Package: iSEEid (via r-universe)

June 18, 2026

Title iSEE extension to assist in identifying sets of samples/cells

Version 0.99.1

Description This package provides a dedicated panel to assist the sample identification within a single iSEE web-application. The main functionality of this package can be adopted to efficiently select samples (e.g. cells) that need to be identified and annotated in the analysis workflow. With iSEEid, the iSEE framework fully qualifies to be an ideal companion for assigning appropriate labels to large omics datasets.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

Depends iSEE, SummarizedExperiment

Imports methods, shiny, shinyAce

Suggests scRNAseq, scater, knitr, rmarkdown, BiocStyle, testthat (>= 3.0.0), scrapper

URL `https://github.com/iSEE/iSEEid`

BugReports `https://github.com/iSEE/iSEEid/issues`

VignetteBuilder knitr

biocViews CellBasedAssays, Clustering, DimensionReduction, FeatureExtraction, GeneExpression, GUI, ImmunoOncology, ShinyApps, SingleCell, Transcription, Transcriptomics, Visualization

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Contents

`SampleIdentificationCenter-class`

The SampleIdentificationCenter class

Description

The SampleIdentificationCenter is a iSEE::Panel subclass that is dedicated to generating ready-to-use R code for assigning a sample label to samples received by a selection from another panel.

Value

A panel designed to work within the iSEE framework

Slot overview

The following slots control the behavior of the panel:

- `EditorUsageMode`, a logical scalar determining whether to show the full R command for making the sample label assignments (if `FALSE`, displays the sample id list as plain text).
- `AnnotationRationale`, a string specifying the rationale for the sample label assignment.
- `CellTypeLabel`, a string providing the label to assign to the selected samples.
- `ColDataColumn`, a string indicating the name of the colData column to store the assigned labels.

In addition, this class inherits all slots from its parent iSEE::Panel class.

Constructor

`SampleIdentificationCenter(...)` creates an instance of a `SampleIdentificationCenter` class, where any slot and its value can be passed to `...` as a named argument.

Supported methods

In the following code snippets, `x` is an instance of a SampleIdentificationCenter class.

Author(s)

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See Also

iSEE::Panel, for the base class.

Examples

```
library(iSEE)
library(scRNAseq)

# Example data ----
sce <- ReprocessedAllenData(assays = "tophat_counts")
class(sce)

library(scater)
library(scrapper)
sce <- normalizeRnaCounts.se(sce, assay.type = "tophat_counts", size.factors = NULL)

sce <- runPCA(sce, ncomponents=4)
sce <- runTSNE(sce)
rowData(sce)$ave_count <- rowMeans(assay(sce, "tophat_counts"))
rowData(sce)$n_cells <- rowSums(assay(sce, "tophat_counts") > 0)

# launch the app itself ----

if (interactive()) {
  iSEE(sce, initial = list(
       ReducedDimensionPlot(),
       SampleIdentificationCenter(
         ColumnSelectionSource = "ReducedDimensionPlot1"
      )
    )
  )
}
```

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