Package 'simplextree'

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Type Package

Title Provides Tools for Working with General Simplicial Complexes

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Description Provides an interface to a Simplex Tree data structure, which is
a data structure aimed at enabling efficient manipulation of simplicial complexes
of any dimension. The Simplex Tree data structure was originally introduced by
Jean-Daniel Boissonnat and Clément Maria (2014) <doi:10.1007/s00453-014-9887-3>.

Language en-US

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URL https://github.com/peekxc/simplextree

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Contents

simplextree-package *simplextree package*

Description

Provides an R/Rcpp implementation of a Simplex Tree data structure and its related tools.

Details

This package provides a lightweight implementation of a Simplex Tree data structure, exported as an Rcpp Module. The current implementation provides a limited API and a subset of the functionality described in the paper.

Author(s)

Matt Piekenbrock

adjacent *Adjacent vertices.*

Description

Returns a vector of vertex ids that are immediately adjacent to a given vertex.

Usage

```
adjacent(st, vertices)
```

Arguments

st	a simplex tree.
vertices	vertex ids.

Examples

```
st <- simplex_tree(1:3)
st %>% adjacent(2)
# 1 3
```

as.list.st_traversal *as.list.st_traversal*

Description

as.list.st_traversal

Usage

```
## S3 method for class 'st_traversal'
as.list(x, ...)
```

Arguments

x	traversal object.
...	unused.

clear *Clears the simplex tree*

Description

Removes all simplices from the simplex tree, except the root node.

Usage

```
clear(st)
```

Arguments

st	a simplex tree object.

Examples

```
st <- simplex_tree()
st %>% insert(1:3)
print(st) ## Simplex Tree with (3, 3, 1) (0, 1, 2)-simplices
st %>% clear()
print(st) ## < empty simplex tree >
```

clone *Clones the given simplex tree.*

Description

Performs a deep-copy on the supplied simplicial complex.

Usage

```
clone(st)
```

Arguments

st	a simplex tree.

cofaces *Generates a coface traversal on the simplex tree.*

Description

Generates a coface traversal on the simplex tree.

Usage

```
cofaces(st, sigma)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

coface_roots *Generates a coface roots traversal on the simplex tree.*

Description

The coface roots of a given simplex sigma are the roots of subtrees in the trie whose descendents (including the roots themselves) are cofaces of sigma. This traversal is more useful when used in conjunction with other traversals, e.g. a *preorder* or *level_order* traversal at the roots enumerates the cofaces of sigma.

Usage

```
coface_roots(st, sigma)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

---

collapse *Elementary collapse*

Description

Performs an elementary collapse.

Usage

```
collapse(st, pair, w = NULL)
```

Arguments

st	a simplex tree.
pair	list of simplices to collapse.
w	vertex to collapse to, if performing a vertex collapse.

Details

This function provides two types of *elementary collapses*.

The first type of collapse is in the sense described by (1), which is summarized here. A simplex σ is said to be collapsible through one of its faces τ if σ is the only coface of τ (excluding τ itself). This function checks whether its possible to collapse σ through τ, (if τ has σ as its only coface), and if so, both simplices are removed. `tau` and `sigma` are sorted before comparison. To perform this kind of elementary collapse, call `collapse` with two simplices as arguments, i.e. `tau` before `sigma`.

Alternatively, this method supports another type of elementary collapse, also called a *vertex collapse*, as described in (2). This type of collapse maps a pair of vertices into a single vertex. To use this collapse, specify three vertex ids, the first two representing the free pair, and the last representing the target vertex to collapse to.

Value

boolean indicating whether the collapse was performed.

References

1. Boissonnat, Jean-Daniel, and Clement Maria. "The simplex tree: An efficient data structure for general simplicial complexes." Algorithmica 70.3 (2014): 406-427.

2. Dey, Tamal K., Fengtao Fan, and Yusu Wang. "Computing topological persistence for simplicial maps." Proceedings of the thirtieth annual symposium on Computational geometry. ACM, 2014.

Examples

```
st <- simplextree::simplex_tree(1:3)
st %>% print_simplices()
# 1, 2, 3, 1 2, 1 3, 2 3, 1 2 3
st %>% collapse(list(1:2, 1:3))
# 1, 2, 3, 1 3, 2 3=

st %>% insert(list(1:3, 2:5))
st %>% print_simplices("column")
# 1 2 3 4 5 1 1 2 2 2 3 3 4 1 2 2 2 3 2
#           2 3 3 4 5 4 5 5 2 3 3 4 4 3
#                           3 4 5 5 5 4
#                                     5

st %>% collapse(list(2:4, 2:5))
st %>% print_simplices("column")
# 1 2 3 4 5 1 1 2 2 2 3 3 4 1 2 2 3
#           2 3 3 4 5 4 5 5 2 3 4 4
#                           3 5 5 5
```

`contract` *Edge contraction*

Description

Performs an edge contraction.

Usage

```
contract(st, edge)
```

Arguments

`st`	a simplex tree.
`edge`	an edge to contract, as a 2-length vector.

Details

This function performs an *edge contraction* in the sense described by (1), which is summarized here. Given an edge va, vb, vb is contracted to va if vb is removed from the complex and the link of va is augmented with the link of vb. This may be thought as applying the mapping:

$$f(u) = va$$

if $u = vb$ and identity otherwise, to all simplices in the complex.
`edge` is **not** sorted prior to contraction: the second vertex of the edge is always contracted to the first. Note that edge contraction is not symmetric.

References

1. Boissonnat, Jean-Daniel, and Clement Maria. "The simplex tree: An efficient data structure for general simplicial complexes." Algorithmica 70.3 (2014): 406-427.

Examples

```
st <- simplex_tree(1:3)
st %>% print_simplices()
# 1, 2, 3, 1 2, 1 3, 2 3, 1 2 3
st %>% contract(c(1, 3)) %>% print_simplices()
# 1, 2, 1 2
```

`degree` *The vertex degree.*

Description

Returns the number of edges (degree) for each given vertex id.

Usage

```
degree(st, vertices)
```

Arguments

`st`	a simplex tree.
`vertices`	the vertex ids to check the degree of.

`deserialize` *Deserializes the simplex tree.*

Description

Provides a compressed serialization interface for the simplex tree.

Usage

```
deserialize(complex, st = NULL)
```

Arguments

`complex`	The result of `serialize`.
`st`	optionally, the simplex tree to insert into. Otherwise a new one is created.

Details

The serialize/deserialize commands can be used to compress/uncompress the complex into smaller form amenable for e.g. storing on disk (see `saveRDS`) or saving for later use.

See Also

Other serialization: `serialize()`

`empty_face` *empty_face*

Description

Alias to the empty integer vector (integer(0L)). Used to indicate the empty face of the tree.

Usage

```
empty_face
```

Format

An object of class `integer` of length 0.

See Also

traverse

`enclosing_radius` *enclosing_radius*

Description

Computes the enclosing radius of a set of distances.

Usage

```
enclosing_radius(d)
```

Arguments

`d`	a `dist` object.

Details

The enclosing radius is useful as an upper bound of the scale parameter for the rips filtration. Scales above the enclosing radius render the Vietoris–Rips complex as a simplicial cone, beyond which the homology is trivial.

expand *k-expansion.*

Description

Performs a k-expansion on the 1-skeleton of the complex, adding k-simplices if all combinations of edges are included. Because this operation uses the edges alone to infer the existence of higher order simplices, the expansion assumes the underlying complex is a flag complex.

Usage

```
expand(st, k = 2)
```

Arguments

st	a simplex tree.
k	the target dimension of the expansion.

faces *Generates a face traversal on the simplex tree.*

Description

Generates a face traversal on the simplex tree.

Usage

```
faces(st, sigma)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

`find` *Find simplices*

Description

Returns whether supplied simplices exist in the complex.

Usage

```
find(st, simplices)
```

Arguments

`st`	a simplex tree.
`simplices`	simplices to insert, either as a vector, a list of vectors, or a column-matrix. See details.

Details

Traverses the simplex tree looking for `simplex`, returning whether or not it exists. `simplex` can be specified as vector to represent a single simplex, and a list to represent a set of simplices. Each `simplex` is sorted before traversing the trie.

If `simplices` is a vector, it's assumed to be a simplex. If a list, its assumed each element in the list represents a simplex (as vectors). If the simplices to insert are all of the same dimension, you can also optionally use a matrix, where each column is assumed to be a simplex.

Value

boolean indicating whether or not `simplex` exists in the tree.

Usage

st

See Also

insert remove

`flag` *flag*

Description

Creates a filtration of flag complexes

Usage

```
flag(st, d)
```

Arguments

`st`	a simplex tree. See details.
`d`	a vector of edge weights, or a 'dist' object.

Details

A flag complex is a simplicial complex whose k-simplices for k >= 2 are completely determined by edges/graph of the complex. This function creates filtered simplicial complex using the supplied edge weights. The resulting complex is a simplex tree object endowed with additional structure; see. Vertices have their weights set to 0, and k-simplices w/ k >= 2 have their weights set to the maximum weight of any of its edges.

`generate_ids` *Generates vertex ids.*

Description

Generates vertex ids representing 0-simplices not in the tree.

Usage

```
generate_ids(st, n)
```

Arguments

`st`	a simplex tree.
`n`	the number of ids to generate.

Details

This function generates new vertex ids for use in situations which involve generating new new 0-simplices, e.g. insertions, contractions, collapses, etc. There are two 'policies' which designate the generating mechanism of these ids: 'compressed' and 'unique'. 'compressed' generates vertex ids sequentially, starting at 0. 'unique' tracks an incremental internal counter, which is updated on every call to `generate_ids`. The new ids under the 'unique' policy generates the first sequential `n` ids that are strictly greater `max`(*counter*, *max vertex id*).

Examples

```
st <- simplex_tree()
print(st$id_policy)
## "compressed"
st %>% generate_ids(3)
## 0 1 2
st %>% generate_ids(3)
## 0 1 2
st %>% insert(list(1,2,3))
print(st$vertices)
## 1 2 3
st %>% insert(as.list(st %>% generate_ids(2)))
st %>% print_simplices()
# 0, 1, 2, 3, 4
st %>% remove(4)
st %>% generate_ids(1)
# 4
```

`insert` *Insert simplices*

Description

Inserts simplices into the simplex tree. Individual simplices are specified as vectors, and a set of simplices as a list of vectors.

Usage

```
insert(st, simplices)
```

Arguments

`st`	a simplex tree.
`simplices`	simplices to insert, either as a vector, a list of vectors, or a column-matrix. See details.

Details

This function allows insertion of arbitrary order simplices. If the simplex already exists in the tree, no insertion is made, and the tree is not modified. `simplex` is sorted before traversing the trie. Faces of `simplex` not in the simplex tree are inserted as needed.

If `simplices` is a vector, it's assumed to be a simplex. If a list, its assumed each element in the list represents a simplex (as vectors). If the simplices to insert are all of the same dimension, you can also optionally use a matrix, where each column is assumed to be a simplex.

See Also

find remove

Examples

```
st <- simplex_tree()
st %>% insert(1:3) ## inserts the 2-simplex { 1, 2, 3 }
st %>% insert(list(4:5, 6)) ## inserts a 1-simplex { 4, 5 } and a 0-simplex { 6 }.
st %>% insert(combn(5,3)) ## inserts all the 2-faces of a 4-simplex
```

---

inverse.choose *inverse.choose*

Description

Inverts the binomial coefficient for general (n,k).

Usage

```
inverse.choose(x, k)
```

Arguments

x	the binomial coefficient.
k	the denominator of the binomial coefficient x.

Details

Given a quantity x = choose(n, k) with fixed k, finds n.

Value

the numerator of the binomial coefficient, if the Otherwise

Examples

```
100 == inverse.choose(choose(100,2), k = 2)
# TRUE
12345 == inverse.choose(choose(12345, 5), k = 5)
# TRUE
```

`is_face` *Is face*

Description

Checks whether a simplex is a face of another simplex and is in the complex.

Usage

```
is_face(st, tau, sigma)
```

Arguments

`st`	a simplex tree.
`tau`	a simplex which may contain `sigma` as a coface.
`sigma`	a simplex which may contain `tau` as a face.

Details

A simplex τ is a face of σ if $\tau \subset \sigma$. This function checks whether that is true. `tau` and `sigma` are sorted before comparison.

Value

boolean indicating whether `tau` is a face of `sigma`.

See Also

std::includes

Examples

```
st <- simplex_tree()
st %>% insert(1:3)
st %>% is_face(2:3, 1:3)
st %>% is_face(1:3, 2:3)
```

is_tree *Checks if the simplicial complex is a tree.*

Description

This function performs a breadth-first search on the simplicial complex, checking if the complex is acyclic.

Usage

```
is_tree(st)
```

Arguments

st	a simplex tree.

Examples

```
st <- simplex_tree()
st %>% insert(list(1:2, 2:3))
st %>% is_tree() # true
st %>% insert(c(1, 3))
st %>% is_tree() # false
```

k_simplices *Generates a traversal on the k-simplices of the simplex tree.*

Description

Generates a traversal on the k-simplices of the simplex tree.

Usage

```
k_simplices(st, k, sigma = NULL)
```

Arguments

st	the simplex tree to traverse.
k	the dimension of the skeleton to include.
sigma	simplex to start the traversal at.

k_skeleton *Generates a k-skeleton traversal on the simplex tree.*

Description

Generates a k-skeleton traversal on the simplex tree.

Usage

```
k_skeleton(st, k, sigma = NULL)
```

Arguments

st	the simplex tree to traverse.
k	the dimension of the skeleton to include.
sigma	simplex to start the traversal at.

level_order *Generates a level order traversal on the simplex tree.*

Description

Generates a level order traversal on the simplex tree.

Usage

```
level_order(st, sigma = NULL)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

link *Generates a traversal on the link of a given simplex in the simplex tree.*

Description

Generates a traversal on the link of a given simplex in the simplex tree.

Usage

```
link(st, sigma)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

maximal *Generates a traversal on the maximal of the simplex tree.*

Description

Generates a traversal on the maximal of the simplex tree.

Usage

```
maximal(st, sigma = NULL)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

nat_to_sub *nat_to_sub*

Description

Computes the x^th (n choose 2) combination.

Usage

```
nat_to_sub(x, n, k)
```

Arguments

x	non-negative integers in the range c(1, choose(n, k))
n	numerator of the binomial coefficient
k	denominator of the binomial coefficient

Details

The mapping is done via an lexicographically-ordered combinadic mapping.
In general, this function is *not* intended to be used to *generate* all (n choose k) combinations in the combinadic mapping.

Value

integer matrix whose columns give the combinadics of x.

References

McCaffrey, J. D. "Generating the mth lexicographical element of a mathematical combination." MSDN Library (2004).

Examples

```
library(simplextree)
all(nat_to_sub(seq(choose(100,2)), n = 100, k = 2) == combn(100,2))

## Generating pairwise combinadics is particularly fast
## Below: test to generate ~ 45k combinadics (note: better to use microbenchmark)
system.time({
  x <- seq(choose(300,2))
  nat_to_sub(x, n = 300, k = 2L)
})

## Compare with generating raw combinations
system.time(combn(300,2))
```

nerve *nerve*

Description

Compute the nerve of a given cover.

Usage

```
nerve(st, cover, k = st$dimension, threshold = 1L, neighborhood = NULL)
```

Arguments

st	a simplex tree.
cover	list of integers indicating set membership. See details.
k	max simplex dimension to consider.
threshold	the number of elements in common for k sets to be considered intersecting. Defaults to 1.
neighborhood	which combinations of sets to check. See details.

Details

This computes the nerve of a given cover, adding a *k*-simplex for each combination of *k+1* sets in the given cover that have at least threshold elements in their common intersection.

If neighborhood is supplied, it can be either 1) a matrix, 2) a list, or 3) a function. Each type parameterizes which sets in the cover need be checked for to see if they have at least threshold elements in their common intersection. If a matrix is supplied, the columns should indicate the indices of the cover to check (e.g if neighborhood = matrix(c(1,2), nrow = 2), then only the first two sets of cover are tested.). Similarly, if a list is supplied, each element in the list should give the indices to test.

The most flexible option is supplying a function to neighborhood. If a function is passed, it's assumed to accept an integer vector of *k* indices (of the cover) and return a boolean indicating whether or not to *test* if they have at least threshold elements in their common intersection. This can be used to filter out subsets of the cover the user knows are The indices are generated using the same code that performs expand.

plot.Rcpp_Filtration *plot.Rcpp_Filtration*

Description

plot.Rcpp_Filtration

Usage

```
## S3 method for class 'Rcpp_Filtration'
plot(...)
```

Arguments

`...`	passed to `plot.Rcpp_SimplexTree`

Functions

- `plot.Rcpp_Filtration`: family of plotting methods.

plot.simplextree *Plots the simplex tree*

Description

Plots the simplex tree

Usage

```
## S3 method for class 'Rcpp_SimplexTree'
plot(
  x,
  coords = NULL,
  vertex_opt = NULL,
  text_opt = NULL,
  edge_opt = NULL,
  polygon_opt = NULL,
  color_pal = NULL,
  maximal = TRUE,
  by_dim = TRUE,
  add = FALSE,
  ...
)
```

Arguments

x	a simplex tree.
coords	Optional (n x 2) matrix of coordinates, where n is the number of 0-simplices.
vertex_opt	Optional parameters to modify default vertex plotting options. Passed to points.
text_opt	Optional parameters to modify default vertex text plotting options. Passed to text.
edge_opt	Optional parameters to modify default edge plotting options. Passed to segments.
polygon_opt	Optional parameters to modify default k-simplex plotting options for k > 1. Passed to polygon.
color_pal	Optional vector of colors. See details.
maximal	Whether to draw only the maximal faces of the complex. Defaults to true.
by_dim	Whether to apply (and recycle or truncate) the color palette to the dimensions rather than to the individual simplices. Defaults to true.
add	Whether to add to the plot or redraw. Defaults to false. See details.
...	unused

Details

This function allows generic plotting of simplicial complexes using base graphics.
If not (x,y) coordinates are supplied via coords, a default layout is generated via phyllotaxis arrangement. This layout is not in general does not optimize the embedding towards any usual visualization criteria e.g. it doesn't try to separate connected components, minimize the number of crossings, etc. For those, the user is recommended to look in existing code graph drawing libraries, e.g. igraphs 'layout.auto' function, etc. The primary benefit of the default phyllotaxis arrangement is that it is deterministic and fast to generate.
All parameters passed via list to vertex_opt, text_opt, edge_opt, polygon_opt override default parameters and are passed to points, text, segments, and polygon, respectively.

If add is true, the plot is not redrawn.

If maximal is true, only the maximal simplices are drawn.

The color_pal argument controls how the simplicial complex is colored. It can be specified in multiple ways.

1. A vector of colors of length *dim+1*, where *dim*=x$dimension
2. A vector of colors of length *n*, where *n*=sum(x$n_simplices)
3. A named list of colors

Option (1) assigns every simplex a color based on its dimension.

Option (2) assigns each individual simplex a color. The vector must be specified in level-order (see ltraverse or examples below).

Option (3) allows specifying individual simplices to draw. It expects a named list, where the names

must correspond to simplices in x as comma-separated strings and whose values are colors. If option (3) is specified, this method will *only* draw the simplices given in color_pal.

If length(color_pal) does not match the dimension or the number of simplices in the complex, the color palette is recyled and simplices are as such.

Examples

```
## Simple 3-simplex
st <- simplex_tree() %>% insert(list(1:4))

## Default is categorical colors w/ diminishing opacity
plot(st)

## If supplied colors have alpha defined, use that
vpal <- rainbow(st$dimension + 1)
plot(st, color_pal = vpal)

## If alpha not supplied, decreasing opacity applied
plot(st, color_pal = substring(vpal, first=1, last=7))

## Bigger example; observe only maximal faces (+vertices and edges) are drawn
st <- simplex_tree(list(1:3, 2:5, 5:9, 7:8, 10))
plot(st, color_pal = rainbow(st$dimension + 1))

## If maximal == FALSE, every simplex is drawn (even on top of each other)
vpal <- rainbow(st$dimension + 1)[c(1,2,5,4,3)]
pal_alpha <- c(1, 1, 0.2, 0.35, 0.35)
vpal <- sapply(seq_along(vpal), function(i) adjustcolor(vpal[i], alpha.f = pal_alpha[i]))
plot(st, color_pal = vpal, maximal = FALSE)

## You can also color each simplex individually by supplying a vector
## of the same length as the number of simplices.
plot(st, color_pal = sample(rainbow(sum(st$n_simplices))))

## The order is assumed to follow the level order traversal (first 0-simplices, 1-, etc.)
## This example colors simplices on a rainbow gradient based on the sum of their labels
si_sum <- straverse(st %>% level_order, sum)
rbw_pal <- rev(rainbow(50, start=0,end=4/6))
plot(st, color_pal=rbw_pal[cut(si_sum, breaks=50, labels = FALSE)])

## This also makes highlighting simplicial operations fairly trivial
four_cofaces <- as.list(cofaces(st, 4))
coface_pal <- straverse(level_order(st), function(simplex){
    ifelse(list(simplex) %in% four_cofaces, "orange", "blue")
})
plot(st, color_pal=unlist(coface_pal))

## You can also give a named list to draw individual simplices.
## **Only the maximal simplices in the list are drawn**
blue_vertices <- structure(as.list(rep("blue", 5)), names=as.character(seq(5, 9)))
plot(st, color_pal=append(blue_vertices, list("5,6,7,8,9"="red")))
```

preorder *Generates a preorder traversal on the simplex tree.*

Description

Generates a preorder traversal on the simplex tree.

Usage

```
preorder(st, sigma = NULL)
```

Arguments

st	the simplex tree to traverse.
sigma	simplex to start the traversal at.

print.st_traversal *print.st_traversal*

Description

print.st_traversal

Usage

```
## S3 method for class 'st_traversal'
print(x, ...)
```

Arguments

x	traversal object.
...	unused.

`print_simplices` *Print simplices to the console*

Description

Prints simplices in a formatted way

Prints a traversal, a simplex tree, or a list of simplices to the R console, with options to customize how the simplices are printed. The `format` must be one of "summary", "tree", "cousins", "short", "column", or "row", with the default being "short". In general, the "tree" and "cousins" format give more details on the structure of the trie, whereas the other formats just change how the given set of simplices are formatted.
The "tree" method prints the nodes grouped by the same last label and indexed by depth. The printed format is:

[vertex] (h = [subtree height]): [subtree depth]([subtree])

Where each lists the top node (*vertex*) and its corresponding subtree. The *subtree height* displays the highest order k-simplex in that subtree. Each level in the subtree tree is a set of sibling k-simplices whose order is given by the number of dots ('.') proceeding the print level.

The "cousin" format prints the simplex relations used by various algorithms to speed up finding adjacencies in the complex. The cousins are grouped by label and depth.
The format looks like:
(last=[label], depth=[depth of label]): [simplex]

This function is useful for understanding how the simplex tree is stored, and for debugging purposes.

Usage

```
print_simplices(
  st,
  format = c("summary", "tree", "cousins", "short", "column", "row")
)
```

Arguments

`st`	a simplex tree.
`format`	the choice of how to format the printing. See details.

reindex *reindexes vertex ids*

Description

This function allows one to 'reorder' or 'reindex' vertex ids.

Usage

```
reindex(st, ids)
```

Arguments

st	a simplex tree.
ids	vector of new vertex ids. See details.

Details

The ids parameter must be a sorted integer vector of new ids with length matching the number of vertices. The simplex tree is modified to replace the vertex label at index i with ids[i]. See examples.

Examples

```
st <- simplex_tree()
st %>% insert(1:3) %>% print_simplices("tree")
# 1 (h = 2): .( 2 3 )..( 3 )
# 2 (h = 1): .( 3 )
# 3 (h = 0):
st %>% reindex(4:6) %>% print_simplices("tree")
# 4 (h = 2): .( 5 6 )..( 6 )
# 5 (h = 1): .( 6 )
# 6 (h = 0):
```

remove *Remove simplices*

Description

Removes simplices from the simplex tree. Individual simplices are specified as vectors, and a set of simplices as a list of vectors.

Usage

```
remove(st, simplices)
```

Arguments

st	a simplex tree.
simplices	simplices to insert, either as a vector, a list of vectors, or a column-matrix. See details.

Details

This function allows removal of a arbitrary order simplices. If simplex already exists in the tree, it is removed, otherwise the tree is not modified. simplex is sorted before traversing the trie. Cofaces of simplex are also removed.

If simplices is a vector, it's assumed to be a simplex. If a list, its assumed each element in the list represents a simplex (as vectors). If the simplices to insert are all of the same dimension, you can also optionally use a matrix, where each column is assumed to be a simplex.

See Also

find remove

---

rips *rips*

Description

Constructs the Vietoris-Rips complex.

Usage

```
rips(d, eps = enclosing_radius(d), dim = 1L, filtered = FALSE)
```

Arguments

d	a numeric 'dist' vector.
eps	diameter parameter.
dim	maximum dimension to construct up to. Defaults to 1 (edges only).
filtered	whether to construct the filtration. Defaults to false. See details.

`serialize` *Serializes the simplex tree.*

Description

Provides a compressed serialization interface for the simplex tree.

Usage

```
serialize(st)
```

Arguments

`st`	a simplex tree.

Details

The serialize/deserialize commands can be used to compress/uncompress the complex into smaller form amenable for e.g. storing on disk (see `saveRDS`) or saving for later use. The serialization.

See Also

Other serialization: `deserialize()`

Examples

```
st <- simplex_tree(list(1:5, 7:9))
st2 <- deserialize(serialize(st))
all.equal(as.list(preorder(st)), as.list(preorder(st2)))
# TRUE

set.seed(1234)
R <- rips(dist(replicate(2, rnorm(100))), eps = pnorm(0.10), dim = 2)
print(R$n_simplices)
# 100 384 851

## Approx. size of the full complex
print(utils::object.size(as.list(preorder(R))), units = "Kb")
# 106.4 Kb

## Approx. size of serialized version
print(utils::object.size(serialize(R)), units = "Kb")
# 5.4 Kb
## You can save these to disk via e.g. saveRDS(serialize(R), ...)
```

`simplex_tree` *Simplex Tree*

Description

Simplex tree class exposed as an Rcpp Module.

Usage

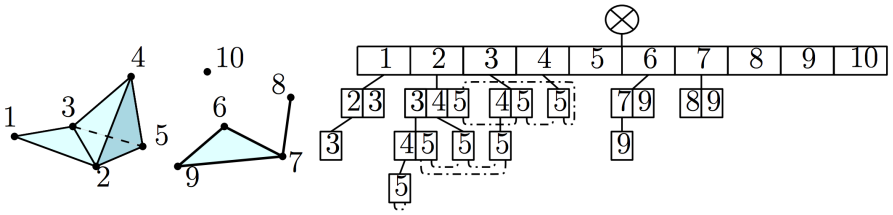
```
simplex_tree(simplices = NULL)
```

Arguments

`simplices`	optional simplices to initialize the simplex tree with. See `insert`.

Details

A simplex tree is an ordered trie-like structure specialized for storing and doing general computation simplicial complexes. Here is figure of a simplex tree, taken from the original paper (see 1):



The current implementation provides a subset of the functionality described in the paper.

Value

A queryable simplex tree, as a `Rcpp_SimplexTree` object (Rcpp module).

Fields

`n_simplices` A vector, where each index k denotes the number (k-1)-simplices.

`dimension` The dimension of the simplicial complex.

Properties

Properties are actively bound shortcuts to various methods of the simplex tree that may be thought of as fields. Unlike fields, however, properties are not explicitly stored: they are generated on access.

`$id_policy` The policy used to generate new vertex ids. May be assigned "compressed" or "unique". See `generate_ids`.

`$vertices` The 0-simplices of the simplicial complex, as a matrix.

`$edges` The 1-simplices of the simplicial complex, as a matrix.

$triangles The 2-simplices of the simplicial complex, as a matrix.

$quads The 3-simplices of the simplicial complex, as a matrix.

$connected_components The connected components of the simplicial complex.

Methods

$as_XPtr Creates an external pointer.

$clear Clears the simplex tree.

$generate_ids Generates new vertex ids according to the set policy.

$degree Returns the degree of each given vertex.

$adjacent Returns vertices adjacent to a given vertex.

$insert Inserts a simplex into the trie.

$remove Removes a simplex from the trie.

$find Returns whether a simplex exists in the trie.

$collapse Performs an elementary collapse.

$contract Performs an edge contraction.

$expand Performs an k-expansion.

$traverse Traverses a subset of the simplex tree, applying a function to each simplex.

$ltraverse Traverses a subset of the simplex tree, applying a function to each simplex and returning the result as a list.

$is_face Checks for faces.

$is_tree Checks if the simplicial complex is a tree.

$as_list Converts the simplicial complex to a list.

$as_adjacency_matrix Converts the 1-skeleton to an adjacency matrix.

$as_adjacency_list Converts the 1-skeleton to an adjacency list.

$as_edgelist Converts the 1-skeleton to an edgelist.

Author(s)

Matt Piekenbrock

References

Boissonnat, Jean-Daniel, and Clement Maria. "The simplex tree: An efficient data structure for general simplicial complexes." Algorithmica 70.3 (2014): 406-427.

Examples

```
## Recreating simplex tree from figure.
st <- simplex_tree()
st %>% insert(list(1:3, 2:5, c(6, 7, 9), 7:8, 10))
plot(st)

## Example insertion
```

```
st <- simplex_tree(list(1:3, 4:5, 6)) ## Inserts one 2-simplex, one 1-simplex, and one 0-simplex
print(st)
# Simplex Tree with (6, 4, 1) (0, 1, 2)-simplices

## More detailed look at structure
print_simplices(st, "tree")
# 1 (h = 2): .( 2 3 )..( 3 )
# 2 (h = 1): .( 3 )
# 3 (h = 0):
# 4 (h = 1): .( 5 )
# 5 (h = 0):
# 6 (h = 0):
## Print the set of simplices making up the star of the simplex '2'
print_simplices(st %>% cofaces(2))
# 2, 2 3, 1 2, 1 2 3

## Retrieves list of all simplices in DFS order, starting with the empty face
dfs_list <- ltraverse(st %>% preorder(empty_face), identity)

## Get connected components
print(st$connected_components)
# [1] 1 1 1 4 4 5

## Use clone() to make copies of the complex (don't use the assignment `<-`)
new_st <- st %>% clone()

## Other more internal methods available via `$`
list_of_simplices <- st$as_list()
adj_matrix <- st$as_adjacency_matrix()
# ... see also as_adjacency_list(), as_edge_list(), etc
```

---

sub_to_nat *sub_to_nat*

Description

Given a combination x, computes its position out of all lexicographically-ordered (n choose 2) combinations.

Usage

```
sub_to_nat(x, n)
```

Arguments

x	matrix whose columns represent k-combinations.
n	numerator of the binomial coefficient

Details

The mapping is done via an lexicographically-ordered combinadic mapping.

Value

integer vector of the positions of the given combinations.

References

McCaffrey, J. D. "Generating the mth lexicographical element of a mathematical combination." MSDN Library (2004).

`threshold` *threshold*

Description

Thresholds a given filtered simplicial complex.

Usage

```
threshold(st, index = NULL, value = NULL)
```

Arguments

`st`	simplex tree.
`index`	integer index to threshold to.
`value`	numeric index to threshold filtration.

`traverse` *traverse*

Description

Traverses specific subsets of a simplicial complex.

Usage

```
traverse(traversal, f, ...)

straverse(traversal, f, ...)

ltraverse(traversal, f, ...)
```

Arguments

traversal	the type of traversal.
f	the function to apply to each simplex.
...	unused.

Details

traverse allows for traversing ordered subsets of the simplex tree. The specific subset and order are determined by the choice of *traversal*: examples include the preorder traversal, the cofaces traversal, etc. See the links below. Each simplex in the traversal is passed as the first and only argument to f, one per simplex in the traversal. traverse does nothing with the result; if you want to collect the results of applying f to each simplex into a list, use ltraverse (or straverse), which are meant to be used like lapply and sapply, respectively.

Value

NULL; for list or vector-valued returns, use ltraverse and straverse respectively.

Examples

```
## Starter example complex
st <- simplex_tree()
st %>% insert(list(1:3, 2:5))

## Print out complex using depth-first traversal.
st %>% preorder() %>% traverse(print)

## Collect the last labels of each simplex in the tree.
last_labels <- st %>% preorder() %>% straverse(function(simplex){ tail(simplex, 1) })
```

---

union_find *UnionFind*

Description

Union find structure exposed as an Rcpp Module.

Usage

```
union_find(n = 0L)
```

Arguments

n	Number of elements in the set.

Value

A disjoint set, as a Rcpp_UnionFind object (Rcpp module).

Methods

$`print.simplextree` S3 method to print a basic summary of the simplex tree.

Author(s)

Matt Piekenbrock

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