Package: immGLIPH (via r-universe)

June 2, 2026

Title Grouping of Lymphocyte Interactions by Paratope Hotspots

Version 0.99.5

Description An R implementation of the GLIPH and GLIPH2 algorithms for clustering T cell receptors (TCRs) predicted to bind the same HLA-restricted peptide antigen. Identifies specificity groups based on local (motif-based) and global (sequence-based) CDR3 similarities. Integrates with the scRepertoire ecosystem via immApex for single-cell immune repertoire analysis. Users should cite the original GLIPH algorithm papers: Glanville et al. (2017) <doi:10.1038/nature22976> and Huang et al. (2020) <doi:10.1038/s41587-020-0505-4>.

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biocViews Software, ImmunoOncology, Clustering, SingleCell, Sequencing, Visualization

Depends R (>= 4.5.0)

Imports stringdist, igraph, BiocParallel, parallel, stringr, stats, utils, graphics, grDevices, viridis, visNetwork, plotfunctions, immApex

Suggests BiocFileCache, scRepertoire, SeuratObject, Seurat, SingleCellExperiment, testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Config/testthat/edition 3

VignetteBuilder knitr

URL https://github.com/BorchLab/immGLIPH, https://github.com/BorchLab/scRepertoire, https://github.com/BorchLab/immApex

BugReports https://github.com/BorchLab/immGLIPH/issues

Config/pak/sysreqs cmake libglpk-dev make libicu-dev libuv1-dev libxml2-dev libssl-dev zlib1g-dev

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

Date/Publication 2026-05-20 12:06:01 UTC

RemoteUrl https://github.com/bioc/immGLIPH

RemoteRef HEAD

RemoteSha 17636de1dcad06e64a93a739d88bf90eb2d41c83

Contents

`clusterScoring` *Score CDR3 clusters using the GLIPH or GLIPH2 algorithm*

Description

Calculates scores for CDR3 clusters following the GLIPH and GLIPH2 scoring procedures. Depending on the information provided, a final score is computed from up to five cluster properties: cluster size, enrichment of CDR3 lengths, enrichment of V genes, enrichment of clonal expansions, and enrichment of common HLA alleles.

Usage

```
clusterScoring(
  cluster_list,
  cdr3_sequences,
  refdb_beta = "human_v2.0_CD48",
  v_usage_freq = NULL,
  cdr3_length_freq = NULL,
  ref_cluster_size = "original",
  gliph_version = 1,
  sim_depth = 1000,
```

```
  hla_cutoff = 0.1,
  n_cores = 1
)
```

Arguments

cluster_list	A list where each element contains a data.frame of CDR3b sequences and additional information needed for scoring. Corresponds to the $cluster_list element returned by runGLIPH.
cdr3_sequences	A vector or data.frame of CDR3 sequences and optional metadata. The columns must be named as specified below in arbitrary order: "CDR3b" CDR3 sequences of beta chains. "TRBV" Optional. V-genes of beta chains. "patient" Optional. Donor index for the corresponding sequence, composed of a donor identifier and an optional experimental condition separated by a colon (e.g., 09/0410:MtbLys). Only the identifier before the colon is used for HLA scoring. "HLA" Optional. Comma-separated HLA alleles for the corresponding donor in standard notation (e.g., DPA1*01:03). Information after the colon in each allele is ignored during HLA scoring. "counts" Optional. Clone frequency.
refdb_beta	A character string or data.frame specifying the reference database. When a data.frame is supplied, CDR3b sequences must be in the first column and V-gene information (if available) in the second column. Built-in databases include "human_v1.0_CD4", "human_v1.0_CD8", "human_v1.0_CD48", "human_v2.0_CD4", "human_v2.0_CD8", "human_v2.0_CD48", "mouse_v1.0_CD4", "mouse_v1.0_CD8", "mouse_v1.0_CD48", and the legacy alias "gliph_reference" (= "human_v1.0_CD48"). See reference_list for details. **Default:** "human_v2.0_CD48"
v_usage_freq	A data.frame with V-gene alleles in the first column and their naive-repertoire frequencies in the second column. **Default:** NULL
cdr3_length_freq	A data.frame with CDR3 lengths in the first column and their naive-repertoire frequencies in the second column. **Default:** NULL
ref_cluster_size	A character string defining which cluster-size probabilities to use for scoring. "original" Standard probabilities from the original algorithm, constant across sample sizes. "simulated" Probabilities estimated for different sample sizes via a 500-step simulation using random sequences from the reference database. **Default:** "original"
gliph_version	A numeric value indicating the algorithm version. 1 GLIPH scoring (product of individual scores multiplied by 0.064). 2 GLIPH2 scoring (product of individual scores only). **Default:** 1

sim_depth	A numeric value for simulated resampling depth in non-parametric convergence significance tests. Higher values increase runtime but improve reproducibility. **Default:** 1000
hla_cutoff	A numeric threshold below which HLA probability scores are considered significant. **Default:** 0.1
n_cores	A numeric value for the number of cores to use. When NULL, it is set to the number of available cores minus two. **Default:** 1

Value

A data.frame of cluster scoring results. The first column contains the total score and additional columns contain up to five individual scores (cluster size, CDR3 length enrichment, V-gene enrichment, clonal expansion enrichment, and common HLA enrichment).

References

Glanville, Jacob, et al. "Identifying specificity groups in the T cell receptor repertoire." Nature 547.7661 (2017): 94.

https://github.com/immunoengineer/gliph

Examples

```
utils::data("gliph_input_data")
ref_df <- gliph_input_data[, c("CDR3b", "TRBV")]

res <- runGLIPH(cdr3_sequences = gliph_input_data[seq_len(200), ],
                refdb_beta = ref_df,
                sim_depth = 100,
                n_cores = 1)

scoring_results <- clusterScoring(
    cluster_list = res$cluster_list,
    cdr3_sequences = gliph_input_data[seq_len(200), ],
    refdb_beta = ref_df,
    gliph_version = 1,
    sim_depth = 100,
    n_cores = 1)
```

---

deNovoTCRs *Generate de novo TCR sequences*

Description

De novo generation of CDR3 sequences based on GLIPH or GLIPH2 clustering results. Using the position-specific abundance of amino acids in the CDR3 region of sequences within a convergence group, artificial sequences are simulated following the approach established in Glanville et al. The generated sequences are scored by a positional weight matrix (PWM) derived from the convergence group, and optionally normalized against a reference database. The top-scoring sequences are returned.

Usage

```
deNovoTCRs(
  convergence_group_tag,
  result_folder = "",
  clustering_output = NULL,
  refdb_beta = "gliph_reference",
  normalization = FALSE,
  accept_sequences_with_C_F_start_end = TRUE,
  sims = 1e+05,
  num_tops = 1000,
  min_length = 10,
  make_figure = FALSE,
  n_cores = 1
)
```

Arguments

`convergence_group_tag`
: Character. Tag of the convergence group to use for prediction.

`result_folder`
: Character. Path to the folder containing clustering output files and where results will be saved. If the value is `""`, results are not saved to disk and the clustering output must be provided via `clustering_output`. **Default:** `""`

`clustering_output`
: List. The output list from `runGLIPH`. Required when `result_folder` is `""`. **Default:** `NULL`

`refdb_beta`
: Character or data.frame. Specifies the reference database to use. When a data.frame is provided, the first column should contain CDR3b sequences and the second column (optional) should contain V genes. The following keyword can be used to select a built-in database:

  - `"gliph_reference"`: 162,165 CDR3b sequences of naive human CD4+ or CD8+ T cells from two individuals (GLIPH paper).

  Default: `"gliph_reference"`

`normalization`
: Logical. If `TRUE`, calculated scores are normalized to the reference database. The returned value represents the probability that a reference sequence has a score greater than or equal to the sample sequence score. When V gene information is available, only sequences with identical V genes are compared. **Default:** `FALSE`

`accept_sequences_with_C_F_start_end`
: Logical. If `TRUE`, only sequences beginning with cysteine (C) and ending with phenylalanine (F) are accepted. **Default:** `TRUE`

`sims`
: Numeric. Number of de novo CDR3 sequences to generate. **Default:** `100000`

`num_tops`
: Numeric. Number of top-scoring de novo sequences to return. **Default:** `1000`

`min_length`
: Numeric. Minimum CDR3 sequence length; also determines the number of N-terminal positions used for PWM scoring. **Default:** `10`

`make_figure`
: Logical. Whether to plot the `num_tops` best-scoring de novo sequences as a function of rank. **Default:** `FALSE`

n_cores Numeric. Number of cores for parallel computation. If NULL, the number of available cores minus two is used. **Default:** 1

Value

A list with the following elements:

de_novo_sequences A data.frame of the num_tops best-scoring generated sequences and their corresponding scores.

sample_sequences_scores A data.frame of the convergence group sequences and their corresponding scores.

cdr3_length_probability A data.frame with each observed CDR3 length and its probability of occurrence in the convergence group. The length distribution of generated sequences mirrors this distribution.

PWM_Scoring A data.frame containing the positional weight matrix used for scoring. Columns represent amino acids and rows represent positions relative to the N-terminus.

PWM_Prediction A list of data.frames containing the positional weight matrices used for sequence generation, one per observed CDR3 length. Columns represent amino acids and rows represent positions relative to the N-terminus.

If result_folder is specified, a tab-delimited file named <convergence_group_tag>_de_novo.txt is also written to disk.

References

Glanville, Jacob, et al. "Identifying specificity groups in the T cell receptor repertoire." Nature 547.7661 (2017): 94.

https://github.com/immunoengineer/gliph

Examples

```
# Build a minimal clustering output to demonstrate deNovoTCRs
fake_cluster <- data.frame(
  CDR3b = c("CASSLAPGATNEKLFF", "CASSLAPGGTNEKLFF",
            "CASSLAPGDTNEKLFF", "CASSLAPGETNEKLFF",
            "CASSLAPGANEKLFF",  "CASSLAPGVTNEKLFF"),
  TRBV  = rep("TRBV5-1", 6),
  stringsAsFactors = FALSE
)
fake_output <- list(cluster_list = list("motif-LAP" = fake_cluster))
ref_seqs <- fake_cluster[, c("CDR3b", "TRBV")]
new_seqs <- deNovoTCRs(
  convergence_group_tag = "motif-LAP",
  clustering_output = fake_output,
  refdb_beta = ref_seqs,
  sims = 100,
  num_tops = 10,
  min_length = 8,
  make_figure = FALSE,
  n_cores = 1
```

```
)
```

`findMotifs` *Find continuous and discontinuous sequence motifs*

Description

Searches a character vector of amino acid sequences for k-mer motifs and returns their frequencies. Both continuous and discontinuous (gapped) motifs are supported. When **immApex** (>= 2.0.0) is installed, the C++-accelerated `immApex::calculateMotif()` backend is used automatically for improved performance; otherwise the function falls back to a pure-R implementation based on `qgrams`.

Usage

```
findMotifs(seqs, q = 2:4, kmer_mindepth = NULL, discontinuous = FALSE)
```

Arguments

`seqs`	A character vector of amino acid sequences in which motifs will be identified and counted.
`q`	A numeric vector of motif lengths to search for. **Default:** `2:4`.
`kmer_mindepth`	The minimum number of times a k-mer must be observed in `seqs` for it to be included in the output. **Default:** `NULL` (no filtering).
`discontinuous`	Whether to include discontinuous (gapped) motifs in the search. **Default:** `FALSE`.

Value

A `data.frame` with two columns: `motif` (the k-mer string) and `V1` (the observed frequency).

Examples

```
utils::data("gliph_input_data")
sample_seqs <- as.character(gliph_input_data$CDR3b)
res <- findMotifs(seqs = sample_seqs)
```

`getGLIPHreference` *Get or download the immGLIPH reference list*

Description

Downloads the reference repertoire data from Zenodo on first use and caches locally via **BiocFileCache**. Subsequent calls load from the cache without re-downloading.

Usage

```
getGLIPHreference(force_download = FALSE, verbose = TRUE)
```

Arguments

`force_download`	Logical. If `TRUE`, re-download even if cached. **Default:** `FALSE`
`verbose`	Logical. Print messages. **Default:** `TRUE`

Details

The cached file contains a named `list` with entries for each built-in reference database (see `.valid_reference_names`).

Value

A named `list` of reference databases. Each element is a list with `refseqs`, `vgene_frequencies`, and `cdr3_length_frequencies`.

Examples

```
# Available reference database names
c("human_v1.0_CD4", "human_v1.0_CD8", "human_v1.0_CD48",
  "human_v2.0_CD4", "human_v2.0_CD8", "human_v2.0_CD48",
  "mouse_v1.0_CD4", "mouse_v1.0_CD8", "mouse_v1.0_CD48",
  "gliph_reference")


ref <- getGLIPHreference()
names(ref)
head(ref[["human_v2.0_CD48"]]$refseqs)
```

`getRandomSubsample` *Draw a stratified random subsample from the reference repertoire*

Description

Draws a random subset of reference motif regions with the same size as the sample set. When `cdr3_len_stratify` and/or `vgene_stratify` are enabled, the function preserves the CDR3 length and/or V-gene distribution of the sample in the subsample. This is used internally by the repeated random sampling (RRS) local-similarity method in `runGLIPH`.

Usage

```
getRandomSubsample(
  cdr3_len_stratify = FALSE,
  vgene_stratify = FALSE,
  refseqs_motif_region,
  motif_region,
  motif_lengths_list,
  ref_motif_lengths_id_list,
  motif_region_vgenes_list,
  ref_motif_vgenes_id_list,
  ref_lengths_vgenes_list,
  lengths_vgenes_list
)
```

Arguments

`cdr3_len_stratify`
: Whether to preserve the CDR3 length distribution. **Default:** `FALSE`

`vgene_stratify`
: Whether to preserve the V-gene distribution. **Default:** `FALSE`

`refseqs_motif_region`
: Character vector of reference motif regions.

`motif_region`
: Character vector of sample motif regions.

`motif_lengths_list`
: Named list mapping CDR3 lengths to their frequency in `motif_region`. Required when `cdr3_len_stratify = TRUE`.

`ref_motif_lengths_id_list`
: Named list mapping CDR3 lengths to indices in `refseqs_motif_region`. Required when `cdr3_len_stratify = TRUE`.

`motif_region_vgenes_list`
: Named list mapping V-genes to their frequency in `motif_region`. Required when `vgene_stratify = TRUE`.

`ref_motif_vgenes_id_list`
: Named list mapping V-genes to indices in `refseqs_motif_region`. Required when `vgene_stratify = TRUE`.

`ref_lengths_vgenes_list`
: Nested list mapping CDR3 length x V-gene combinations to indices in `refseqs_motif_region`. Required when both stratification flags are `TRUE`.

`lengths_vgenes_list`
: Nested list mapping CDR3 length x V-gene combinations to their frequency in the sample. Required when both stratification flags are `TRUE`.

Value

A character vector of length `length(motif_region)` drawn from `refseqs_motif_region`.

Examples

```
ref_seqs <- c("ASSG", "ASSD", "ASSE", "ASSF", "ASSK", "ASSL")
sample_seqs <- c("ASSG", "ASSF", "ASSL")
sub <- getRandomSubsample(
  refseqs_motif_region = ref_seqs,
  motif_region = sample_seqs
)
```

---

gliph_input_data *Example TCR input data*

Description

A `data.frame` of 365 TRB CDR3 sequences with V-gene and patient annotations, derived from the **scRepertoire** example dataset (Yost et al. 2021). The data were extracted from the `gliph_sce` SingleCellExperiment object using `immApex::getIR()`.

Usage

```
data(gliph_input_data)
```

Format

A data.frame with 365 rows and 3 columns (CDR3b, TRBV, patient).

Details

`CDR3b` Amino acid sequence of the TRB CDR3 region.

`TRBV` TRBV gene name (e.g. `"TRBV9"`).

`patient` Patient/sample identifier (e.g. `"P17B"`, `"P19L"`).

Source

Yost, K. E. et al. Clonal replacement of tumor-specific T cells following PD-1 blockade. *Nature Medicine* 25, 1251–1259 (2019).

Built from **scRepertoire** example data; see `data-raw/build_example_data.R`.

See Also

gliph_sce for the parent SingleCellExperiment object, runGLIPH for the main analysis function.

---

gliph_sce *Example SingleCellExperiment with TCR clonal information*

Description

A SingleCellExperiment object containing 2,000 genes across 500 cells, with T-cell receptor clonotype information stored in the colData. Built from the **scRepertoire** example dataset using combineTCR() and combineExpression().

Usage

```
data(gliph_sce)
```

Format

A SingleCellExperiment with 2000 genes and 500 cells.

Details

The colData includes scRepertoire columns such as CTaa (amino acid clonotype), CTgene (gene-level clonotype), CTnt (nucleotide clonotype), CTstrict (strict clonotype), and clone frequency/proportion columns. These can be parsed by immApex::getIR() to extract chain-specific TCR data.

This object demonstrates how to pass a SingleCellExperiment directly to runGLIPH.

Source

Yost, K. E. et al. Clonal replacement of tumor-specific T cells following PD-1 blockade. *Nature Medicine* 25, 1251–1259 (2019).

Built from **scRepertoire** example data; see data-raw/build_example_data.R.

See Also

gliph_input_data for a plain data.frame extracted from this object, runGLIPH for the main analysis function.

gTRB *Germline TCR-beta CDR3 fragments*

Description

A `list` of three `data.frames` containing germline-encoded fragments of V (`gTRV`), D (`gTRD`), and J (`gTRJ`) gene segments that may appear in the CDR3 region. These fragments are used by the GLIPH2 algorithm to identify germline-encoded sequence segments.

Usage

```
data(gTRB)
```

Format

A list of 3 data.frames: gTRV, gTRD, and gTRJ.

Source

Lefranc, M.-P. IMGT, the international ImMunoGeneTics database. *Nucl. Acids Res.* 29, 207–209 (2001).

loadGLIPH *Load saved GLIPH results from disk*

Description

Reads the tab-delimited output files produced by `runGLIPH` (when `result_folder` was specified) and reconstructs the same list structure that `runGLIPH()` returns.

Usage

```
loadGLIPH(result_folder = "")
```

Arguments

`result_folder`	Path to the folder containing the saved GLIPH output files.

Value

A `list` with the same structure as the return value of `runGLIPH`, including elements such as `cluster_list`, `cluster_properties`, `motif_enrichment`, `connections`, and `parameters`.

Examples

```
utils::data("gliph_input_data")
ref_df <- gliph_input_data[, c("CDR3b", "TRBV")]
tmp_dir <- tempfile("gliph_out_")
res <- runGLIPH(
  cdr3_sequences = gliph_input_data[seq_len(200), ],
  method = "gliph1",
  refdb_beta = ref_df,
  result_folder = tmp_dir,
  sim_depth = 50,
  n_cores = 1
)
reloaded <- loadGLIPH(result_folder = tmp_dir)
unlink(tmp_dir, recursive = TRUE)
```

---

plotNetwork *Visualize TCR convergence group network*

Description

Uses the visNetwork package to build an interactive network graph from the clustering results produced by runGLIPH. Nodes represent individual CDR3b sequences and edges encode local or global sequence similarities. The resulting visualization is fully interactive: scroll to zoom, hover over a node for details, and click a node to highlight its direct neighbors.

Usage

```
plotNetwork(
  clustering_output = NULL,
  result_folder = "",
  show_additional_columns = NULL,
  color_info = "total.score",
  color_palette = viridis::viridis,
  local_edge_color = "orange",
  global_edge_color = "#68bceb",
  size_info = NULL,
  absolute_size = FALSE,
  cluster_min_size = 3,
  n_cores = 1
)
```

Arguments

`clustering_output`
: Output list returned by runGLIPH. **Default:** `NULL`

`result_folder` Path to the folder containing saved GLIPH output files. When a non-empty path is supplied the results are loaded from disk and `clustering_output` is ignored. **Default:** `""`

`show_additional_columns` Character vector of extra column names whose values should be displayed in the node tooltips. Column names from the original `cdr3_sequences` data frame and from `clustering_output$cluster_properties` are accepted. **Default:** `NULL`

`color_info` Column name used to colour the nodes. Accepts any column from the input `cdr3_sequences` or `clustering_output$cluster_properties`. Set to `"none"` to colour all nodes grey, or `"color"` to use pre-assigned colour values stored in that column. For numeric columns the viridis palette is applied automatically (purple = low, yellow = high). **Default:** `"total.score"`

`color_palette` A function that accepts a single integer `n` and returns `n` colour values. **Default:** `viridis::viridis`

`local_edge_color` Colour applied to edges representing local similarities. **Default:** `"orange"`

`global_edge_color` Colour applied to edges representing global similarities. **Default:** `"#68bceb"`

`size_info` Column name whose numeric values determine node sizes. Accepts columns from `cdr3_sequences` or `clustering_output$cluster_properties`. **Default:** `NULL`

`absolute_size` If `TRUE` the raw values from the `size_info` column are used as node sizes; otherwise the values are linearly scaled to the range 12–20. **Default:** `FALSE`

`cluster_min_size` Minimum number of members a cluster must contain to be included in the plot. **Default:** `3`

`n_cores` Number of cores for parallel processing. When `NULL` the number of available cores minus two is used. **Default:** `1`

Value

A `visNetwork` object containing the interactive network graph.

Examples

```
utils::data("gliph_input_data")
ref_df <- gliph_input_data[, c("CDR3b", "TRBV")]
res <- runGLIPH(cdr3_sequences = gliph_input_data[seq_len(200),],
                method = "gliph1",
                refdb_beta = ref_df,
                sim_depth = 100,
                n_cores = 1)

plotNetwork(clustering_output = res,
            n_cores = 1)
```

ref_cluster_sizes *Cluster size probabilities in naive reference repertoire*

Description

A `list` with two elements providing expected cluster-size probabilities under the null model (no true convergence):

`original` Probabilities from the original GLIPH algorithm, applied uniformly across all sample sizes.

`simulated` Probabilities estimated from 500-step simulations at sample sizes of 125, 250, 500, 1000, 2000, 4000, 6000, 8000, and 10000 random reference sequences. During scoring the row closest to the actual sample size is used.

Usage

```
data(ref_cluster_sizes)
```

Format

A list with 2 elements: original and simulated.

Source

Glanville, J. et al. Identifying specificity groups in the T cell receptor repertoire. *Nature* 547, 94–98 (2017).

reference_list *GLIPH reference repertoire list (external data)*

Description

A named `list` of naive TCR repertoire reference databases used for motif enrichment testing and cluster scoring. The data is **not** bundled with the package; it is downloaded on first use from Zenodo and cached locally via **BiocFileCache** (see `getGLIPHreference`).

Format

NULL. Data is downloaded on first use via `getGLIPHreference`.

Details

Each element is itself a list with three components:

`refseqs` A `data.frame` with columns `CDR3b` (amino acid sequence) and `TRBV` (V-gene name).

`vgene_frequencies` A `data.frame` with columns `vgene` and `freq` giving the relative frequency of each V gene in the reference repertoire.

`cdr3_length_frequencies` A `data.frame` with columns `len` and `freq` giving the relative frequency of each CDR3 length in the reference repertoire.

The following named entries are available:

- `"human_v1.0_CD4"`, `"human_v1.0_CD8"`, `"human_v1.0_CD48"` – Glanville et al. (2017)
- `"human_v2.0_CD4"`, `"human_v2.0_CD8"`, `"human_v2.0_CD48"` – Huang et al. (2020)
- `"mouse_v1.0_CD4"`, `"mouse_v1.0_CD8"`, `"mouse_v1.0_CD48"` – Glanville et al. (2017)
- `"gliph_reference"` – Legacy alias for `"human_v1.0_CD48"`

Value

No return value. This documents the `reference_list` object which is downloaded at runtime by `getGLIPHreference`.

Source

Glanville, J. et al. Identifying specificity groups in the T cell receptor repertoire. *Nature* 547, 94–98 (2017).

Huang, H. et al. Analyzing the *Mycobacterium tuberculosis* immune response by T-cell receptor clustering with GLIPH2 and genome-wide antigen screening. *Nature Biotechnology* 38, 1194–1202 (2020).

Raw data downloaded from `http://50.255.35.37:8080/tools`.

See Also

`getGLIPHreference` to download or load the data, `runGLIPH` and `clusterScoring` which use the reference internally via the `refdb_beta` parameter.

`runGLIPH` *Run the GLIPH or GLIPH2 TCR clustering algorithm*

Description

Unified entry point for the GLIPH/GLIPH2 algorithm for grouping T cell receptors by antigen specificity. The function identifies locally and globally similar CDR3b sequences, clusters them into convergence groups, and scores each group for biological relevance.

Usage

```
runGLIPH(
  cdr3_sequences,
  method = c("gliph2", "gliph1", "custom"),
  chains = "TRB",
  result_folder = "",
  refdb_beta = "human_v2.0_CD48",
  v_usage_freq = NULL,
  cdr3_length_freq = NULL,
  ref_cluster_size = "original",
  sim_depth = 1000,
  lcminp = 0.01,
  lcminove = c(1000, 100, 10),
  kmer_mindepth = 3,
  accept_CF = TRUE,
  min_seq_length = 8,
  gccutoff = NULL,
  structboundaries = TRUE,
  boundary_size = 3,
  motif_length = c(2, 3, 4),
  local_similarities = TRUE,
  global_similarities = TRUE,
  local_method = NULL,
  global_method = NULL,
  clustering_method = NULL,
  scoring_method = NULL,
  cluster_min_size = 2,
  hla_cutoff = 0.1,
  n_cores = 1,
  motif_distance_cutoff = 3,
  discontinuous_motifs = FALSE,
  all_aa_interchangeable = FALSE,
  boost_local_significance = FALSE,
  global_vgene = FALSE,
  cdr3_len_stratify = FALSE,
  vgene_stratify = FALSE,
  public_tcrs = TRUE,
  vgene_match = "none",
  scoring_sim_depth = 1000,
  verbose = TRUE
)
```

Arguments

`cdr3_sequences`	Input data containing CDR3b amino acid sequences. Accepts a character vector, a `data.frame` with columns described below, a `Seurat` object, a `SingleCellExperiment` object, or a list returned by `scRepertoire::combineTCR()/combineBCR()`. When a `data.frame` is supplied, the following column names are recognized

(alternative names in parentheses are mapped automatically):

CDR3b (cdr3, cdr3_aa, CDR3.beta, junction_aa) Required. CDR3 beta-chain amino acid sequences.

TRBV (v_gene, v.gene, Vgene, v_call) Optional. V-gene usage.

patient (sample, donor, sample_id) Optional. Donor index.

HLA (hla, HLA_alleles) Optional. HLA alleles, comma-separated.

counts (frequency, clone_count, cloneCount) Optional. Clone frequency.

`method` Character. Algorithm preset to use.

`"gliph2"` Fisher-based local and global similarity, GLIPH2-style isolated clustering and scoring.

`"gliph1"` Repeated random sampling for local similarity, Hamming distance cutoff for global similarity, GLIPH1-style connected-component clustering.

`"custom"` All parameters can be set independently.

Default: `"gliph2"`

`chains` Character. Chain type for extraction from `Seurat` or `SingleCellExperiment` objects via `immApex::getIR()`. **Default:** `"TRB"`

`result_folder` Character. Path to output folder. If `""`, results are not saved to disk. **Default:** `""`

`refdb_beta` Character or `data.frame`. Reference database for motif enrichment testing. Built-in databases include `"human_v1.0_CD4"`, `"human_v1.0_CD8"`, `"human_v1.0_CD48"`, `"human_v2.0_CD4"`, `"human_v2.0_CD8"`, `"human_v2.0_CD48"`, `"mouse_v1.0_CD4"`, `"mouse_v1.0_CD8"`, `"mouse_v1.0_CD48"`, and the legacy alias `"gliph_reference"` (= `"human_v1.0_CD48"`). Alternatively, supply a `data.frame` with CDR3b in the first column and optional V-gene in the second. See `reference_list` for details. **Default:** `"human_v2.0_CD48"`

`v_usage_freq` `data.frame` or `NULL`. V-gene frequencies for scoring. If `NULL`, built-in defaults are used. **Default:** `NULL`

`cdr3_length_freq`
`data.frame` or `NULL`. CDR3 length frequencies for scoring. If `NULL`, built-in defaults are used. **Default:** `NULL`

`ref_cluster_size`
Character. Reference cluster size strategy.

`"original"` Use the original sample size.

`"simulated"` Use simulated cluster sizes.

Default: `"original"`

`sim_depth` Integer. Simulation depth for repeated random sampling (local method `"rrs"`) or cluster scoring. **Default:** `1000`

`lcminp` Numeric. Local convergence maximum p-value threshold. **Default:** `0.01`

`lcminove` Numeric vector. Local convergence minimum fold-change per motif length (lengths 2, 3, and 4 respectively). **Default:** `c(1000, 100, 10)`

`kmer_mindepth` Integer. Minimum number of kmer observations required to consider a motif. **Default:** `3`

`accept_CF` Logical. If `TRUE`, accept only sequences starting with C and ending with F. **Default:** `TRUE`

`min_seq_length` Integer. Minimum CDR3b sequence length to retain. **Default:** `8`

`gccutoff` Numeric or `NULL`. Global convergence Hamming distance cutoff (used when `global_method = "cutoff"`). If `NULL`, the cutoff is auto-selected based on sample size. **Default:** `NULL`

`structboundaries` Logical. If `TRUE`, trim structural boundaries from CDR3b sequences before motif search. **Default:** `TRUE`

`boundary_size` Integer. Number of positions to trim from each end when `structboundaries = TRUE`. **Default:** `3`

`motif_length` Numeric vector. Motif lengths to search. **Default:** `c(2, 3, 4)`

`local_similarities` Logical. If `TRUE`, search for locally similar CDR3b sequences. **Default:** `TRUE`

`global_similarities` Logical. If `TRUE`, search for globally similar CDR3b sequences. **Default:** `TRUE`

`local_method` Character or `NULL`. Method for local similarity detection. If `NULL`, set by the `method` preset.

`"fisher"` Fisher exact test for motif enrichment.

`"rrs"` Repeated random sampling.

Default: `NULL`

`global_method` Character or `NULL`. Method for global similarity detection. If `NULL`, set by the `method` preset.

`"fisher"` Fisher exact test for struct enrichment.

`"cutoff"` Hamming distance cutoff.

Default: `NULL`

`clustering_method` Character or `NULL`. Clustering strategy. If `NULL`, set by the `method` preset.

`"GLIPH1.0"` Connected-component clustering.

`"GLIPH2.0"` Isolated clustering with merging.

Default: `NULL`

`scoring_method` Character or `NULL`. Scoring strategy. If `NULL`, set by the `method` preset.

`"GLIPH1.0"` GLIPH1-style scoring.

`"GLIPH2.0"` GLIPH2-style scoring.

Default: `NULL`

`cluster_min_size` Integer. Minimum number of unique CDR3b sequences required to retain a convergence group. **Default:** `2`

`hla_cutoff` Numeric. Significance cutoff for HLA enrichment testing. **Default:** `0.1`

`n_cores` Integer or `NULL`. Number of cores for parallel processing. If `NULL`, the number of available cores is auto-detected. **Default:** `1`

`motif_distance_cutoff` Integer. Maximum positional distance between shared motifs for two CDR3b sequences to be linked (GLIPH2). **Default:** `3`

discontinuous_motifs
: Logical. If TRUE, allow discontinuous motif patterns during local similarity search. **Default:** FALSE

all_aa_interchangeable
: Logical. If FALSE, BLOSUM62 filtering is applied to global similarities, restricting substitutions to biochemically similar amino acids. **Default:** FALSE

boost_local_significance
: Logical. If TRUE, boost local p-values using germline N-nucleotide insertion information. **Default:** FALSE

global_vgene
: Logical. If TRUE, restrict global similarity edges to pairs sharing the same V-gene. **Default:** FALSE

cdr3_len_stratify
: Logical. If TRUE, stratify random subsamples by CDR3 length (used with local_method = "rrs"). **Default:** FALSE

vgene_stratify
: Logical. If TRUE, stratify random subsamples by V-gene usage (used with local_method = "rrs"). **Default:** FALSE

public_tcrs
: Logical or character. Controls cross-donor edge filtering. For method = "gliph1" or "gliph2": if FALSE, restrict edges to same donor. For method = "custom":

  "all" Allow cross-donor edges for all similarity types.

  "local" Allow cross-donor edges for local only.

  "global" Allow cross-donor edges for global only.

  "none" Restrict all edges to same donor.

  Default: TRUE

vgene_match
: Character. V-gene matching requirement for custom clustering.

  "none" No V-gene matching required.

  "local" Require V-gene match for local edges.

  "global" Require V-gene match for global edges.

  "all" Require V-gene match for all edges.

  Default: "none"

scoring_sim_depth
: Integer. Simulation depth used specifically for convergence group scoring. **Default:** 1000

verbose
: Logical. If TRUE, print progress messages to the console. **Default:** TRUE

Value

A list with the following elements:

sample_log data.frame. Motif counts per simulation iteration (only present when local_method = "rrs").

motif_enrichment list with two elements:

- selected_motifs data.frame of significantly enriched motifs passing all thresholds.
- all_motifs data.frame of all evaluated motifs with enrichment statistics.

global_enrichment list. Global struct enrichment results (GLIPH2 only; NULL otherwise).

`connections` `data.frame`. Edge list representing the clone network.

`cluster_properties` `data.frame`. Convergence group properties and scores.

`cluster_list` Named `list` of `data.frame` objects with per-cluster member details.

`parameters` `list`. All input parameters used for the run.

References

Glanville, J. et al. (2017). Identifying specificity groups in the T cell receptor repertoire. *Nature*, 547, 94–98. doi:10.1038/nature22976

Huang, H. et al. (2020). Analyzing the Mycobacterium tuberculosis immune response by T-cell receptor clustering with GLIPH2 and genome-wide antigen screening. *Nature Biotechnology*, 38, 1194–1202. doi:10.1038/s4158702005054

Examples

```
utils::data("gliph_input_data")
ref_df <- gliph_input_data[, c("CDR3b", "TRBV")]
res <- runGLIPH(
  cdr3_sequences = gliph_input_data[seq_len(200), ],
  method = "gliph2",
  refdb_beta = ref_df,
  sim_depth = 50,
  n_cores = 1
)
```

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