

Package ‘jvecfor’

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Type Package

Title Fast K-Nearest Neighbor Search for Single-Cell Analysis

Version 1.0.0

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Description Drop-in replacement for BiocNeighbors::findKNN using the jvecfor Java library, which builds on the jvector library to leverage the Java Vector API for portable SIMD acceleration across AVX2, AVX-512, and ARM NEON hardware. jvecfor/jvector implements HNSW-DiskANN approximate search and VP-tree exact search. The package achieves approximately 2x speedup over Annoy-based search at $n \geq 50K$ cells while returning output structurally identical to BiocNeighbors, making it suitable for seamless integration into existing Bioconductor single-cell workflows. Convenience wrappers delegate shared nearest-neighbor (SNN) and k-nearest-neighbor (KNN) graph construction to the bluster package.

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Imports BiocNeighbors, BiocParallel, Matrix, bluster, data.table, methods, processx

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URL <https://github.com/gkanogiannis/jvecfor>

BugReports <https://github.com/gkanogiannis/jvecfor/issues>

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jvecfor-package	<i>jvecfor: Fast K-Nearest Neighbor Search for Single-Cell Analysis</i>
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Description

Drop-in replacement for `BiocNeighbors::findKNN` using the `jvecfor` Java library (HNSW-DiskANN approximate and VP-tree exact methods). Achieves approximately 2x speedup over Annoy-based search at $n \geq 50K$ cells. Convenience wrappers delegate SNN/KNN graph construction to the `bluster` package.

Main functions

`fastFindKNN` KNN search – returns index + distance matrices.

`fastMakeSNNGraph` KNN -> SNN graph via `bluster`.

`fastMakeKNNGraph` KNN -> KNN graph via `bluster`.

`JvecforParam` `BiocNeighbors` parameter class for drop-in integration with `scran`, `scater`, etc.

`jvecfor_setup` Install a custom `jvecfor` JAR.

Options

`jvecfor.verbose` Logical. Enable Java/`jvecfor` progress logging globally. Default FALSE.

`jvecfor.jar` Character. Path to a custom `jvecfor` JAR file. Overrides the bundled JAR in `inst/java/`.

Author(s)

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See Also

Useful links:

- <https://github.com/gkanogiannis/jvecfor>
- Report bugs at <https://github.com/gkanogiannis/jvecfor/issues>

fastFindKNN

Fast K-Nearest Neighbor Search

Description

Drop-in replacement for `BiocNeighbors::findKNN` using the `jvecfor` Java library. Supports HNSW-DiskANN approximate search (`type="ann"`) and VP-tree exact search (`type="knn"`).

Usage

```
fastFindKNN(
  X,
  k = 15L,
  type = c("ann", "knn"),
  metric = c("euclidean", "cosine", "dot_product"),
  num.threads = NULL,
  BPPARAM = BiocParallel::bpparam(),
  ef.search = 0L,
  M = 16L,
  oversample.factor = 1,
  pq.subspaces = 0L,
  get.distance = TRUE,
  verbose = getOption("jvecfor.verbose", FALSE)
)
```

Arguments

<code>X</code>	A numeric matrix, data.frame, or sparse matrix (<code>Matrix::dgCMatrix</code>) with rows = observations, cols = features. Sparse matrices are written in MatrixMarket format and densified in the Java backend, avoiding R-side memory allocation of the full dense matrix.
<code>k</code>	Integer. Number of nearest neighbors to find (excluding self). Default 15.
<code>type</code>	Character. "ann" for approximate (HNSW-DiskANN) or "knn" for exact (VP-tree). Default "ann".
<code>metric</code>	Character. Distance metric: "euclidean", "cosine", or "dot_product". Default "euclidean". Note: "dot_product" is only valid when type = "ann"; it is not a proper metric and cannot be used with the VP-tree exact search.

num.threads	Integer or NULL. Number of Java threads. If NULL, defaults to <code>BiocParallel::bpworkers(BPPARAM)</code> .
BPPARAM	A <code>BiocParallelParam</code> object controlling the thread count. Defaults to <code>bpparam()</code> .
ef.search	Integer. HNSW-DiskANN beam width override (0 = auto: $\max(k+1, 3k)$). Only meaningful when <code>type = "ann"</code> . Default 0L.
M	Integer. HNSW-DiskANN maximum connections per node. Higher values (e.g. 32) improve recall for high-dimensional data at the cost of more memory and a slower build. Only meaningful when <code>type = "ann"</code> . Default 16L.
oversample.factor	Numeric. Oversampling multiplier for the ANN beam width. When > 1.0 , fetches <code>ceil(ef * oversample.factor)</code> candidates and returns the top <code>k</code> , improving recall at proportional cost. Only meaningful when <code>type = "ann"</code> . Default 1.0.
pq.subspaces	Integer. Number of Product Quantization subspaces for approximate ANN scoring (0 = disabled). Typical value: $\text{ncol}(X) / 2$. Reduces search time approximately 4-8x with minimal recall loss. Only meaningful when <code>type = "ann"</code> . Default 0L.
get.distance	Logical. Return distance matrix alongside index? Default TRUE.
verbose	Logical. Pass <code>--verbose</code> to the Java process, enabling HNSW-DiskANN build progress logging on stderr. Overrides the <code>jvecfor.verbose</code> global option when set explicitly. Default <code>getOption("jvecfor.verbose", FALSE)</code> .

Value

A named list:

index $n \times k$ integer matrix of 1-indexed neighbor indices.

distance $n \times k$ numeric matrix of distances/similarities, or NULL if `get.distance=FALSE`.

Examples

```
set.seed(42)
X <- matrix(rnorm(200), nrow = 20, ncol = 10)

# Full examples require Java >= 20 on PATH
nn <- fastFindKNN(X, k = 3)
dim(nn$index) # 20 x 3
dim(nn$distance) # 20 x 3

# High-recall HNSW-DiskANN with wider beam and more connections
nn2 <- fastFindKNN(X, k = 3, M = 32, ef.search = 100,
                   oversample.factor = 2.0)

# Dot-product similarity (ANN only)
nn3 <- fastFindKNN(X, k = 3, metric = "dot_product")
```

fastMakeKNNGraph *Build a K-Nearest Neighbor Graph*

Description

Convenience wrapper that calls `fastFindKNN` then delegates graph construction to `bluster::neighborsToKNNGraph`.

Usage

```
fastMakeKNNGraph(
  X,
  k = 15L,
  type = c("ann", "knn"),
  metric = c("euclidean", "cosine", "dot_product"),
  num.threads = NULL,
  BPPARAM = BiocParallel::bpparam(),
  ef.search = 0L,
  M = 16L,
  oversample.factor = 1,
  pq.subspaces = 0L,
  verbose = getOption("jvecfor.verbose", FALSE),
  directed = FALSE,
  ...
)
```

Arguments

<code>X</code>	A numeric matrix, data.frame, or sparse matrix (<code>Matrix::dgCMatrix</code>) with <code>rows = cells</code> , <code>cols = features/PCs</code> .
<code>k</code>	Integer. Number of nearest neighbors. Default 15.
<code>type</code>	Character. "ann" or "knn". Default "ann".
<code>metric</code>	Character. "euclidean", "cosine", or "dot_product". Default "euclidean". See fastFindKNN for the dot_product restriction.
<code>num.threads</code>	Integer or NULL. Number of Java threads. If NULL, defaults to <code>BiocParallel::bpworkers(BPPARAM)</code> .
<code>BPPARAM</code>	A <code>BiocParallelParam</code> object controlling the thread count. Defaults to <code>bpparam()</code> .
<code>ef.search</code>	Integer. HNSW-DiskANN beam width override (0 = auto). Default 0L.
<code>M</code>	Integer. HNSW-DiskANN max connections per node. Default 16L.
<code>oversample.factor</code>	Numeric. Oversampling multiplier. Default 1.0.
<code>pq.subspaces</code>	Integer. PQ subspaces (0 = disabled). Default 0L.
<code>verbose</code>	Logical. Enable Java verbose logging. Default <code>getOption("jvecfor.verbose", FALSE)</code> .
<code>directed</code>	Logical. Build directed graph? Default FALSE.
<code>...</code>	Additional arguments forwarded to <code>bluster::neighborsToKNNGraph</code> .

Value

An igraph object (KNN graph).

Examples

```
set.seed(42)
X <- matrix(rnorm(5000), nrow = 100, ncol = 50)

# Full examples require Java >= 20 on PATH
g <- fastMakeKNNGraph(X, k = 10)
igraph::vcount(g) # 100
```

fastMakeSNNGraph *Build a Shared Nearest-Neighbor Graph*

Description

Convenience wrapper that calls `fastFindKNN` then delegates graph construction to `bluster::neighborsToSNNGraph`.

Usage

```
fastMakeSNNGraph(
  X,
  k = 15L,
  type = c("ann", "knn"),
  metric = c("euclidean", "cosine", "dot_product"),
  num.threads = NULL,
  BPPARAM = BiocParallel::bpparam(),
  ef.search = 0L,
  M = 16L,
  oversample.factor = 1,
  pq.subspaces = 0L,
  verbose = getOption("jvecfor.verbose", FALSE),
  snn.type = "rank",
  ...
)
```

Arguments

<code>X</code>	A numeric matrix, data.frame, or sparse matrix (<code>Matrix::dgCMatrix</code>) with <code>rows = cells</code> , <code>cols = features/PCs</code> .
<code>k</code>	Integer. Number of nearest neighbors. Default 15.
<code>type</code>	Character. "ann" or "knn". Default "ann".
<code>metric</code>	Character. "euclidean", "cosine", or "dot_product". Default "euclidean". See fastFindKNN for the dot_product restriction.

num.threads	Integer or NULL. Number of Java threads. If NULL, defaults to <code>BiocParallel::bpworkers(BPPARAM)</code> .
BPPARAM	A <code>BiocParallelParam</code> object controlling the thread count. Defaults to <code>bpparam()</code> .
ef.search	Integer. HNSW-DiskANN beam width override (0 = auto). Default 0L.
M	Integer. HNSW-DiskANN max connections per node. Default 16L.
oversample.factor	Numeric. Oversampling multiplier. Default 1.0.
pq.subspaces	Integer. PQ subspaces (0 = disabled). Default 0L.
verbose	Logical. Enable Java verbose logging. Default <code>getOption("jvecfor.verbose", FALSE)</code> .
snn.type	Character. SNN weighting scheme passed to <code>bluster::neighborsToSNNGraph</code> : "rank", "jaccard", or "number". Default "rank".
...	Additional arguments forwarded to <code>bluster::neighborsToSNNGraph</code> .

Value

An `igraph` object (weighted, undirected SNN graph).

Examples

```
set.seed(42)
X <- matrix(rnorm(5000), nrow = 100, ncol = 50)

# Full examples require Java >= 20 on PATH
g <- fastMakeSNNGraph(X, k = 10)
igraph::vcount(g) # 100

# Higher recall with larger beam and more connections
g2 <- fastMakeSNNGraph(X, k = 10, M = 32, oversample.factor = 2.0)
```

`JvecforIndex-class` *JvecforIndex: BiocNeighbors Index Class for jvecfor*

Description

A `BiocNeighborIndex` subclass storing the data matrix and `JvecforParam` parameters. The actual Java HNSW/VP-tree index is built on-the-fly when `findKNN` is called.

Slots

`data` Numeric matrix (rows = observations, cols = features).
`param` A `JvecforParam` object.
`names` Row names from the original matrix, or NULL.

See Also

[JvecforParam](#)

JvecforParam-class *JvecforParam: BiocNeighbors Parameter Class for jvecfor*

Description

A [BiocNeighborParam](#) subclass for the jvecfor Java backend. Passing a JvecforParam object as the BNPARAM argument to [findKNN](#) or higher-level functions (e.g. `scran::buildSNNGraph`, `scater::runUMAP`) routes neighbor search through jvecfor's HNSW-DiskANN or VP-tree engine.

Usage

```
JvecforParam(
  type = "ann",
  distance = "Euclidean",
  M = 16L,
  ef.search = 0L,
  oversample.factor = 1,
  pq.subspaces = 0L,
  verbose = FALSE
)

## S4 method for signature 'JvecforParam'
show(object)

## S4 method for signature 'JvecforParam'
buildIndex(X, BNPARAM, transposed = FALSE, ...)

## S4 method for signature 'JvecforIndex'
findKnnFromIndex(
  BNINDEX,
  k,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  ...
)
```

Arguments

<code>type</code>	Character. "ann" (default) or "knn".
<code>distance</code>	Character. "Euclidean" (default) or "Cosine".
<code>M</code>	Integer. HNSW max connections per node. Default 16L.
<code>ef.search</code>	Integer. HNSW beam width (0 = auto). Default 0L.
<code>oversample.factor</code>	Numeric. Oversampling multiplier. Default 1.0.

pq.subspaces	Integer. PQ subspaces (0 = disabled). Default 0L.
verbose	Logical. Java progress logging. Default FALSE.
object	A JvecforParam object.
X	A numeric matrix (rows = observations, cols = features).
BNPARAM	A JvecforParam object.
transposed	Logical. If TRUE, X is features-by-obs and will be transposed. Default FALSE.
...	Ignored.
BNINDEX	A JvecforIndex object.
k	Integer. Number of nearest neighbors.
get.index	Logical. Return index matrix? Default TRUE.
get.distance	Logical. Return distance matrix? Default TRUE.
num.threads	Integer. Thread count. Default 1.
subset	Integer vector. Row indices to return results for. All rows are computed; this filters the output. Default NULL (all rows).

Value

A JvecforParam object.

A [JvecforIndex](#) object.

A named list with index (n-by-k integer matrix or NULL) and distance (n-by-k numeric matrix or NULL).

Methods (by generic)

- show(JvecforParam): Print a summary of the parameter object.
- buildIndex(JvecforParam): Build a JvecforIndex from a data matrix.
- findKnnFromIndex(JvecforIndex): Find k-nearest neighbors using a JvecforIndex.

Functions

- JvecforParam(): Constructor for JvecforParam objects.

Slots

type Character. "ann" (HNSW-DiskANN, default) or "knn" (VP-tree exact).

M Integer. HNSW max connections per node. Default 16L.

ef.search Integer. HNSW beam width (0 = auto). Default 0L.

oversample.factor Numeric. Oversampling multiplier (≥ 1). Default 1.0.

pq.subspaces Integer. Product-quantization subspaces (0 = disabled). Default 0L.

verbose Logical. Enable Java progress logging. Default FALSE.

Supported distance metrics

"Euclidean" and "Cosine" (title-case, following BiocNeighbors convention). The jvecfor-specific "dot_product" metric is only available via `fastFindKNN` directly.

Limitations

- queryKNN is not supported. The Java backend performs self-KNN only (all points query against all points in a single JVM invocation).
- The index built by `buildIndex` stores the data matrix in R memory; the actual Java HNSW/VP-tree index is rebuilt each time `findKNN` is called.

See Also

`fastFindKNN` for the standalone function with full parameter control including `dot_product` metric.

Examples

```
library(BiocNeighbors)
p <- JvecforParam()
p

# Custom parameters
p2 <- JvecforParam(type = "knn", distance = "Cosine", M = 32L)

# Use with BiocNeighbors (requires Java >= 20):
# res <- findKNN(X, k = 10, BNPARAM = JvecforParam())
```

jvecfor_setup

Install a Custom jvecfor JAR

Description

Copies a custom jvecfor JAR to the user data directory (`tools::R_user_dir("jvecfor", "data")`). The bundled JAR in `inst/java/` is used by default; call `jvecfor_setup()` only to override it with a custom build. Alternatively, set `options(jvecfor.jar = "/path/to/jvecfor.jar")` for a session-level override without copying.

Usage

```
jvecfor_setup(jar_path = NULL)
```

Arguments

`jar_path` Path to the jvecfor JAR. If `NULL`, auto-searches `java/jvecfor/target/jvecfor-*.jar` relative to the working directory (works when developing inside the source tree).

Value

Invisibly returns the path to the installed JAR.

Examples

```
# Show where custom JARs are stored
tools::R_user_dir("jvecfor", "data")

# List bundled JARs
dir(system.file("java", package = "jvecfor"), pattern = "*.jar")
```

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