file is read and processed; or \* a single rMATS results data.frame, in which case 'event\_type' must be supplied.

For each event, the function constructs paired INC and EXC entries: \* 'inc' contains genomic segments included in the form \* 'exc' contains the excluded segment(s) \* 'delta\_psi', 'p.value', and 'padj' are assigned using the rMATS-reported values

Event IDs are automatically generated (event\_type:N) if not supplied

### Usage

```
get_rmats_post_di(input, event_type = NULL)
```

### Arguments

input	Either: * a data.frame with columns 'path', 'grp1', 'grp2', 'event_type', or * a data.frame of rMATS post-DI results.
event_type	Optional event type when 'input' contains a single rMATS data.frame. Ignored when file metadata table is supplied.

### Value

A 'data.table' with columns:

**event\_id** unique event identifier

**event\_type** splicing event type

**form** "INC" or "EXC"

**gene\_id** gene ID

**chr** chromosome

**strand** strand

**inc** genomic coordinates of included segment(s)

**exc** genomic coordinates of excluded segment(s)

**p.value** rMATS p-value

**padj** FDR

**delta\_psi** signed PSI change (+INC, -EXC)

**Examples**

```

# # Multiple files
# input <- data.frame(
#   path = c('/path/A3SS.MATS.JC.txt', '/path2/A5SS.MATS.JC.txt'),
#   grp1 = c("WT", "WT"),
#   grp2 = c("KO", "KO"),
#   event_type = c("A3SS", "A5SS")
# )
# res <- get_rmats_post_di(meta)

# Single rMATS table already loaded as df
df <- data.frame(
  ID = 1L,
  GeneID = "ENSG00000182871",
  geneSymbol = "COL18A1",
  chr = "chr21",
  strand = "+",
  longExonStart_0base = 45505834L,
  longExonEnd = 45505966L,
  shortES = 45505837L,
  shortEE = 45505966L,
  flankingES = 45505357L,
  flankingEE = 45505431L,
  ID.2 = 2L,
  IJC_SAMPLE_1 = "4,1,0",
  SJC_SAMPLE_1 = "9,12,3",
  IJC_SAMPLE_2 = "0,4,5",
  SJC_SAMPLE_2 = "11,15,15",
  IncFormLen = 52L,
  SkipFormLen = 49L,
  PValue = 0.6967562,
  FDR = 1,
  IncLevel1 = "0.295,0.073,0.0",
  IncLevel2 = "0.0,0.201,0.239",
  IncLevelDifference = -0.024,
  stringsAsFactors = FALSE
)
res2 <- get_rmats_post_di(df, event_type = "A3SS")
print(res2)

```

---

get\_sequences

*Retrieve transcript and protein sequences (internal)*


---

**Description**

Internal helper that calls [load\_seq\_map()] to obtain transcript and protein sequences for a given GTF annotation and corresponding FASTA files. Used within higher-level SpliceImpactR workflows.

**Usage**

```
get_sequences(gtf_df, transcript_path, translation_path)
```

**Arguments**

gtf\_df            A data.frame or data.table containing GTF annotation data, typically from [load\_gtf\_long()].

transcript\_path            Path to the transcript FASTA file (e.g. gencode.v45.pc.transcripts.fa.gz).

translation\_path            Path to the protein translation FASTA file (e.g. gencode.v45.pc.translations.fa.gz).

**Value**

A data.table with gene, transcript, and protein IDs and their corresponding nucleotide and amino acid sequences.

---

get\_splicing\_impact    *End-to-end SpliceImpactR wrapper with selectable output class*

---

**Description**

Runs the core SpliceImpactR pipeline from raw event table (or sample paths) through paired domain/PPI calls, then returns either a compact 'data.table' bundle ('data', 'res', 'hits\_final') or an S4 [SpliceImpactResult].

**Usage**

```
get_splicing_impact(
  sample_frame = NULL,
  data = NULL,
  res = NULL,
  annotation_df = NULL,
  protein_feature_total = NULL,
  exon_features = NULL,
  ppi = NULL,
  source_data = c("rmats_hit", "hitindex", "rmats", "both"),
  event_types = c("ALE", "AFE", "MXE", "SE", "A3SS", "A5SS", "RI", "HFE", "HLE"),
  use = "JCEC",
  keep_annotated_first_last = FALSE,
  min_total_reads = 10L,
  minimum_proportion_containing_event = 0.5,
  terminal_fill = "event_max",
  cooks_cutoff = "Inf",
  adjust_method = "fdr",
  fdr_threshold = 0.05,
```

```

delta_psi_threshold = 0.1,
parallel_glm = TRUE,
chunk_size_glm = 1000L,
BPPARAM = BiocParallel::SerialParam(),
chunk_size_match = 2000L,
source_pairs = c("multi", "paired"),
show_protein_domains = FALSE,
return_class = c("data.table", "S4"),
debug_steps = FALSE,
metadata = list(),
verbose = TRUE
)

```

### Arguments

sample_frame	Optional sample manifest for [get_hitindex()] / [get_rmats_hit()]. Must include 'path', 'condition', and optional 'sample_name'.
data	Optional precomputed raw event-level table.
res	Optional precomputed differential inclusion table.
annotation_df	Optional annotation list from [get_annotation()] with 'annotations' and 'sequences'.
protein_feature_total	Optional protein feature table from [get_comprehensive_annotations()]. Required if 'exon_features' is not supplied and domain/PPI steps are run.
exon_features	Optional precomputed exon-feature overlap table from [get_exon_features()].
ppi	Optional preloaded PPI table. If 'NULL', [get_ppi_interactions()] is used when needed.
source_data	Which ingestion route to use when 'data' is 'NULL'. One of "hitindex", "rmats", "both", or legacy alias "rmats_hit".
event_types	Event types for [get_rmats_hit()] / [load_rmats()]. Use both terminal and non-terminal types for 'source_data = "both"'.
use	Junction count mode for rMATS ingestion ("JC" or "JCEC").
keep_annotated_first_last	Passed to [get_hitindex()] for terminal events.
min_total_reads	Passed to [get_differential_inclusion()].
minimum_proportion_containing_event	Passed to [get_differential_inclusion()].
terminal_fill	Passed to [get_differential_inclusion()].
cooks_cutoff	Passed to [get_differential_inclusion()].
adjust_method	Passed to [get_differential_inclusion()].
fdr_threshold	Passed to [keep_sig_pairs()] as the adjusted p-value cutoff.
delta_psi_threshold	Passed to [keep_sig_pairs()] as the absolute delta-psi cutoff.
parallel_glm	Passed to [get_differential_inclusion()].

chunk_size_glm	Passed to [get_differential_inclusion()].
BPPARAM	Passed to [get_differential_inclusion()]. Use a [BiocParallel::BiocParallelParam-class] object (for example [BiocParallel::SerialParam()], [BiocParallel::SnowParam()], or [BiocParallel::MulticoreParam()]).
chunk_size_match	Chunk size for [get_matched_events_chunked()].
source_pairs	Pairing mode for [get_pairs()] ("multi" or "paired").
show_protein_domains	Passed to [get_domains()].
return_class	One of "data.table" or "S4".
debug_steps	Logical; if 'TRUE', includes intermediates ('matched', 'hits_sequences', 'pairs', 'seq_compare', 'hits_domain') in data.table mode.
metadata	Optional list attached to 'SpliceImpactResult@metadata'.
verbose	Logical; emit progress messages.

### Value

If 'return\_class = "data.table"', returns a named list with 'data', 'res', and 'hits\_final'.

If 'return\_class = "S4"', returns a [SpliceImpactResult] containing 'raw\_events', 'di\_events', and 'paired\_hits' slots.

### Examples

```
ex <- load_example_data(
  c("sample_frame", "annotation_df", "protein_feature_total", "ppi")
)
out <- get_splicing_impact(
  sample_frame = ex$sample_frame,
  annotation_df = ex$annotation_df,
  protein_feature_total = ex$protein_feature_total,
  ppi = ex$ppi,
  source_data = "rmats",
  event_types = c("SE"),
  use = "JCEC",
  parallel_glm = FALSE,
  BPPARAM = BiocParallel::SerialParam(),
  verbose = FALSE
)
print(names(out))
```

get\_user\_data

*Get User-Supplied Splicing Event Data***Description**

SpliceImpactR accepts user-supplied splicing data in the same structure produced by `get_rmats_hit()`. Each event must be represented at the event-form and sample level.

**\*\*Event representation\*\*** - Each splicing event must be split into two forms: - INC: the inclusion isoform - EXC: the exclusion isoform - Alternative first/last exon events (AFE/ALE) or more abstract events may instead provide a single SITE form.

**\*\*Coordinates\*\*** - inc column: genomic coordinates included in the given form - exc column: genomic coordinates excluded in the given form - Coordinates may be one or multiple ranges (e.g., "100-200" or "100-150;300-350") - User must supply at least an inc and if supplying an exc, accompany with an inc coord

**\*\*Counts and PSI\*\*** - inclusion\_reads and exclusion\_reads must be provided per form - psi must be provided per sample (range 0-1) If psi isn't given, it will be extracted through inclusion\_reads/exclusion\_reads

**\*\*Sample structure\*\*** - Each event must have INC and EXC rows (or just SITE) - Each event must have >1 sample per condition (e.g., case vs control) - Required sample annotations: sample, condition

**\*\*Required columns\*\*** event\_id, event\_type, form, gene\_id, chr, strand, inc, exc, inclusion\_reads, exclusion\_reads, psi, sample, condition

**\*\*Defaults\*\*** - If event\_type not supplied: filled as "unknown" - If source\_file not supplied: filled with empty string

This format enables downstream functionality including PSI modeling, annotation integration, and protein consequence prediction.

**Usage**

```
get_user_data(df)
```

**Arguments**

df                      Data frame with splicing events. Detailed in description

**Value**

data.table with cols, detailed above: "event\_id", "event\_type", "form", "gene\_id", "chr", "strand", "inc", "exc", "inclusion\_reads", "exclusion\_reads", "psi", "sample", "condition", "source\_file" – designed to match get\_rmats\_hit output

**Examples**

```
example_df <- data.frame(
  event_id = rep("A3SS:1", 8),
  event_type = "A3SS",
```

```

form = rep(c("INC", "EXC"), each = 4),
gene_id = "ENSG00000158286",
chr = "chrX",
strand = "-",
inc = c(rep("149608626-149608834", 4), rep("149608626-149608829", 4)),
exc = c(rep("", 4), rep("149608830-149608834", 4)),
inclusion_reads = c(30, 32, 29, 31, 2, 3, 4, 3),
exclusion_reads = c(1, 1, 2, 1, 28, 27, 26, 30),
sample = c("S1", "S2", "S3", "S4", "S1", "S2", "S3", "S4"),
condition = rep(c("case", "case", "control", "control"), 2),
stringsAsFactors = FALSE
)
example_df$psi <- example_df$inclusion_reads / example_df$exclusion_reads
user_data <- get_user_data(example_df)
print(user_data)

```

---

get\_user\_data\_post\_di *Format user-supplied post-DI (post-differential-inclusion) splicing results*

---

## Description

This function converts user-supplied event results into the internal SpliceImpactR DI format. It accepts per-event statistics and ensures each splicing event contains valid inclusion/exclusion structure.

**## Requirements** *\*\*Event representation\*\** - Each splicing event must be split into two forms: - INC: the inclusion isoform - EXC: the exclusion isoform - Alternative first/last exon events (AFE/ALE) or more abstract events may instead provide a single SITE form.

*\*\*Coordinates\*\** - inc column: genomic coordinates included in the given form - exc column: genomic coordinates excluded in the given form - Coordinates may be one or multiple ranges (e.g., "100-200" or "100-150;300-350")

- User **must supply** 'event\_id' (unique ID per splicing event, event\_id = event\_type:x for form != SITE. event\_id = gene:event\_type for form = SITE. Look at example output from get\_differential\_inclusion using test data for more examples) - Each event must be either: - **INC + EXC** forms (paired isoforms), or - **SITE** (single isoform) - Required columns: 'gene\_id, chr, strand, inc, exc, form, event\_id'

**## Behavior** - Does **not** generate event IDs: user must provide them - Constructs 'site\_id = event\_type|gene\_id|chr|inc|exc|form' - 'delta\_psi': - If missing: INC = +1, EXC = -1, SITE expands to +1 and -1 each to get all relevant comparisons - 'p.value', 'padj': - If missing: set to 0 - All diagnostic fields ('cooks\_max, n, n\_used, n\_samples, n\_case, mean\_psi\_ctrl, mean\_psi\_case, n\_control') set to -1 if missing

**## Validation** - Throws error if: - Any event lacks **INC+EXC** or **SITE** - An event mixes SITE with INC/EXC

**## Output** Returns a 'data.table' formatted like SpliceImpactR DI output. Ready for annotation, pairing, enrichment, and PPI analysis.

**Usage**

```
get_user_data_post_di(df)
```

**Arguments**

df                    Data frame of post-DI results, detailed in description

**Value**

A data.table formatted like SpliceImpactR DI output (get\_differential\_inclusion)

**Examples**

```
example_user_data <- data.frame(
  event_id = rep("A3SS:1", 8),
  event_type = "A3SS",
  gene_id = "ENSG00000158286",
  chr = "chrX",
  strand = "-",
  form = rep(c("INC", "EXC"), each = 4),
  inc = c(
    rep("149608626-149608834", 4),
    rep("149608626-149608829", 4)
  ),
  exc = c(
    rep("", 4),
    rep("149608830-149608834", 4)
  ),
  inclusion_reads = c(30, 28, 25, 32, 2, 3, 4, 3),
  exclusion_reads = c(1, 2, 1, 1, 28, 27, 26, 30),
  sample = c("S1", "S2", "S3", "S4", "S1", "S2", "S3", "S4"),
  condition = rep(c("case", "case", "control", "control"), 2),
  stringsAsFactors = FALSE
)

# compute psi if missing, just for demo

post_di_user_data <- get_user_data_post_di(example_user_data)
print(post_di_user_data)
```

---

```
identify_hybrid_exons_split
```

*Identify potential hybrid exons (internal)*

---

**Description**

Internal helper to find exons that overlap between internal and terminal (first/last) exons of different transcripts within the same gene. Used to detect possible hybrid exon configurations.

**Usage**

```
identify_hybrid_exons_split(gtf_df)
```

**Arguments**

`gtf_df` A `data.frame` or `data.table` containing GTF annotations with `gene_id`, `transcript_id`, `exon_id`, `chr`, `start`, `end`, and `absolute_exon_class`.

**Details**

Uses `data.table::foverlaps()` to identify exons that share genomic coordinates but belong to different transcripts within the same gene.

**Value**

A list of two `data.tables`:

- `first_hybrids` overlaps between first and internal exons
- `last_hybrids` overlaps between last and internal exons

Each includes transcript IDs, exon IDs, and mapped transcript `row_uids`.

---

<code>import_di_table</code>	<i>Standardize a differential inclusion (DI) result table</i>
------------------------------	---

---

**Description**

Converts an arbitrary differential inclusion result table into the standardized column format expected by SpliceImpactR functions.

**Usage**

```
import_di_table(
  df,
  colmap = list(gene_id = "gene_id", chr = "chr", strand = "strand", inc = "inc", exc =
    "exc", delta_psi = "delta_psi", pvalue = "p.value", event_type = NULL),
  default_event_type = "SITE",
  adjust_method = "fdr",
  add_chr_prefix = FALSE
)
```

**Arguments**

<code>df</code>	A 'data.frame' or 'data.table' containing differential inclusion results.
<code>colmap</code>	A named list mapping required fields in 'df' to standard names ('gene_id', 'chr', 'strand', 'inc', 'exc', 'delta_psi', 'pvalue', and optionally 'event_type').
<code>default_event_type</code>	Character. Default 'event_type' to assign if none provided (default "SITE").
<code>adjust_method</code>	Character. Multiple-testing correction method passed to [stats::p.adjust()] (default "fdr").
<code>add_chr_prefix</code>	Logical. Add "chr" prefix if absent (default 'FALSE').

**Details**

This function provides a uniform interface for importing external DI results (e.g. from rMATS, MAJIQ, or SUPPA2) so they can be compared or plotted alongside SpliceImpactR outputs.

**Value**

A standardized 'data.table' with columns: 'site\_id', 'event\_type', 'gene\_id', 'chr', 'strand', 'inc', 'exc', 'delta\_psi', 'p.value', 'padj', and 'form'.

**Examples**

```
df <- data.frame(
  gene_id = "ENSG00000280071",
  chr = "7",
  strand = "+",
  inc = "1940088-1940549",
  exc = "",
  delta_psi = 0.25,
  p.value = 0.01
)
di_std <- import_di_table(df)
head(di_std)
```

---

integrated\_event\_summary

*Integrated summary of event classification, alignment, and domain changes*

---

**Description**

Provides a comprehensive visualization and summary of event classification outcomes (frame shifts, rescues, matches, etc.), alignment quality, and domain change prevalence across alternative splicing event types. Integrates results from [`compare_sequence_frame()`] with pre-filter event tables to display pre- vs post-filter usage, event coordination, and gene/domain overlaps.

**Usage**

```
integrated_event_summary(hits, pre_filter_hits)
```

**Arguments**

**hits** 'data.frame', 'data.table', or 'SpliceImpactResult' output from [`'compare_sequence_frame()'`], containing per-event alignment and domain information (e.g. `'summary_classification'`, `'prot_score'`, `'event_type'`, `'case_only_n'`, `'control_only_n'`, etc.).

**pre\_filter\_hits** 'data.frame', 'data.table', or 'SpliceImpactResult' representing the unfiltered input events (e.g. raw differential inclusion table prior to sequence comparison).

**Details**

The function integrates multiple layers of event-level characterization:

- Event-type composition and class proportions
- Protein alignment quality distribution
- Domain-change prevalence (case/control/both)
- Event-type coordination heatmap (Jaccard similarity across genes)
- Relative event retention pre- vs post-filtering

**Value**

A named list with:

**'summaries'** List containing per-type tables: `by_type`, `class_counts`, `score_summary`, `domain_prevalence`, and `relative_use`.

**'plot'** A multi-panel [`'patchwork'`] composite summarizing classification, alignment, domain changes, and coordination.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)
```

```
ppi <- get_ppi_interactions()
hits_final <- get_ppi_switches(hits_domain, ppi, protein_feature_total)
int_summary <- integrated_event_summary(hits_final, res)
print(int_summary)
```

---

iwr\_to\_pfam

*Convert InterPro IDs to PFAM IDs*


---

### Description

Convert InterPro IDs to PFAM IDs

### Usage

```
iwr_to_pfam(iwr_ids)
```

### Arguments

iwr\_ids            Character vector of InterPro IDs (for example, "IPR000719").

### Value

Character vector of PFAM IDs mapped from 'iwr\_ids'.

---

keep\_sig\_pairs

*Filter event pairs by significance and deltaPSI thresholds*


---

### Description

Keeps all rows belonging to events where at least one isoform or site passes adjusted p-value and deltaPSI significance criteria.

### Usage

```
keep_sig_pairs(
  DT,
  padj_thr = 0.05,
  dpsr_thr = 0.1,
  return_class = c("auto", "data.table", "S4")
)
```

**Arguments**

DT	A 'data.frame' or 'data.table' containing at least 'event_id', 'padj', and 'delta_psi' columns.
padj_thr	Numeric. Adjusted p-value threshold (default '0.05').
dpsi_thr	Numeric. Absolute deltaPSI threshold (default '0.1').
return_class	Character. Output mode: "data.table", "S4", or "auto" (default). In 'auto', S4 input returns updated S4 output.

**Value**

A 'data.table' (or updated 'SpliceImpactResult' when 'return\_class' resolves to S4) containing all rows from event pairs in which at least one row meets the significance criteria.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
sig_di <- keep_sig_pairs(res)
print(sig_di)
```

---

load\_example\_data      *Load bundled example inputs for documentation*

---

**Description**

Returns commonly used example objects (sample manifest, test annotations, optional feature mappings, optional PPI table) so man-page examples can stay focused on the documented function rather than setup boilerplate.

**Usage**

```
load_example_data(
  include = c("sample_frame", "annotation_df"),
  biomaRt_databases = c("interpro"),
  test = TRUE
)
```

**Arguments**

include	Character vector selecting which objects to return. Supported values are "sample_frame", "annotation_df", "protein_feature_total", "exon_features", "ppi", and "all". If "all" is present, it expands to 'c("sample_frame", "annotation_df", "protein_feature_total", "exon_features")'.
---------	--

`biomaRt_databases` Character vector passed to `[get_protein_features()]` when protein features are requested. Default is `"interpro"`.

`test` Logical passed to `[get_protein_features()]` (default `'TRUE'`).

**Value**

Named list containing the requested objects.

**Examples**

```
ex <- load_example_data(c("sample_frame", "annotation_df"))
sample_frame <- ex$sample_frame
annotation_df <- ex$annotation_df

ex2 <- load_example_data(c("annotation_df", "exon_features"))
exon_features <- ex2$exon_features
print(exon_features)
```

---

<code>load_gtf_long</code>	<i>Load a GTF file into a long-form data.table (internal)</i>
----------------------------	---

---

**Description**

Internal helper to read a GTF or GFF file (optionally gzipped) and return it as a tidy **data.table**. Ensures consistent column naming, fills in missing identifiers from the `'attributes'` column, and optionally adds a unique row identifier.

**Usage**

```
load_gtf_long(gtf_path_or_df, add_row_uid = TRUE)
```

**Arguments**

`gtf_path_or_df` Character string giving the path or URL to a GTF/GFF file (optionally prefixed with `'file://'`), or an existing `data.frame/data.table` containing GTF-like data.

`add_row_uid` Logical; if `'TRUE'`, adds a unique `'row_uid'` column for reference.

**Details**

The function uses **rtracklayer** to import GTF/GFF files, which returns an S4 `DataFrame`. It is then coerced to a standard `data.table`. When certain ID columns are missing, they are extracted from the `'attributes'` column using `[attr_get()]`.

**Value**

A `data.table` with standardized GTF fields and a consistent set of identifier columns.

**Examples**

```
## Not run:
gtf_dt <- load_gtf_long("gencode.v45.annotation.gtf.gz")
data.table::head(gtf_dt)

## End(Not run)
```

load\_rmats

*Load rMATS event files into standardized data.tables***Description**

Parses rMATS output (.MATS.JC.txt or .MATS.JCEC.txt) for multiple event types and returns unified event tables ready for downstream inclusion/exclusion processing.

**Usage**

```
load_rmats(
  paths,
  use = c("JC", "JCEC"),
  event_types = c("SE", "RI", "A5SS", "A3SS", "MXE")
)
```

**Arguments**

**paths** A data.frame with columns path, sample\_name, and condition.

**use** Character scalar, one of "JC" or "JCEC".

**event\_types** Event types to include: one or more of c("SE", "RI", "A5SS", "A3SS", "MXE").

**Value**

A 'data.table' with unified rMATS event annotations, including columns:

- event\_type, event\_id, gene\_id, chr, strand
- sample, condition (if applicable)
- delta\_psi, pvalue, fdr (if present)
- inclusion/exclusion read counts

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
rmats <- load_rmats(sample_frame, use = "JCEC", event_types = c("MXE", "SE", "A3SS", "A5SS", "RI"))
print(rmats)
```

---

load_seq_map	<i>Build a compact transcript protein sequence map (internal)</i>
--------------	---

---

## Description

Internal helper that integrates information from a GTF, transcript FASTA, and protein FASTA to produce a compact mapping of genes, transcripts, and proteins, optionally including nucleotide and amino-acid sequences.

## Usage

```
load_seq_map(
  gtf_df,
  txfa_path,
  aafa_path,
  take_tx_cds_slice = TRUE,
  keep_sequences = TRUE,
  add_row_uids = TRUE
)
```

## Arguments

gtf_df	A <code>data.frame</code> or <code>data.table</code> produced by <code>[load_gtf_long()]</code> , containing at least <code>gene_id</code> , <code>transcript_id</code> , <code>protein_id</code> , and optionally <code>row_uid</code> .
txfa_path	Character string giving the path to the GENCODE transcript FASTA file (e.g. <code>gencode.v45.pc.transcripts.fa.gz</code> ).
aafa_path	Character string giving the path to the GENCODE protein FASTA file (e.g. <code>gencode.v45.pc.translations.fa.gz</code> ).
take_tx_cds_slice	Logical; if TRUE, restricts transcript sequences to their coding region based on the <code>CDS:start-end</code> annotation in the FASTA header.
keep_sequences	Logical; if TRUE, include sequence strings in the output table, otherwise store <code>NA_character_</code> .
add_row_uids	Logical; if TRUE, attaches corresponding <code>row_uids</code> for genes and transcripts from <code>gtf_df</code> .

## Details

The function combines identifiers from GTF features, transcript FASTA headers, and protein FASTA headers to construct a unified mapping. It uses **Biostrings** to load FASTA data and **data.table** for efficient joins.

**Value**

A data.table containing, for each transcript:

**row\_uid** Row index within the output mapping.

**gene\_id, transcript\_id, protein\_id** Identifiers from GENCODE.

**transcript\_seq, protein\_seq** Optional sequence strings.

**gene\_row\_uid, transcript\_row\_uid** Original UID references (if added).

---

mark\_changing\_partners\_split

*Helper to annotate PPI changes from DDI and DMI*

---

**Description**

Helper to annotate PPI changes from DDI and DMI

**Usage**

```
mark_changing_partners_split(
  ppi,
  gene_id,
  changed_pfam_case,
  changed_pfam_control,
  changed_motif_case = character(),
  changed_motif_control = character()
)
```

---

match\_events\_to\_annotations\_vec

*Match alternative splicing events to annotated exons and transcripts*

---

**Description**

Performs vectorized overlap mapping between event coordinates (e.g. inclusion or exclusion intervals) and exons from an annotation resource. Returns the best-matching transcript and exon set per event based on coverage, exon classification, and protein-coding preference.

**Usage**

```
match_events_to_annotations_vec(events, annotations, minOverlap = 0.05)
```

**Arguments**

events	A 'data.frame' or 'data.table' containing splicing events with columns 'chr', 'strand', 'gene_id', and coordinate fields 'inc' and 'exc' (semicolon-delimited "start-end" strings).
annotations	A gene annotation table (e.g. from [rtracklayer::import()] on a GTF file) with exon and transcript rows, passed to [build_from_annotations()].
minOverlap	Minimum fractional overlap (0-1) required between an inclusion segment and an annotated exon to count as a hit. Default '0.05'.

**Details**

The function uses [GenomicRanges::findOverlaps()] to match event inclusion intervals to exons. Candidate transcripts are filtered to ensure sufficient coverage and absence of overlaps with exclusion coordinates.

The algorithm prioritizes exon classification ('first', 'internal', 'last') consistent with the event type (AFE, ALE, SE, etc.), followed by reciprocal overlap fractions, intersection width, and protein-coding status.

**Value**

A 'data.table' containing one row per input event with the following appended columns:

**'transcript\_id'** The best matching transcript ID.

**'exons'** Semicolon delimited list of exon IDs covered by the event.

**'inc\_exons\_by\_idx'** Semicolon delimited exon IDs per inclusion index (maintaining order).

**'inc\_rows\_by\_idx'** Semicolon delimited exon row indices matching inclusion order.

---

overview\_spicing\_comparison

*Overview of global splicing event distributions between conditions*

---

**Description**

Generates a multi-panel comparison summarizing global splicing characteristics (event counts, events-per-gene, PSI distributions) between experimental and control conditions, normalized by sequencing depth.

**Usage**

```
overview_spicing_comparison(
  events,
  sample_df,
  depth_norm = c("exon_files", "user-given"),
  event_type = "AFE",
  conditions = c(control = "control", experimental = "case"),
  minReads = 10,
  output_file = NULL
)
```

## Arguments

events	'data.frame' or 'data.table' of splicing events with at least: 'sample', 'condition', 'gene_id', 'inclusion_reads', 'exclusion_reads', 'psi', 'inc', 'exc'.
sample_df	Metadata 'data.frame' with sample-level paths and conditions.
depth_norm	Normalization mode: "exon_files" (compute from read files) or "user-given" (use provided size factors).
event_type	Character string specifying the event class (e.g., "AFE", "ALE").
conditions	Named character vector mapping 'control' and 'experimental' condition labels.
minReads	Minimum reads required for inclusion or exclusion (default = 10).
output_file	Optional path to save a combined summary figure.

## Details

The output combines: - **Panel A:** Depth-normalized event counts per sample (Wilcoxon test) - **Panel B:** Mean events per gene per sample (Wilcoxon test) - **Panel D:** PSI cumulative distribution comparison (K-S test)

Size factors are computed internally using [.get\_size\_factors\_from\_exons()], enabling robust normalization.

## Value

Invisibly returns a combined ['patchwork'] plot object.

## See Also

[.get\_size\_factors\_from\_exons()], [getSizeFactors()]

## Examples

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
ov <- overview_splicing_comparison(hit_index, sample_frame, 'exon_files')
print(ov)
```

---

plot\_alignment\_summary

*Plot alignment score distribution and coding summary*

---

## Description

Visualizes alignment scores ('prot\_pid' or 'dna\_pid') and coding class composition of hits, showing both the categorical composition and histogram of alignment identity values.

**Usage**

```
plot_alignment_summary(
  hits,
  mode = c("protein", "transcript"),
  output_file = NULL
)
```

**Arguments**

`hits`            'data.frame' or 'data.table' containing 'prot\_pid' or 'dna\_pid' and 'summary\_classification' columns.

`mode`            Character, either "protein" (uses 'prot\_pid') or "transcript" (uses 'dna\_pid').

`output_file`    Optional path to save the combined plot.

**Value**

A composite 'ggplot' object (from 'ggpubr::ggarrange') showing stacked bar counts by coding class and histogram of alignment identity scores.

**See Also**

[plot\_length\_comparison()]

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
alignment_summary <- plot_alignment_summary(seq_compare)
print(alignment_summary)
```

---

plot\_di\_volcano\_dt      *Volcano plot for differential inclusion results*

---

**Description**

Generates a volcano plot of deltaPSI vs.  $-\log_{10}(\text{FDR})$  highlighting significant events.

**Usage**

```
plot_di_volcano_dt(di, padj_thr = 0.05, dps_i_thr = 0.1)
```

**Arguments**

di	A 'data.frame' or 'data.table' containing at least 'delta_psi' and 'padj' columns (optionally 'event_type').
padj_thr	Numeric. Adjusted p-value threshold (default '0.05').
dpsi_thr	Numeric. Absolute deltaPSI threshold (default '0.1').

**Details**

Significant sites are colored in 'deeppink4'; nonsignificant sites are shown in light grey. Dashed and dotted lines indicate deltaPSI and FDR thresholds.

**Value**

A 'ggplot2' object showing differential inclusion significance.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
plot_di_volcano_dt(res)
```

---

plot\_enriched\_domains\_counts

*Plot enriched domains by associated event count*

---

**Description**

Visualizes the top enriched protein domains based on the number of events contributing to each domain's enrichment, optionally coloring by  $-\log_{10}$  adjusted p-value.

**Usage**

```
plot_enriched_domains_counts(enriched_domains, top_n = 25)
```

**Arguments**

enriched_domains	'data.frame' or 'data.table' Output table from [enrich_domains_hypergeo()], including at least columns 'domain_id' and 'events'. Optional columns 'padj' and 'OR' are used for coloring and labeling.
top_n	Integer (default '25') Number of top domains to display, ranked by increasing 'padj'.

**Details**

The function expects the output of `[enrich_domains_hypergeo()]`, typically a 'data.table' or 'data.frame' containing 'domain\_id', 'events', and optionally 'padj' and 'OR'.

Each bar corresponds to one domain, with height proportional to the number of unique 'event\_id's contributing to that domain. Bars are ordered by ascending adjusted p-value ('padj'), and colored by  $-\log_{10}(\text{padj})$  if available. When no 'padj' column is present, the bars are shown in a uniform fill color.

**Value**

A 'ggplot' object showing bars of domain counts colored by enrichment significance.

**See Also**

`[enrich_domains_hypergeo()]`, `[enrich_by_event()]`, `[enrich_by_db()]`

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)
bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
enriched_domains <- enrich_domains_hypergeo(hits_domain, bg, db_filter = 'interpro')
plot_enriched_domains_counts(enriched_domains, top_n = 20)
```

---

plot\_length\_comparison

*Compare inclusion vs. exclusion isoform lengths*

---

**Description**

Generates a multi-panel summary comparing isoform lengths between inclusion (INC) and exclusion (EXC) events for either protein or transcript modes.

**Usage**

```
plot_length_comparison(
  hits,
  phenotypes = c(control = "control", experimental = "case"),
  mode = c("protein", "transcript"),
  output_file = NULL
)
```

**Arguments**

hits	'data.frame' or 'data.table' containing event-level results, including at least 'prot_len_case', 'prot_len_control', and 'prot_len_diff' for 'mode = "protein"', or their transcript analogues 'tx_len_case', 'tx_len_control', and 'tx_len_diff'.
phenotypes	Named character vector of length 2 giving labels for control and experimental phenotypes. Must have names "control" and "experimental".
mode	Character, one of "protein" or "transcript". Determines which length columns to use and whether to derive protein-coding categories.
output_file	Optional path for saving the combined plot (e.g., "length_summary.png").

**Details**

Produces three coordinated panels:

1. Paired boxplot showing INC vs EXC lengths per event with Wilcoxon paired test annotation.
2. Density plot of delta length (INC - EXC).
3. Barplot summarizing protein-coding categories.

**Value**

A composite 'ggplot' object (assembled with 'patchwork') showing paired boxplots, delta-length density, and protein-coding class distribution.

**See Also**

[plot\_alignment\_summary()]

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
```

```
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)
proximal_output <- plot_length_comparison(seq_compare)
print(proximal_output)
```

---

plot_ppi_summary	<i>Plot summary of altered PPI interactions</i>
------------------	---

---

### Description

Visualizes the frequency and magnitude of gained/lost PPIs per event, using a dual-panel layout: - left: proportion of events with any PPI change - right: histograms of CASE and CONTROL partner counts (non-zero only)

### Usage

```
plot_ppi_summary(
  df,
  bins = 30,
  palette = c(no = "grey80", yes = "deeppink4", CASE = "#2b8cbe", CONTROL = "#e34a33"),
  output_file = NULL,
  width = 9,
  height = 4.8
)
```

### Arguments

df	‘data.table’ or ‘data.frame’ with PPI counts per event, as returned by [ppi_switches_for_hits()].
bins	Integer; number of histogram bins (default ‘30’).
palette	Named character vector of fill colors for the plot (default includes “no”, “yes”, “CASE”, “CONTROL”).
output_file	Optional path to save the figure (‘.png’ or ‘.pdf’).
width, height	Numeric dimensions (in inches) for saved plot.

### Value

A ‘ggplot’ object combining two panels (using ‘patchwork’).

### See Also

[ppi\_switches\_for\_hits()]

**Examples**

```

ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
annotation_df <- load_example_data("annotation_df")$annotation_df
matched <- get_matched_events_chunked(res, annotation_df$annotations, chunk_size = 2000)
x_seq <- attach_sequences(matched, annotation_df$sequences)
pairs <- get_pairs(x_seq, source="multi")
seq_compare <- compare_sequence_frame(pairs, annotation_df$annotations)

annotation_df <- get_annotation(load = 'test')
interpro_features <- get_protein_features(c("interpro"), annotation_df$annotations, timeout = 600, test = TRUE)
protein_feature_total <- get_comprehensive_annotations(list(interpro_features))

exon_features <- get_exon_features(annotation_df$annotations, protein_feature_total)

hits_domain <- get_domains(seq_compare, exon_features)

bg <- get_background(source = "hit_index",
                    input = sample_frame,
                    annotations = annotation_df$annotations,
                    protein_features = protein_feature_total)
ppi <- get_ppi_interactions()
hits_final <- get_ppi_switches(hits_domain, ppi, protein_feature_total)
ppi_plot <- plot_ppi_summary(hits_final)
print(ppi_plot)

```

---

plot\_prox\_dist

*Plot proximal vs distal exon usage*


---

**Description**

Creates a donut-style summary plot showing the number of events classified as proximal or distal for each event type (AFE, ALE).

**Usage**

```
plot_prox_dist(res)
```

**Arguments**

`res` 'data.table' output from [get\_proximal\_shift\_from\_hits()], containing at least columns 'event\_type' and 'V1' (proximal/distal label).

**Details**

The plot shows each event type as a donut chart:

- Inner label = total number of events.
- Slices = counts of proximal and distal events.

Only event types with at least one valid classification are shown.

**Value**

A ‘ggplot’ object (donut-style bar chart).

**See Also**

[get\_proximal\_shift\_from\_hits()]

---

plot\_two\_transcripts\_with\_domains\_unified

*Plot two transcripts with exon structure and protein feature tracks  
(unified view)*

---

**Description**

Visualize **two Ensembl transcripts** side-by-side with their exon structures and optional **protein feature/domain tracks** (e.g., InterPro, Pfam, ELM, SEG, SignalP), using a single endpoint. The plot can be rendered in either:

**Usage**

```
plot_two_transcripts_with_domains_unified(
  ...,
  view = c("transcript", "protein")
)
```

**Arguments**

... Additional arguments forwarded to the internal workhorse plot\_two\_transcripts\_with\_features(). Common arguments include:

**transcripts** Character vector of length 2 of Ensembl transcript IDs.

**gtf\_df** GTF-like exon annotation table containing at least transcript\_id, type=="exon", exon\_number, chr, strand, start, end.

**protein\_features** Protein feature table with at least ensembl\_transcript\_id, name, feature\_id, database.

**feature\_db** Optional character vector of databases to retain (e.g., c("interpro", "pfam", "elm", "seg", ...)).

**wrap\_width** Integer; width for wrapping long domain labels.

	<b>highlight_hits</b> Optional data.frame/data.table of event rows used for highlighting.
	<b>highlight_event_id</b> Optional event ID to select from highlight_hits.
	<b>highlight_alpha</b> Alpha transparency for highlight bands.
	<b>highlight_box</b> Logical; draw dashed vertical bounds around highlighted spans.
	<b>highlight_box_pad_frac</b> Fraction of total x-range used to pad highlight bounds.
	<b>highlight_box_lwd</b> Line width for highlight bounding lines.
	<b>combine_domains</b> Logical; combine identical domain labels onto shared tracks.
	<b>domain_base_gap</b> Vertical gap between transcript backbone and first domain track.
	<b>domain_track_step</b> Vertical spacing between stacked domain tracks.
	<b>domain_label_dy</b> Vertical offset used to place domain labels.
view	Character scalar selecting the visualization coordinate system: "transcript" (genomic/intron-aware) or "protein" (compact/exonic).

## Details

- **Transcript view** ('view = "transcript"): genomic x-axis with introns drawn and, when both transcripts are negative-strand, a strand-aware x-axis reversal so the display reads left-to-right in **5'→3'** direction. - **Protein view** ('view = "protein"): compact, intron-free x-axis where exons are concatenated end-to-end (exonic coordinates), making it easier to compare protein feature locations across isoforms without large genomic intron gaps.

Optionally, event-specific genomic spans (e.g., inclusion/exclusion regions) can be overlaid as translucent highlight bands per transcript.

### **What gets drawn**

- Exons as black rectangles (alternating alpha in protein/compact view).
- Introns as grey connector segments (transcript/genomic view only).
- Protein features as stacked rectangles under each transcript (if present).
- Domain labels anchored to the left edge (or right when the x-axis is reversed).
- Optional highlighted spans with dashed bounding lines.

**Protein/domain tracks** Protein features are filtered to the two transcripts and optionally filtered by feature\_db. Features are clipped to exons in transcript/genomic view, and projected into compact/exonic coordinates in protein view.

- If combine\_domains = TRUE, identical domain labels share a common vertical track to reduce redundancy.
- If combine\_domains = FALSE, each feature instance is assigned its own track (potentially more vertical space, but preserves instance-level separation).

**Event highlighting** If highlight\_hits and highlight\_event\_id are provided, event spans are parsed from inc\_case, exc\_case, inc\_control, exc\_control columns. In transcript/genomic view spans are used directly; in protein/compact view spans are projected into compact coordinates per transcript using exon maps.

**Value**

A ggplot object, or NULL if no drawable content is available (e.g., when both transcripts have zero features and you have configured internal logic to early-return on missing domains).

**Expected input formats**

**protein\_features name column:** The internal parser expects feature genomic coordinates encoded in the name field formatted as "`<label>;chr:start-end`" (e.g. "PF00069;chr7:123-456").

**highlight\_hits span columns:** Span columns are expected as strings "start-end" using genomic coordinates. Missing spans should be `NA_character_`.

**Highlight input (custom\_hits\_domain) example**

The `highlight_hits` object is expected to be a table (`data.frame/data.table`) with at least one row per event. Use `highlight_event_id` to select the row to plot. Required columns are `event_id`, `event_type_control`, `transcript_id_case`, `transcript_id_control`. Span columns may include `inc_case`, `exc_case`, `inc_control`, `exc_control` and should be genomic coordinate strings of the form "start-end" (or `NA_character_` when absent).

```
custom_hits_domain <- data.table::data.table(
  event_id = event:n,
  event_type = event,
  transcript_id_case = transcript_id,
  transcript_id_control = transcript_id,
  inc_case = inc_case,
  inc_control = inc_control,
  exc_case = exc_case,
  exc_control = exc_control
)
```

**See Also**

[ggplot](#) for rendering and theming.

**Examples**

```
# Example highlight row (skipped exon / SE), but can usually just use
# hits_domain/hits_final and supply the event_id in highlight_event_id
custom_hits_domain <- data.table::data.table(
  event_id = "AFE:1",
  event_type = "AFE",
  transcript_id_case = "ENST00000337907",
  transcript_id_control = "ENST00000476556",
  inc_case = "8655973-8656441",
  inc_control = "8423561-8423666",
  exc_case = NA,
  exc_control = NA
)
```

```

# Transcript (genomic) view: introns included, strand-aware axis
p_tx <- plot_two_transcripts_with_domains_unified(
  gtf_df = annotation_df$annotations,
  protein_features = protein_feature_total,
  feature_db = c("interpro", "pfam"),
  highlight_hits = custom_hits_domain,
  highlight_event_id = "AFE:1",
  combine_domains = FALSE,
  view = "protein"
)

# Protein (compact) view: introns removed
p_prot <- plot_two_transcripts_with_domains_unified(
  gtf_df = annotation_df$annotations,
  protein_features = protein_feature_total,
  feature_db = c("interpro", "pfam", "elm", "seg"),
  highlight_hits = hits_final,
  highlight_event_id = "ENSG00000142599:AFE",
  combine_domains = TRUE,
  view = "transcript"
)

# We are also able to just probe 2 random transcripts from annotations
p_prot <- plot_two_transcripts_with_domains_unified(
  transcripts = c("ENST00000337907", "ENST00000476556"),
  gtf_df = annotation_df$annotations,
  protein_features = protein_feature_total,
  feature_db = c("interpro", "pfam", "elm", "seg"),
  combine_domains = TRUE,
  view = "protein"
)

```

---

```
probe_individual_event
```

*Visualize PSI values for a single splicing event*

---

### Description

Creates a per-event PSI summary across samples. For **AFE** and **ALE** events, the plot separates PSI by 'inc' entry to distinguish alternative terminal exons; other event types are summarized by 'event\_id'.

### Usage

```
probe_individual_event(data, event, fill_zeros = TRUE)
```

**Arguments**

data	'data.frame' or 'data.table' containing at least the columns 'event_id', 'event_type', 'psi', 'condition', and 'sample'. For terminal events, an 'inc' column is also required.
event	Character scalar specifying the 'event_id' to visualize.
fill_zeros	Logical indicating whether to fill missing PSI values with zeros for samples that contain any observation of the event (default: 'TRUE').

**Value**

A list with elements:

- 'plot': 'ggplot' box/point plot of PSI per sample group.
- 'data': 'data.table' used to build the plot.

**Examples**

```
ex <- load_example_data("sample_frame")
sample_frame <- ex$sample_frame
hit_index <- get_hitindex(sample_frame)
res <- get_differential_inclusion(hit_index)
event_probe <- "ENSG00000117632:AFE"
probe_individual_event(hit_index, event = event_probe)
```

---

prot_hdr_to_enst	<i>Extract transcript identifier from protein FASTA header</i>
------------------	--

---

**Description**

Extract transcript identifier from protein FASTA header

**Usage**

```
prot_hdr_to_enst(h)
```

**Arguments**

h	Character string giving a single FASTA header line (including the leading '>' symbol if present).
---	---

**Details**

GENCODE protein FASTA headers typically contain a transcript reference such as:

```
“>ENSP00000369497.3|ENST00000355832.3|ENSG00000141510.15|...”
```

or may encode it in tagged fields like 'transcript:ENST...' or 'transcript\_id=ENSMUST...'. This function uses regular-expression pattern matching to locate the transcript identifier, strips the version suffix (e.g. '.3'), and returns the cleaned transcript ID.

**Value**

A character string containing the transcript identifier (without version suffix). Returns an empty string if no match is found.

---

restrict\_gtf\_genetype *Restrict GTF entries by gene type (internal)*

---

**Description**

Internal helper to subset a GTF `data.frame` or `data.table` to include only selected gene biotypes (e.g. `protein_coding`, `lncRNA`).

**Usage**

```
restrict_gtf_genetype(
  gtf_df,
  restrictions = c("protein_coding", "lncRNA", "snoRNA", "snRNA", "rRNA", "miRNA",
                  "MT_tRNA", "MT_rRNA")
)
```

**Arguments**

`gtf_df` A `data.frame` or `data.table` containing a `gene_type` column.

`restrictions` Character vector of allowed `gene_type` values. Defaults to common gene biotypes.

**Value**

A subset of `gtf_df` containing only rows whose `gene_type` matches one of the specified restrictions.

---

restrict\_gtf\_rowtype *Restrict GTF entries by feature type (internal)*

---

**Description**

Internal helper to subset a GTF `data.frame` or `data.table` to retain only gene, exon, and transcript rows.

**Usage**

```
restrict_gtf_rowtype(gtf_df)
```

**Arguments**

`gtf_df` A `data.frame` or `data.table` containing a `type` column (e.g. output of `[load_gtf_long()]`).

**Value**

A subset of gtf\_df including only rows where type is one of "gene", "exon", or "transcript".

---

SpliceImpactResult-class

*SpliceImpact result container (S4)*

---

**Description**

SpliceImpact result container (S4)

**Slots**

raw\_events 'SummarizedExperiment' of sample/form-level rows.

di\_events 'GRanges' of differential inclusion rows.

res\_di 'GRanges' of threshold-filtered differential rows.

matched 'S4Vectors::DataFrame' of annotation-matched DI rows.

sample\_frame 'S4Vectors::DataFrame' sample manifest ('path', 'sample\_name', 'condition') when available.

paired\_hits 'GRanges' of paired event-level rows.

segments 'GRangesList' of per-event segment parts ('inc\_case', etc.).

metadata list with flags and optional provenance.

---

spliceimpact\_hit\_colsets

*List predefined paired-hit column subsets*

---

**Description**

List predefined paired-hit column subsets

**Usage**

```
spliceimpact_hit_colsets()
```

**Value**

Named list of predefined column vectors for paired-hit accessors.

---

spliceimpact\_s4\_guide *Detailed guide for using SpliceImpactResult*

---

**Description**

Prints practical guidance on slots, assays, key columns, and common access patterns for conversion between S4 and 'data.table'.

**Usage**

```
spliceimpact_s4_guide(as_markdown = FALSE)
```

**Arguments**

as\_markdown      Logical; if 'TRUE', returns guide text instead of printing.

**Value**

Invisible character guide text (or visible text if 'as\_markdown = TRUE').

**Examples**

```
guide_txt <- spliceimpact_s4_guide(as_markdown = TRUE)
cat(substr(guide_txt, 1, 80), "\n")
```

---

spliceimpact\_s4\_schema  
*S4 slot and key schema for SpliceImpactResult*

---

**Description**

S4 slot and key schema for SpliceImpactResult

**Usage**

```
spliceimpact_s4_schema()
```

**Value**

Named list describing slots, core key columns, and assay names.

**Examples**

```
schema <- spliceimpact_s4_schema()
names(schema)
```

---

split_into_bits	<i>Split GTF transcripts into balanced chromosome groups (internal)</i>
-----------------	---

---

**Description**

Internal helper that groups protein-coding transcripts by chromosome, ensuring that each group remains below a cumulative size threshold. Useful for dividing GTF processing or annotation tasks into balanced batches.

**Usage**

```
split_into_bits(gtf_df, max_group_size)
```

**Arguments**

gtf_df	A data.frame or data.table containing GTF annotations, typically from [load_gtf_long()].
max_group_size	Numeric scalar giving the maximum total number of transcripts allowed per group (passed to bin_under_cap()).

**Details**

The function considers only transcripts where type == "transcript", transcript\_type == "protein\_coding". Chromosome names are simplified by removing a leading "chr" prefix before grouping.

**Value**

A list of character vectors, where each element corresponds to a bin of chromosome names grouped under the cumulative cap.

---

strip_ver	<i>Strip version suffix from identifiers (internal)</i>
-----------	---

---

**Description**

Removes trailing version components (e.g., ".1", ".2") from Ensembl or similar identifiers.

**Usage**

```
strip_ver(x)
```

**Arguments**

x	Character vector of identifiers.
---	----------------------------------

**Value**

A character vector with version suffixes removed.

---

to_long_features	<i>Convert wide BioMart feature table to long format (internal)</i>
------------------	---

---

### Description

Internal helper that reshapes a wide BioMart results table containing per-feature columns (e.g. InterPro, Pfam, TMHMM) into a unified long format suitable for downstream annotation or visualization.

### Usage

```
to_long_features(  
  ipr,  
  features = c("mobidblite", "seg", "ncoils", "tmhmm", "signalp"),  
  include_interpro = TRUE  
)
```

### Arguments

ipr	A data.frame or data.table returned from [biomaRt::getBM()] containing per-transcript protein feature data.
features	Character vector of feature prefixes to include (default: c("mobidblite", "seg", "ncoils", "tmhmm", "signalp")).
include_interpro	Logical; whether to also include InterPro annotations if present (default TRUE).

### Details

For each feature type *x*, the function expects columns *x*, *x\_start*, and *x\_end*. These are combined into a single long table. Non-InterPro features use the feature ID for all name fields. InterPro entries optionally use the description fields *interpro\_description* and *interpro\_short\_description* if available.

### Value

A data.table in long format with columns: *ensembl\_transcript\_id*, *ensembl\_peptide\_id*, *database*, *feature\_id*, *name*, *alt\_name*, *start*, *stop*, and *method* = "biomaRt".

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