

# Package ‘concordexR’

January 27, 2025

**Title** Identify Spatial Homogeneous Regions with concordex

**Version** 1.7.1

**Description** Spatial homogeneous regions (SHRs) in tissues are domains that are homogenous with respect to cell type composition. We present a method for identifying SHRs using spatial transcriptomics data, and demonstrate that it is efficient and effective at finding SHRs for a wide variety of tissue types. concordex relies on analysis of k-nearest-neighbor (kNN) graphs. The tool is also useful for analysis of non-spatial transcriptomics data, and can elucidate the extent of concordance between partitions of cells derived from clustering algorithms, and transcriptomic similarity as represented in kNN graphs.

**License** Artistic-2.0

**URL** <https://github.com/pachterlab/concordexR>,  
<https://pachterlab.github.io/concordexR/>

**BugReports** <https://github.com/pachterlab/concordexR/issues>

**Depends** R (>= 4.4.0)

**Imports** BiocGenerics, BiocNeighbors, BiocParallel, bluster, cli,  
DelayedArray, Matrix, methods, purrr, rlang,  
SingleCellExperiment, sparseMatrixStats, SpatialExperiment,  
SummarizedExperiment

**Suggests** BiocManager, BiocStyle, ggplot2, glue, knitr, mbkmeans,  
patchwork, rmarkdown, scater, SFEData,  
SpatialFeatureExperiment, TENxPBMCDData, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**biocViews** SingleCell, Clustering, Spatial, Transcriptomics

**Config/testthat/edition** 3

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|                    |  |
|--------------------|--|
| calculateConcordex | <i>Identify Spatially Homogeneous Regions with concordex</i> |
|--------------------|--|

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## Description

Compute the neighborhood consolidation matrix and identify spatial homogeneous regions.

## Usage

```
calculateConcordex(x, ...)
```

```
runConcordex(x, ...)
```

```
## S4 method for signature 'ANY'
```

```
calculateConcordex(
  x,
  labels,
  ...,
  n_neighbors = 30,
  compute_similarity = FALSE,
```

```

    BLUSPARAM,
    BNINDEX,
    BNPARAM = KmknParam(),
    BPPARAM = SerialParam()
)

## S4 method for signature 'SummarizedExperiment'
calculateConcordex(x, labels, ..., assay.type = "logcounts")

## S4 method for signature 'SingleCellExperiment'
calculateConcordex(x, labels, ..., use.dimred = NULL)

## S4 method for signature 'SpatialExperiment'
calculateConcordex(x, labels, ..., use.spatial = TRUE)

## S4 method for signature 'SpatialExperiment'
runConcordex(x, labels, ..., name = "NBC")

## S4 method for signature 'SingleCellExperiment'
runConcordex(x, labels, ..., name = "NBC")

```

## Arguments

|                    |   |
|--------------------|---|
| x                  | A <a href="#">SpatialExperiment</a> , <a href="#">SpatialFeatureExperiment</a> , <a href="#">SingleCellExperiment</a> , or <a href="#">SummarizedExperiment</a> object containing a count matrix. Otherwise, a numeric matrix-like object containing counts for observations (e.g. cells/spots) on the rows and features on the columns.  |
| ...                | Other parameters passed to default method   |
| labels             | Observation labels used to compute the neighborhood consolidation matrix. Continuous or discrete labels are allowed, and typically, integer labels are assumed to be discrete.<br>Labels can be specified as follows: <ul style="list-style-type: none"> <li>• A vector or matrix-like object with one entry per observation. If a matrix, the observations should be on the rows and the label identifiers on the columns.</li> <li>• If x inherits from <a href="#">SummarizedExperiment-class</a>, a string or character vector specifying the names of columns in <code>colData(x)</code> or the name of a dimensionality reduction result (see <a href="#">reducedDimNames</a>)</li> </ul> |
| n_neighbors        | Number of neighbors to expect for each observation. Defaults to 30.   |
| compute_similarity | Logical. Whether to return the label similarity matrix. Only useful if discrete labels are provided.  |
| BLUSPARAM          | A <a href="#">BlusterParam-class</a> object specifying the clustering algorithm to use to identify spatial homogeneous regions. If this parameter is not specified, then regions are not returned. By default, this parameter is missing.   |
| BNINDEX            | A <a href="#">BiocNeighborIndex</a> object containing the precomputed index information, see <a href="#">findKNN</a> .  |

|             |  |
|-------------|--|
| BNPARAM     | A <a href="#">BiocNeighborParam</a> object specifying the algorithm to use. This can be missing if BNINDEX is supplied, see <a href="#">findKNN</a> .  |
| BPPARAM     | A <a href="#">BiocParallelParam</a> object specifying whether and how computing the metric for numerous observations shall be parallelized (see <a href="#">bpparam</a> ).   |
| assay.type  | String or integer scalar indicating the assay of <code>x</code> containing the counts.   |
| use.dimred  | Integer or string specifying the reduced dimensions to use for construction of the k-nearest neighbor graph. Note that if this is not NULL, reduced dimensions can not be used as labels to compute the neighborhood consolidation matrix. |
| use.spatial | Logical, should the spatial coordinates be used to compute the k-nearest neighbor graph?   |
| name        | String specifying the name to be used to store the result in the <a href="#">reducedDims</a> of the output.  |

### Value

A sparse matrix

### Examples

```
example(read10xVisium, "SpatialExperiment")
library(bluster)

## Setting BLUSPARAM clusters the consolidation
## matrix into SHRs
cdx <- calculateConcordex(
  spe, "in_tissue",
  n_neighbors=10,
  BLUSPARAM=KmeansParam(3)
)

## SHRs are an attribute of the result
shr <- attr(cdx, "shr")

## The label similarity matrix can be computed
## with `compute_similarity=TRUE`
cdx <- calculateConcordex(
  spe, "in_tissue",
  n_neighbors=10,
  compute_similarity=TRUE,
  BLUSPARAM=KmeansParam(3)
)
```

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