Package ‘stIHC’

May 9, 2026

Type Package

Title Spatial Transcriptomics Iterative Hierarchical Clustering

Version 0.1.0

Description
Spatial transcriptomics iterative hierarchical clustering ('stIHC'), is a method for identifying spatial gene co-expression modules, defined as groups of genes with shared spatial expression patterns. The method is applicable across spatial transcriptomics technologies with differing spatial resolution, and provides a framework for investigating the spatial organisation of gene expression in tissues. For further details, see Higgins C., Li J.J., Carey M. <doi:10.1002/qub2.70011>.

License MIT + file LICENSE

Encoding UTF-8

Depends R (>= 4.0.0)

Imports fdaPDE, stats, cluster, mclust

Suggests testthat (>= 3.0.0), knitr, rmarkdown, covr

RoxygenNote 7.3.3

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

Author Catherine Higgins [aut, cre],
Jingyi Jessica Li [aut],
Michelle Carey [aut]

Maintainer Catherine Higgins <`catherine.higgins@ucd.ie`>

Repository CRAN

Date/Publication 2026-01-12 18:50:10 UTC

Contents

`stIHC` *Spatial Transcriptomics Iterative Hierarchical Clustering*

Description

Spatial Transcriptomics Iterative Hierarchical Clustering

Usage

```
stIHC(data)
```

Arguments

`data`	data frame with columns `x`, `y` for spatial coordinates and subsequent columns containing observations.

Value

A list with elements:

`label`	Vector of cluster labels.
`mean_clusters_mat`	Matrix of cluster means.
`clusters`	List of matrices, each matrix contains the observations belonging to that cluster.

Examples

```
## Load example data within the package
rds_path <- system.file("extdata", "spatial_data.rds", package = "stIHC")
example_data <- readRDS(rds_path)

## Run stIHC
stihc = stIHC(example_data)

## Inspect cluster assignments
table(stihc$label)
```

Index