Package 'fastRanges'

April 23, 2026

Type Package

Title Deterministic Multithreaded Genomic Interval Operations

Version 0.99.2

Description High-performance interval overlap and join operations for 'IRanges' and 'GenomicRanges'. The package provides deterministic multithreaded overlap computation, reusable subject indexes for repeated queries, and join helpers that keep range metadata in a consistent output grammar.

URL https://github.com/cparsania/fastRanges, https://cparsania.github.io/fastRanges/

BugReports https://github.com/cparsania/fastRanges/issues

License Artistic-2.0

Encoding UTF-8

Depends R (>= 4.5.0)

Imports methods, S4Vectors, IRanges, GenomicRanges, GenomeInfoDb, Rcpp

LinkingTo Rcpp

Suggests BiocStyle, testthat (>= 3.0.0), knitr, rmarkdown, pkgdown, XVector, ggplot2, dplyr, tidyr, scales

VignetteBuilder knitr

SystemRequirements quarto

biocViews Software, Infrastructure, Sequencing

Config/testthat/edition 3

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

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

git_branch devel

git_last_commit 8e74a30

git_last_commit_date 2026-03-27

Repository Bioconductor 3.23

Date/Publication 2026-04-23

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Contents

`fast_anti_overlap_join` *Anti Overlap Join*

Description

Return query rows that do not overlap any subject ranges.

Usage

```
fast_anti_overlap_join(
  query,
  subject,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  query_prefix = "query_"
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object.
`subject`	An `IRanges`/`GRanges` object or a `fast_ranges_index`. Use `fast_build_index(subject)` when the same subject is reused across many overlap queries.
`max_gap`	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use `-1` to require a true overlap. Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.
`min_overlap`	Integer scalar minimum overlap width, in bases. `0` is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected `type` allows an actual overlap width to be measured.
`type`	Character scalar describing what "match" means. `"any"` matches any overlap that satisfies `max_gap` / `min_overlap`. `"start"` matches ranges with compatible start coordinates.

"end" matches ranges with compatible end coordinates.

"within" matches queries contained inside subjects.

"equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.

ignore_strand — Logical scalar controlling strand handling for genomic ranges.

For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules.

TRUE means strand is ignored and only genomic coordinates are compared.

For IRanges, this argument has no effect because there is no strand.

threads — Integer scalar number of worker threads to use.

Use 1 for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware.

fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

deterministic — Logical scalar controlling output order.

TRUE returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

FALSE allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

query_prefix — Prefix applied to query columns.

Details

This is similar to a SQL ANTI JOIN.

It keeps only query rows with zero overlap hits.

overlap_count is always 0 in the returned table and is included to keep the result grammar parallel to fast_semi_overlap_join().

Value

A data.frame containing query rows with zero overlaps.

Overlap semantics

query is the range set you ask about. subject is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
```

```
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_anti_overlap_join(q, s)
```

---

fast_build_index *Build a Reusable Subject Index*

Description

Build a sorted subject index that can be reused across repeated overlap queries.

Usage

```
fast_build_index(subject)
```

Arguments

subject	An IRanges or GRanges object.

Details

The index stores a sorted representation of subject that is optimized for repeated overlap queries.

Build the index once, then pass it as subject to fast_find_overlaps(), fast_count_overlaps(), or other overlap-summary functions.

Use the raw subject object, not the index, when you need subject metadata in the output table, for example with overlap joins.

Value

A fast_ranges_index object.

Examples

```
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
idx <- fast_build_index(s)
idx
```

---

fast_cluster_overlaps *Cluster Overlapping Ranges*

Description

Assign each range to an overlap-connected component.

Usage

```
fast_cluster_overlaps(
  x,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  return = c("vector", "data.frame")
)
```

Arguments

x	An IRanges or GRanges object.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with IRanges::findOverlaps() / GenomicRanges::findOverlaps().
min_overlap	Integer scalar minimum overlap width, in bases. 0 is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected type allows an actual overlap width to be measured.
type	Character scalar describing what "match" means. "any" matches any overlap that satisfies max_gap / min_overlap. "start" matches ranges with compatible start coordinates. "end" matches ranges with compatible end coordinates. "within" matches queries contained inside subjects. "equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.
ignore_strand	Logical scalar controlling strand handling for genomic ranges. For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules. TRUE means strand is ignored and only genomic coordinates are compared. For IRanges, this argument has no effect because there is no strand.
threads	Integer scalar number of worker threads to use. Use 1 for the most conservative behavior and easiest debugging. Use larger values on multicore machines when throughput matters. For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware. fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.
deterministic	Logical scalar controlling output order. TRUE returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts. FALSE allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.
return	One of "vector" or "data.frame".

Details

Two ranges are assigned to the same cluster when they are connected by a chain of overlaps under the provided overlap settings.

Two ranges can end up in the same cluster even if they do not overlap directly, as long as they are linked by intermediate overlaps.

Example: if range 1 overlaps range 2, and range 2 overlaps range 3, then all three belong to one cluster.

Value

If `return = "vector"`, an integer vector of cluster IDs with one element per range in `x`. If `return = "data.frame"`, a `data.frame` with `range_id`, `cluster_id`, and `cluster_size`.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

type = "start" and type = "end" are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

type = "within" asks whether each query lies inside a subject interval.

type = "equal" asks whether query and subject describe the same interval, optionally with endpoint tolerance when max_gap >= 0.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (IRanges / GenomicRanges).

Examples

```
x <- IRanges::IRanges(start = c(1, 3, 10, 11, 20), end = c(5, 8, 12, 14, 22))
fast_cluster_overlaps(x)
```

---

fast_count_overlaps *Count Overlaps*

Description

Count subject overlaps per query range.

Usage

```
fast_count_overlaps(
  query,
  subject,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges/GRanges object or a fast_ranges_index. Use fast_build_index(subject) when the same subject is reused across many overlap queries.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with IRanges::findOverlaps() / GenomicRanges::findOverlaps().

`min_overlap` Integer scalar minimum overlap width, in bases.

`0` is the least strict setting.

Larger values require wider shared overlap and therefore return fewer hits.

This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

Details

`deterministic` does not change returned counts for this summary output.

Returns one integer per query range.

A value of `0` means that query had no matching subjects.

A value of `5` means that query matched five subject ranges under the chosen overlap rule.

Value

Integer vector with one element per query range.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_count_overlaps(q, s, threads = 1)
```

`fast_count_overlaps_by_group` *Count Overlaps by Subject Group*

Description

Count overlaps per query and per subject metadata group.

Usage

```
fast_count_overlaps_by_group(
  query,
  subject,
  group_col,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  include_na_group = FALSE
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object.
`subject`	An `IRanges`/`GRanges` object or a `fast_ranges_index`. Use `fast_build_index(subject)` when the same subject is reused across many overlap queries.
`group_col`	Subject metadata column name used for grouping. This must be present in `mcols(subject)`.
`max_gap`	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use `-1` to require a true overlap. Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.
`min_overlap`	Integer scalar minimum overlap width, in bases. `0` is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

`include_na_group`

Logical scalar. If `TRUE`, missing group values are counted as `"<NA>"` instead of being dropped.

Details

`deterministic` does not change returned group counts for this summary output.

This function answers the question: "for each query, how many overlaps came from each subject group?"

Rows correspond to query ranges.

Columns correspond to distinct values in `mcols(subject)[[group_col]]`.

Value

Integer matrix with one row per query and one column per group.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- GenomicRanges::GRanges("chr1", IRanges::IRanges(c(1, 10), width = 5))
s <- GenomicRanges::GRanges("chr1", IRanges::IRanges(c(2, 9), width = 5))
S4Vectors::mcols(s)$grp <- c("A", "B")
fast_count_overlaps_by_group(q, s, group_col = "grp")
```

`fast_coverage` *Coverage Across Ranges*

Description

Compute per-position coverage for input ranges.

Usage

```
fast_coverage(
  x,
  shift = 0L,
  width = NULL,
  weight = 1L,
  method = c("auto", "sort", "hash"),
  threads = fast_default_threads()
)
```

Arguments

`x`	An `IRanges` or `GRanges` object.
`shift`	Passed to `coverage()`. Use this to shift intervals before computing coverage.
`width`	Passed to `coverage()`. Use this to force the output length.
`weight`	Passed to `coverage()`. This can be a scalar or vector and is useful when intervals should contribute weighted counts instead of `1`.
`method`	Coverage method.
`threads`	Integer scalar thread count. Reserved for API consistency.

Details

Coverage answers the question: "how many ranges cover each position?"

For `IRanges`, the result is one `Rle`.

For `GRanges`, the result is an `RleList`, usually one coverage track per sequence level.

Value

`Rle` (for `IRanges`) or `RleList` (for `GRanges`).

Examples

```
x <- IRanges::IRanges(start = c(1, 4, 10), end = c(5, 8, 12))
fast_coverage(x)
```

fast_default_threads *Default Thread Count*

Description

Returns the default thread count used by fastRanges overlap routines.

Usage

```
fast_default_threads()
```

Details

The default is controlled by getOption("fastRanges.threads") and falls back to 1L.

This helper is mainly useful when you want package-wide thread control without passing threads = to every call.

Example:

options(fastRanges.threads = 8L) sets the default thread count for later calls that do not specify threads explicitly.

Value

Integer scalar thread count.

Examples

```
fast_default_threads()
old_threads <- getOption("fastRanges.threads")
options(fastRanges.threads = 3L)
fast_default_threads()
options(fastRanges.threads = old_threads)
```

fast_disjoin *Disjoin Ranges*

Description

Return non-overlapping segments induced by input ranges.

Usage

```
fast_disjoin(x, ignore_strand = FALSE, with_revmap = FALSE)
```

Arguments

x	An IRanges or GRanges object.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.
with_revmap	Logical scalar. If TRUE, include reverse mapping from each output range back to contributing input ranges.

Details

fast_disjoin() cuts the covered span of x into the smallest non-overlapping pieces.

Value

An object of the same range class as x.

Examples

```
x <- IRanges::IRanges(start = c(1, 4, 10), end = c(5, 8, 12))
fast_disjoin(x)
```

---

fast_distance_to_nearest

Distance to Nearest Subject Range

Description

Compute nearest-neighbor mapping from query ranges to subject ranges.

Usage

```
fast_distance_to_nearest(
  query,
  subject,
  ignore_strand = FALSE,
  threads = fast_default_threads()
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges or GRanges subject object.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.
threads	Integer scalar thread count. Included for API consistency.

Details

This function currently returns the same object shape as fast_nearest(). It is provided so users can choose the more explicit name when they care about the distance column.

Value

A S4Vectors::DataFrame with query_id, subject_id, and distance columns.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_distance_to_nearest(q, s)
```

---

fast_find_overlaps *Find Overlaps with Deterministic Multithreading*

Description

Compute overlap pairs between query and subject using a multithreaded C++ backend. The result is a Hits object compatible with Bioconductor workflows.

Usage

```
fast_find_overlaps(
  query,
  subject,
  select = c("all", "first", "last", "arbitrary"),
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges/GRanges object or a fast_ranges_index. Use fast_build_index(subject) when the same subject is reused across many overlap queries.
select	Character scalar controlling whether all hits are returned or a single subject match is selected per query. Use "all" to return a Hits object. Use "first", "last", or "arbitrary" to return an integer vector with one selected subject index per query and NA for queries with no hit.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes.

Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly.

Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.

`min_overlap` Integer scalar minimum overlap width, in bases.

`0` is the least strict setting.

Larger values require wider shared overlap and therefore return fewer hits.

This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

Details

This is the core matching function in `fastRanges`.

Think of it as answering the question: "for each query range, which subject ranges satisfy my overlap rule?"

The return value is a `Hits` object. The important pieces are:

`queryHits(h)` gives the row numbers from `query`.

`subjectHits(h)` gives the matching row numbers from `subject`.

If you need only counts or a yes/no answer, prefer `fast_count_overlaps()` or `fast_overlaps_any()`, because they return simpler summaries.

Compatibility notes:

`fastRanges` aims to stay close to Bioconductor overlap semantics for supported inputs, and its outputs are routinely validated against `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.

Currently supported core input types are `IRanges` and `GRanges`.

Empty-range semantics are delegated to Bioconductor-compatible reference behavior.

Circular genomic sequences are not currently supported and will raise an explicit error.

`GRangesList` inputs are not currently supported and will raise an explicit error.

Performance notes:

For one-off overlap calls, use the raw `subject`.

For repeated-query or throughput-oriented workloads, build a reusable index once with `fast_build_index(subject)` and pass that index as `subject`.

For maximum multithreaded throughput, consider `deterministic = FALSE` when output order is not important.

Value

If `select = "all"`, a `S4Vectors::Hits` object.

Otherwise, an integer vector of length `length(query)` containing one selected subject index per query and `NA` when no subject matched.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
```

```
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
h <- fast_find_overlaps(q, s, threads = 1)
length(h)
```

---

fast_find_overlaps_iter

Create an Overlap Iterator

Description

Create an iterator that computes overlaps in query chunks.

Usage

```
fast_find_overlaps_iter(
  query,
  subject,
  chunk_size = 50000L,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges/GRanges object or a fast_ranges_index.
chunk_size	Integer scalar number of query ranges to process in one iterator step. Smaller values use less memory and give more frequent progress points. Larger values usually improve throughput but each call to fast_iter_next() does more work.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with IRanges::findOverlaps() / GenomicRanges::findOverlaps().
min_overlap	Integer scalar minimum overlap width, in bases. 0 is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected type allows an actual overlap width to be measured.
type	Character scalar describing what "match" means. "any" matches any overlap that satisfies max_gap / min_overlap. "start" matches ranges with compatible start coordinates. "end" matches ranges with compatible end coordinates. "within" matches queries contained inside subjects. "equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.
ignore_strand	Logical scalar controlling strand handling for genomic ranges. For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules. TRUE means strand is ignored and only genomic coordinates are compared. For IRanges, this argument has no effect because there is no strand.
threads	Integer scalar number of worker threads to use. Use 1 for the most conservative behavior and easiest debugging. Use larger values on multicore machines when throughput matters. For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware. fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

Details

Use the iterator API when `query` is large and you do not want to materialize all overlap hits in one call.

Typical workflow:

create the iterator with `fast_find_overlaps_iter()`

inspect progress with `fast_iter_has_next()`

pull one chunk with `fast_iter_next()`

or collect all remaining chunks with `fast_iter_collect()`

Value

A `fast_ranges_iter` iterator object.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
```

```
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
it <- fast_find_overlaps_iter(q, s, chunk_size = 2L)
fast_iter_has_next(it)
```

---

fast_follow *Follow Query Ranges*

Description

Return the index of the first subject range that is strictly before each query range.

Usage

```
fast_follow(
  query,
  subject,
  ignore_strand = FALSE,
  threads = fast_default_threads()
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object.
`subject`	An `IRanges` or `GRanges` subject object.
`ignore_strand`	Logical scalar. Ignored for non-genomic ranges.
`threads`	Integer scalar thread count. Included for API consistency.

Details

For each query range, return the index of the first subject range that comes strictly before the query.

Value

Integer vector of subject indices, with NA for unmatched queries.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_follow(q, s)
```

---

fast_gaps *Gaps Between Ranges*

Description

Compute uncovered regions between ranges.

Usage

```
fast_gaps(x, start = NULL, end = NULL, ignore_strand = FALSE)
```

Arguments

x	An IRanges or GRanges object.
start, end	Optional integer bounds for non-genomic ranges. These are most useful for IRanges. For GRanges, sequence lengths are usually taken from seqinfo(x).
ignore_strand	Logical scalar. Ignored for non-genomic ranges.

Details

fast_gaps() returns the regions not covered by x inside the requested bounds.

Value

An object of the same range class as x.

Examples

```
x <- IRanges::IRanges(start = c(1, 4, 10), end = c(5, 8, 12))
fast_gaps(x, start = 1L, end = 15L)
```

`fast_index_stats` *Index Summary Statistics*

Description

Summarize index size and partition structure.

Usage

```
fast_index_stats(index, detailed = FALSE)
```

Arguments

`index`	A `fast_ranges_index` object.
`detailed`	Logical scalar. If `TRUE`, returns partition-level details.

Details

Use this function to inspect how the subject was partitioned internally and to get a rough sense of memory footprint.

`subject_n` is the number of indexed ranges.

`partition_n` is the number of internal partitions, usually driven by sequence structure.

`index_size_mb` is the in-memory object size, not the serialized file size.

Value

By default, a one-row `S4Vectors::DataFrame` with summary fields. If `detailed = TRUE`, returns a list with `summary` and `partitions`.

Examples

```
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
idx <- fast_build_index(s)
fast_index_stats(idx)
```

fast_inner_overlap_join *Inner Overlap Join*

Description

Convenience wrapper for `fast_overlap_join(..., join = "inner")`.

Usage

```
fast_inner_overlap_join(
  query,
  subject,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  query_prefix = "query_",
  subject_prefix = "subject_"
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object.
`subject`	An `IRanges`/`GRanges` object or a `fast_ranges_index`. Use `fast_build_index(subject)` when the same subject is reused across many overlap queries.
`max_gap`	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use `-1` to require a true overlap. Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.
`min_overlap`	Integer scalar minimum overlap width, in bases. `0` is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected `type` allows an actual overlap width to be measured.
`type`	Character scalar describing what "match" means. `"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

	"start" matches ranges with compatible start coordinates. "end" matches ranges with compatible end coordinates. "within" matches queries contained inside subjects. "equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.
ignore_strand	Logical scalar controlling strand handling for genomic ranges. For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules. TRUE means strand is ignored and only genomic coordinates are compared. For IRanges, this argument has no effect because there is no strand.
threads	Integer scalar number of worker threads to use. Use 1 for the most conservative behavior and easiest debugging. Use larger values on multicore machines when throughput matters. For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware. fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.
deterministic	Logical scalar controlling output order. TRUE returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts. FALSE allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.
query_prefix	Prefix added to columns derived from query. This helps you see which output columns came from the query object.
subject_prefix	Prefix added to columns derived from subject. This helps you see which output columns came from the subject object.

Value

A data.frame overlap join result.

Overlap semantics

query is the range set you ask about. subject is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|
```

```
type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
               < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_inner_overlap_join(q, s)
```

`fast_iter_collect` *Collect All Iterator Chunks*

Description

Materialize all overlap chunks from an iterator into a single `Hits` object.

Usage

```
fast_iter_collect(iter)
```

Arguments

`iter`	A `fast_ranges_iter` object.

Details

This collects only the chunks that have not yet been consumed.

If you want all hits from the beginning after some chunks were already read, call `fast_iter_reset(iter)` first and then `fast_iter_collect(iter)`.

Value

A `S4Vectors::Hits` object.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
it <- fast_find_overlaps_iter(q, s, chunk_size = 2L)
fast_iter_collect(it)
```

---

fast_iter_has_next *Check if an Iterator Has Remaining Chunks*

Description

Check if an Iterator Has Remaining Chunks

Usage

```
fast_iter_has_next(iter)
```

Arguments

`iter`	A `fast_ranges_iter` object.

Value

Logical scalar indicating whether more query chunks remain.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
it <- fast_find_overlaps_iter(q, s, chunk_size = 2L)
fast_iter_has_next(it)
```

fast_iter_next *Advance an Overlap Iterator*

Description

Compute overlaps for the next query chunk.

Usage

```
fast_iter_next(iter)
```

Arguments

iter	A fast_ranges_iter object.

Details

Each call advances the iterator state.

The returned Hits object uses global query indices, not chunk-local indices, so you can combine chunk outputs safely.

Value

A S4Vectors::Hits object for the next chunk, with global query indices.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
it <- fast_find_overlaps_iter(q, s, chunk_size = 2L)
fast_iter_next(it)
```

fast_iter_reset *Reset an Overlap Iterator*

Description

Reset iterator position to the first query chunk.

Usage

```
fast_iter_reset(iter)
```

Arguments

iter	A fast_ranges_iter object.

Details

After reset, the next call to `fast_iter_next()` starts again from the first query chunk.

Value

Invisibly returns `iter`.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
it <- fast_find_overlaps_iter(q, s, chunk_size = 2L)
fast_iter_reset(it)
```

---

fast_left_overlap_join

Left Overlap Join

Description

Convenience wrapper for `fast_overlap_join(..., join = "left")`.

Usage

```
fast_left_overlap_join(
  query,
  subject,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  query_prefix = "query_",
  subject_prefix = "subject_"
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object.
`subject`	An `IRanges`/`GRanges` object or a `fast_ranges_index`. Use `fast_build_index(subject)` when the same subject is reused across many overlap queries.
`max_gap`	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use `-1` to require a true overlap. Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes.

Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly.

Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.

`min_overlap` Integer scalar minimum overlap width, in bases.

`0` is the least strict setting.

Larger values require wider shared overlap and therefore return fewer hits.

This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

`query_prefix` Prefix added to columns derived from `query`. This helps you see which output columns came from the query object.

`subject_prefix` Prefix added to columns derived from `subject`. This helps you see which output columns came from the subject object.

Value

A `data.frame` overlap join result.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_left_overlap_join(q, s)
```

fast_load_index *Load a Reusable Subject Index*

Description

Load a fast_ranges_index object saved with fast_save_index().

Usage

```
fast_load_index(path)
```

Arguments

path	File path to a serialized index.

Details

This function validates that the file contains the fields required by fastRanges before returning the object.

Value

A fast_ranges_index object.

Examples

```
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
idx <- fast_build_index(s)
f <- tempfile(fileext = ".rds")
fast_save_index(idx, f)
idx2 <- fast_load_index(f)
unlink(f)
print(idx2)
```

fast_nearest *Nearest Subject Range per Query*

Description

Compute nearest-neighbor mapping from query ranges to subject ranges.

Usage

```
fast_nearest(
  query,
  subject,
  ignore_strand = FALSE,
  threads = fast_default_threads()
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges or GRanges subject object.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.
threads	Integer scalar thread count. Included for API consistency.

Details

These functions answer nearest-neighbor questions rather than overlap questions.

fast_nearest() and fast_distance_to_nearest() return one row per matched query.

query_id is the row index in query.

subject_id is the row index of the nearest subject.

distance is 0 when the query overlaps the subject and positive when the nearest subject is separated by a gap.

Value

A S4Vectors::DataFrame with query_id, subject_id, and distance columns.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_nearest(q, s)
```

---

fast_overlaps_any *Overlap Existence per Query*

Description

Return TRUE for queries that overlap at least one subject range.

Usage

```
fast_overlaps_any(
  query,
  subject,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges/GRanges object or a fast_ranges_index. Use fast_build_index(subject) when the same subject is reused across many overlap queries.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with IRanges::findOverlaps() / GenomicRanges::findOverlaps().
min_overlap	Integer scalar minimum overlap width, in bases. 0 is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected type allows an actual overlap width to be measured.
type	Character scalar describing what "match" means. "any" matches any overlap that satisfies max_gap / min_overlap. "start" matches ranges with compatible start coordinates. "end" matches ranges with compatible end coordinates. "within" matches queries contained inside subjects. "equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.
ignore_strand	Logical scalar controlling strand handling for genomic ranges. For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules. TRUE means strand is ignored and only genomic coordinates are compared. For IRanges, this argument has no effect because there is no strand.
threads	Integer scalar number of worker threads to use. Use 1 for the most conservative behavior and easiest debugging. Use larger values on multicore machines when throughput matters. For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware. fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.
deterministic	Logical scalar controlling output order. TRUE returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts. FALSE allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

Details

`deterministic` does not change returned logical values for this summary output.

Returns one logical value per query range.

`TRUE` means at least one subject range matched.

`FALSE` means no subject range matched.

Value

Logical vector with one element per query range.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

type = "equal" asks whether query and subject describe the same interval, optionally with endpoint tolerance when max_gap >= 0.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (IRanges / GenomicRanges).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_overlaps_any(q, s, threads = 1)
```

---

fast_overlap_aggregate

Aggregate Subject Metadata Over Overlaps

Description

Aggregate a numeric subject metadata column across overlaps for each query.

Usage

```
fast_overlap_aggregate(
  query,
  subject,
  value_col = NULL,
  fun = c("count", "sum", "mean", "min", "max"),
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  na_rm = TRUE
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges/GRanges object or a fast_ranges_index. Use fast_build_index(subject) when the same subject is reused across many overlap queries.
value_col	Subject metadata column name containing numeric values. This is required unless fun = "count".
fun	Aggregation function: one of "count", "sum", "mean", "min", or "max".
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap.

Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes.

Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly.

Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.

`min_overlap` Integer scalar minimum overlap width, in bases.

`0` is the least strict setting.

Larger values require wider shared overlap and therefore return fewer hits.

This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

`na_rm` Logical scalar. If `TRUE`, remove missing values in aggregation.

Details

`deterministic` does not change returned aggregate values for this summary output.

This function summarizes subject metadata over the overlap hits of each query.

Examples:

use `fun = "count"` to count overlaps

use `fun = "sum"` to sum a signal column over matched subjects

use `fun = "mean"` to compute average matched score per query

Value

Numeric vector with one value per query.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- GenomicRanges::GRanges("chr1", IRanges::IRanges(c(1, 10), width = 5))
s <- GenomicRanges::GRanges("chr1", IRanges::IRanges(c(2, 9), width = 5))
S4Vectors::mcols(s)$score <- c(2, 5)
fast_overlap_aggregate(q, s, value_col = "score", fun = "sum")
```

---

fast_overlap_join *Join Ranges by Overlap*

Description

Build a metadata-preserving overlap join with a consistent, tidy tabular output grammar.

Usage

```
fast_overlap_join(
  query,
  subject,
  join = c("inner", "left"),
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  query_prefix = "query_",
  subject_prefix = "subject_"
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges/GRanges object or a fast_ranges_index. Use fast_build_index(subject) when the same subject is reused across many overlap queries.
join	Join mode. "inner" returns one row per overlap hit and drops queries with no hit. "left" keeps every query at least once. Queries with no hit get NA values in subject columns.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with IRanges::findOverlaps() / GenomicRanges::findOverlaps().

min_overlap	Integer scalar minimum overlap width, in bases. 0 is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected type allows an actual overlap width to be measured.
type	Character scalar describing what "match" means. "any" matches any overlap that satisfies max_gap / min_overlap. "start" matches ranges with compatible start coordinates. "end" matches ranges with compatible end coordinates. "within" matches queries contained inside subjects. "equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.
ignore_strand	Logical scalar controlling strand handling for genomic ranges. For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules. TRUE means strand is ignored and only genomic coordinates are compared. For IRanges, this argument has no effect because there is no strand.
threads	Integer scalar number of worker threads to use. Use 1 for the most conservative behavior and easiest debugging. Use larger values on multicore machines when throughput matters. For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware. fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.
deterministic	Logical scalar controlling output order. TRUE returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts. FALSE allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.
query_prefix	Prefix added to columns derived from query. This helps you see which output columns came from the query object.
subject_prefix	Prefix added to columns derived from subject. This helps you see which output columns came from the subject object.

Details

The join family turns overlap hits into beginner-friendly tabular output.

Output always starts with query_id and subject_id.

query_id is the 1-based row index from query.

subject_id is the 1-based row index from subject, or NA for unmatched queries in a left join.

The remaining columns are prefixed copies of the original range columns and metadata columns.

Value

A `data.frame` with overlap ids and prefixed query/subject columns.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_overlap_join(q, s, join = "inner", threads = 1)
```

---

fast_precede *Precede Query Ranges*

Description

Return the index of the first subject range that is strictly after each query range.

Usage

```
fast_precede(
  query,
  subject,
  ignore_strand = FALSE,
  threads = fast_default_threads()
)
```

Arguments

query	An IRanges or GRanges query object.
subject	An IRanges or GRanges subject object.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.
threads	Integer scalar thread count. Included for API consistency.

Details

For each query range, return the index of the first subject range that comes strictly after the query.

Value

Integer vector of subject indices, with NA for unmatched queries.

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_precede(q, s)
```

fast_ranges_example *Example Genomic Ranges for Documentation, Tests, and Tutorials*

Description

fast_ranges_example is a small reproducible dataset shipped with the package. It is intended for documentation examples, teaching, unit tests, and quick smoke checks of overlap workflows.

Format

A named list with two components:

query A GRanges object with 6 genomic intervals and metadata columns query_id and score.

subject A GRanges object with 7 genomic intervals and metadata columns gene_id and biotype.

Details

The object is a named list with two GRanges components:

- query: six example genomic intervals that behave like user-supplied peaks, windows, or regions of interest.
- subject: seven example genomic intervals that behave like annotation features such as genes, promoters, enhancers, or other reference ranges.

Metadata columns are included so examples can demonstrate joins, grouped summaries, and overlap aggregation:

- query contains query_id and score
- subject contains gene_id and biotype

The same records are also distributed as plain BED files in inst/extdata/query_peaks.bed and inst/extdata/subject_genes.bed. Use the in-memory dataset when you want a ready-to-run example in R, and use the BED files when you want to demonstrate file import or command-line workflows.

This dataset is intentionally small and synthetic. It is designed for examples and tests, not as a biological reference resource.

Source

Generated from data-raw/make_example_data.R, which also writes matching BED files to inst/extdata/.

Examples

```
data("fast_ranges_example", package = "fastRanges")
query <- fast_ranges_example$query
subject <- fast_ranges_example$subject

query
```

```
subject

fast_find_overlaps(query, subject, threads = 1)
```

---

fast_range_intersect *Intersection of Two Range Sets*

Description

Compute range-wise intersection.

Usage

```
fast_range_intersect(x, y, ignore_strand = FALSE)
```

Arguments

x, y	IRanges or GRanges objects of compatible class.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.

Details

fast_range_intersect() keeps only the coordinate span shared by x and y.

Value

An object of the same range class as x and y.

Examples

```
x <- IRanges::IRanges(start = c(1, 10), end = c(5, 12))
y <- IRanges::IRanges(start = c(3, 20), end = c(8, 21))
fast_range_intersect(x, y)
```

---

fast_range_setdiff *Set Difference of Two Range Sets*

Description

Compute ranges in x that are not covered by y.

Usage

```
fast_range_setdiff(x, y, ignore_strand = FALSE)
```

Arguments

x, y	IRanges or GRanges objects of compatible class.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.

Details

fast_range_setdiff() subtracts the covered span of y from x.

Value

An object of the same range class as x.

Examples

```
x <- IRanges::IRanges(start = c(1, 10), end = c(5, 12))
y <- IRanges::IRanges(start = c(3, 20), end = c(8, 21))
fast_range_setdiff(x, y)
```

---

fast_range_union *Union of Two Range Sets*

Description

Compute range-wise union.

Usage

```
fast_range_union(x, y, ignore_strand = FALSE)
```

Arguments

x, y	IRanges or GRanges objects of compatible class.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.

Details

fast_range_union() returns the combined interval coverage of x and y.

Value

An object of the same range class as x and y.

Examples

```
x <- IRanges::IRanges(start = c(1, 10), end = c(5, 12))
y <- IRanges::IRanges(start = c(3, 20), end = c(8, 21))
fast_range_union(x, y)
```

fast_reduce *Reduce Overlapping Ranges*

Description

Merge overlapping or adjacent ranges.

Usage

```
fast_reduce(x, ignore_strand = FALSE, min_gap_width = 1L, with_revmap = FALSE)
```

Arguments

x	An IRanges or GRanges object.
ignore_strand	Logical scalar. Ignored for non-genomic ranges.
min_gap_width	Integer scalar controlling when nearby ranges should be merged. 1 merges overlapping or directly adjacent ranges. Larger values require larger gaps before two ranges are kept separate.
with_revmap	Logical scalar. If TRUE, include reverse mapping from each output range back to contributing input ranges.

Details

fast_reduce() simplifies a range set by merging runs of overlapping or near-adjacent intervals.

Value

An object of the same range class as x.

Examples

```
x <- IRanges::IRanges(start = c(1, 4, 10), end = c(5, 8, 12))
fast_reduce(x)
```

fast_save_index *Save a Reusable Subject Index*

Description

Save a fast_ranges_index object to disk for reuse across sessions.

Usage

```
fast_save_index(index, path, compress = TRUE)
```

Arguments

index	A fast_ranges_index object created by fast_build_index().
path	Output file path for the serialized index.
compress	Logical scalar. If TRUE, uses xz compression.

Details

Saving an index is useful when index construction is expensive and the same subject set will be queried again in a later R session.

Value

Invisibly returns path.

Examples

```
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
idx <- fast_build_index(s)
f <- tempfile(fileext = ".rds")
fast_save_index(idx, f)
unlink(f)
```

---

fast_self_overlaps *Self Overlaps*

Description

Find overlaps within a single range object.

Usage

```
fast_self_overlaps(
  x,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  drop_self = TRUE,
  drop_redundant = TRUE
)
```

Arguments

x	An IRanges or GRanges object.
max_gap	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use -1 to require a true overlap. Use 0 to allow touching ranges for "any" and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with IRanges::findOverlaps() / GenomicRanges::findOverlaps().
min_overlap	Integer scalar minimum overlap width, in bases. 0 is the least strict setting. Larger values require wider shared overlap and therefore return fewer hits. This argument matters only when the selected type allows an actual overlap width to be measured.
type	Character scalar describing what "match" means. "any" matches any overlap that satisfies max_gap / min_overlap. "start" matches ranges with compatible start coordinates. "end" matches ranges with compatible end coordinates. "within" matches queries contained inside subjects. "equal" matches queries and subjects with the same interval, or with start/end differences no larger than max_gap when tolerance is allowed.
ignore_strand	Logical scalar controlling strand handling for genomic ranges. For GRanges, FALSE means "+", "-", and "*" are interpreted using standard Bioconductor strand rules. TRUE means strand is ignored and only genomic coordinates are compared. For IRanges, this argument has no effect because there is no strand.
threads	Integer scalar number of worker threads to use. Use 1 for the most conservative behavior and easiest debugging. Use larger values on multicore machines when throughput matters. For repeated-query workloads, combine a prebuilt index from fast_build_index(subject) with a thread count chosen empirically on your hardware. fastRanges is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.
deterministic	Logical scalar controlling output order. TRUE returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts. FALSE allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.
drop_self	Logical scalar. If TRUE, self-hits (i vs i) are removed.
drop_redundant	Logical scalar. If TRUE, redundant pairs are removed for self-comparisons by keeping only query_id < subject_id.

Details

`fast_self_overlaps()` compares a range object to itself.

This is useful when you want to know which ranges in one set overlap each other rather than overlap another object.

Value

A `S4Vectors::Hits` object.

Overlap semantics

`query` is the range set you ask about. `subject` is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is `<= max_gap` (for `max_gap >= 0`), and overlap width is `>= min_overlap`.

Beginner-friendly interpretation:

`type = "any"` asks "do these ranges touch or overlap closely enough to count?"

`type = "start"` and `type = "end"` are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

`type = "within"` asks whether each query lies inside a subject interval.

`type = "equal"` asks whether query and subject describe the same interval, optionally with endpoint tolerance when `max_gap >= 0`.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (`IRanges` / `GenomicRanges`).

Examples

```
x <- IRanges::IRanges(start = c(1, 3, 10), end = c(5, 8, 12))
fast_self_overlaps(x)
```

`fast_semi_overlap_join` *Semi Overlap Join*

Description

Return query rows that overlap at least one subject range.

Usage

```
fast_semi_overlap_join(
  query,
  subject,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE,
  query_prefix = "query_"
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object.
`subject`	An `IRanges`/`GRanges` object or a `fast_ranges_index`. Use `fast_build_index(subject)` when the same subject is reused across many overlap queries.
`max_gap`	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use `-1` to require a true overlap. Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.

`min_overlap` Integer scalar minimum overlap width, in bases.

`0` is the least strict setting.

Larger values require wider shared overlap and therefore return fewer hits.

This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

`query_prefix` Prefix applied to query columns.

Details

This is similar to a SQL `SEMI JOIN`.

It keeps only query rows that have at least one overlap hit.

`overlap_count` tells you how many subject ranges matched each retained query row.

Value

A `data.frame` containing matching query rows and overlap counts.

Overlap semantics

query is the range set you ask about. subject is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is <= max_gap (for max_gap >= 0), and overlap width is >= min_overlap.

Beginner-friendly interpretation:

type = "any" asks "do these ranges touch or overlap closely enough to count?"

type = "start" and type = "end" are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

type = "within" asks whether each query lies inside a subject interval.

type = "equal" asks whether query and subject describe the same interval, optionally with endpoint tolerance when max_gap >= 0.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (IRanges / GenomicRanges).

Examples

```
q <- IRanges::IRanges(start = c(1, 10, 20), width = c(5, 4, 3))
s <- IRanges::IRanges(start = c(3, 9, 18), width = c(4, 6, 5))
fast_semi_overlap_join(q, s)
```

`fast_tile_coverage` *Tile-Based Coverage Summary*

Description

Aggregate coverage into fixed-width tiles.

Usage

```
fast_tile_coverage(
  x,
  tile_width,
  step_width = tile_width,
  shift = 0L,
  width = NULL,
  weight = 1L,
  method = c("auto", "sort", "hash"),
  threads = fast_default_threads()
)
```

Arguments

`x`	An `IRanges` or `GRanges` object.
`tile_width`	Integer scalar tile width.
`step_width`	Integer scalar step width. Use a value smaller than `tile_width` for overlapping tiles and the same value for adjacent tiles.
`shift`	Passed to `coverage()`.
`width`	Passed to `coverage()`.
`weight`	Passed to `coverage()`.
`method`	Coverage method.
`threads`	Integer scalar thread count. Reserved for API consistency.

Details

`fast_tile_coverage()` converts base-resolution coverage into a simpler table of fixed-width summaries.

Each row in the result is one tile.

`coverage_sum` is the sum of coverage values across that tile.

For `GRanges`, the output also includes `seqnames`.

Value

A `data.frame` with tile coordinates and `coverage_sum`.

Examples

```
x <- IRanges::IRanges(start = c(1, 4, 10), end = c(5, 8, 12))
fast_tile_coverage(x, tile_width = 5L)
```

`fast_window_count_overlaps` *Windowed Overlap Counts*

Description

Count overlaps in sliding windows across the coordinate span of `query`.

Usage

```
fast_window_count_overlaps(
  query,
  subject,
  window_width,
  step_width = window_width,
  max_gap = -1L,
  min_overlap = 0L,
  type = c("any", "start", "end", "within", "equal"),
  ignore_strand = FALSE,
  threads = fast_default_threads(),
  deterministic = TRUE
)
```

Arguments

`query`	An `IRanges` or `GRanges` query object. Windows are generated from `min(start(query))` to `max(end(query))`, separately by chromosome for `GRanges`.
`subject`	An `IRanges` or `GRanges` subject object.
`window_width`	Integer scalar window width.
`step_width`	Integer scalar window step. Use a value smaller than `window_width` for sliding windows and the same value for non-overlapping windows.
`max_gap`	Integer scalar controlling how far apart two ranges may be and still count as a hit. Use `-1` to require a true overlap. Use `0` to allow touching ranges for `"any"` and to keep Bioconductor's default tolerance behavior for the other overlap modes. Use positive values when you want "nearby" ranges to count as matches even if they do not overlap directly. Units are bases. The meaning is intentionally aligned with `IRanges::findOverlaps()` / `GenomicRanges::findOverlaps()`.

`min_overlap` Integer scalar minimum overlap width, in bases.

`0` is the least strict setting.

Larger values require wider shared overlap and therefore return fewer hits.

This argument matters only when the selected `type` allows an actual overlap width to be measured.

`type` Character scalar describing what "match" means.

`"any"` matches any overlap that satisfies `max_gap` / `min_overlap`.

`"start"` matches ranges with compatible start coordinates.

`"end"` matches ranges with compatible end coordinates.

`"within"` matches queries contained inside subjects.

`"equal"` matches queries and subjects with the same interval, or with start/end differences no larger than `max_gap` when tolerance is allowed.

`ignore_strand` Logical scalar controlling strand handling for genomic ranges.

For `GRanges`, `FALSE` means `"+"`, `"-"`, and `"*"` are interpreted using standard Bioconductor strand rules.

`TRUE` means strand is ignored and only genomic coordinates are compared.

For `IRanges`, this argument has no effect because there is no strand.

`threads` Integer scalar number of worker threads to use.

Use `1` for the most conservative behavior and easiest debugging.

Use larger values on multicore machines when throughput matters.

For repeated-query workloads, combine a prebuilt index from `fast_build_index(subject)` with a thread count chosen empirically on your hardware.

`fastRanges` is optimized for large and throughput-oriented workloads. For one-off or small jobs, Bioconductor's native overlap routines may be competitive.

`deterministic` Logical scalar controlling output order.

`TRUE` returns a stable order, which is useful for testing, reproducible reports, and direct comparison across thread counts.

`FALSE` allows the implementation to return hits in an unspecified order, which can be noticeably faster for large multithreaded jobs because it avoids extra global ordering work.

Details

Windows are generated across the span of `query`, then overlap counts are measured between those windows and `subject`.

The result is a table rather than a `Hits` object because the main goal is summary, not individual hit inspection.

Value

A `data.frame` containing window coordinates and overlap counts.

Overlap semantics

query is the range set you ask about. subject is the range set you compare it against.

Core interval semantics (ASCII schematic):

```
type = "any"
query  :    |------|
subject: |------|

type = "within"
subject: |--------------|
query  :    |------|

type = "start"
query  :    |------|
subject:    |------------|

type = "end"
query  :       |------|
subject: |------------|

type = "equal"
query  :    |------|
subject:    |------|

gap / min_overlap controls
query  : |------|      |------| : subject
              < gap >
```

The middle distance is the gap. A hit is allowed when this distance is <= max_gap (for max_gap >= 0), and overlap width is >= min_overlap.

Beginner-friendly interpretation:

type = "any" asks "do these ranges touch or overlap closely enough to count?"

type = "start" and type = "end" are useful when interval boundaries are biologically meaningful, for example transcription start or end sites.

type = "within" asks whether each query lies inside a subject interval.

type = "equal" asks whether query and subject describe the same interval, optionally with endpoint tolerance when max_gap >= 0.

This argument grammar is intentionally aligned with Bioconductor overlap APIs (IRanges / GenomicRanges).

Examples

```
q <- IRanges::IRanges(start = c(1, 12), end = c(10, 20))
s <- IRanges::IRanges(start = c(2, 5, 15), end = c(3, 6, 16))
fast_window_count_overlaps(q, s, window_width = 5L, step_width = 5L)
```

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