Package: gstsm (via r-universe)

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Title Generalized Spatial-Time Sequence Miner

Version 1.0.0

Description Implementations of the algorithms present article Generalized Spatial-Time Sequence Miner, original title (Castro, Antonio; Borges, Heraldo ; Pacitti, Esther ; Porto, Fabio ; Coutinho, Rafaelli ; Ogasawara, Eduardo . Generalização de Mineração de Sequências Restritas no Espaço e no Tempo. In: XXXVI SBBD - Simpósio Brasileiro de Banco de Dados, 2021 <doi:10.5753/sbbd.2021.17891>).

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`find` *Find - definition*

Description

S3 class definition for find method.

Usage

```
find(object, ck)
```

Arguments

`object`	a GSTSM object
`ck`	set of candidates

Value

Solid Ranged-Group(s) of all candidate sequences

`find.default` *Find - default*

Description

Default method for find. Does nothing.

Usage

```
## Default S3 method:
find(object, ck)
```

Arguments

`object`	a GSTSM object
`ck`	set of candidates

Value

Solid Ranged-Group(s) of all candidate sequences

`find.gstsm` *Find - GSTSM implementation*

Description

GSTSM implementationfor for find method. Does nothing. The goal is to find the Ranged Groups information for a candidate c.

Usage

```
## S3 method for class 'gstsm'
find(object, ck)
```

Arguments

`object`	a GSTSM object
`ck`	set of candidates

Value

Solid Ranged-Group(s) of all candidate sequences

`find_kernel_ranged_group`

Find Kernel Ranged Group

Description

The goal is to find the Kernel Ranged Group information for a candidate c.

Usage

```
find_kernel_ranged_group(c, d, gamma, beta, adjacency_matrix)
```

Arguments

`c`	candidate
`d`	set of transactions
`gamma`	minimum temporal frequency
`beta`	minimum group size
`adjacency_matrix`	adjacency matrix

Value

Kernel Ranged-Group(s) of c updated

`generate_adjacency_matrix`

Generate Adjacency Matrix

Description

Helper function that generates an adjacency matrix.

Usage

```
generate_adjacency_matrix(spatial_positions, sigma)
```

Arguments

`spatial_positions`	set of spatial positions
`sigma`	max distance between group points

Value

Adjacency Matrix

`generate_candidates` *Generate Candidates - definition*

Description

S3 class definition for generate_candidates method.

Usage

```
generate_candidates(object, srg)
```

Arguments

`object`	a GSTSM object
`srg`	set of Solid Ranged Groups

Value

candidate sequences of size k + 1

`generate_candidates.default` *Generate Candidates - default*

Description

Default method for generate_candidates. Does nothing.

Usage

```
## Default S3 method:
generate_candidates(object, srg)
```

Arguments

`object`	a GSTSM object
`srg`	set of Solid Ranged Groups

Value

candidate sequences of size k + 1

`generate_candidates.gstsm` *Generate Candidates - GSTSM implementation*

Description

The algorithm combines SRGs that have sequences of size k, received as input, to generate candidates with sequences of size k + 1. Let x and y be SRGs, the conditions for this to occur are: that we have an intersection of candidates over the time range, intersection over the set of spatial positions (x.g n y.g), and a common subsequence: <x.s2, . . . , x.sk>=<y.s1, . . . , y.sk-1>.

Usage

```
## S3 method for class 'gstsm'
generate_candidates(object, srg)
```

Arguments

`object`	a GSTSM object
`srg`	set of Solid Ranged Groups

Value

candidate sequences of size k + 1

`gstsm` *GSTSM*

Description

S3 class definition for GSTSM.

Usage

```
gstsm(sts_dataset, spatial_positions, gamma, beta, sigma)
```

Arguments

`sts_dataset`	STS dataset
`spatial_positions`	set of spatial positions
`gamma`	minimum temporal frequency
`beta`	minimum group size
`sigma`	maximum distance between group points

Details

This algorithm is designed to the identification of frequent sequences in STS datasets from the concept of Solid Ranged Groups (SRG). GSTSM is based on the candidate-generating principle. The goal is to start finding SRGs for sequences of size one. Then it explores the support and the number of occurrences of SRGs for larger sequences with a limited number of scans over the database.

Value

a GSTSM object

Examples

```
library("gstsm")

D <- as.data.frame(matrix(c("B", "B", "A", "C", "A",
              "C", "B", "C", "A", "B",
              "C", "C", "A", "C", "A",
              "B", "B", "D", "A", "B",
              "B", "D", "D", "B", "D"
            ), nrow = 5, ncol = 5, byrow = TRUE))

ponto <- c("p1", "p2", "p3", "p4", "p5")
x <- c(1, 2, 3, 4, 5)
y <- c(0, 0, 0, 0, 0)
z <- y
P <- data.frame(ponto=ponto, x=x, y=y, z=z, stringsAsFactors = FALSE)

gamma <- 0.8
beta <- 2
sigma <- 1

gstsm_object <- gstsm(D, P, gamma, beta, sigma)

result <- mine(gstsm_object)
```

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merge *Merge - definition*

Description

S3 class definition for merge method.

Usage

```
merge(object, ck)
```

Arguments

`object`	a GSTSM object
`ck`	set of candidates

Value

Solid Ranged-Group(s) of all candidate sequences

`merge.default` *Merge - default*

Description

Default method for merge. Does nothing.

Usage

```
## Default S3 method:
merge(object, ck)
```

Arguments

`object`	a GSTSM object
`ck`	set of candidates

Value

Solid Ranged-Group(s) of all candidate sequences

`merge.gstsm` *Merge - GSTSM implementation*

Description

Merge - GSTSM implementation

Usage

```
## S3 method for class 'gstsm'
merge(object, ck)
```

Arguments

`object`	a GSTSM object
`ck`	set of candidates

Value

Solid Ranged-Group(s) of all candidate sequences

`merge_kernel_ranged_groups`

Merge Kernel Ranged Groups

Description

The goal is to merge KRGs. Let q and u be two different KRGs from the same candidate sequence. They can be merged into a group qu = q U u as long as they have an intersection and qu has a frequency greater than or equal to the minimum frequency defined by the user.

Usage

```
merge_kernel_ranged_groups(c, gamma)
```

Arguments

`c`	candidate
`gamma`	minimum temporal frequency

Value

KRG

`merge_open_kernel_ranged_groups`

Merge Kernel Ranged Groups

Description

The goal of is to stretch KRGs of the same candidate sequence. Its possible if two KRGs have intersection in space and the resulting KRG keeps its frequency equal to or greater than beta.

Usage

```
merge_open_kernel_ranged_groups(c, timestamp, gamma, beta, adjacency_matrix)
```

Arguments

`c`	candidate.
`timestamp`	current timestamp
`gamma`	minimum temporal frequency
`beta`	minimum group size
`adjacency_matrix`	adjacency matrix

Value

Set of updated KRGs

`mine` *Mine - definition*

Description

S3 class definition for mine method.

Usage

```
mine(object)
```

Arguments

`object`	a GSTSM object

Value

all Solid Ranged Group(s) found, of all sizes

`mine.default` *Mine - default*

Description

Default method for mine. Does nothing.

Usage

```
## Default S3 method:
mine(object)
```

Arguments

`object`	a GSTSM object

Value

all Solid Ranged Group(s) found, of all sizes

`mine.gstsm` *Mine - GSTSM implementation*

Description

Mine - GSTSM implementation

Usage

```
## S3 method for class 'gstsm'
mine(object)
```

Arguments

`object`	a GSTSM object

Value

all Solid Ranged Group(s) found, of all sizes

`split_groups` *Split Groups*

Description

Helper function that splits groups.

Usage

```
split_groups(pos, adjacency_matrix)
```

Arguments

`pos`	sequence occurrence index
`adjacency_matrix`	possible connection between positions

Value

new set based on candidate c found in d.

`validate_and_close` *Validate and Close*

Description

The function receives as input the set of RGs (RG) from a candidate and the minimum size of a group (beta). It starts defining a set of elements that will be removed from the set of RGs, if it does not have the minimum group size.

Usage

```
validate_and_close(c, gamma, beta)
```

Arguments

`c`	candidate
`gamma`	minimum temporal frequency
`beta`	minimum group size

Value

validated Greedy-Ranged-Groups.

`validate_kernel_ranged_groups`
Validate Kernel Ranged Groups

Description

Its objective is to verify that the user thresholds were observed in each RGs, checking if they can still be stretched by keeping the frequency greater than or equal to the minimum gamma and if the minimum group size beta occurs. It takes as input a set of RGs RG of a candidate sequence, the timestamp of the start of the current sliding window timestamp, the user-defined thresholds gamma and beta.

Usage

```
validate_kernel_ranged_groups(c, timestamp, gamma, beta)
```

Arguments

`c`	candidate
`timestamp`	current timestamp
`gamma`	minimum temporal frequency
`beta`	minimum group size

Value

Validated Kernel-Ranged-Groups.

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