Package: clusterWebApp (via r-universe)

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Title Universal Clustering Analysis Platform

Version 0.1.3

Description An interactive platform for clustering analysis and teaching based on the 'shiny' web application framework. Supports multiple popular clustering algorithms including k-means, hierarchical clustering, DBSCAN (Density-Based Spatial Clustering of Applications with Noise), PAM (Partitioning Around Medoids), GMM (Gaussian Mixture Model), and spectral clustering. Users can upload datasets or use built-in ones, visualize clustering results using dimensionality reduction methods such as Principal Component Analysis (PCA) and t-distributed Stochastic Neighbor Embedding (t-SNE), evaluate clustering quality via silhouette plots, and explore method-specific visualizations and guides. For details on implemented methods, see: Reynolds (2009, ISBN:9781598296975) for GMM; Luxburg (2007) <doi:10.1007/s11222-007-9033-z> for spectral clustering.

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Imports shiny, shinythemes, shinycssloaders, cluster, factoextra, datasets, ggplot2, dbscan, mclust, kernlab, Rtsne, DT, dplyr, tidyr, mlbench, magrittr

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`compute_silhouette` *Compute Average Silhouette Width*

Description

Calculates the average silhouette coefficient from a silhouette object.

Usage

```
compute_silhouette(sil)
```

Arguments

`sil`	A silhouette object as returned by `silhouette`.

Value

A numeric value indicating the average silhouette width, or `NA` if input is `NULL`.

Examples

```
data <- scale(iris[, 1:4])
cl <- kmeans(data, 3)$cluster
sil <- cluster::silhouette(cl, dist(data))
if (interactive()) {
  compute_silhouette(sil)
}
```

plot_elbow *Plot Elbow Method for KMeans*

Description

Uses within-cluster sum of squares (WSS) to help determine the optimal number of clusters.

Usage

```
plot_elbow(data)
```

Arguments

data	A numeric matrix or data frame for clustering.

Value

A ggplot object showing the elbow plot.

Examples

```
data <- scale(iris[, 1:4])
if (interactive()) {
  plot_elbow(data)
}
```

plot_radar *Plot Radar Chart for PAM Cluster Centers*

Description

Displays the medoids of each PAM cluster using a polar radar chart.

Usage

```
plot_radar(data, clusters)
```

Arguments

data	A numeric matrix or data frame for clustering.
clusters	An integer indicating the number of clusters.

Value

A ggplot object showing the radar chart of cluster medoids.

Examples

```
data <- scale(iris[, 1:4])
if (interactive()) {
  plot_radar(data, clusters = 3)
}
```

`plot_silhouette` *Plot Silhouette Diagram*

Description

Plots the silhouette diagram for a given clustering result.

Usage

```
plot_silhouette(sil)
```

Arguments

`sil`	A silhouette object as returned by `silhouette`.

Value

A silhouette plot if input is not NULL, otherwise a placeholder text.

Examples

```
data <- scale(iris[, 1:4])
cl <- kmeans(data, 3)$cluster
sil <- cluster::silhouette(cl, dist(data))
if (interactive()) {
  plot_silhouette(sil)
}
```

`prepare_data` *Prepare Built-in Datasets for Clustering*

Description

Loads and preprocesses a built-in dataset for clustering analysis. Depending on the dataset name provided, different cleaning steps are applied.

Usage

```
prepare_data(dataset)
```

Arguments

`dataset`	A string specifying the dataset name. Options are: "iris", "USArrests", "mtcars", "CO2", "swiss", "Moons".

Details

iris The classic iris dataset, excluding the species column.

USArrests State-wise arrest data. Missing values are removed.

mtcars Motor trend car data set. No transformation applied.

CO2 CO2 uptake in grass plants. Only numeric columns are selected and rows with missing values are removed.

swiss Swiss fertility and socio-economic indicators. Used as-is.

Moons Synthetic non-linear dataset generated by `mlbench::mlbench.smiley()`.

Value

A cleaned `data.frame` containing only numeric variables and no missing values.

Examples

```
data <- prepare_data("iris")
head(data)
```

run_app *Launch the Shiny Clustering Web App*

Description

This function launches the Shiny web application located in the `inst/app` directory of the installed package. The application provides an interactive interface for clustering analysis.

Usage

```
run_app()
```

Value

No return value. This function is called for its side effect (launching the app).

Examples

```
if (interactive()) {
  run_app()
}
```

run_clustering *Perform clustering analysis*

Description

This function performs clustering on a numeric matrix using one of six common clustering methods: KMeans, Hierarchical, DBSCAN, PAM, Gaussian Mixture Model (GMM), or Spectral Clustering.

Usage

```
run_clustering(data, method, k = 3, eps = 0.5, minPts = 5)
```

Arguments

`data`	A numeric matrix or data frame, typically standardized, to be clustered.
`method`	A string indicating the clustering method to use. Options are: "KMeans", "Hierarchical", "DBSCAN", "PAM", "GMM", "Spectral".
`k`	An integer specifying the number of clusters. Required for KMeans, Hierarchical, PAM, GMM, and Spectral.
`eps`	A numeric value specifying the epsilon parameter for DBSCAN. Default is 0.5.
`minPts`	An integer specifying the minimum number of points for DBSCAN. Default is 5.

Value

A list containing two elements:

cluster A vector of cluster labels assigned to each observation.

silhouette An object of class `silhouette` representing silhouette widths.

Examples

```
data(iris)
result <- run_clustering(scale(iris[, 1:4]), method = "KMeans", k = 3)
print(result$cluster)
if (interactive()) {
  plot(result$silhouette)
}
```

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