Package ‘immLynx’

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Title Linking Advanced TCR Python Pipelines and Hugging Face Models in R

Version 0.99.4

Description A comprehensive toolkit that bridges popular Python-based immune repertoire analysis tools and Hugging Face protein language models into the R environment. Provides unified interfaces for TCR distance calculations (tcrdist3), sequence generation probability (OLGA), selection inference (soNNia), clustering (clusTCR), protein embeddings (ESM-2), metaclone discovery (metaclonotypist). Fully compatible with the scRepertoire and immApex ecosystem for single-cell
immune repertoire analysis.

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Author Nick Borcherding [aut, cre] (ORCID: <https://orcid.org/0000-0003-1427-6342>)

Maintainer Nick Borcherding <ncborch@gmail.com>

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immLynx-package *immLynx: Advanced Analysis Pipelines for single-cell immune repertoire data*

Description

immLynx provides a unified interface for running multiple analysis pipelines on single-cell sequencing data in the scRepertoire format. The package wraps several popular Python-based tools and makes them accessible within R workflows.

Main Functions

Clustering & Grouping:

- `runClustTCR`: Cluster TCRs using clusTCR (MCL or DBSCAN)
- `runMetaclonotypist`: Identify metaclones with metaclonotypist

Distance Metrics:

- `runTCRdist`: Calculate TCR distances with tcrdist3

Generation Probability:

- `runOLGA`: Calculate Pgen using OLGA
- `generateOLGA`: Generate random TCR sequences

Embeddings:

- `runEmbeddings`: Generate protein embeddings using ESM-2

Selection Inference:

- `runSoNNia`: Infer selection with soNNia

Utility Functions:

- `extractTCRdata`: Extract TCR data from SingleCellExperiment objects
- `validateTCRdata`: Validate TCR data format
- `convertToTcrdist`: Convert to tcrdist3 format
- `summarizeTCRrepertoire`: Generate repertoire statistics

Data Format

All functions expect SingleCellExperiment objects with scRepertoire TCR data stored in the metadata. The functions use `immApex::getIR()` to extract TCR sequences in the format:

- `barcode`: Cell barcode
- `cdr3_aa`: CDR3 amino acid sequence
- `v`: V gene

- d: D gene (if applicable)
- j: J gene
- c: C gene
- chain: Chain type (TRA/TRB)

Python Dependencies

Python packages are managed automatically by basilisk. The following are included:

- clustcr - TCR clustering
- tcrdist3 - TCR distance calculations
- olga - Generation probability
- sonnia - Selection inference
- metaclonotypist - Metaclone discovery
- transformers - Hugging Face models
- torch - PyTorch for GPU support

Author(s)

Maintainer: Nick Borcherding <ncborch@gmail.com> (ORCID)

See Also

Useful links:

- scRepertoire: https://github.com/BorchLab/scRepertoire
- immApex: https://github.com/BorchLab/immApex

---

calculate.clustcr *Cluster TCRs using clusTCR*

Description

Internal function that calls clusTCR via basilisk.

Usage

```
calculate.clustcr(
  sequences,
  method = "mcl",
  inflation = 2,
  eps = 0.5,
  min_samples = 2
)
```

Arguments

sequences	Character vector of CDR3 amino acid sequences
method	Clustering method: "mcl" or "dbscan"
inflation	MCL inflation parameter (for mcl method)
eps	DBSCAN epsilon parameter (for dbscan method)
min_samples	DBSCAN minimum samples parameter (for dbscan method)

Value

Integer vector of cluster assignments

---

calculate.metaclonotypist

Internal Metaclonotypist Calculation Function

Description

Calls metaclonotypist Python package via basilisk

Usage

```
calculate.metaclonotypist(
  cdr3_sequences,
  v_genes = NULL,
  j_genes = NULL,
  chain = "beta",
  method = "tcrdist",
  max_edits = 2,
  max_dist = 20,
  clustering = "leiden",
  resolution = 1
)
```

Arguments

cdr3_sequences	Character vector of CDR3 amino acid sequences
v_genes	Character vector of V gene names (optional)
j_genes	Character vector of J gene names (optional)
chain	Chain type: "alpha" or "beta"
method	Distance method: "tcrdist" or "sceptr"
max_edits	Maximum edit distance for screening
max_dist	Maximum distance for clustering
clustering	Clustering algorithm
resolution	Clustering resolution

Value

List with cluster assignments

---

calculate.olga *Calculate Generation Probability using OLGA*

Description

Internal function that calls OLGA via basilisk.

Usage

```
calculate.olga(
  action = c("pgen", "generate"),
  model = "humanTRB",
  sequences = NULL,
  v_genes = NULL,
  j_genes = NULL,
  n = 100
)
```

Arguments

action	Either "pgen" to calculate probability or "generate" to generate sequences
model	OLGA model name
sequences	Character vector of CDR3 sequences (for pgen)
v_genes	Optional V gene annotations
j_genes	Optional J gene annotations
n	Number of sequences to generate (for generate action)

Value

For pgen: numeric vector of probabilities. For generate: data.frame

calculate.sonia *Run soNNia Selection Analysis*

Description

Internal function that calls soNNia via basilisk.

Usage

```
calculate.sonia(
  data_folder,
  data_filename,
  pgen_filename,
  organism = "human",
  dataset_type = "TCR",
  n_epochs = 100,
  save_folder = "sonia_output"
)
```

Arguments

data_folder	Directory containing data files
data_filename	Name of selected TCR data file
pgen_filename	Name of background Pgen file
organism	Organism: "human" or "mouse"
dataset_type	Type of dataset: "TCR" or "BCR"
n_epochs	Number of training epochs
save_folder	Directory for saving outputs

Value

List with selection model results

calculate.tcrDist *Calculate TCR Distances using tcrdist3*

Description

Internal function that calls tcrdist3 via basilisk.

Usage

```
calculate.tcrDist(
  df,
  organism = "human",
  chains = "beta",
  compute_distances = TRUE
)
```

Arguments

`df`	A data.frame with TCR sequences in tcrdist3 format
`organism`	Character: "human" or "mouse"
`chains`	Character vector: "alpha", "beta", or c("alpha", "beta")
`compute_distances`	Logical: whether to compute full distance matrix

Value

A list containing distance matrices

`calculate_helpers` *Internal Python Bridge Functions*

Description

Internal functions that use basilisk to call Python libraries. These functions are not exported and are used by the run* wrapper functions.

`convertToTcrdist` *Convert TCR Data to tcrdist3 Format*

Description

Converts TCR data from immLynx/scRepertoire format to the format required by tcrdist3 for distance calculations.

Usage

```
convertToTcrdist(
  tcr_data,
  chains = c("beta", "alpha", "both"),
  include_count = TRUE
)
```

Arguments

`tcr_data`	A data.frame from extractTCRdata() or similar source
`chains`	Which chains to include: "alpha", "beta", or "both". Default is "beta".
`include_count`	Logical. If TRUE, adds a 'count' column (default 1). Default is TRUE.

Value

A data.frame in tcrdist3 format with columns:

count Clone count (default 1)

v_a_gene Alpha V gene (if alpha chain included)

j_a_gene Alpha J gene (if alpha chain included)

cdr3_a_aa Alpha CDR3 amino acid sequence (if alpha chain included)

v_b_gene Beta V gene (if beta chain included)

j_b_gene Beta J gene (if beta chain included)

cdr3_b_aa Beta CDR3 amino acid sequence (if beta chain included)

Examples

```
# Convert long-format TCR data to tcrdist3 format
tcr_data <- data.frame(
  barcode = paste0("cell_", 1:5),
  cdr3_aa = c("CASSLGTGELFF", "CASSIRSSYEQYF", "CASSYSTGELFF",
              "CASNQGLNEKLFF", "CASSLDRNEQFF"),
  v = paste0("TRBV", c("7-2", "12-3", "5-1", "28", "7-9")),
  j = paste0("TRBJ", c("2-2", "1-1", "2-7", "1-5", "2-1")),
  chain = rep("TRB", 5),
  stringsAsFactors = FALSE
)
tcrdist_format <- convertToTcrdist(tcr_data, chains = "beta")
head(tcrdist_format)
```

`extractTCRdata` *Extract TCR Data from SingleCellExperiment Object*

Description

Extracts T-cell receptor data from a SingleCellExperiment object that has been processed with scRepertoire. This is a convenience wrapper around `immApex::getIR()` that provides additional formatting options.

Usage

```
extractTCRdata(
  input,
  chains = c("TRB", "TRA", "TRG", "TRD", "IGH", "IGL", "IGK", "both"),
  format = c("long", "wide"),
  remove_na = TRUE
)
```

Arguments

`input`	A SingleCellExperiment object containing scRepertoire TCR data in metadata.
`chains`	Which chains to extract: "TRA", "TRB", "TRG", "TRD", "IGH", "IGL", "IGK", or "both" (for TRA and TRB). Default is "TRB".
`format`	Output format: "long" (one row per chain) or "wide" (one row per cell with columns for each chain). Default is "long".
`remove_na`	Logical. If TRUE, removes rows with NA CDR3 sequences. Default is TRUE.

Value

A data.frame containing:

barcode Cell barcode

cdr3_aa CDR3 amino acid sequence

cdr3_nt CDR3 nucleotide sequence (if available)

v V gene

d D gene (if applicable)

j J gene

c C gene (if available)

chain Chain type (TRA, TRB, etc.)

Examples

```
# Extract beta chain data
data(immLynx_example)
tcr_data <- extractTCRdata(immLynx_example, chains = "TRB")
head(tcr_data)
```

generateOLGA — *Generate Random TCR Sequences using OLGA*

Description

Generate random TCR sequences from OLGA's generative model.

Usage

```
generateOLGA(n = 100, model = "humanTRB")
```

Arguments

n	Number of sequences to generate.
model	OLGA model to use: "humanTRB", "humanTRA", "humanIGH", "mouseTRB".

Value

Data.frame with generated sequences (nt_seq, aa_seq, v_index, j_index).

Examples

```
# Available models
models <- c("humanTRB", "humanTRA", "humanIGH", "mouseTRB")

  # Generate 100 random human TRB sequences
  random_seqs <- generateOLGA(n = 100, model = "humanTRB")
  head(random_seqs)

  # Generate human TRA sequences
  tra_seqs <- generateOLGA(n = 50, model = "humanTRA")

  # Generate mouse TRB sequences
  mouse_seqs <- generateOLGA(n = 200, model = "mouseTRB")
```

huggingModel — *Initialize a Hugging Face Model and Tokenizer*

Description

Downloads or loads a cached pre-trained model and its corresponding tokenizer from the Hugging Face Hub. Uses the basilisk-managed Python environment which includes `transformers` and `torch`.

Usage

```
huggingModel(model_name = "facebook/esm2_t12_35M_UR50D")
```

Arguments

model_name	A string specifying the model identifier from the Hugging Face Hub. For ESM-2 35M, this is "facebook/esm2_t12_35M_UR50D". Other options include "facebook/esm2_t33_650M_UR50D" for larger models.

Value

A list containing the R-wrapped Python objects for the 'model' and 'tokenizer', along with the basilisk process handle. The process must be stopped when no longer needed via `basilisk::basiliskStop()`.

See Also

tokenizeSequences, proteinEmbeddings, runEmbeddings

Examples

```
# Default model is ESM-2 35M
model_name <- "facebook/esm2_t12_35M_UR50D"

  # Load the default ESM-2 35M model
  hf_components <- huggingModel(model_name)
  names(hf_components)  # "model", "tokenizer", "proc"

  # Use with tokenizeSequences and proteinEmbeddings
  sequences <- c("CASSLGTGELFF", "CASSIRSSYEQYF")
  tokenized <- tokenizeSequences(hf_components$tokenizer,
                                 sequences)
  embeddings <- proteinEmbeddings(hf_components$model,
                                  tokenized,
                                  pool = "mean",
                                  chunk_size = 32)

  # Clean up the basilisk process when done
  basilisk::basiliskStop(hf_components$proc)
```

---

immLynx_example *Example Single-Cell RNA-seq Data with TCR Information*

Description

An SCE object containing single-cell RNA-seq data from multiple patients with integrated T-cell receptor (TCR) repertoire data from scRepertoire. This dataset is useful for demonstrating the functionality of immLynx analysis functions.

Usage

```
data(immLynx_example)
```

Format

An SCE object with the following components:

Assays RNA expression data

Metadata Cell-level metadata including:

- `orig.ident`: Original sample identifier (e.g., "P17B", "P17L")
- `nCount_RNA`: Total RNA counts per cell
- `nFeature_RNA`: Number of detected genes per cell
- `CTgene`: TCR gene information (V/J genes)
- `CTnt`: TCR CDR3 nucleotide sequences
- `CTaa`: TCR CDR3 amino acid sequences
- `CTstrict`: Strict TCR identifier combining gene and sequence
- `clonalFrequency`: Number of cells sharing the same TCR
- `clonalProportion`: Proportion of cells with the same TCR
- `cloneSize`: Categorical clone size (Small, Medium, Large, Hyperexpanded)
- `Patient`: Patient identifier (P17, P18, P19, P20)
- `Type`: Sample type (B = Blood, L = Lymph node)
- `clusters`: Cell cluster assignments

Details

This dataset was created by combining 10X Genomics single-cell gene expression and VDJ sequencing data from 8 samples across 4 patients. Each patient contributed two samples: blood (B) and lymph node (L) tissue. More information on the data can be found in the following [manuscript](https://pubmed.ncbi.nlm.nih.gov/33622974/).

Examples

```
data(immLynx_example)
immLynx_example
```

`proteinEmbeddings` *Get Protein Embeddings from a Model*

Description

Applies a pre-trained model to a batch of tokenized sequences to generate embeddings. This is the core embedding function used by `runEmbeddings`.

Usage

```
proteinEmbeddings(
  model,
  tokenized.batch,
  pool = c("none", "mean", "cls"),
  chunk_size = NULL,
  prefer_dtype = c("float16", "bfloat16", "float32"),
  prefer_device = c("auto", "cuda", "mps", "cpu")
)
```

Arguments

model	HF model (from AutoModel or similar), typically obtained via huggingModel.
tokenized.batch	A *list* of tokenized tensors OR a list of such lists (i.e., already minibatched). If you pass a single big batch, set chunk_size. Typically obtained via tokenizeSequences.
pool	One of "mean", "cls", or "none". "mean" is recommended for sequence-level embeddings.
chunk_size	If tokenized.batch is a single big batch, split it into chunks of this many sequences. Ignored if you pre-batched upstream.
prefer_dtype	One of "float16", "bfloat16", "float32". Lower precision uses less memory but may reduce accuracy.
prefer_device	One of "auto", "cuda", "mps", "cpu". "auto" will select the best available device.

Value

An R matrix [n_sequences x hidden] if pool != "none". If pool == "none", returns a list of arrays per chunk.

See Also

runEmbeddings for a higher-level wrapper that works directly with SingleCellExperiment objects.

Examples

```
sequences <- c("CASSLGTGELFF", "CASSIRSSYEQYF", "CASSYSTGELFF")

  # Full workflow: load model, tokenize, embed
  hf_components <- huggingModel()
  tokenized <- tokenizeSequences(hf_components$tokenizer,
                                 sequences)

  # Mean pooling (recommended for sequence-level tasks)
  embeddings <- proteinEmbeddings(hf_components$model,
                                  tokenized,
                                  pool = "mean",
                                  chunk_size = 32)
  dim(embeddings)  # [n_sequences x hidden_dim]
```

```
# CLS token embedding
cls_emb <- proteinEmbeddings(hf_components$model,
                             tokenized,
                             pool = "cls",
                             chunk_size = 32)

# Per-token embeddings (no pooling)
token_emb <- proteinEmbeddings(hf_components$model,
                               tokenized,
                               pool = "none",
                               chunk_size = 32)

# Use GPU with half precision for speed
embeddings_gpu <- proteinEmbeddings(
    hf_components$model, tokenized,
    pool = "mean", chunk_size = 64,
    prefer_device = "cuda",
    prefer_dtype = "float16")
```

`runClustTCR` *Run clusTCR Clustering on scRepertoire Data*

Description

This function extracts TCR sequences from a SingleCellExperiment object with scRepertoire data and performs clustering using the clusTCR algorithm.

Usage

```
runClustTCR(
  input,
  chains = c("TRB", "TRA", "both"),
  method = "mcl",
  combine_chains = FALSE,
  return_object = TRUE,
  column_prefix = "clustcr",
  ...
)
```

Arguments

`input`	A SingleCellExperiment object containing scRepertoire TCR data in the metadata.
`chains`	Character string specifying which chains to use: "TRA", "TRB", or "both". Default is "TRB".
`method`	Clustering method passed to clusTCR. Default is "mcl" (Markov Clustering), which is accurate for typical repertoire datasets.

combine_chains	Logical. If TRUE and chains="both", concatenates alpha and beta sequences with "_". Default is FALSE (clusters chains separately).
return_object	Logical. If TRUE, adds cluster assignments back to the input object metadata. If FALSE, returns only the clustering results. Default is TRUE.
column_prefix	Prefix for the new metadata column(s). Default is "clustcr".
...	Additional arguments passed to calculate.clustcr (e.g., inflation).

Value

If return_object=TRUE, returns the input object with cluster assignments added to metadata. If return_object=FALSE, returns a data.frame with barcodes and cluster assignments.

Examples

```
data(immLynx_example)

  # Cluster TRB chain using MCL algorithm
  sce <- runClustTCR(immLynx_example,
                          chains = "TRB")

  # Adjust MCL inflation parameter
  sce <- runClustTCR(immLynx_example,
                          chains = "TRB",
                          inflation = 3.0)

  # Cluster both chains separately
  sce <- runClustTCR(immLynx_example,
                          chains = "both")

  # Combine alpha and beta chains before clustering
  sce <- runClustTCR(immLynx_example,
                          chains = "both",
                          combine_chains = TRUE)

  # Get results as data.frame
  clusters_df <- runClustTCR(immLynx_example,
                           chains = "TRB",
                           return_object = FALSE)
```

---

runEmbeddings *Generate Protein Language Model Embeddings for TCR Sequences*

Description

Extracts TCR CDR3 sequences from a SingleCellExperiment object and generates embeddings using a protein language model (e.g., ESM-2).

Usage

```
runEmbeddings(
  input,
  chains = c("TRB", "TRA", "both"),
  model_name = "facebook/esm2_t12_35M_UR50D",
  pool = "mean",
  chunk_size = 32,
  reduction_name = "tcr_esm",
  reduction_key = "ESM_",
  return_object = TRUE,
  ...
)
```

Arguments

input	A SingleCellExperiment object containing scRepertoire TCR data.
chains	Which chain(s) to embed: "TRB", "TRA", or "both". Default is "TRB".
model_name	Hugging Face model name. Default is "facebook/esm2_t12_35M_UR50D". Other options: "facebook/esm2_t33_650M_UR50D", "facebook/esm2_t36_3B_UR50D"
pool	Pooling method: "mean", "cls", or "none". Default is "mean".
chunk_size	Number of sequences to process at once. Default is 32.
reduction_name	Name for the dimensional reduction. Default is "tcr_esm".
reduction_key	Key prefix for embeddings in reduction. Default is "ESM_".
return_object	Logical. If TRUE, adds embeddings as dimensional reduction. If FALSE, returns list with embeddings and metadata. Default is TRUE.
...	Additional arguments passed to proteinEmbeddings().

Details

This function uses protein language models to generate dense vector representations of TCR CDR3 sequences. These embeddings can be used for: - Dimensionality reduction and visualization - Clustering TCRs by sequence similarity - Downstream machine learning tasks

Value

If return_object=TRUE, returns input object with embeddings added as a dimensional reduction. If FALSE, returns list with embeddings matrix and metadata.

Examples

```
data(immLynx_example)

  # Generate ESM-2 embeddings for TRB chain
  sce <- runEmbeddings(immLynx_example,
                               chains = "TRB")

  # Use a larger ESM-2 model
```

```
sce <- runEmbeddings(immLynx_example,
                             chains = "TRB",
                             model_name = "facebook/esm2_t33_650M_UR50D")

# Embed both chains together
sce <- runEmbeddings(immLynx_example,
                             chains = "both")

# Use CLS pooling instead of mean pooling
sce <- runEmbeddings(immLynx_example,
                             chains = "TRB",
                             pool = "cls")

# Get raw embeddings as a list
emb_list <- runEmbeddings(immLynx_example,
                           chains = "TRB",
                           return_object = FALSE)
dim(emb_list$embeddings)
```

`runHLAassociation` *Perform HLA Association Analysis on Metaclones*

Description

Tests associations between metaclone membership and HLA alleles using Fisher's exact test with FDR correction.

Usage

```
runHLAassociation(
  metaclone_data,
  hla_data,
  by = "barcode",
  fdr_threshold = 0.05
)
```

Arguments

`metaclone_data`	A data.frame with metaclone assignments, typically from runMetaclonotypist() with return_input=FALSE.
`hla_data`	A data.frame with HLA typing information. Must have a 'barcode' or 'sample' column for matching and columns for each HLA allele.
`by`	Column name to use for matching between datasets. Default is "barcode".
`fdr_threshold`	FDR threshold for significance. Default is 0.05.

Value

A data.frame with HLA association results:

metaclone Metaclone identifier

hla_allele HLA allele tested

odds_ratio Association odds ratio

pvalue Raw p-value from Fisher's exact test

fdr FDR-adjusted p-value

significant Whether FDR < threshold

Examples

```
# Create example metaclone and HLA data
metaclone_data <- data.frame(
  barcode = paste0("cell_", 1:20),
  metaclone = rep(c("MC1", "MC2"), each = 10),
  stringsAsFactors = FALSE
)
hla_data <- data.frame(
  barcode = paste0("cell_", 1:20),
  HLA_A = c(rep("A*02:01", 8), rep("A*01:01", 4),
            rep("A*02:01", 3), rep("A*01:01", 5)),
  stringsAsFactors = FALSE
)
results <- runHLAassociation(metaclone_data, hla_data)
```

---

runMetaclonotypist *Run Metaclonotypist for TCR Metaclone Discovery*

Description

Identifies TCR metaclones (groups of related T cell receptors) using the metaclonotypist pipeline. Metaclonotypist uses a two-stage approach: fast edit-distance-based screening followed by TCRdist or SCEPTR refinement.

Usage

```
runMetaclonotypist(
  input,
  chains = c("beta", "alpha"),
  method = c("tcrdist", "sceptr"),
  max_edits = 2,
  max_dist = NULL,
  clustering = c("cc", "leiden", "louvain", "mcl"),
  resolution = 1,
  return_input = TRUE,
  column_name = "metaclone"
)
```

Arguments

`input`	A SingleCellExperiment object with scRepertoire data, or a data.frame with TCR data.
`chains`	Which chain to analyze: "alpha" or "beta". Default is "beta".
`method`	Distance metric for refinement: "tcrdist" (default) or "sceptr".
`max_edits`	Maximum CDR3 edit distance for initial screening. Default is 2.
`max_dist`	Maximum distance threshold for clustering. Default is 20 for tcrdist, 1.5 for sceptr.
`clustering`	Clustering algorithm: "cc" (connected components, default), "leiden", "louvain", or "mcl".
`resolution`	Resolution parameter for leiden/louvain clustering. Default is 1.0.
`return_input`	Logical. If TRUE and input is a SingleCellExperiment object, adds metaclone assignments to metadata. Default is TRUE.
`column_name`	Name for the metadata column. Default is "metaclone".

Details

Metaclonotypist identifies groups of related TCRs that may recognize similar antigens. The algorithm: 1. Uses the Symdel algorithm for fast edit-distance-based candidate identification 2. Refines candidates using TCRdist or SCEPTR similarity metrics 3. Applies graph-based clustering (Leiden by default) to identify metaclones

Value

If return_input=TRUE and input is a SingleCellExperiment, returns the object with metaclone assignments added to metadata. Otherwise returns a data.frame with:

barcode Cell barcode

cdr3_aa CDR3 amino acid sequence

metaclone Metaclone cluster assignment

metaclone_size Number of cells in the metaclone

References

Metaclonotypist: https://github.com/qimmuno/metaclonotypist

Examples

```
data(immLynx_example)

  # Run metaclonotypist on beta chain
  sce <- runMetaclonotypist(immLynx_example, chains = "beta")

  # Get results as data.frame instead of adding to object
  metaclones <- runMetaclonotypist(immLynx_example,
                                   return_input = FALSE)
```

```
# Adjust edit distance threshold
sce <- runMetaclonotypist(immLynx_example,
                                max_edits = 3,
                                max_dist = 50)
```

---

runOLGA *Calculate Generation Probability (Pgen) for TCRs in scRepertoire Data*

Description

Extracts TCR sequences from a SingleCellExperiment object and calculates their generation probability using OLGA.

Usage

```
runOLGA(
  input,
  chains = c("TRB", "TRA"),
  model = NULL,
  organism = "human",
  use_vj_genes = FALSE,
  return_object = TRUE,
  column_name = "olga_pgen"
)
```

Arguments

input	A SingleCellExperiment object containing scRepertoire TCR data.
chains	Which chain to analyze: "TRA" or "TRB". Default is "TRB".
model	OLGA model to use. Options: "humanTRB", "humanTRA", "humanIGH", "mouseTRB". If NULL, will be inferred from organism and chains parameters.
organism	Organism: "human" or "mouse". Used if model is NULL. Default is "human".
use_vj_genes	Logical. If TRUE, includes V and J gene information in Pgen calculation. Default is FALSE (sequence-only Pgen).
return_object	Logical. If TRUE, adds Pgen values to metadata. Default is TRUE.
column_name	Name for the metadata column. Default is "olga_pgen".

Value

If return_object=TRUE, returns input object with Pgen added to metadata. If FALSE, returns data.frame with barcodes, sequences, and Pgen values.

Examples

```
data(immLynx_example)

  # Calculate Pgen for TRB chain
  sce <- runOLGA(immLynx_example, chains = "TRB")

  # Calculate Pgen for TRA chain
  sce <- runOLGA(immLynx_example, chains = "TRA")

  # Include V and J gene information
  sce <- runOLGA(immLynx_example,
                      chains = "TRB",
                      use_vj_genes = TRUE)

  # Get results as data.frame
  pgen_df <- runOLGA(immLynx_example,
                    chains = "TRB",
                    return_object = FALSE)

  # Specify model explicitly for mouse data
  sce <- runOLGA(immLynx_example,
                      model = "mouseTRB")
```

---

runSoNNia *Run soNNia Selection Analysis*

Description

Infer selection pressures on TCRs using soNNia. Requires a background dataset of unselected sequences (generated by OLGA).

Usage

```
runSoNNia(
  input,
  chains = c("TRB", "TRA"),
  background_file,
  organism = "human",
  save_folder = "sonia_output",
  n_epochs = 100,
  return_object = TRUE
)
```

Arguments

input	A SingleCellExperiment object containing scRepertoire TCR data.
chains	Which chain to analyze: "TRB" or "TRA". Default is "TRB".

background_file	Path to CSV file with background sequences (from generateOLGA).
organism	Organism: "human" or "mouse". Default is "human".
save_folder	Directory to save soNNia model. Default is "sonia_output".
n_epochs	Number of training epochs. Default is 100.
return_object	If TRUE, adds selection scores to metadata. Default is TRUE.

Details

This function requires a background dataset of unselected TCR sequences, which can be generated using generateOLGA(). The selected sequences are extracted from the input object and compared to this background to infer selection pressures.

Value

If return_object=TRUE, returns input object with selection scores in metadata. Otherwise returns the soNNia results.

Examples

```
data(immLynx_example)
## Not run:
  # Step 1: Generate background sequences with OLGA
  background <- generateOLGA(n = 1000, model = "humanTRB")
  bg_file <- tempfile(fileext = ".csv")
  utils::write.csv(background, bg_file, row.names = FALSE)

  # Step 2: Run soNNia selection analysis
  sce <- runSoNNia(immLynx_example,
                        chains = "TRB",
                        background_file = bg_file)

  # Get raw results instead of adding to object
  sonia_results <- runSoNNia(immLynx_example,
                             chains = "TRB",
                             background_file = bg_file,
                             return_object = FALSE)

## End(Not run)
```

---

runTCRdist *Calculate TCR Distances on scRepertoire Data*

Description

This function extracts TCR sequences from a SingleCellExperiment object with scRepertoire data and calculates pairwise TCR distances using tcrdist3.

Usage

```
runTCRdist(
  input,
  chains = "beta",
  organism = "human",
  compute_distances = TRUE,
  add_to_object = FALSE
)
```

Arguments

input	A SingleCellExperiment object containing scRepertoire TCR data.
chains	Character vector specifying chains: "alpha", "beta", or c("alpha", "beta"). Default is "beta".
organism	Organism: "human" or "mouse". Default is "human".
compute_distances	Logical. Whether to compute full distance matrix. Default TRUE.
add_to_object	Logical. If TRUE, attempts to add distance matrix to object (stored in metadata for SCE). Default is FALSE due to large matrix size.

Value

A list containing:

distances	Distance matrices (pw_alpha, pw_beta, pw_cdr3_a_aa, pw_cdr3_b_aa)
barcodes	Cell barcodes corresponding to matrix rows/columns
tcr_data	The formatted TCR data.frame used for analysis

If add_to_object=TRUE, returns the input object with distances stored.

Examples

```
data(immLynx_example)

  # Calculate TCR distances for beta chain
  dist_results <- runTCRdist(immLynx_example,
                             chains = "beta")

  # Access the distance matrix
  dist_matrix <- dist_results$distances
  barcodes <- dist_results$barcodes

  # Calculate for both chains
  dist_both <- runTCRdist(immLynx_example,
                          chains = c("alpha", "beta"))

  # Add distances directly to the object
  sce <- runTCRdist(immLynx_example,
                            chains = "beta",
```

```
add_to_object = TRUE)
```

---

summarizeTCRrepertoire

Summarize TCR Repertoire Statistics

Description

Generates summary statistics for TCR repertoire data including diversity metrics, clonality measures, and sequence characteristics.

Usage

```
summarizeTCRrepertoire(
  input,
  chains = c("TRB", "TRA", "both"),
  group.by = NULL,
  calculate_diversity = TRUE
)
```

Arguments

input	A SingleCellExperiment object with scRepertoire data, or a data.frame from extractTCRdata().
chains	Which chains to summarize: "TRB", "TRA", or "both". Default is "TRB".
group.by	Optional metadata column for grouping (SingleCellExperiment objects only).
calculate_diversity	Logical. If TRUE, calculates diversity indices. Default is TRUE.

Value

An object of class TCR_summary containing summary statistics for the TCR repertoire.

Examples

```
# Summarize from a data.frame
tcr_data <- data.frame(
  barcode = paste0("cell_", 1:10),
  cdr3_aa = c("CASSLGTGELFF", "CASSIRSSYEQYF", "CASSLGTGELFF",
              "CASSYSTGELFF", "CASSIRSSYEQYF", "CASSLGTGELFF",
              "CASNQGLNEKLFF", "CASSYSTGELFF", "CASSLGTGELFF",
              "CASSIRSSYEQYF"),
  v = rep("TRBV7-2", 10),
  j = rep("TRBJ2-2", 10),
  chain = rep("TRB", 10),
  stringsAsFactors = FALSE
)
```

```
summary <- summarizeTCRrepertoire(tcr_data)
print(summary)
```

TCR_summary-class *S4 Class for TCR Repertoire Summary*

Description

Formal S4 class to store summary statistics for a TCR repertoire, including diversity metrics, clonality measures, and sequence characteristics.

Usage

```
## S4 method for signature 'TCR_summary'
show(object)
```

Arguments

object	A TCR_summary object.

Value

An S4 object of class TCR_summary containing the summary statistics described in the slots. The show method prints a formatted summary to the console and returns invisible(NULL).

Slots

total_cells Integer. Total number of cells with TCR data.

unique_clonotypes Integer. Number of unique clonotypes.

clonotype_ratio Numeric. Ratio of unique clonotypes to total cells.

diversity List of diversity indices (Shannon, Simpson, etc.), or NULL.

top_clones Data.frame of the top 10 most frequent clonotypes.

cdr3_length List with CDR3 length distribution statistics.

gene_usage List of V and J gene usage data.frames.

chains Character. Chain(s) summarized.

tokenizeSequences *Tokenize Amino Acid Sequences*

Description

Takes a vector of amino acid sequences and uses a Hugging Face tokenizer to convert them into numerical input IDs suitable for model input. The tokenizer should be obtained from huggingModel, which manages the Python environment via basilisk.

Usage

```
tokenizeSequences(
  tokenizer,
  aa_sequences,
  padding = TRUE,
  truncation = TRUE,
  return_tensors = "pt"
)
```

Arguments

tokenizer	The tokenizer object returned by huggingModel.
aa_sequences	A character vector of amino acid sequences (e.g., CDR3 sequences).
padding	A logical or string. If TRUE, pads sequences to the length of the longest sequence in the batch. Defaults to TRUE.
truncation	A logical. If TRUE, truncates sequences to the model's maximum input length. Defaults to TRUE.
return_tensors	A string specifying the format for the returned tensors. "pt" for PyTorch tensors, "tf" for TensorFlow. Defaults to "pt".

Value

The tokenized output, typically a dictionary-like object containing 'input_ids' and 'attention_mask'.

See Also

huggingModel, proteinEmbeddings, runEmbeddings

Examples

```
sequences <- c("CASSLGTGELFF", "CASSIRSSYEQYF", "CASSYSTGELFF")

  # Initialize model and tokenizer
  hf_components <- huggingModel()

  # Tokenize CDR3 sequences
  tokenized <- tokenizeSequences(hf_components$tokenizer,
```

```
                                sequences)

# Tokenize without padding (variable-length output)
tokenized_nopad <- tokenizeSequences(
    hf_components$tokenizer,
    sequences,
    padding = FALSE)

# Pass tokenized output to proteinEmbeddings
embeddings <- proteinEmbeddings(hf_components$model,
                                tokenized,
                                pool = "mean",
                                chunk_size = 32)

# Clean up
basilisk::basiliskStop(hf_components$proc)
```

---

validateTCRdata *Validate TCR Data Format*

Description

Validates that TCR data is in the correct format for immLynx analysis functions. Checks for required columns, valid sequence formats, and gene nomenclature.

Usage

```
validateTCRdata(
  tcr_data,
  check_genes = FALSE,
  check_sequences = TRUE,
  strict = FALSE
)
```

Arguments

tcr_data	A data.frame containing TCR data
check_genes	Logical. If TRUE, validates gene names against IMGT nomenclature. Default is FALSE.
check_sequences	Logical. If TRUE, validates that CDR3 sequences contain only valid amino acids. Default is TRUE.
strict	Logical. If TRUE, stops with error on validation failure. If FALSE, returns validation report. Default is FALSE.

Value

If strict=FALSE, returns a list with:

valid Logical indicating overall validity

errors Character vector of error messages

warnings Character vector of warning messages

summary Summary statistics of the data

If strict=TRUE, returns TRUE invisibly on success or stops with error.

Examples

```
# Create example TCR data
tcr_data <- data.frame(
  barcode = paste0("cell_", 1:5),
  cdr3_aa = c("CASSLGTGELFF", "CASSIRSSYEQYF", "CASSYSTGELFF",
              "CASNQGLNEKLFF", "CASSLDRNEQFF"),
  v = paste0("TRBV", c("7-2", "12-3", "5-1", "28", "7-9")),
  j = paste0("TRBJ", c("2-2", "1-1", "2-7", "1-5", "2-1")),
  chain = rep("TRB", 5),
  stringsAsFactors = FALSE
)
report <- validateTCRdata(tcr_data, strict = FALSE)
report$valid
report$summary
```

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