

Package ‘BiocNeighbors’

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Description Implements exact and approximate methods for nearest neighbor detection, in a framework that allows them to be easily switched within Bioconductor packages or workflows.

Exact searches can be performed using the k-means for k-nearest neighbors algorithm, vantage point trees, or an exhaustive search.

Approximate searches can be performed using the Annoy or HNSW libraries.

Each search can be performed with a variety of different distance metrics, parallelization, and variable numbers of neighbors.

Range-based searches (to find all neighbors within a certain distance) are also supported.

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LinkingTo Rcpp, assorthead, beachmat

URL <https://github.com/knncolle/BiocNeighbors>

BugReports <https://github.com/knncolle/BiocNeighbors/issues>

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BiocNeighbors-package *BiocNeighbors: Nearest Neighbor Detection for Bioconductor Packages*

Description

Implements exact and approximate methods for nearest neighbor detection, in a framework that allows them to be easily switched within Bioconductor packages or workflows. Exact searches can be performed using the k-means for k-nearest neighbors algorithm, vantage point trees, or an exhaustive search. Approximate searches can be performed using the Annoy or HNSW libraries. Each search can be performed with a variety of different distance metrics, parallelization, and variable numbers of neighbors. Range-based searches (to find all neighbors within a certain distance) are also supported.

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See Also

Useful links:

- <https://github.com/knncolle/BiocNeighbors>
- Report bugs at <https://github.com/knncolle/BiocNeighbors/issues>

AnnoyParam

*The AnnoyParam class***Description**

A class to hold parameters for the Annoy algorithm for approximate nearest neighbor identification.

Usage

```
AnnoyParam(
  ntrees = 50,
  search.mult = ntrees,
  distance = c("Euclidean", "Manhattan", "Cosine")
)

## S4 method for signature 'AnnoyParam'
defineBuilder(BNPARAM)
```

Arguments

<code>ntrees</code>	Integer scalar, number of trees to use for index generation.
<code>search.mult</code>	Numeric scalar, multiplier for the number of points to search.
<code>distance</code>	String specifying the distance metric to use. Cosine distances are implemented as Euclidean distances on L2-normalized coordinates.
<code>BNPARAM</code>	An AnnoyParam instance.

Details

The Approximate nearest neighbors Oh Yeah (Annoy) algorithm is based on recursive hyperplane partitions. Briefly, a tree is constructed where a random hyperplane splits the points into two subsets at each internal node. Leaf nodes are defined when the number of points in a subset falls below a threshold (close to twice the number of dimensions for the settings used here). Multiple trees are constructed in this manner, each of which is different due to the random choice of hyperplanes. For a given query point, each tree is searched to identify the subset of all points in the same leaf node as the query point. The union of these subsets across all trees is exhaustively searched to identify the actual nearest neighbors to the query.

The `ntrees` parameter controls the trade-off between accuracy and computational work. More trees provide greater accuracy at the cost of more computational work (both in terms of the indexing time and search speed in downstream functions).

The `search.mult` controls the parameter known as `search_k` in the original Annoy documentation. Specifically, `search_k` is defined as $k * \text{search.mult}$ where k is the number of nearest neighbors to identify in downstream functions. This represents the number of points to search exhaustively and determines the run-time balance between speed and accuracy. The default `search.mult=ntrees` is based on the Annoy library defaults. Note that this parameter is not actually used in the index construction itself, and is only included here so that the output index fully parametrizes the search.

Technically, the index construction algorithm is stochastic but, for various logistical reasons, the seed is hard-coded into the C++ code. This means that the results of the Annoy neighbor searches will be fully deterministic for the same inputs, even though the theory provides no such guarantees.

Value

The AnnoyParam constructor returns an instance of the AnnoyParam class.

The `defineBuilder` method returns a list that can be used in `buildIndex` to construct an Annoy index.

Author(s)

Aaron Lun

See Also

[BiocNeighborParam](#), for the parent class and its available methods.

<https://github.com/spotify/annoy>, for details on the underlying algorithm.

Examples

```
(out <- AnnoyParam())
out[['ntrees']]

out[['ntrees']] <- 20L
out
```

BiocNeighborIndex

The BiocNeighborIndex class

Description

A virtual class for indexing structures of different nearest-neighbor search algorithms. Developers should define subclasses for their own `buildIndex` and/or `defineBuilder` methods.

Details

In general, the internal structure of a BiocNeighborIndex class is arbitrary and left to the discretion of the developer. If an arbitrary structure is used, the associated methods should be written for all downstream generics like `findKNN`, etc.

Alternatively, developers may choose to derive from the BiocNeighborGenericIndex class. This expects:

- A ptr slot containing an external pointer that refers to a BiocNeighbors::Prebuilt object (see definition in `system.file("include", "BiocNeighbors.h", package="BiocNeighbors")`).
- A names slot containing a character vector with the names of the observations, or NULL if no names are available. This is used by `subset=` in the various `find*` generics.

In this case, no additional methods are required for the downstream generics.

Author(s)

Aaron Lun

BiocNeighborParam *The BiocNeighborParam class*

Description

A virtual class for specifying the type of nearest-neighbor search algorithm and associated parameters.

Details

The BiocNeighborParam class is a virtual base class on which other parameter objects are built. There are currently 5 concrete subclasses in **BiocNeighbors**:

[KmknnParam](#): Exact nearest-neighbor search with the KMKNN algorithm.

[VptreeParam](#): Exact nearest-neighbor search with the tree algorithm.

[ExhaustiveParam](#): Exact nearest-neighbor search via brute-force.

[AnnoyParam](#): Approximate nearest-neighbor search with the Annoy algorithm.

[HnswParam](#): Approximate nearest-neighbor search with the HNSW algorithm.

These objects hold parameters specifying how each algorithm should be run on an arbitrary data set. See the associated documentation pages for more details.

Methods

In the following code snippets, `x` and `object` are BiocNeighborParam objects.

`show(object)`: Display the class and arguments of `object`.

`bandistance(object)`: Return a string specifying the distance metric to be used for searching. This should be one of "Euclidean", "Manhattan" or "Cosine".

`x[[i]]`: Return the value of slot `i`, as used in the constructor for `x`.

`x[[i]] <- value`: Set slot `i` to the specified value.

Author(s)

Aaron Lun

See Also

[KmknnParam](#), [VptreeParam](#), [AnnoyParam](#), and [HnswParam](#) for constructors.

[buildIndex](#), [findKNN](#) and [queryKNN](#) for dispatch.

buildIndex	<i>Build a nearest-neighbor index</i>
------------	---------------------------------------

Description

Build indices for nearest-neighbor searching with different algorithms.

Usage

```
buildIndex(X, BNPARAM, transposed = FALSE, ...)

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

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

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

## S4 method for signature 'list'
buildIndex(X, BNPARAM, transposed = FALSE, ..., .check.nonfinite = TRUE)
```

Arguments

X	A numeric matrix or matrix-like object where rows correspond to data points and columns correspond to variables (i.e., dimensions).
BNPARAM	A BiocNeighborParam object specifying the type of index to be constructed. If NULL or missing, this defaults to a KmknnParam object. Alternatively, this may be a list returned by defineBuilder .
transposed	Logical scalar indicating whether X is transposed, i.e., rows are variables and columns are data points.
...	Further arguments to be passed to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., <code>vptree.foo.bar</code> .
.check.nonfinite	Boolean indicating whether to check for non-finite values in X. This can be set to FALSE for greater efficiency.

Details

Each `buildIndex` method is expected to return an instance of a [BiocNeighborIndex](#) subclass. The structure of this subclass is arbitrary and left to the discretion of the method developer.

If a `buildIndex` method returns a [BiocNeighborGenericIndex](#) subclass, the index can be used with the existing methods for [findKnnFromIndex](#), etc. without further effort. Otherwise, developers are responsible for defining methods for their subclass in each of the relevant generics.

Users should assume that the index is not serializable (i.e., saved or transferred between processes) via R's usual mechanisms. If the index must be saved to disk, consider using [saveIndex](#) instead.

Value

A [BiocNeighborIndex](#) object can be used in [findKNN](#) and related functions as the X= argument, or in [findKnnFromIndex](#) and related generics as the BNINDEX= argument.

Author(s)

Aaron Lun

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
(k.out <- buildIndex(Y))
(a.out <- buildIndex(Y, BNPARAM=AnnoyParam()))
```

defineBuilder	<i>Define an index builder</i>
---------------	--------------------------------

Description

Define a builder object that can construct C++ indices for neighbor searches.

Usage

```
defineBuilder(BNPARAM)

## S4 method for signature 'NULL'
defineBuilder(BNPARAM)

## S4 method for signature 'missing'
defineBuilder(BNPARAM)
```

Arguments

BNPARAM A [BiocNeighborParam](#) object specifying the type of index to be constructed. If NULL, this defaults to a [KmknnParam](#) object.

Details

The external pointer returned in builder should refer to a `BiocNeighbors::Builder` object, see the definition in `system.file("include", "BiocNeighbors.h", package="BiocNeighbors")` for details. If a developer defines a `defineBuilder` method for a search algorithm, they do not have to define a new `buildIndex` method. The existing `buildIndex` methods will automatically create an instance of the appropriate [BiocNeighborGenericIndex](#) subclass based on `class`, which can be immediately used in all generics (e.g., [findKNN](#), [queryNeighbors](#)) without further effort.

Note that the pointer returned by `defineBuilder` should *not* be used as the `ptr` in the [BiocNeighborIndex](#) subclasses. The `ptr` slot is expected to contain a pointer referring to a `BiocNeighbors::Prebuilt` object, as returned by the default `buildIndex`. Using the pointer from builder will probably crash the R session.

Needless to say, users should not attempt to serialize the external pointer returned by this generic. Attempting to use a deserialized pointer in `buildIndex` will cause the R session to crash.

Value

List containing:

- `builder`, a pointer to a builder instance that can be used to construct a prebuilt index in [buildIndex](#).
- `class`, the constructor for a [BiocNeighborGenericIndex](#) subclass that accepts `ptr` and `names` arguments.

Author(s)

Aaron Lun

See Also

[defineBuilder, KmknnParam-method](#), [defineBuilder, VptreeParam-method](#), [defineBuilder, AnnoyParam-method](#) and [defineBuilder, HnswParam-method](#) for specific methods.

Examples

```
(out <- defineBuilder())
(out2 <- defineBuilder(AnnoyParam()))
```

ExhaustiveParam

The ExhaustiveParam class

Description

A class to hold parameters for the exhaustive algorithm for exact nearest neighbor identification.

Usage

```
ExhaustiveParam(distance = c("Euclidean", "Manhattan", "Cosine"))
```

```
## S4 method for signature 'ExhaustiveParam'
defineBuilder(BNPARAM)
```

Arguments

<code>distance</code>	String specifying the distance metric to use. Cosine distances are implemented as Euclidean distances on L2-normalized coordinates.
<code>BNPARAM</code>	An ExhaustiveParam instance.

Details

The exhaustive search computes all pairwise distances between data and query points to identify nearest neighbors of the latter. It has quadratic complexity and is theoretically the worst-performing method; however, it has effectively no overhead from constructing or querying indexing structures, making it faster for in situations where indexing provides little benefit. This includes queries against datasets with few data points or very high dimensionality.

All that said, this algorithm is largely provided as a baseline for comparing against the other algorithms.

Value

The ExhaustiveParam constructor returns an instance of the ExhaustiveParam class.

The `defineBuilder` method returns an external pointer that can be used in `buildIndex` to construct an exhaustive index.

Author(s)

Allison Vuong

See Also

[BiocNeighborParam](#), for the parent class and its available methods.

Examples

```
(out <- ExhaustiveParam())
```

findDistanceFromIndex *Distance to the k-th nearest neighbor*

Description

Find the distance to the k-th nearest neighbor for each point in a dataset.

Usage

```
findDistanceFromIndex(BNINDEX, k, num.threads = 1, subset = NULL, ...)
```

```
## S4 method for signature 'BiocNeighborGenericIndex'
```

```
findDistanceFromIndex(BNINDEX, k, num.threads = 1, subset = NULL, ...)
```

```
findDistance(X, k, num.threads = 1, subset = NULL, ..., BNPARAM = NULL)
```

Arguments

BNINDEX	A BiocNeighborIndex object, typically created by <code>buildIndex</code> .
k	A positive integer scalar specifying the number of nearest neighbors to retrieve. Alternatively, an integer vector of length equal to the number of points in X, specifying the number of neighbors to identify for each point. If subset is provided, this should have length equal to the length of subset. Users should wrap this vector in an AsIs class to distinguish length-1 vectors from integer scalars. All k should be less than or equal to the number of points in X minus 1, otherwise the former will be capped at the latter with a warning.
num.threads	Integer scalar specifying the number of threads to use for the search.
subset	An integer, logical or character vector specifying the indices of points in X for which the nearest neighbors should be identified. This yields the same result as (but is more efficient than) subsetting the output matrices after computing neighbors for all points.

...	For <code>findDistanceFromIndex</code> , further arguments to pass to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., <code>vptree.foo.bar</code> . For <code>findDistance</code> , further arguments to pass to <code>findDistanceFromIndex</code> . These are also passed to <code>buildIndex</code> when <code>X</code> is not an external pointer.
<code>X</code>	A numeric matrix or matrix-like object where rows correspond to data points and columns correspond to variables (i.e., dimensions). Alternatively, a prebuilt <code>BiocNeighborIndex</code> object from <code>buildIndex</code> .
<code>BNPARAM</code>	A <code>BiocNeighborParam</code> object specifying how the index should be constructed. If <code>NULL</code> , this defaults to a <code>KmknParam</code> . Ignored if <code>X</code> contains a prebuilt index.

Details

If multiple queries are to be performed to the same `X`, it may be beneficial to build the index from `X` with `buildIndex`. The resulting pointer object can be supplied as `X` to multiple `findDistance` calls, avoiding the need to repeat index construction in each call.

Value

Numeric vector of length equal to the number of points in `X` (or subset, if provided), containing the distance from each point to its `k`-th nearest neighbor. This is equivalent to but more memory efficient than using `findKNN` and subsetting to the last distance.

Author(s)

Aaron Lun

See Also

`buildIndex`, to build an index ahead of time.

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
out <- findDistance(Y, k=8)
summary(out)
```

findKnnFromIndex	<i>Find k-nearest neighbors</i>
------------------	---------------------------------

Description

Find the `k`-nearest neighbors of each point in a dataset.

Usage

```

findKnnFromIndex(
  BNINDEX,
  k,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  ...
)

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

findKNN(
  X,
  k,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  ...,
  BPPARAM = NULL,
  BNPARAM = NULL
)

```

Arguments

BNINDEX	A BiocNeighborIndex object, typically created by buildIndex .
k	A positive integer scalar specifying the number of nearest neighbors to retrieve. Alternatively, an integer vector of length equal to the number of points in X, specifying the number of neighbors to identify for each point. If subset is provided, this should have length equal to the length of subset. Users should wrap this vector in an AsIs class to distinguish length-1 vectors from integer scalars. All k should be less than or equal to the number of points in X minus 1, otherwise the former will be capped at the latter with a warning.
get.index	A logical scalar indicating whether the indices of the nearest neighbors should be recorded. Setting this to FALSE improves efficiency if the indices are not of interest. Alternatively, if k is an integer scalar, this may be a string containing "normal" or "transposed". The former is the same as TRUE, while the latter returns the index matrix in transposed format.

get.distance	<p>A logical scalar indicating whether distances to the nearest neighbors should be recorded. Setting this to FALSE improves efficiency if the distances are not of interest.</p> <p>Alternatively, if k is an integer scalar, this may be a string containing "normal" or "transposed". The former is the same as TRUE, while the latter returns the distance matrix in transposed format.</p>
num.threads	Integer scalar specifying the number of threads to use for the search.
subset	An integer, logical or character vector specifying the indices of points in X for which the nearest neighbors should be identified. This yields the same result as (but is more efficient than) subsetting the output matrices after computing neighbors for all points.
...	<p>For findKnnFromIndex, further arguments to pass to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., vptree.foo.bar.</p> <p>For findKNN, further arguments to pass to findKnnFromIndex. These are also passed to buildIndex when X is not an external pointer.</p>
X	A numeric matrix or matrix-like object where rows correspond to data points and columns correspond to variables (i.e., dimensions). Alternatively, a prebuilt BiocNeighborIndex object from buildIndex .
BPPARAM	Soft-deprecated, use num.threads instead.
BNPARAM	A BiocNeighborParam object specifying how the index should be constructed. If NULL, this defaults to a KmknnParam . Ignored if X contains a prebuilt index.

Value

List containing index (if get.index is not FALSE) and distance (if get.distance is not FALSE).

- If get.index=TRUE or "normal" and k is an integer scalar, index is an integer matrix with k columns where each row corresponds to a point (denoted here as i) in X. The i -th row contains the indices of points in X that are the nearest neighbors to point i , sorted by increasing distance from i . i will *not* be included in its own set of nearest neighbors.
If get.index=FALSE or "transposed" and k is an integer scalar, index is as described above but transposed, i.e., the i -th column contains the indices of neighboring points in X.
- If get.distance=TRUE or "normal" and k is an integer scalar, distance is a numeric matrix of the same dimensions as index. The i -th row contains the distances of neighboring points in X to the point i , sorted in increasing order.
If get.distance=FALSE or "transposed" and k is an integer scalar, distance is as described above but transposed, i.e., the i -th column contains the distances to neighboring points in X.
- If get.index is not FALSE and k is an integer vector, index is a list of integer vectors where each vector corresponds to a point (denoted here as i) in X. The i -th vector has length $k[i]$ and contains the indices of points in X that are the nearest neighbors to point i , sorted by increasing distance from i .
- If get.distance is not FALSE and k is an integer vector, distance is a list of numeric vectors of the same lengths as those in index. The i -th vector contains the distances of neighboring points in X to the point i , sorted in increasing order.

Author(s)

Aaron Lun

See Also

[buildIndex](#), to build an index ahead of time.

[findDistance](#), to efficiently obtain the distance to the k-th nearest neighbor.

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
out <- findKNN(Y, k=8)
head(out$index)
head(out$distance)
```

findMutualINN	<i>Find mutual nearest neighbors</i>
---------------	--------------------------------------

Description

Find mutual nearest neighbors (MNN) across two data sets.

Usage

```
findMutualINN(data1, data2, k1, k2 = k1, BNINDEX1 = NULL, BNINDEX2 = NULL, ...)
```

Arguments

data1	A numeric matrix containing points in the rows and variables/dimensions in the columns.
data2	A numeric matrix like data1 for another dataset with the same variables/dimensions.
k1	Integer scalar specifying the number of neighbors to search for in data1.
k2	Integer scalar specifying the number of neighbors to search for in data2.
BNINDEX1	A pre-built index for data1. If NULL, this is constructed from data1 within the internal queryKNN call.
BNINDEX2	A pre-built index for data2. If NULL, this is constructed from data2 within the internal queryKNN call.
...	Other arguments to be passed to the underlying queryKNN calls, e.g., BNPARAM, .

Details

For each point in dataset 1, the set of k2 nearest points in dataset 2 is identified. For each point in dataset 2, the set of k1 nearest points in dataset 1 is similarly identified. Two points in different datasets are considered to be part of an MNN pair if each point lies in the other's set of neighbors. This concept allows us to identify matching points across datasets, which is useful for, e.g., batch correction.

Any values for the BNINDEX1 and BNINDEX2 arguments should be equal to the output of [buildIndex](#) for the respective matrices, using the algorithm specified with BNPARAM. These arguments are only provided to improve efficiency during repeated searches on the same datasets (e.g., for comparisons between all pairs). The specification of these arguments should not, generally speaking, alter the output of the function.

Value

A list containing the integer vectors `first` and `second`, containing row indices from `data1` and `data2` respectively. Corresponding entries in `first` and `second` specify a MNN pair consisting of the specified rows from each matrix.

Author(s)

Aaron Lun

See Also

[queryKNN](#) for the underlying neighbor search code.

`fastMNN` and related functions from the **batchelor** package, from which this code was originally derived.

Examples

```
B1 <- matrix(rnorm(10000), ncol=50) # Batch 1
B2 <- matrix(rnorm(10000), ncol=50) # Batch 2
out <- findMutualNN(B1, B2, k1=20)
head(out$first)
head(out$second)
```

findNeighborsFromIndex

Find neighbors within a threshold distance

Description

Find all neighbors within a threshold distance of each point of a dataset.

Usage

```
findNeighborsFromIndex(
  BNINDEX,
  threshold,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  ...
)

## S4 method for signature 'BiocNeighborGenericIndex'
findNeighborsFromIndex(
  BNINDEX,
  threshold,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
```

```

    subset = NULL,
    ...
)

findNeighbors(
  X,
  threshold,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  ...,
  BPPARAM = NULL,
  BNPARAM = NULL
)

```

Arguments

BNINDEX	A BiocNeighborIndex object, typically created by buildIndex .
threshold	A positive numeric scalar specifying the maximum distance at which a point is considered a neighbor. Alternatively, a vector containing a different distance threshold for each point.
get.index	A logical scalar indicating whether the indices of the neighbors should be recorded.
get.distance	A logical scalar indicating whether distances to the neighbors should be recorded.
num.threads	Integer scalar specifying the number of threads to use for the search.
subset	An integer, logical or character vector specifying the indices of points in X for which the nearest neighbors should be identified. This yields the same result as (but is more efficient than) subsetting the output matrices after computing neighbors for all points.
...	For <code>findNeighborsFromIndex</code> , further arguments to pass to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., <code>vptree.foo.bar</code> . For <code>findNeighbors</code> , further arguments to pass to <code>findNeighborsFromIndex</code> . These are also passed to buildIndex when X is not an external pointer.
X	A numeric matrix or matrix-like object where rows correspond to data points and columns correspond to variables (i.e., dimensions). Alternatively, a prebuilt BiocNeighborIndex object from buildIndex .
BPPARAM	Soft-deprecated, use <code>num.threads</code> instead.
BNPARAM	A BiocNeighborParam object specifying how the index should be constructed. If NULL, this defaults to a KmknnParam . Ignored if X contains a prebuilt index.

Details

This function identifies all points in X that within threshold of each point in X. For Euclidean distances, this is equivalent to identifying all points in a hypersphere centered around the point of interest. Not all implementations support this search mode, but we can use [KmknnParam](#) and [VptreeParam](#).

If `threshold` is a vector, each entry is assumed to specify a (possibly different) threshold for each point in X. If `subset` is also specified, each entry is assumed to specify a threshold for each point in `subset`. An error will be raised if `threshold` is a vector of incorrect length.

If multiple queries are to be performed to the same X , it may be beneficial to build the index from X with `buildIndex`. The resulting pointer object can be supplied as X to multiple `findNeighbors` calls, avoiding the need to repeat index construction in each call.

Value

A list is returned containing:

- `index`, if `get.index=TRUE`. This is a list of integer vectors where each entry corresponds to a point (denoted here as i) in X . The vector for i contains the set of row indices of all points in X that lie within threshold of point i . Neighbors for i are sorted by increasing distance.
- `distance`, if `get.distance=TRUE`. This is a list of numeric vectors where each entry corresponds to a point (as above) and contains the distances of the neighbors from i . Elements of each vector in `distance` match to elements of the corresponding vector in `index`.

If both `get.index=FALSE` and `get.distance=FALSE`, an integer vector is returned of length equal to the number of observations. The i -th entry contains the number of neighbors of i within threshold.

If `subset` is not `NULL`, each entry of the above vector/lists corresponds to a point in the subset, in the same order as supplied in `subset`.

Author(s)

Aaron Lun

See Also

`buildIndex`, to build an index ahead of time.

Examples

```
Y <- matrix(runif(100000), ncol=20)
out <- findNeighbors(Y, threshold=1)
summary(lengths(out$index))
```

`findResultsToMatrix` *Convert neighbor search results to alternative representations*

Description

Convert the results of various neighbor search functions to alternative representations for more convenient downstream use.

Usage

```
findResultsToMatrix(
  results,
  num.pts = NULL,
  index.transposed = FALSE,
  distance.transposed = FALSE,
  query.rows = TRUE,
```

```

    repr = "C"
  )

  findResultsToHits(
    results,
    num.pts = NULL,
    index.transposed = FALSE,
    distance.transposed = FALSE,
    query.from = TRUE
  )

  queryResultsToMatrix(
    results,
    num.pts,
    index.transposed = FALSE,
    distance.transposed = FALSE,
    query.rows = TRUE,
    repr = "C"
  )

  queryResultsToHits(
    results,
    num.pts,
    index.transposed = FALSE,
    distance.transposed = FALSE,
    query.from = TRUE
  )

```

Arguments

- | | |
|---------------------|--|
| results | <p>For <code>findResultsToMatrix</code> and <code>findResultsToHits</code>, a named list containing the output from <code>findKNN</code>, <code>findNeighbors</code> or related functions.</p> <p>For <code>queryResultsToMatrix</code> and <code>queryResultsToHits</code>, a named list containing the output from <code>queryKNN</code>, <code>queryNeighbors</code> or related functions.</p> <p>In both cases, the list should contain an <code>index</code> entry, and may optionally contain a <code>distance</code> entry.</p> |
| num.pts | <p>Integer specifying the number of data points in the X dataset (see the argument of the same name in <code>findKNN</code>, <code>queryKNN</code> and <code>friends</code>).</p> <p>For <code>findResultsToMatrix</code> and <code>findResultsToHits</code>, this can be <code>NULL</code>, in which case the number of data points is assumed to be the same as the number of query points in <code>results</code>. Note that users should specify <code>num.pts</code> if <code>subset=</code> is used in <code>findKNN</code> or related functions.</p> <p>For <code>queryResultsToMatrix</code> and <code>queryResultsToHits</code>, this is a required argument.</p> |
| index.transposed | <p>Boolean indicating whether <code>results\$index</code> is a transposed matrix, i.e., each column corresponds to a query point. This should be set to <code>TRUE</code> if <code>get.index="transposed"</code> in <code>findKNN</code> or <code>queryKNN</code>. Only relevant if <code>results\$index</code> is a matrix.</p> |
| distance.transposed | <p>Boolean indicating whether <code>results\$distance</code> is a transposed matrix, i.e., each column corresponds to a query point. This should be set to <code>TRUE</code> if <code>get.distance="transposed"</code>.</p> |

	in <code>findKNN</code> or <code>queryKNN</code> . Only relevant if <code>results\$distance</code> is present and a matrix.
<code>query.rows</code>	Boolean indicating whether query points should be represented as rows in the returned matrix.
<code>repr</code>	String specifying the type of sparse matrix, see <code>?sparseMatrix</code> for more details.
<code>query.from</code>	Boolean indicating whether query points should be stored as <code>from</code> in the returned <code>Hits</code> object.

Value

For `findResultsToMatrix` and `queryResultsToMatrix`, a sparse matrix from the **Matrix** package is returned.

- If `query.rows=TRUE`, each row corresponds to a query point and the columns with non-zero entries represent the nearest neighbors. Otherwise, each column corresponds to a query point.
- If `results` contains `distance`, the value of each non-zero entry contains the distance to that neighbor. Otherwise, a pattern matrix is returned indicating whether each entry is a nearest neighbor.

For `findResultsToHits` and `queryResultsToHits`, a `Hits` object is returned.

- If `query.from=TRUE`, `from` contains the observations and `to` contains the identities of the neighbors. Otherwise, the query points are stored in `to`.
- If `results` contains `distance`, a `distance` field will be present in `mcols`, containing the distance from each observation to each of its neighbors.

The output will be a `SelfHits` instance if `num.obs=NULL` for `findResultsToHits`.

See Also

The `colPairs` slot of the `SingleCellExperiment` class, from the **SingleCellExperiment** package.

Examples

```
X <- matrix(rnorm(10000), ncol=20)
out <- findKNN(X, k=5)
sm <- findResultsToMatrix(out)
str(sm)
sh <- findResultsToHits(out)
sh

Y <- matrix(rnorm(1000), ncol=20)
out2 <- queryKNN(query=Y, X=X, k=5)
sm2 <- queryResultsToMatrix(out2, num.pts = nrow(X))
str(sm2)
h2 <- queryResultsToHits(out2, num.pts = nrow(X))
h2
```

`getLoadGenericIndexRegistry`*Load indices from extension packages*

Description

Extend `loadIndex` to work with algorithms from **BiocNeighbors** extension packages.

Usage

```
getLoadGenericIndexRegistry()
registerLoadGenericIndexClass(name, class)
registerLoadIndexFunction(name, fun)
```

Arguments

<code>name</code>	String containing the name of the neighbor search algorithm, e.g., "knncolle::Vptree".
<code>class</code>	Function that accepts a single argument (the external pointer to a <code>knncolle::Prebuilt</code> instance) and returns an instance of the appropriate <code>BiocNeighborGenericIndex</code> subclass.
<code>fun</code>	Function that accepts a directory path (see <code>loadIndex</code>) plus any number of additional arguments via <code>...</code> , and returns an instance of the <code>BiocNeighborIndex</code> subclass corresponding to <code>name</code> .

Details

If the extension developer implements their search algorithm in the form of C++ subclasses of the various `knncolle` interfaces, they can call `getLoadGenericIndexRegistry` in their package's `.onLoad` to access the registry and add a loading method for their algorithm. They should also call `registerLoadGenericIndexClass` to specify a constructor function for the corresponding `BiocNeighborGenericIndex` subclass.

If the extension developer implements their search algorithm by subclassing **BiocNeighbors** generics at the R level, they should call `registerLoadIndexFunction` in their package's `.onLoad`. This function is responsible for reading the on-disk contents from the specified directory and using them to construct a `BiocNeighborIndex` instance.

Value

For `getLoadGenericIndexRegistry`, an external pointer to the global `knncolle::load_prebuilt_registry()` object in C++.

For `registerLoadGenericIndexClass`, the name and class are registered with `loadIndex`.

For `registerLoadIndexFunction`, the name and function are registered with `loadIndex`.

Author(s)

Aaron Lun

Examples

```
getLoadGenericIndexRegistry()
registerLoadGenericIndexClass("knncolle_annoy::Annoy", AnnoyIndex)
```

HnswParam

*The HnswParam class***Description**

A class to hold parameters for the HNSW algorithm for approximate nearest neighbor identification.

Usage

```
HnswParam(
  nlinks = 16,
  ef.construction = 200,
  ef.search = 10,
  distance = c("Euclidean", "Manhattan", "Cosine")
)

## S4 method for signature 'HnswParam'
defineBuilder(BNPARAM)
```

Arguments

nlinks	Integer scalar, number of bi-directional links per element for index generation.
ef.construction	Integer scalar, size of the dynamic list for index generation.
ef.search	Integer scalar, size of the dynamic list for neighbor searching.
distance	String specifying the distance metric to use. Cosine distances are implemented as Euclidean distances on L2-normalized coordinates.
BNPARAM	A HsnwParam instance.

Details

In the HNSW algorithm (Malkov and Yashunin, 2016), each point is a node in a “navigable small world” graph. The nearest neighbor search proceeds by starting at a node and walking through the graph to obtain closer neighbors to a given query point. Navigable small world graphs are used to maintain connectivity across the data set by creating links between distant points. This speeds up the search by ensuring that the algorithm does not need to take many small steps to move from one cluster to another. The HNSW algorithm extends this idea by using a hierarchy of such graphs containing links of different lengths, which avoids wasting time on small steps in the early stages of the search where the current node position is far from the query.

Larger values of nlinks improve accuracy at the expense of speed and memory usage. Larger values of ef.construction improve index quality at the expense of indexing time. The value of ef.search controls the accuracy of the neighbor search at run time, where larger values improve accuracy at the expense of a slower search.

Technically, the index construction algorithm is stochastic but, for various logistical reasons, the seed is hard-coded into the C++ code. This means that the results of the HNSW neighbor searches will be fully deterministic for the same inputs, even though the theory provides no such guarantees.

Value

The HnswParam constructor returns an instance of the HnswParam class.

The `defineBuilder` method returns an external pointer that can be used in `buildIndex` to construct a HNSW index.

Author(s)

Aaron Lun

See Also

[BiocNeighborParam](#), for the parent class and its available methods.

<https://github.com/nmslib/hnswlib>, for details on the underlying algorithm.

Examples

```
(out <- HnswParam())
out[['nlinks']]

out[['nlinks']] <- 20L
out
```

KmknnParam

The KmknnParam class

Description

A class to hold parameters for the k-means k-nearest-neighbors (KMKNN) algorithm for exact nearest neighbor identification.

Usage

```
KmknnParam(..., distance = c("Euclidean", "Manhattan", "Cosine"))
```

```
## S4 method for signature 'KmknnParam'
defineBuilder(BNPARAM)
```

Arguments

...	Further arguments, ignored.
distance	String specifying the distance metric to use. Cosine distances are implemented as Euclidean distances on L2-normalized coordinates.
BNPARAM	A KmknnParam instance.

Details

In the KMKNN algorithm (Wang, 2012), k-means clustering is first applied to the data points using the square root of the number of points as the number of cluster centers. The cluster assignment and distance to the assigned cluster center for each point represent the KMKNN indexing information. This speeds up the nearest neighbor search by exploiting the triangle inequality between cluster centers, the query point and each point in the cluster to narrow the search space. The advantage of the KMKNN approach is its simplicity and minimal overhead, resulting in performance improvements over conventional tree-based methods for high-dimensional data where most points need to be searched anyway. It is also trivially extended to find all neighbors within a threshold distance from a query point.

Note that KMKNN operates much more naturally with Euclidean distances. Computational efficiency may not be optimal when using it with other choices of distance, though the results will still be exact.

Value

The `KmknnParam` constructor returns an instance of the `KmknnParam` class.

The `defineBuilder` method returns a list that can be used in `buildIndex` to construct a KMKNN index.

Author(s)

Aaron Lun, using code from the **cydar** package.

References

Wang X (2012). A fast exact k-nearest neighbors algorithm for high dimensional search using k-means clustering and triangle inequality. *Proc Int Jt Conf Neural Netw*, 43, 6:2351-2358.

See Also

[BiocNeighborParam](#), for the parent class and its available methods.

Examples

```
(out <- KmknnParam(iter.max=100))
```

loadIndex

Load a prebuilt search index from disk

Description

Load a [BiocNeighborIndex](#) object from its on-disk representation back into the current R session.

Usage

```
loadIndex(dir, ...)
```

Arguments

`dir` String containing the path to a directory in which the original index was saved. This should be the same as the argument passed to [saveIndex](#).

`...` Additional arguments passed to specific methods.

Details

As discussed in [saveIndex](#), it is expected that the on-disk representation is loaded in the same R environment that was used to save it.

Developers are directed to [getLoadGenericIndexRegistry](#) to add loading functions for their own search algorithms.

Value

A [BiocNeighborIndex](#) object, created from files inside `dir`.

Author(s)

Aaron Lun

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
k.out <- buildIndex(Y)
k.nn <- findKNN(k.out, k=5)

tmp <- tempfile()
dir.create(tmp)
saveIndex(k.out, tmp)

reloaded <- loadIndex(tmp)
re.nn <- findKNN(reloaded, k=5)
identical(k.nn, re.nn)
```

queryDistanceFromIndex

Distance to the k-th nearest neighbor to query points

Description

Query a reference dataset to determine the distance to the k-th nearest neighbor of each point in a query dataset.

Usage

```
queryDistanceFromIndex(
  BNINDEX,
  query,
  k,
  num.threads = 1,
  subset = NULL,
```

```

    transposed = FALSE,
    ...
)

## S4 method for signature 'BiocNeighborGenericIndex'
queryDistanceFromIndex(
  BNINDEX,
  query,
  k,
  num.threads = 1,
  subset = NULL,
  transposed = FALSE,
  ...,
  .check.nonfinite = TRUE
)

queryDistance(
  X,
  query,
  k,
  num.threads = 1,
  ...,
  subset = NULL,
  transposed = FALSE,
  BNPARAM = NULL
)

```

Arguments

BNINDEX	A BiocNeighborIndex object, typically created by buildIndex .
query	A numeric matrix or matrix-like object of query points, containing the same number of columns as X.
k	A positive integer scalar specifying the number of nearest neighbors to retrieve. Alternatively, an integer vector of length equal to the number of points in query, specifying the number of neighbors to identify for each point. If subset is provided, this should have length equal to the length of subset. Users should wrap this vector in an AsIs class to distinguish length-1 vectors from integer scalars. All k should be less than or equal to the number of points in X, otherwise the former will be capped at the latter with a warning.
num.threads	Integer scalar specifying the number of threads to use for the search.
subset	An integer, logical or character vector indicating the rows of query (or columns, if transposed=TRUE) for which the nearest neighbors should be identified.
transposed	A logical scalar indicating whether query is transposed, in which case it contains dimensions in the rows and data points in the columns. For queryKNN, setting transposed=TRUE also indicates that X is also transposed.
...	For queryDistanceFromIndex, further arguments to pass to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., <code>vptree.foo.bar</code> . For queryDistance, further arguments to pass to queryDistanceFromIndex. These are also passed to buildIndex when X is not an external pointer.

<code>.check.nonfinite</code>	Boolean indicating whether to check for non-finite values in query. This can be set to FALSE for greater efficiency.
<code>X</code>	The reference dataset to be queried. This should be a numeric matrix or matrix-like object where rows correspond to reference points and columns correspond to variables (i.e., dimensions). Alternatively, a prebuilt BiocNeighborIndex object from buildIndex .
<code>BNPARAM</code>	A BiocNeighborParam object specifying how the index should be constructed. If NULL, this defaults to a KmknnParam . Ignored if X contains a prebuilt index.

Details

If multiple queries are to be performed to the same X, it may be beneficial to build the index from X with [buildIndex](#). The resulting pointer object can be supplied as X to multiple queryKNN calls, avoiding the need to repeat index construction in each call.

Value

Numeric vector of length equal to the number of points in query (or subset, if provided), containing the distance from each point to its k-th nearest neighbor. This is equivalent to but more memory efficient than using [queryKNN](#) and subsetting to the last distance.

Author(s)

Aaron Lun

See Also

[buildIndex](#), to build an index ahead of time.

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
Z <- matrix(rnorm(20000), ncol=20)
out <- queryDistance(Y, query=Z, k=5)
head(out)
```

queryKnnFromIndex *Query k-nearest neighbors*

Description

Query a reference dataset for the k-nearest neighbors of each point in a query dataset.

Usage

```

queryKnnFromIndex(
  BNINDEX,
  query,
  k,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  transposed = FALSE,
  ...
)

## S4 method for signature 'BiocNeighborGenericIndex'
queryKnnFromIndex(
  BNINDEX,
  query,
  k,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  transposed = FALSE,
  ...,
  .check.nonfinite = TRUE
)

queryKNN(
  X,
  query,
  k,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  transposed = FALSE,
  ...,
  BPPARAM = NULL,
  BNPARAM = NULL
)

```

Arguments

BNINDEX	A BiocNeighborIndex object, typically created by buildIndex .
query	A numeric matrix or matrix-like object of query points, containing the same number of columns as X.
k	A positive integer scalar specifying the number of nearest neighbors to retrieve. Alternatively, an integer vector of length equal to the number of points in query, specifying the number of neighbors to identify for each point. If subset is provided, this should have length equal to the length of subset. Users should wrap this vector in an AsIs class to distinguish length-1 vectors from integer scalars.

	All k should be less than or equal to the number of points in X , otherwise the former will be capped at the latter with a warning.
<code>get.index</code>	A logical scalar indicating whether the indices of the nearest neighbors should be recorded. Setting this to <code>FALSE</code> improves efficiency if the indices are not of interest. Alternatively, if k is an integer scalar, this may be a string containing "normal" or "transposed". The former is the same as <code>TRUE</code> , while the latter returns the index matrix in transposed format.
<code>get.distance</code>	A logical scalar indicating whether distances to the nearest neighbors should be recorded. Setting this to <code>FALSE</code> improves efficiency if the distances are not of interest. Alternatively, if k is an integer scalar, this may be a string containing "normal" or "transposed". The former is the same as <code>TRUE</code> , while the latter returns the distance matrix in transposed format.
<code>num.threads</code>	Integer scalar specifying the number of threads to use for the search.
<code>subset</code>	An integer, logical or character vector indicating the rows of query (or columns, if <code>transposed=TRUE</code>) for which the nearest neighbors should be identified.
<code>transposed</code>	A logical scalar indicating whether query is transposed, in which case it contains dimensions in the rows and data points in the columns. For queryKNN, setting <code>transposed=TRUE</code> also indicates that X is also transposed.
<code>...</code>	For queryKnnFromIndex, further arguments to pass to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., <code>vptree.foo.bar</code> . For queryKNN, further arguments to pass to queryKnnFromIndex. These are also passed to <code>buildIndex</code> when X is not an external pointer.
<code>.check.nonfinite</code>	Boolean indicating whether to check for non-finite values in query. This can be set to <code>FALSE</code> for greater efficiency.
<code>X</code>	The reference dataset to be queried. This should be a numeric matrix or matrix-like object where rows correspond to reference points and columns correspond to variables (i.e., dimensions). Alternatively, a prebuilt <code>BiocNeighborIndex</code> object from <code>buildIndex</code> .
<code>BPPARAM</code>	Soft-deprecated, use <code>num.threads</code> instead.
<code>BNPARAM</code>	A <code>BiocNeighborParam</code> object specifying how the index should be constructed. If <code>NULL</code> , this defaults to a <code>KmknParam</code> . Ignored if X contains a prebuilt index.

Details

If multiple queries are to be performed to the same X , it may be beneficial to build the index from X with `buildIndex`. The resulting pointer object can be supplied as X to multiple queryKNN calls, avoiding the need to repeat index construction in each call.

Value

List containing `index` (if `get.index` is not `FALSE`) and `distance` (if `get.distance` is not `FALSE`).

- If `get.index=TRUE` or "normal" and k is an integer scalar, `index` is an integer matrix with k columns where each row corresponds to a point (denoted here as i) in query. The i -th row contains the indices of points in X that are the nearest neighbors to point i , sorted by increasing distance from i .

If `get.index=FALSE` or `"transposed"` and `k` is an integer scalar, `index` is as described above but transposed, i.e., the i -th column contains the indices of neighboring points in X .

- If `get.distance=TRUE` or `"normal"` and `k` is an integer scalar, `distance` is a numeric matrix of the same dimensions as `index`. The i -th row contains the distances of neighboring points in X to the point i , sorted in increasing order.

If `get.distance=FALSE` or `"transposed"` and `k` is an integer scalar, `distance` is as described above but transposed, i.e., the i -th column contains the distances to neighboring points in X .

- If `get.index` is not `FALSE` and `k` is an integer vector, `index` is a list of integer vectors where each vector corresponds to a point (denoted here as i) in X . The i -th vector has length `k[i]` and contains the indices of points in X that are the nearest neighbors to point i , sorted by increasing distance from i .
- If `get.distance` is not `FALSE` and `k` is an integer vector, `distance` is a list of numeric vectors of the same lengths as those in `index`. The i -th vector contains the distances of neighboring points in X to the point i , sorted in increasing order.

Author(s)

Aaron Lun

See Also

[buildIndex](#), to build an index ahead of time.

[queryDistance](#), to obtain the distance from each query point to its k -th nearest neighbor.

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
Z <- matrix(rnorm(20000), ncol=20)
out <- queryKNN(Y, query=Z, k=5)
head(out$index)
head(out$distance)
```

queryNeighborsFromIndex

Query neighbors within a threshold distance

Description

Find all points in a reference dataset that lie within a threshold distance of each point in a query dataset.

Usage

```
queryNeighborsFromIndex(
  BNINDEX,
  query,
  threshold,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
```

```

subset = NULL,
transposed = FALSE,
...
)

## S4 method for signature 'BiocNeighborGenericIndex'
queryNeighborsFromIndex(
  BNINDEX,
  query,
  threshold,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  transposed = FALSE,
  ...,
  .check.nonfinite = TRUE
)

queryNeighbors(
  X,
  query,
  threshold,
  get.index = TRUE,
  get.distance = TRUE,
  num.threads = 1,
  subset = NULL,
  transposed = FALSE,
  ...,
  BPPARAM = NULL,
  BNPARAM = NULL
)

```

Arguments

BNINDEX	A BiocNeighborIndex object, typically created by buildIndex .
query	A numeric matrix or matrix-like object of query points, containing the same number of columns as X.
threshold	A positive numeric scalar specifying the maximum distance at which a point is considered a neighbor. Alternatively, a vector containing a different distance threshold for each query point.
get.index	A logical scalar indicating whether the indices of the neighbors should be recorded.
get.distance	A logical scalar indicating whether distances to the neighbors should be recorded.
num.threads	Integer scalar specifying the number of threads to use for the search.
subset	An integer, logical or character vector indicating the rows of query (or columns, if transposed=TRUE) for which the nearest neighbors should be identified.
transposed	A logical scalar indicating whether query is transposed, in which case it contains dimensions in the rows and data points in the columns. For queryKNN, setting transposed=TRUE also indicates that X is also transposed.

...	For queryNeighborsFromIndex, further arguments to pass to individual methods. If a method accepts arguments here, it should prefix these arguments with the algorithm name to avoid conflicts, e.g., vptree.foo.bar. For queryNeighbors, further arguments to pass to queryNeighborsFromIndex. These are also passed to buildIndex when X is not an external pointer.
.check.nonfinite	Boolean indicating whether to check for non-finite values in query. This can be set to FALSE for greater efficiency.
X	The reference dataset to be queried. This should be a numeric matrix or matrix-like object where rows correspond to reference points and columns correspond to variables (i.e., dimensions). Alternatively, a prebuilt BiocNeighborIndex object from buildIndex .
BPPARAM	Soft-deprecated, use num.threads instead.
BNPARAM	A BiocNeighborParam object specifying how the index should be constructed. If NULL, this defaults to a KmknnParam . Ignored if X contains a prebuilt index.

Details

This function identifies all points in X that within threshold of each point in query. For Euclidean distances, this is equivalent to identifying all points in a hypersphere centered around the point of interest. Not all implementations support this search mode, but we can use [KmknnParam](#) and [VptreeParam](#).

If threshold is a vector, each entry is assumed to specify a (possibly different) threshold for each point in query. If subset is also specified, each entry is assumed to specify a threshold for each point in subset. An error will be raised if threshold is a vector of incorrect length.

If multiple queries are to be performed to the same X, it may be beneficial to build the index from X with [buildIndex](#). The resulting pointer object can be supplied as X to multiple queryKNN calls, avoiding the need to repeat index construction in each call.

Value

A list is returned containing:

- index, if get.index=TRUE. This is a list of integer vectors where each entry corresponds to a point (denoted here as *i*) in query. The vector for *i* contains the set of row indices of all points in X that lie within threshold of point *i*. Neighbors for *i* are sorted by increasing distance from *i*.
- distance, if get.distance=TRUE. This is a list of numeric vectors where each entry corresponds to a point (as above) and contains the distances of the neighbors from *i*. Elements of each vector in distance match to elements of the corresponding vector in index.

If both get.index=FALSE and get.distance=FALSE, an integer vector is returned of length equal to the number of observations. The *i*-th entry contains the number of neighbors of *i* within threshold.

If subset is not NULL, each entry of the above vector/lists refers to a point in the subset, in the same order as supplied in subset.

Author(s)

Aaron Lun

See Also

[buildIndex](#), to build an index ahead of time.

Examples

```
Y <- matrix(rnorm(100000), ncol=20)
Z <- matrix(rnorm(20000), ncol=20)
out <- queryNeighbors(Y, query=Z, threshold=3)
summary(lengths(out$index))
```

saveIndex	<i>Save a nearest-neighbor index</i>
-----------	--------------------------------------

Description

Save an index for nearest-neighbor searching to disk.

Usage

```
saveIndex(BNINDEX, dir, ...)
```

S4 method for signature 'BiocNeighborGenericIndex'

```
saveIndex(BNINDEX, dir, ...)
```

Arguments

BNINDEX	A BiocNeighborIndex object representing a pre-built index, typically from buildIndex .
dir	String containing the path to a directory in which to save the index. This directory should already exist.
...	Further arguments to pass to specific methods.

Details

Files generated by `saveIndex` are not guaranteed to be portable across architectures, compilers, or even versions of **BiocNeighbors**. An index saved in this manner is only intended to be read back to the same R environment on the same machine.

Value

One or more files are created on disk inside `dir`. These can be used to reconstitute `BNINDEX` by calling [loadIndex](#).

Author(s)

Aaron Lun

Examples

```

Y <- matrix(rnorm(100000), ncol=20)
k.out <- buildIndex(Y)

tmp <- tempfile()
dir.create(tmp)
saveIndex(k.out, tmp)
list.files(tmp, recursive=TRUE)

```

VptreeParam

*The VptreeParam class***Description**

A class to hold parameters for the vantage point (VP) tree algorithm for exact nearest neighbor identification.

Usage

```

VptreeParam(distance = c("Euclidean", "Manhattan", "Cosine"))

## S4 method for signature 'VptreeParam'
defineBuilder(BNPARAM)

```

Arguments

distance	String specifying the distance metric to use. Cosine distances are implemented as Euclidean distances on L2-normalized coordinates.
BNPARAM	A VptreeParam instance.

Details

In a VP tree (Yianilos, 1993), each node contains a subset of points that is split into two further partitions. The split is determined by picking an arbitrary point inside that subset as the node center, computing the distance to all other points from the center, and taking the median as the “radius”. The left child of this node contains all points within the median distance from the radius, while the right child contains the remaining points. This is applied recursively until all points resolve to individual nodes. The nearest neighbor search traverses the tree and exploits the triangle inequality between query points, node centers and thresholds to narrow the search space.

VP trees are often faster than more conventional KD-trees or ball trees as the former uses the points themselves as the nodes of the tree, avoiding the need to create many intermediate nodes and reducing the total number of distance calculations. Like KMKNN, it is also trivially extended to find all neighbors within a threshold distance from a query point.

Value

The VptreeParam constructor returns an instance of the VptreeParam class.

The `defineBuilder` method returns an external pointer that can be used in `buildIndex` to construct a VP tree index.

Author(s)

Aaron Lun

References

Yianilos PN (1993). Data structures and algorithms for nearest neighbor search in general metric spaces. *Proceedings of the Fourth Annual ACM-SIAM Symposium on Discrete Algorithms*, 311-321.

See Also

[BiocNeighborParam](#), for the parent class and its available methods.

<https://stevehanov.ca/blog/index.php?id=130>, for a description of the algorithm.

Examples

```
(out <- VptreeParam())
```

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