Package ‘sketchR’

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Title An R interface for python subsampling/sketching algorithms
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Description Provides an R interface for various subsampling algorithms implemented in python packages. Currently, interfaces to the geosketch and scSampler python packages are implemented. In addition it also provides diagnostic plots to evaluate the subsampling.
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sketchR-package

sketchR - an R interface for python subsampling/sketching algorithms

Description

The sketchR package provides an R interface for various subsampling algorithms implemented in python packages. Currently, interfaces to the geosketch and scSampler python packages are implemented, in the functions geosketch() and scsampler(), respectively. In addition the package also provides diagnostic plots to evaluate the subsampling. More details on how to get started and incorporate the subsampling into an scRNA-seq workflow are provided in the vignette.

Author(s)

Charlotte Soneson
Michael Stadler

See Also

Useful links:

- https://github.com/fmicompbio/sketchR
- Report bugs at https://github.com/fmicompbio/sketchR/issues

compareCompositionPlot

Compare the compositions of a data set and a subset

Description

Plot the composition of a data set (e.g., the number of cells from each cell type) and contrast it with the corresponding composition of a subset.
Usage

```r
compareCompositionPlot(
  df,
  idx,
  column,
  showPercentages = TRUE,
  fontSizePercentages = 4
)
```

Arguments

- **df**: A `data.frame`-like object (such that `df[[column]]` works).
- **idx**: A numeric vector representing the row indexes of `df` corresponding to the subset of interest. Can also be a named list of index vectors if multiple subsets are of interest.
- **column**: A character scalar corresponding to a column of `df` and representing the variable for which the composition should be calculated.
- **showPercentages**: Logical scalar, indicating whether relative frequencies of each category should be shown in the plot.
- **fontSizePercentages**: Numerical scalar, indicating the font size of the relative frequencies, if `showPercentages` is `TRUE`.

Value

A `ggplot` object.

Author(s)

Charlotte Soneson

Examples

```r
df <- data.frame(celltype = sample(LETTERS[1:5], 1000, replace = TRUE,
  prob = c(0.1, 0.2, 0.5, 0.05, 0.15)))
idx <- sample(seq_len(1000), 200)
compareCompositionPlot(df, idx, "celltype")
```
Run geosketch to subsample a matrix

Description

Perform geometric sketching with the geosketch python package.

Usage

geosketch(
  mat,
  N,
  replace = FALSE,
  k = "auto",
  alpha = 0.1,
  seed = NULL,
  max_iter = 200,
  one_indexed = TRUE,
  verbose = FALSE
)

Arguments

mat          m x n matrix. Samples (the dimension along which to subsample) should be in
             the rows, features in the columns.
N            Numeric scalar, the number of samples to retain.
replace      Logical scalar, whether to sample with replacement.
k            Numeric scalar or "auto", specifying the number of covering. If k = "auto"
             (the default), it is set to sqrt(nrow(mat)) for replace = TRUE and to N for
             replace = FALSE.
alpha        Numeric scalar defining the acceptable interval around k. Binary search halts
             when it obtains between k * (1 - alpha) and k * (1 + alpha) covering boxes.
seed         Numeric scalar or NULL (default). If not NULL, it will be converted to integer
             and passed to numpy to seed the random number generator.
max_iter     Numeric scalar giving the maximum iterations at which to terminate binary
             search in rare cases of non-monotonicity of covering boxes.
one_indexed   Logical scalar, whether to return one-indexed indices.
verbose      Logical scalar, whether to print logging output while running.

Details

The first time this function is run, it will create a conda environment containing the geosketch
package. This is done via the basilisk R/Bioconductor package - see the documentation for that
package for troubleshooting.
Value

A numeric vector with indices to retain.

Author(s)

Charlotte Soneson, Michael Stadler

References


Examples

\[
x <- \text{matrix(rnorm(500), nrow = 100)}
\]
\[
\text{geosketch(mat = x, N = 10, seed = 42)}
\]
getScSamplerNames  Get names of scSampler functions

Description
Get names of scSampler functions

Usage
getScSamplerNames()

Value
A list of names of objects exposed in the scSampler module

Author(s)
Charlotte Soneson

Examples
getScSamplerNames()

hausdorffDistPlot  Create diagnostic plot of Hausdorff distances

Description
Create diagnostic plot showing the Hausdorff distance between a sketch and the full data set, for varying sketch sizes. For reproducibility, seed the random number generator before calling this function using set.seed.

Usage
hausdorffDistPlot(
    mat, 
    Nvec, 
    Nrep = 5, 
    q = 1e-04, 
    methods = c("geosketch", "scsampler", "uniform"), 
    extraArgs = list()
)
Arguments

mat m x n matrix. Samples (the dimension along which to subsample) should be in the rows, features in the columns.

Nvec Numeric vector of sketch sizes.

Nrep Numeric scalar indicating the number of sketches to draw for each sketch size.

q Numeric scalar in [0,1], indicating the fraction of largest minimum distances to discard when calculating the robust Hausdorff distance. Setting q=0 gives the classical Hausdorff distance. The default is 1e-4, as suggested by Hie et al (2019).

methods Character vector, indicating which method(s) to include in the plot. Should be a subset of c("geosketch", "scsampler", "uniform"), where "uniform" randomly samples from input features with uniform probabilities.

extraArgs Named list providing extra arguments to the respective methods (beyond the matrix and the sketch size). The names of the list should be the method names (currently, "geosketch" or "scsampler"), and each list element should be a named list of argument values. See the examples for an illustration of how to use this argument. Note that the seed argument, if provided to any of the methods, will be ignored (since it would imply providing the same seed for each repeated run of the sketching).

Value

A ggplot object.

Author(s)

Charlotte Soneson, Michael Stadler

References


Song et al (2022): scSampler: fast diversity-preserving subsampling of large-scale single-cell transcriptomic data. bioRxiv doi:10.1101/2022.01.15.476407


Examples

```r
## Generate example data matrix
mat <- matrix(rnorm(1000), nrow = 100)

## Generate diagnostic Hausdorff distance plot
## (including all available methods)
hausdorffDistPlot(mat, Nvec = c(10, 25, 50))

## Provide additional arguments for geosketch
```
hausdorffDistPlot(mat, Nvec = c(10, 25, 50), Nrep = 2,
extraArgs = list(geosketch = list(max_iter = 100)))

scsampler Run scSampler to subsample a matrix

Description
Perform subsampling with the scSampler python package.

Usage
scsampler(mat, N, random_split = 1, seed = 0)

Arguments
mat m x n matrix. Samples (the dimension along which to subsample) should be in
the rows, features in the columns.
N Numeric scalar, the number of samples to retain.
random_split Numeric scalar, the number of parts to randomly split the data into before sub-
sampling within each part. A larger value will speed up computations, but give
less optimal results.
seed Numeric scalar, passed to scsampler to seed the random number generator.

Details
The first time this function is run, it will create a conda environment containing the scSampler
package. This is done via the basilisk R/Bioconductor package - see the documentation for that
package for troubleshooting.

Value
A numeric vector with indices to retain.

Author(s)
Charlotte Soneson, Michael Stadler

References
Song et al (2022): scSampler: fast diversity-preserving subsampling of large-scale single-cell tran-
scriptomic data. bioRxiv doi:10.1101/2022.01.15.476407

Examples
x <- matrix(rnorm(500), nrow = 100)
scsampler(mat = x, N = 10)
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