Package: scCertify (via r-universe)

July 1, 2026

Title Explainable Confidence Scoring for Single-Cell Annotations

Version 0.99.1

Description cellCertR provides an explainable confidence scoring framework for single-cell RNA sequencing annotations using marker enrichment, neighborhood agreement, entropy-based uncertainty estimation, and ontology-aware label matching.

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Imports Seurat, FNN, entropy, UCell

Suggests SingleR, celldex, SingleCellExperiment, ggplot2, knitr, rmarkdown, scDblFinder, testthat (>= 3.0.0)

biocViews Software, SingleCell, RNASeq, GeneExpression, Sequencing

URL `https://github.com/Jaya-Surya-dev/scCertify`

BugReports `https://github.com/Jaya-Surya-dev/scCertify/issues`

VignetteBuilder knitr

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Repository https://biocstaging.r-universe.dev

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RemoteUrl https://github.com/BiocStaging/scCertify

RemoteRef HEAD

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Contents

`calibrate_confidence` *Calibrate Confidence Scores*

Description

Converts raw confidence scores into calibrated percentile scores.

Usage

```
calibrate_confidence(scores)
```

Arguments

`scores`	Numeric vector

Value

Numeric vector

Examples

```
scores <- c(
  0.2,
  0.5,
  0.8
)

calibrate_confidence(
  scores
)
```

`cell_certify` *Cell Annotation Confidence*

Description

Main confidence scoring framework.

Usage

```
cell_certify(object, markers, label_column = "predicted_label")
```

Arguments

`object`	Seurat object
`markers`	Named marker list
`label_column`	Metadata label column

Value

Seurat object

Examples

```
NULL
```

`classify_confidence` *Classify Confidence Levels*

Description

Converts confidence scores into confidence classes.

Usage

```
classify_confidence(scores)
```

Arguments

`scores`	Numeric vector

Value

Character vector

Examples

```
scores <- c(
  0.2,
  0.7,
  0.9
)

classify_confidence(
  scores
)
```

`entropy_score` *Entropy-Based Uncertainty Score*

Description

Calculates entropy from prediction score matrices.

Usage

```
entropy_score(score_matrix)
```

Arguments

`score_matrix`	Numeric matrix

Value

Numeric vector

Examples

```
mat <- matrix(
  runif(20),
  nrow = 5
)

entropy_score(
  mat
)
```

`explain_cell` *Explain Cell Annotation Confidence*

Description

Provides interpretable explanation for confidence scores.

Usage

```
explain_cell(object, cell_id)
```

Arguments

`object`	Seurat object
`cell_id`	Cell barcode

Value

Character vector

Examples

```
NULL
```

`explain_confidence` *Explain Confidence Attribution*

Description

Explains why a cell received its confidence score.

Usage

```
explain_confidence(object, cell_id)
```

Arguments

`object`	Seurat object
`cell_id`	Cell barcode

Value

Character vector

Examples

```
NULL
```

`marker_score` *Marker Consistency Score*

Description

Uses UCell enrichment scoring for marker evaluation.

Usage

```
marker_score(object, markers, label_column = "predicted_label")
```

Arguments

`object`	Seurat object
`markers`	Named marker list
`label_column`	Metadata label column

Value

Numeric vector

Examples

```
NULL
```

`match_labels` *Ontology Label Matching*

Description

Matches predicted labels to marker database labels.

Usage

```
match_labels(label, marker_names)
```

Arguments

`label`	Character label
`marker_names`	Character vector

Value

Character vector

Examples

```
match_labels(
  "T_cells",
  c(
    "T_cell",
    "B_cell"
  )
)
```

`neighbor_score` *Neighbor Agreement Score*

Description

Computes local neighborhood agreement scores.

Usage

```
neighbor_score(
  object,
  reduction = "pca",
  dims = NULL,
  k = 10,
  label_column = "predicted_label"
)
```

Arguments

`object`	Seurat object
`reduction`	Reduction method
`dims`	PCA dimensions
`k`	Number of neighbors
`label_column`	Metadata label column

Value

Numeric vector

Examples

```
NULL
```

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