

Package ‘MatchAlign’

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Title Parsing GFA and GAF Alignment Files

Version 0.1.2

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Description Provides tools for extracting segment paths from Graphical Fragment Assembly ('GFA') and Graph Alignment Format ('GAF') files. `parse_paths_gfa()` reads P (path) and W (walk) records and returns a named list of segment identifiers for each accession. `parse_paths_gaf()` parses the path string from each alignment and returns a named list of segments traversed by each query. `parse_segment_lengths_gfa()` reads S records and returns a named list of segment lengths keyed by segment identifier. These tools are intended to simplify downstream interpretation and analysis of pangenome graphs.

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Encoding UTF-8

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

URL <https://github.com/cromazurek/MatchAlign>

BugReports <https://github.com/cromazurek/MatchAlign/issues>

Config/roxygen2/version 8.0.0

NeedsCompilation no

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Repository CRAN

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parse_paths_gaf	Create a list where each alignment is an element with an associated list of the segments used
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Description

Create a list where each alignment is an element with an associated list of the segments used

Usage

```
parse_paths_gaf(gaf_file)
```

Arguments

gaf_file A gaf file

Value

A list where each alignment is an element with an associated list of segments used

Examples

```
example_gaf <- system.file("extdata", "example.gaf", package = "MatchAlign")
alignment_paths <- parse_paths_gaf(example_gaf)
```

parse_paths_gfa	Create a list where each accession is an element with an associated list of the segments
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Description

Create a list where each accession is an element with an associated list of the segments

Usage

```
parse_paths_gfa(gfa_file)
```

Arguments

gfa_file A gfa file

Value

A list where each accession is an element with an associated list of segments

Examples

```
example_gfa <- system.file("extdata", "example.gfa", package = "MatchAlign")
accession_paths <- parse_paths_gfa(example_gfa)
```

`parse_segment_lengths_gfa`*Create a list of segment lengths from a GFA file*

Description

Create a list of segment lengths from a GFA file

Usage

```
parse_segment_lengths_gfa(gfa_file)
```

Arguments

`gfa_file` A gfa file

Value

A named list where each segment is an element with its length

Examples

```
example_gfa <- system.file("extdata", "example.gfa", package = "MatchAlign")
segment_lengths <- parse_segment_lengths_gfa(example_gfa)
```

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