Package ‘BioGSP’

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Description Implementation of Graph Signal Processing (GSP) methods including Spectral Graph Wavelet Transform (SGWT) for analyzing spatial patterns in biological data. Based on Hammond, Vandergheynst, and Gribonval (2011) ``Wavelets on Graphs via Spectral Graph Theory''. Provides tools for multi-scale analysis of spatial signals, including forward and inverse transforms, energy analysis, and visualization functions tailored for biological applications.

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URL `https://github.com/BMEngineeR/BioGSP`

BugReports `https://github.com/BMEngineeR/BioGSP/issues`

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`BioGSP-package` *BioGSP: Biological Graph Signal Processing for Spatial Data Analysis*

Description

The BioGSP package provides a comprehensive implementation of Graph Signal Processing (GSP) methods including Spectral Graph Wavelet Transform (SGWT) for analyzing spatial patterns in biological data. This implementation is based on Hammond, Vandergheynst, and Gribonval (2011) "Wavelets on Graphs via Spectral Graph Theory".

Details

The package enables multi-scale analysis of spatial signals by:

- Building graphs from spatial coordinates using k-nearest neighbors
- Computing graph Laplacian eigendecomposition for spectral analysis
- Designing wavelets in the spectral domain using various kernel functions
- Decomposing signals into scaling and wavelet components at multiple scales
- Providing reconstruction capabilities with error analysis
- Offering comprehensive visualization and analysis tools

Main Functions

`initSGWT` Initialize SGWT object with data and parameters

`runSpecGraph` Build graph and compute eigendecomposition

`runSGWT` Perform forward and inverse SGWT transforms

`runSGCC` Calculate weighted similarity between signals

`sgwt_forward` Forward SGWT transform

`sgwt_inverse` Inverse SGWT transform

`sgwt_energy_analysis` Energy distribution analysis

`plot_sgwt_decomposition` Visualization of SGWT components

`demo_sgwt` Demonstration with synthetic data

Applications

The BioGSP package is particularly useful for:

- Spatial biology: Analyzing cell distribution patterns in tissue imaging (CODEX, Visium, etc.)
- Single-cell genomics: Spatial transcriptomics and proteomics analysis
- Neuroscience: Brain connectivity and signal analysis
- Pathology: Tumor microenvironment and tissue architecture analysis
- Developmental biology: Spatial pattern formation and cell fate mapping
- Immunology: Immune cell spatial organization and interactions

Author(s)

BioGSP Development Team

References

Hammond, D. K., Vandergheynst, P., & Gribonval, R. (2011). Wavelets on graphs via spectral graph theory. Applied and Computational Harmonic Analysis, 30(2), 129-150.

See Also

Useful links:

- `https://github.com/BMEngineeR/BioGSP`
- Report bugs at `https://github.com/BMEngineeR/BioGSP/issues`

Examples

```
## Not run:
# Load the package
library(BioGSP)

# Run a quick demo
demo_result <- demo_sgwt()

# Generate synthetic data
set.seed(123)
n <- 100
```

```
data <- data.frame(
  x = runif(n, 0, 10),
  y = runif(n, 0, 10),
  signal = sin(runif(n, 0, 2*pi))
)

# New workflow: Initialize -> Build Graph -> Run SGWT
SG <- initSGWT(data, signals = "signal", k = 8, J = 4, kernel_type = "heat")
SG <- runSpecGraph(SG)
SG <- runSGWT(SG)

# Analyze results
energy_analysis <- sgwt_energy_analysis(SG)
print(energy_analysis)

## End(Not run)
```

cal_laplacian *Calculate Graph Laplacian Matrix*

Description

Compute unnormalized, normalized, or random-walk Laplacian from an adjacency matrix.

Usage

```
cal_laplacian(W, type = c("unnormalized", "normalized", "randomwalk"))
```

Arguments

`W`	A square adjacency matrix (can be dense or sparse).
`type`	Type of Laplacian to compute: "unnormalized", "normalized", or "randomwalk".

Value

Laplacian matrix of the same class as input.

Examples

```
## Not run:
W <- matrix(c(0, 1, 1, 1, 0, 1, 1, 1, 0), nrow = 3)
cal_laplacian(W, type = "normalized")

## End(Not run)
```

`checkKband` *Check K-band limited property of signals*

Description

Analyze whether signals are k-band limited by comparing low-frequency and high-frequency Fourier coefficients using eigendecomposition and statistical testing. Builds graph and computes Laplacian directly from SGWT data.

Usage

```
checkKband(
  SG,
  signals = NULL,
  alpha = 0.05,
  verbose = TRUE,
  k = 25,
  laplacian_type = "normalized"
)
```

Arguments

`SG`	SGWT object with Data slot (from initSGWT)
`signals`	Character vector of signal names to analyze. If NULL, uses all signals from SG$Data$signals
`alpha`	Significance level for Wilcoxon test (default: 0.05)
`verbose`	Logical; if TRUE, print progress messages (default: TRUE)
`k`	Number of nearest neighbors for graph construction (default: 25)
`laplacian_type`	Type of Laplacian ("unnormalized", "normalized", or "randomwalk") (default: "normalized")

Value

List containing:

is_kband_limited Logical; TRUE if all signals are k-band limited

knee_point_low Integer; knee point index for low-frequency eigenvalues

knee_point_high Integer; knee point index for high-frequency eigenvalues

signal_results List with per-signal test results including p-values and Fourier coefficients

Examples

```
## Not run:
# Initialize SGWT object (no need to run runSpecGraph)
SG <- initSGWT(data, signals = c("signal1", "signal2"))

# Check k-band limited property
result <- checkKband(SG, signals = c("signal1", "signal2"), k = 30)
if (result$is_kband_limited) {
  cat("All signals are k-band limited")
}

## End(Not run)
```

`codex_toy_data` *Toy CODEX Spatial Cell Type Data*

Description

A synthetic dataset mimicking CODEX multiplexed imaging data for demonstrating Spectral Graph Wavelet Transform (SGWT) analysis on spatial cell type distributions. The dataset contains spatial coordinates and cell type annotations for multiple immune cell populations arranged in realistic spatial clusters.

Usage

```
data(codex_toy_data)
```

Format

A data frame with 18604 rows and 5 columns:

cellLabel Character. Unique identifier for each cell

Y_cent Numeric. Y coordinate of cell centroid (0-115 range)

X_cent Numeric. X coordinate of cell centroid (0-116 range)

Annotation5 Character. Full descriptive cell type name

ROI_num Character. Region of interest identifier ("ROI_0" through "ROI_15")

Details

The dataset contains 16 regions of interest (ROI_0 through ROI_15) with different spatial patterns and varying cell counts (945-1497 cells per ROI). Each ROI represents a distinct tissue region with unique spatial arrangements of the same cell types.

ROI Distribution:

- **ROI_0**: 952 cells
- **ROI_1**: 945 cells
- **ROI_2**: 1155 cells
- **ROI_3**: 1421 cells
- **ROI_4**: 1096 cells
- **ROI_5**: 1420 cells
- **ROI_6-ROI_15**: 958-1497 cells each

Cell types across all ROIs include:

- **BCL6- B Cell** (~3719 cells): Primary B cell population
- **CD4 T** (~4092 cells): Helper T cells - largest population
- **CD8 T** (~3346 cells): Cytotoxic T cells

- **DC** (~2233 cells): Dendritic cells
- **M1** (~1490 cells): M1 macrophages
- **CD4 Treg** (~1490 cells): Regulatory T cells
- **BCL6+ B Cell** (~931 cells): Activated B cells
- **Endothelial** (~746 cells): Vascular cells
- **M2** (~370 cells): M2 macrophages
- **Myeloid** (~186 cells): Other myeloid cells
- **Other** (~1 cells): Miscellaneous cell types

This synthetic data is designed to demonstrate:

- Spatial clustering patterns of different cell types
- Multi-scale spatial analysis using SGWT
- Cross-cell type correlation analysis
- Graph construction and eigenvalue analysis
- Wavelet decomposition of spatial signals

Source

Generated synthetically using clustered normal distributions with realistic parameters based on real CODEX data characteristics.

Examples

```
# Load the toy dataset
data(codex_toy_data)

# Examine the structure
str(codex_toy_data)
head(codex_toy_data)

# Summary of cell types
table(codex_toy_data$Annotation5)

# Summary by ROI
table(codex_toy_data$ROI_num)
table(codex_toy_data$ROI_num, codex_toy_data$Annotation5)

# Quick visualization of spatial distribution
if (requireNamespace("ggplot2", quietly = TRUE)) {
  library(ggplot2)
  ggplot(codex_toy_data, aes(x = X_cent, y = Y_cent, color = Annotation5)) +
    geom_point(size = 0.8, alpha = 0.7) +
    facet_wrap(~ROI_num, scales = "free") +
    labs(title = "Toy CODEX Spatial Cell Distribution by ROI",
         x = "X Coordinate", y = "Y Coordinate") +
    theme_minimal() +
    scale_y_reverse()
}

# Basic SGWT analysis example
## Not run:
# Focus on BCL6- B Cell cells in ROI_1 for SGWT analysis
```

```
bcl6nb_data <- codex_toy_data[codex_toy_data$Annotation5 == "BCL6- B Cell" &
                              codex_toy_data$ROI_num == "ROI_1", ]

# Create binned representation
library(dplyr)
binned_data <- codex_toy_data %>%
  filter(Annotation5 == "BCL6- B Cell", ROI_num == "ROI_1") %>%
  mutate(
    x_bin = cut(X_cent, breaks = 20, labels = FALSE),
    y_bin = cut(Y_cent, breaks = 20, labels = FALSE)
  ) %>%
  group_by(x_bin, y_bin) %>%
  summarise(cell_count = n(), .groups = 'drop')

# Prepare for SGWT
complete_grid <- expand.grid(x_bin = 1:20, y_bin = 1:20)
sgwt_data <- complete_grid %>%
  left_join(binned_data, by = c("x_bin", "y_bin")) %>%
  mutate(
    cell_count = ifelse(is.na(cell_count), 0, cell_count),
    x = x_bin,
    y = y_bin,
    signal = cell_count / max(cell_count, na.rm = TRUE)
  ) %>%
  select(x, y, signal)

# Apply SGWT
sgwt_result <- SGWT(data.in = sgwt_data,
                    signal = "signal",
                    k = 8,
                    J = 3,
                    kernel_type = "heat")

## End(Not run)
```

compare_kernel_families

Compare different kernel families

Description

Visualize and compare different kernel families (both scaling and wavelet filters)

Usage

```
compare_kernel_families(
  x_range = c(0, 3),
  scale_param = 1,
  plot_results = TRUE
)
```

Arguments

`x_range`	Range of x values to evaluate (default: c(0, 3))
`scale_param`	Scale parameter for all functions (default: 1)
`plot_results`	Whether to plot the comparison (default: TRUE)

Value

Data frame with x values and kernel values for each family

Examples

```
comparison <- compare_kernel_families()
comparison <- compare_kernel_families(x_range = c(0, 5), scale_param = 1.5)
```

`compute_sgwt_filters` *Compute SGWT filters*

Description

Compute wavelet and scaling function coefficients in the spectral domain

Usage

```
compute_sgwt_filters(eigenvalues, scales, lmax = NULL, kernel_type = "heat")
```

Arguments

`eigenvalues`	Eigenvalues of the graph Laplacian
`scales`	Vector of scales for the wavelets
`lmax`	Maximum eigenvalue (optional)
`kernel_type`	Kernel family that defines both scaling and wavelet filters (default: "mexican_hat", options: "mexican_hat", "meyer", "heat")

Value

List of filters (scaling function + wavelets)

Examples

```
eigenvals <- c(0, 0.1, 0.5, 1.0, 1.5)
scales <- c(2, 1, 0.5)
filters <- compute_sgwt_filters(eigenvals, scales)
filters_meyer <- compute_sgwt_filters(eigenvals, scales, kernel_type = "meyer")
filters_heat <- compute_sgwt_filters(eigenvals, scales, kernel_type = "heat")
```

`cosine_similarity` *Calculate cosine similarity between two vectors*

Description

Calculate cosine similarity between two numeric vectors with numerical stability

Usage

```
cosine_similarity(x, y, eps = 1e-12)
```

Arguments

`x`	First vector
`y`	Second vector
`eps`	Small numeric for numerical stability when norms are near zero (default 1e-12)

Value

Cosine similarity value (between -1 and 1)

Examples

```
x <- c(1, 2, 3)
y <- c(2, 3, 4)
similarity <- cosine_similarity(x, y)
# With custom eps for numerical stability
similarity2 <- cosine_similarity(x, y, eps = 1e-10)
```

`demo_sgwt` *Demo function for SGWT*

Description

Demonstration function showing basic SGWT usage with synthetic data using the new workflow: initSGWT -> runSpecGraph -> runSGWT

Usage

```
demo_sgwt(verbose = TRUE)
```

Arguments

`verbose`	Logical; if TRUE, show progress messages and results (default: TRUE)

Value

SGWT object with complete analysis

Examples

```
## Not run:
SG <- demo_sgwt()
print(SG)

## End(Not run)
```

FastDecompositionLap
Fast eigendecomposition of Laplacian matrix

Description

Perform fast eigendecomposition using RSpectra for large matrices

Usage

```
FastDecompositionLap(
  laplacianMat = NULL,
  k_eigen = 25,
  which = "LM",
  sigma = NULL,
  opts = list(),
  lower = TRUE,
  ...
)
```

Arguments

`laplacianMat`	Laplacian matrix
`k_eigen`	Number of eigenvalues to compute (default: 25)
`which`	Which eigenvalues to compute ("LM", "SM", etc.)
`sigma`	Shift parameter for eigenvalue computation
`opts`	Additional options for eigenvalue computation
`lower`	Whether to compute from lower end of spectrum
`...`	Additional arguments

Value

List with eigenvalues (evalues) and eigenvectors (evectors)

Examples

```
## Not run:
# Create a Laplacian matrix and decompose
L <- matrix(c(2, -1, -1, -1, 2, -1, -1, -1, 2), nrow = 3)
decomp <- FastDecompositionLap(L, k_eigen = 25)

## End(Not run)
```

`find_knee_point` *Find knee point in a curve*

Description

Simple knee point detection using the maximum curvature method

Usage

```
find_knee_point(y, sensitivity = 1)
```

Arguments

`y`	Numeric vector of y values
`sensitivity`	Sensitivity parameter (not used in this simple implementation)

Value

Index of the knee point

Examples

```
y <- c(1, 2, 3, 10, 11, 12)  # curve with a knee
knee_idx <- find_knee_point(y)
```

`gft` *Graph Fourier Transform*

Description

Compute the Graph Fourier Transform (GFT) of a signal using Laplacian eigenvectors.

Usage

```
gft(signal, U)
```

Arguments

`signal`	Input signal (vector or matrix)
`U`	Matrix of eigenvectors (dense matrix preferred)

Value

Transformed signal in the spectral domain (vector or matrix)

`hello_sgwt` *Hello function for SGWT package demonstration*

Description

Simple hello function to demonstrate package loading

Usage

```
hello_sgwt()
```

Value

Character string with greeting

Examples

```
hello_sgwt()
```

`igft` *Inverse Graph Fourier Transform*

Description

Compute the Inverse Graph Fourier Transform (IGFT) of spectral coefficients using Laplacian eigenvectors.

Usage

```
igft(fourier_coeffs, U)
```

Arguments

`fourier_coeffs`	Input Fourier coefficients (vector or matrix)
`U`	Matrix of eigenvectors (dense matrix preferred)

Value

Reconstructed signal in the vertex domain (vector or matrix)

Examples

```
## Not run:
# Single signal
signal_reconstructed <- igft(fourier_coeffs, eigenvectors)

# Multiple signals (batch processing)
signals_reconstructed <- igft(fourier_coeffs_matrix, eigenvectors)

## End(Not run)
```

initSGWT *Initialize SGWT object*

Description

Build an SGWT object with Data and Parameters slots, validate inputs.

Usage

```
initSGWT(
  data.in,
  x_col = "x",
  y_col = "y",
  signals = NULL,
  scales = NULL,
  J = 5,
  scaling_factor = 2,
  kernel_type = "heat"
)
```

Arguments

`data.in`	Data frame containing spatial coordinates and signal data
`x_col`	Character string specifying the column name for X coordinates (default: "x")
`y_col`	Character string specifying the column name for Y coordinates (default: "y")
`signals`	Character vector of signal column names to analyze. If NULL, all non-coordinate columns are used.
`scales`	Vector of scales for the wavelets. If NULL, scales are auto-generated.
`J`	Number of scales to generate if scales is NULL (default: 5)
`scaling_factor`	Scaling factor between consecutive scales (default: 2)
`kernel_type`	Kernel family ("mexican_hat", "meyer", or "heat") (default: "heat")

Value

SGWT object with Data and Parameters slots initialized

Examples

```
## Not run:
# Initialize SGWT object
data <- data.frame(x = runif(100), y = runif(100),
                  signal1 = rnorm(100), signal2 = rnorm(100))
SG <- initSGWT(data, signals = c("signal1", "signal2"))

## End(Not run)
```

`install_and_load` *Install and load packages*

Description

Utility function to install and load packages from CRAN or GitHub

Usage

```
install_and_load(packages)
```

Arguments

`packages`	Named vector where names are package names and values are source URLs

Value

NULL (side effect: installs and loads packages)

Examples

```
## Not run:
packages <- c("ggplot2" = "ggplot2", "devtools" = "r-lib/devtools")
install_and_load(packages)

## End(Not run)
```

`plot_FM` *Plot Fourier modes (eigenvectors) from SGWT object*

Description

Plot low-frequency and high-frequency Fourier modes (eigenvectors) from the graph Laplacian eigendecomposition in an SGWT object

Usage

```
plot_FM(SG, mode_type = "both", n_modes = 6, ncol = 3, point_size = 1.5)
```

Arguments

`SG`	SGWT object with Graph slot computed (from runSpecGraph)
`mode_type`	Type of modes to plot: "low", "high", or "both" (default: "both")
`n_modes`	Number of modes to plot for each type (default: 6)
`ncol`	Number of columns in plot layout (default: 3)
`point_size`	Size of points in the plot (default: 1.5)

Value

Combined plot of Fourier modes

Examples

```
## Not run:
# Plot both low and high frequency modes
SG <- initSGWT(data) %>% runSpecGraph()
plot_FM(SG, mode_type = "both", n_modes = 4)

# Plot only low frequency modes
plot_FM(SG, mode_type = "low", n_modes = 8)

## End(Not run)
```

---

plot_sgwt_decomposition *Plot SGWT decomposition results*

Description

Visualize SGWT decomposition components including original signal, scaling function, wavelet coefficients, and reconstructed signal

Usage

```
plot_sgwt_decomposition(SG, signal_name = NULL, plot_scales = NULL, ncol = 3)
```

Arguments

SG	SGWT object with Forward and Inverse results computed
signal_name	Name of signal to plot (default: first signal)
plot_scales	Which wavelet scales to plot (default: first 4)
ncol	Number of columns in the plot layout (default: 3)

Value

ggplot object with combined plots

Examples

```
## Not run:
# Assuming you have SGWT object
plots <- plot_sgwt_decomposition(SG_object, signal_name = "signal1")
print(plots)

## End(Not run)
```

`print.SGWT` *Print method for SGWT objects*

Description

Print method for SGWT objects

Usage

```
## S3 method for class 'SGWT'
print(x, ...)
```

Arguments

`x`	SGWT object to print
`...`	Additional arguments passed to print methods

`runSGCC` *Run SGCC weighted similarity analysis in Fourier domain*

Description

Calculate energy-normalized weighted similarity between two signals using Fourier domain coefficients directly (no vertex domain reconstruction). Excludes DC component and uses energy-based weighting consistent with Parseval's theorem.

Usage

```
runSGCC(
  signal1,
  signal2,
  SG = NULL,
  eps = 1e-12,
  validate = TRUE,
  return_parts = TRUE,
  low_only = FALSE
)
```

Arguments

`signal1`	Either a signal name (character) for SG object, or SGWT Forward result, or SGWT object
`signal2`	Either a signal name (character) for SG object, or SGWT Forward result, or SGWT object
`SG`	SGWT object (required if signal1/signal2 are signal names)
`eps`	Small numeric for numerical stability (default: 1e-12)
`validate`	Logical; if TRUE, check consistency (default: TRUE)
`return_parts`	Logical; if TRUE, return detailed components (default: TRUE)
`low_only`	Logical; if TRUE, compute only low-frequency similarity (default: FALSE)

Value

Similarity analysis results computed in Fourier domain

Examples

```
## Not run:
# Between two signals in same SGWT object
similarity <- runSGCC("signal1", "signal2", SG = SG_object)

# Between two SGWT objects
similarity <- runSGCC(SG_object1, SG_object2)

## End(Not run)
```

---

runSGWT *Run SGWT forward and inverse transforms for all signals*

Description

Perform SGWT analysis on all signals in the SGWT object. Uses batch processing for multiple signals when possible for efficiency. Assumes Graph slot is populated by runSpecGraph().

Usage

```
runSGWT(SG, use_batch = TRUE, verbose = TRUE)
```

Arguments

SG	SGWT object with Graph slot populated
use_batch	Whether to use batch processing for multiple signals (default: TRUE)
verbose	Whether to print progress messages (default: TRUE)

Value

Updated SGWT object with Forward and Inverse slots populated

Examples

```
## Not run:
SG <- initSGWT(data)
SG <- runSpecGraph(SG)
SG <- runSGWT(SG)  # Uses batch processing by default
SG <- runSGWT(SG, use_batch = FALSE)  # Force individual processing

## End(Not run)
```

runSpecGraph — *Build spectral graph for SGWT object*

Description

Generate Graph slot information including adjacency matrix, Laplacian matrix, eigenvalues, and eigenvectors.

Usage

```
runSpecGraph(
  SG,
  k = 25,
  laplacian_type = "normalized",
  length_eigenvalue = NULL,
  verbose = TRUE
)
```

Arguments

`SG`	SGWT object from initSGWT()
`k`	Number of nearest neighbors for graph construction (default: 25)
`laplacian_type`	Type of graph Laplacian ("unnormalized", "normalized", or "randomwalk") (default: "normalized")
`length_eigenvalue`	Number of eigenvalues/eigenvectors to compute (default: NULL, uses full length)
`verbose`	Whether to print progress messages (default: TRUE)

Value

Updated SGWT object with Graph slot populated

Examples

```
## Not run:
SG <- initSGWT(data)
# Uses full length by default
SG <- runSpecGraph(SG, k = 30, laplacian_type = "normalized")
# Or specify custom length
SG <- runSpecGraph(SG, k = 30, laplacian_type = "normalized",
                   length_eigenvalue = 30)

## End(Not run)
```

sgwt-globals *Global variables used in ggplot2 aesthetics*

Description

This file declares global variables used in ggplot2 aesthetics to avoid R CMD check NOTEs about undefined global functions or variables.

sgwt_auto_scales *Generate automatic scales for SGWT*

Description

Generate logarithmically spaced scales for SGWT

Usage

```
sgwt_auto_scales(lmax, J = 5, scaling_factor = 2)
```

Arguments

`lmax`	Maximum eigenvalue
`J`	Number of scales
`scaling_factor`	Scaling factor between consecutive scales

Value

Vector of scales

Examples

```
scales <- sgwt_auto_scales(lmax = 2.0, J = 5, scaling_factor = 2)
```

sgwt_energy_analysis *Analyze SGWT energy distribution across scales in Fourier domain*

Description

Calculate and analyze energy distribution across different scales using Fourier domain coefficients directly (consistent with Parseval's theorem). Excludes DC component for more accurate energy analysis.

Usage

```
sgwt_energy_analysis(SG, signal_name = NULL)
```

Arguments

`SG`	SGWT object with Forward results computed
`signal_name`	Name of signal to analyze (default: first signal)

Value

Data frame with energy analysis results computed in Fourier domain

Examples

```
## Not run:
# Assuming you have SGWT object
energy_analysis <- sgwt_energy_analysis(SG_object, signal_name = "signal1")
print(energy_analysis)

## End(Not run)
```

`sgwt_forward` *Forward SGWT transform (single or batch)*

Description

Transform signal(s) to spectral domain and apply SGWT filters. Handles both single signals (vector) and multiple signals (matrix) efficiently. Stores original and filtered Fourier coefficients for analysis.

Usage

```
sgwt_forward(
  signal,
  eigenvectors,
  eigenvalues,
  scales,
  lmax = NULL,
  kernel_type = "heat"
)
```

Arguments

`signal`	Input signal vector OR matrix where each column is a signal (n_vertices x n_signals)
`eigenvectors`	Eigenvectors of the graph Laplacian
`eigenvalues`	Eigenvalues of the graph Laplacian
`scales`	Vector of scales for the wavelets
`lmax`	Maximum eigenvalue (optional)
`kernel_type`	Kernel family that defines both scaling and wavelet filters (default: "heat")

Value

List containing:

fourier_coefficients List with original and filtered Fourier coefficients

filters Filter bank used

Examples

```
## Not run:
# Single signal
result <- sgwt_forward(signal, eigenvectors, eigenvalues, scales)

# Multiple signals (batch processing)
signals_matrix <- cbind(signal1, signal2, signal3)
result <- sgwt_forward(signals_matrix, eigenvectors, eigenvalues, scales)

## End(Not run)
```

`sgwt_get_kernels` *Get a unified kernel family (low-pass and band-pass) by kernel_type*

Description

Returns a pair of functions implementing the scaling (low-pass) and wavelet (band-pass) kernels for a given kernel family. This enforces consistency: a single kernel_type defines both filters.

Usage

```
sgwt_get_kernels(kernel_type = "heat")
```

Arguments

`kernel_type`	Kernel family name ("mexican_hat", "meyer", or "heat")

Value

A list with two functions: list(scaling = function(x, scale_param), wavelet = function(x, scale_param))

`sgwt_inverse` *Inverse SGWT transform (single or batch)*

Description

Reconstruct signal(s) from filtered Fourier coefficients using inverse GFT. Handles both single signals and multiple signals efficiently. Returns detailed inverse transform results including low-pass, band-pass approximations, reconstructed signal(s), and reconstruction error(s).

Usage

```
sgwt_inverse(sgwt_decomp, eigenvectors, original_signal = NULL)
```

Arguments

`sgwt_decomp`	SGWT decomposition object from sgwt_forward
`eigenvectors`	Eigenvectors of the graph Laplacian (for inverse GFT)
`original_signal`	Original signal vector OR matrix (n_vertices x n_signals) for error calculation (optional)

Value

List containing:

vertex_approximations Named list with inverse-transformed signals in vertex domain:

- `low_pass`: Low-pass (scaling) approximation
- `wavelet_1`, `wavelet_2`, etc.: Band-pass (wavelet) approximations by scale

reconstructed_signal Full reconstructed signal (vector or matrix)

reconstruction_error RMSE (scalar for single signal, vector for multiple signals)

Examples

```
## Not run:
# Single signal
inverse_result <- sgwt_inverse(sgwt_decomp, eigenvectors, original_signal)

# Multiple signals (batch processing)
inverse_result <- sgwt_inverse(sgwt_decomp, eigenvectors, original_signals_matrix)

## End(Not run)
```

---

simulate_checkerboard

Simulate checkerboard pattern

Description

Generate a checkerboard pattern with alternating signals

Usage

```
simulate_checkerboard(grid_size = 8, tile_size = 1)
```

Arguments

`grid_size`	Number of tiles per row/column (default: 8)
`tile_size`	Resolution of each tile in pixels per side (default: 1)

Value

Data frame with X, Y coordinates and signal_1, signal_2 patterns

Examples

```
## Not run:
# Generate 8x8 checkerboard with 10x10 pixel tiles
df <- simulate_checkerboard(grid_size = 8, tile_size = 10)
p <- visualize_checkerboard(df)
print(p)

## End(Not run)
```

simulate_moving_circles

Simulate Moving Circles Pattern

Description

Generate patterns of two circles moving toward each other horizontally. Creates mutually exclusive signals where overlapping pixels are assigned to signal_1 (circle 1). The circles start at fixed horizontal distances from the midline and move toward the center.

Usage

```
simulate_moving_circles(
  grid_size = 60,
  radius_seq = 6:14,
  n_steps = 10,
  center_distance = 30,
  radius2_factor = 1.5,
  seed = 123,
  verbose = TRUE
)
```

Arguments

`grid_size`	Size of the spatial grid (default: 60)
`radius_seq`	Vector of radii for circle 1 (default: 6:14)
`n_steps`	Number of movement steps (default: 10)
`center_distance`	Initial horizontal distance from midline for both centers (default: 30)
`radius2_factor`	Circle 2 radius = radius_seq * radius2_factor (default: 1.5)
`seed`	Random seed for reproducibility (default: 123)
`verbose`	Logical; if TRUE, show progress bar and messages (default: TRUE)

Value

List of data frames, each containing X, Y coordinates and signal_1, signal_2 binary signals

Examples

```
## Not run:
# Generate moving circles patterns with default parameters
patterns <- simulate_moving_circles()

# Custom parameters
patterns <- simulate_moving_circles(
  grid_size = 80,
  radius_seq = c(8, 12, 16),
  n_steps = 8,
  center_distance = 35,
  radius2_factor = 1.2
)

## End(Not run)
```

`simulate_multiscale` *Simulate Multi-center Multi-scale Concentric Ring Patterns*

Description

Generate multi-center, multi-scale concentric ring simulation data. Creates patterns with inner circles and outer rings where the outer radius shrinks from a fixed starting point to a factor of the inner radius across multiple steps.

Usage

```
simulate_multiscale(
  grid_size = 60,
  Ra_seq = seq(2.5, 20, by = 2.5),
  n_steps = 10,
  n_centers = 1,
  outer_start = 40,
  outer_end_factor = 1.2,
  seed = 123,
  verbose = TRUE
)
```

Arguments

`grid_size`	Size of the spatial grid (default: 60)
`Ra_seq`	Vector of inner circle radii (default: seq(2.5, 20, by = 2.5))
`n_steps`	Number of outer radius shrinkage steps (default: 10)
`n_centers`	Number of circle centers (default: 1)
`outer_start`	Fixed starting outer radius (default: 40)
`outer_end_factor`	Outer radius shrinks to this factor × Ra (default: 1.2)
`seed`	Random seed for reproducible center placement (default: 123)
`verbose`	Logical; if TRUE, show progress bar and messages (default: TRUE)

Value

List of data frames, each containing X, Y coordinates and signal_1, signal_2 binary signals

Examples

```
## Not run:
# Generate multi-center patterns with default parameters
patterns <- simulate_multiscale()

# Custom parameters
patterns <- simulate_multiscale(
  grid_size = 80,
  Ra_seq = seq(5, 25, by = 5),
  n_steps = 8,
  n_centers = 2,
  outer_start = 50
)

## End(Not run)
```

---

simulate_multiscale_overlap

Simulate Multiple Center Patterns with Fixed Centers

Description

Generate spatial patterns with multiple circular centers at fixed positions. Similar to simulate_multiscale but with centers placed at fixed locations for reproducible pattern generation. Creates concentric circle patterns with inner circle A and outer ring B at various radius combinations.

Usage

```
simulate_multiscale_overlap(
  grid_size = 60,
  n_centers = 3,
  Ra_seq = c(10, 5, 1),
  Rb_seq = c(10, 5, 1),
  seed = 123,
  verbose = TRUE
)
```

Arguments

`grid_size`	Size of the spatial grid (default: 60)
`n_centers`	Number of pattern centers to generate. If 1, center is placed at grid center. If > 1, centers are randomly placed but fixed by seed (default: 3)
`Ra_seq`	Vector of inner circle radii (default: c(10, 5, 1))
`Rb_seq`	Vector of outer ring radii (default: c(10, 5, 1))
`seed`	Random seed for reproducible center placement (default: 123)
`verbose`	Logical; if TRUE, show progress bar and messages (default: TRUE)

Value

List of data frames, each containing X, Y coordinates and signal_1, signal_2 binary signals

Examples

```
## Not run:
# Generate multi-center patterns with fixed centers
patterns <- simulate_multiscale_overlap()

# Single center at grid center
patterns_single <- simulate_multiscale_overlap(n_centers = 1)

# Custom parameters with multiple centers
Ra_seq <- seq(from = 10, to = 3, length.out = 4)
Rb_seq <- seq(from = 15, to = 2, length.out = 4)
patterns <- simulate_multiscale_overlap(
  Ra_seq = Ra_seq,
  Rb_seq = Rb_seq,
  n_centers = 2,
  seed = 456
)

## End(Not run)
```

`simulate_stripe_patterns` *Simulate Stripe Patterns*

Description

Generate stripe patterns with two parallel stripes separated by a gap. Creates rotatable stripe patterns with configurable gap, width, and rotation angle.

Usage

```
simulate_stripe_patterns(
  grid_size = 100,
  gap_seq = c(10),
  width_seq = c(5),
  theta_seq = c(0),
  eps = 1e-09,
  verbose = TRUE
)
```

Arguments

`grid_size`	Size of the spatial grid (default: 100)
`gap_seq`	Vector of gap distances between stripe centers (default: c(10))
`width_seq`	Vector of stripe widths (default: c(5))
`theta_seq`	Vector of rotation angles in degrees (default: c(0))
`eps`	Small numeric value for open boundary conditions to avoid overlap at stripe edges (default: 1e-9)
`verbose`	Logical; if TRUE, show progress messages (default: TRUE)

Value

List of data frames, each containing X, Y coordinates and signal_1, signal_2 binary signals

Examples

```
## Not run:
# Generate stripe patterns with default parameters
patterns <- simulate_stripe_patterns()

# Custom parameters
patterns <- simulate_stripe_patterns(
  grid_size = 80,
  gap_seq = c(10, 20),
  width_seq = c(5, 10, 20),
  theta_seq = c(0, 30, 60),
  eps = 1e-9,
  verbose = TRUE
)

## End(Not run)
```

---

visualize_checkerboard

Visualize checkerboard pattern

Description

Create a visualization of checkerboard pattern data

Usage

```
visualize_checkerboard(df, color1 = "black", color2 = "white")
```

Arguments

`df`	Data frame with X, Y coordinates and signal_1, signal_2 columns
`color1`	Color for signal_1 tiles (default: "black")
`color2`	Color for signal_2 tiles (default: "white")

Value

ggplot object showing the checkerboard pattern

Examples

```
## Not run:
df <- simulate_checkerboard(grid_size = 6, tile_size = 5)
p <- visualize_checkerboard(df, color1 = "darkblue", color2 = "lightgray")
print(p)

## End(Not run)
```

`visualize_moving_circles`
Visualize Moving Circles Pattern

Description

Visualize the simulated moving circles patterns from simulate_moving_circles

Usage

```
visualize_moving_circles(
  sim_data,
  bg_color = "grey90",
  signal1_color = "#16964a",
  signal2_color = "#2958a8",
  show_subtitle = TRUE,
  sort_order = c("ascending", "descending"),
  panel_spacing = 0.1,
  title_size = 12
)
```

Arguments

`sim_data`	Output from simulate_moving_circles function
`bg_color`	Background color for plots (default: "grey90")
`signal1_color`	Color for signal 1 (default: "#16964a")
`signal2_color`	Color for signal 2 (default: "#2958a8")
`show_subtitle`	Logical; if TRUE (default), show parameter values in facet labels
`sort_order`	Order for sorting ("ascending" or "descending", default: "ascending")
`panel_spacing`	Control spacing between panels in lines (default: 0.1)
`title_size`	Size of title text (default: 12)

Value

ggplot object with faceted visualization

Examples

```
## Not run:
# Generate and visualize patterns
sim_data <- simulate_moving_circles(
  radius_seq = 6:14,
  n_steps = 10
)
plot_grid <- visualize_moving_circles(sim_data)
print(plot_grid)

## End(Not run)
```

`visualize_multiscale` *Visualize Multi-center Multi-scale Concentric Ring Patterns*

Description

Visualize the simulated concentric ring patterns from simulate_multiscale

Usage

```
visualize_multiscale(
  sim_data,
  Ra_seq,
  n_steps,
  bg_color = "grey90",
  signal1_color = "#16964a",
  signal2_color = "#2958a8",
  show_subtitle = TRUE,
  sort_order = c("ascending", "descending"),
  panel_spacing = 0.1,
  title_size = 12
)
```

Arguments

`sim_data`	Output from simulate_multiscale function
`Ra_seq`	Vector of Ra values used in simulation
`n_steps`	Number of steps used in simulation
`bg_color`	Background color for plots (default: "grey90")
`signal1_color`	Color for signal 1 (default: "#16964a")
`signal2_color`	Color for signal 2 (default: "#2958a8")
`show_subtitle`	Logical; if TRUE (default), show parameter values in facet labels
`sort_order`	Order for sorting ("ascending" or "descending", default: "ascending")
`panel_spacing`	Control spacing between panels in lines (default: 0.1)
`title_size`	Size of title text (default: 12)

Value

ggplot object with faceted visualization

Examples

```
## Not run:
# Generate and visualize patterns
sim_data <- simulate_multiscale(
  Ra_seq = seq(2.5, 20, by = 2.5),
  n_steps = 10
)
plot_grid <- visualize_multiscale(sim_data,
                                  Ra_seq = seq(2.5, 20, by = 2.5),
                                  n_steps = 10)
print(plot_grid)

## End(Not run)
```

`visualize_sgwt_kernels` *Visualize SGWT kernels and scaling functions*

Description

Visualize the scaling function and wavelet kernels used in SGWT based on the eigenvalue spectrum and selected parameters

Usage

```
visualize_sgwt_kernels(
  eigenvalues,
  scales = NULL,
  J = 4,
  scaling_factor = 2,
  kernel_type = "heat",
  lmax = NULL,
  eigenvalue_range = NULL,
  resolution = 1000
)
```

Arguments

`eigenvalues`	Vector of eigenvalues from graph Laplacian
`scales`	Vector of scales for the wavelets (if NULL, auto-generated)
`J`	Number of scales to generate if scales is NULL (default: 4)
`scaling_factor`	Scaling factor between consecutive scales (default: 2)
`kernel_type`	Type of wavelet kernel ("mexican_hat" or "meyer", default: "mexican_hat")
`lmax`	Maximum eigenvalue (optional, computed if NULL)
`eigenvalue_range`	Range of eigenvalues to plot (default: full range)
`resolution`	Number of points for smooth curve plotting (default: 1000)

Value

List containing the filter visualization plot and filter values

Examples

```
## Not run:
# Generate some example eigenvalues
eigenvals <- seq(0, 2, length.out = 100)

# Visualize kernels with specific parameters
viz_result <- visualize_sgwt_kernels(
  eigenvalues = eigenvals,
  J = 4,
  scaling_factor = 2,
  kernel_type = "heat"
)
print(viz_result$plot)

## End(Not run)
```

`visualize_similarity_xy`
Visualize similarity in low vs non-low frequency space

Description

Create a scatter plot with low-frequency similarity (c_low) on x-axis and non-low-frequency similarity (c_nonlow) on y-axis from runSGCC results

Usage

```
visualize_similarity_xy(
  similarity_results,
  point_size = 2,
  point_color = "steelblue",
  add_diagonal = TRUE,
  add_axes_lines = TRUE,
  title = "Low-frequency vs Non-low-frequency Similarity",
  show_labels = FALSE,
  show_names = FALSE
)
```

Arguments

`similarity_results`	List of similarity results from runSGCC function, or a single result
`point_size`	Size of points in the plot (default: 2)
`point_color`	Color of points (default: "steelblue")
`add_diagonal`	Whether to add diagonal reference lines (default: TRUE)
`add_axes_lines`	Whether to add x=0 and y=0 reference lines (default: TRUE)

`title`	Plot title (default: "Low-frequency vs Non-low-frequency Similarity")
`show_labels`	Whether to show point labels if names are available (default: FALSE)
`show_names`	Whether to display data point names as text labels using ggrepel (default: FALSE). If more than 50 points, randomly samples 50 for labeling. Requires ggrepel package.

Value

ggplot object showing similarity space visualization

Examples

```
## Not run:
# Single similarity result
sim_result <- runSGCC("signal1", "signal2", SG = SG_object)
plot <- visualize_similarity_xy(sim_result)
print(plot)

# Multiple similarity results
sim_results <- list(
  pair1 = runSGCC("signal1", "signal2", SG = SG_object1),
  pair2 = runSGCC("signal1", "signal2", SG = SG_object2)
)
plot <- visualize_similarity_xy(sim_results, show_names = TRUE)
print(plot)

# Show both labels and names (for comparison)
plot_both <- visualize_similarity_xy(sim_results, show_labels = TRUE, show_names = TRUE)
print(plot_both)

# With many data points (>50), names will be randomly sampled
# install.packages("ggrepel")  # Required for show_names = TRUE
plot_many <- visualize_similarity_xy(many_sim_results, show_names = TRUE)
print(plot_many)

## End(Not run)
```

`visualize_stripe_patterns`

Visualize Stripe Pattern Simulation Results

Description

Create visualization plots for stripe pattern simulation results

Usage

```
visualize_stripe_patterns(
  sim_data,
  gap_seq,
  width_seq,
  theta_seq,
  bg_color = "grey",
  signal1_color = "#1f6f8b",
  signal2_color = "#e67e22",
  overlap_color = "#7a4dbf",
  show_title = TRUE
)
```

Arguments

`sim_data`	Output from simulate_stripe_patterns function
`gap_seq`	Vector of gap values used in simulation
`width_seq`	Vector of width values used in simulation
`theta_seq`	Vector of theta (rotation angle) values used in simulation
`bg_color`	Background color for plots (default: "grey")
`signal1_color`	Color for signal 1 (default: "#1f6f8b")
`signal2_color`	Color for signal 2 (default: "#e67e22")
`overlap_color`	Color for overlapping regions (default: "#7a4dbf")
`show_title`	Logical; if TRUE (default), add titles to plots with parameter values

Value

Combined ggplot object with all pattern visualizations

Examples

```
## Not run:
# Generate and visualize patterns
sim_data <- simulate_stripe_patterns(
  grid_size = 80,
  gap_seq = c(10, 20),
  width_seq = c(5, 10, 20),
  theta_seq = c(0, 30, 60)
)
plot_grid <- visualize_stripe_patterns(sim_data,
                                       gap_seq = c(10, 20),
                                       width_seq = c(5, 10, 20),
                                       theta_seq = c(0, 30, 60))
print(plot_grid)

## End(Not run)
```

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