

# Package ‘topolow’

June 8, 2025

**Title** Antigenic Mapping Using TopoLow Algorithm

**Version** 0.3.2

**Description** An implementation of the TopoLow algorithm for antigenic cartography mapping and analysis. The package provides tools for:

- \* Optimizing point configurations in high-dimensional spaces
- \* Handling missing and thresholded measurements
- \* Processing antigenic assay data
- \* Visualizing antigenic maps
- \* Cross-validation and error analysis
- \* Network structure analysis

The algorithm uses a physics-inspired approach combining spring forces and repulsive interactions to find optimal point configurations.

Methods are described in Arhami and Rohani (2025) <[doi:10.1101/2025.02.09.637307](https://doi.org/10.1101/2025.02.09.637307)>.

**License** MIT + file LICENSE

**Encoding** UTF-8

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utils,  
plotly (>= 4.10.0),  
Racmacs (>= 1.1.2),  
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**URL** <https://github.com/omid-arhami/topolow>

**BugReports** <https://github.com/omid-arhami/topolow/issues>

**LazyData** true

**Depends** R ( $\geq 4.1.0$ )

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## Description

Main function implementing adaptive Monte Carlo sampling to explore parameter space. Updates sampling distribution based on evaluated likelihoods.

**Usage**

```

adaptive_MC_sampling(
  samples_file,
  distance_matrix,
  iterations = 1,
  batch_size = 1,
  mapping_max_iter,
  relative_epsilon,
  folds = 20,
  num_cores = 1,
  scenario_name,
  output_dir = NULL,
  verbose = FALSE
)

```

**Arguments**

samples_file	Path to CSV with initial samples
distance_matrix	Distance matrix to fit
iterations	Number of sampling iterations per job
batch_size	Samples per iteration (fixed to 1)
mapping_max_iter	Maximum map optimization iterations
relative_epsilon	Convergence threshold
folds	Number of CV folds
num_cores	Number of cores for parallel processing
scenario_name	Name for output files
output_dir	Character. Directory for output files. If NULL, uses current directory
verbose	Logical. Whether to print progress messages. Default: FALSE

**Value**

Data frame of samples with evaluated likelihoods

---

add_noise_bias	<i>Add Noise and Bias to Matrix Data</i>
----------------	--

---

**Description**

Creates noisy versions of a distance matrix by adding random noise and/or systematic bias. Useful for testing robustness of algorithms to measurement errors and systematic biases.

**Usage**

```
add_noise_bias(matrix_data)
```

**Arguments**

matrix\_data      Numeric matrix to add noise to

**Details**

The function generates three variants of the input matrix:

1. n1: Matrix with random Gaussian noise
2. n2: Different realization of random noise
3. nb: Matrix with both random noise and systematic negative bias

The noise level is scaled relative to the data mean to maintain realistic error magnitudes.

**Value**

List containing three matrices:

n1	Matrix with first noise realization
n2	Matrix with second noise realization
nb	Matrix with noise and negative bias

**Examples**

```
## Not run:
# Create sample distance matrix
dist_mat <- matrix(runif(100), 10, 10)
dist_mat[lower.tri(dist_mat)] <- t(dist_mat)[lower.tri(dist_mat)]
diag(dist_mat) <- 0

# Generate noisy versions
noisy_variants <- add_noise_bias(dist_mat)

## End(Not run)
```

---

aggregate\_parameter\_optimization\_results

*Aggregate Results from Parameter Optimization Jobs*

---

**Description**

Combines results from multiple parameter optimization jobs executed via SLURM into a single dataset. This function processes results from jobs submitted by [submit\\_parameter\\_jobs](#).

**Usage**

```
aggregate_parameter_optimization_results(
  scenario_name,
  write_files = TRUE,
  dir = NULL
)
```

**Arguments**

scenario_name	Character. Name used in parameter optimization jobs.
write_files	Logical. Whether to save combined results (default: TRUE).
dir	Character. Directory for output files. If NULL, uses current directory

**Details**

The function looks for CSV files in the init\_param\_optimization directory that match the pattern params\_{scenario\_name}.csv. It combines all results into a single dataset, computes median values across folds, and optionally writes the aggregated results to a file.

The output file is saved as: model\_parameters/{scenario\_name}\_model\_parameters.csv

**Value**

Data frame of aggregated results containing median values across folds:

N	Number of dimensions
k0	Initial spring constant
cooling_rate	Spring decay rate
c_repulsion	Repulsion constant
Holdout_MAE	Median holdout mean absolute error
NLL	negative log likelihood of the fold

**See Also**

[initial\\_parameter\\_optimization](#) for running the optimization [submit\\_parameter\\_jobs](#) for job submission

**Examples**

```
## Not run:
# After running parameter optimization jobs:
results <- aggregate_parameter_optimization_results("optimization_run1")

## End(Not run)
```

---

analyze\_network\_structure

*Calculate Network Analysis Metrics*

---

**Description**

Analyzes the connectivity pattern in a distance matrix by converting it to a network representation. Useful for assessing data completeness and structure.

**Usage**

```
analyze_network_structure(distance_matrix)
```

**Arguments**

distance\_matrix  
Square symmetric matrix of distances

**Value**

List containing:

adjacency      Logical matrix indicating presence of measurements  
connectivity    Data frame with connectivity metrics per point  
summary        List of overall network statistics

**Examples**

```
## Not run:
metrics <- analyze_network_structure(dist_mat)
print(metrics$summary$completeness)

## End(Not run)
```

---

calculate\_annual\_distances

*Calculate Annual Distance Metrics*

---

**Description**

Calculates year-over-year antigenic distances and statistics. Compares each point to the mean coordinates of the previous year.

**Usage**

```
calculate_annual_distances(df_coords, ndim, na.rm = TRUE)
```

**Arguments**

df\_coords      Data frame containing: - V1...Vn coordinate columns - year: Numeric years - name: Point identifiers (will use rownames if missing)  
ndim            Number of coordinate dimensions  
na.rm          Logical indicating whether to remove NA values

**Value**

List containing:

dist\_data      Data frame with columns:

- year: Collection year
- distance: Distance from previous year mean

summary        List with:

- overall\_mean: Mean distance across all years
- overall\_sd: Standard deviation of distances

**Examples**

```
## Not run:
annual_stats <- calculate_annual_distances(coords, ndim=2)
print(annual_stats$summary$overall_mean)

## End(Not run)
```

---

```
calculate_cumulative_distances
```

*Calculate Cumulative Distance Metrics*

---

**Description**

Calculates cumulative distance metrics either from a reference point or between all pairs. Handles both seasonal and year-based analyses.

**Usage**

```
calculate_cumulative_distances(
  df_coords,
  ndim,
  reference_row = FALSE,
  na.rm = TRUE
)
```

**Arguments**

<code>df_coords</code>	Data frame containing: - V1...Vn coordinate columns - year: Numeric years - season: Character season identifiers. - cluster: Factor cluster assignments - color: Character color codes
<code>ndim</code>	Number of coordinate dimensions
<code>reference_row</code>	Integer index of reference row (or FALSE for all-pairs analysis)
<code>na.rm</code>	Logical indicating whether to remove NA values

**Value**

List containing either: If `reference_row` provided:

<code>summary_data</code>	Data frame with columns: <ul style="list-style-type: none"> <li>• <code>season_num</code>: Numeric season identifier based on Influenza A.</li> <li>• <code>cluster</code>: Cluster assignment</li> <li>• <code>color</code>: Point color</li> <li>• <code>avg_euclidean_dist</code>: Mean distance to reference</li> <li>• <code>count</code>: Points per cluster</li> <li>• <code>total_count</code>: Total points per season</li> <li>• <code>fraction</code>: Proportion of points in cluster</li> </ul>
---------------------------	--

If `reference_row = FALSE`:

<code>dist_data</code>	Data frame with columns: <ul style="list-style-type: none"> <li>• <code>year_diff</code>: Years between points</li> <li>• <code>euclidean_dist</code>: Distance between points</li> <li>• <code>ref_year</code>: Reference year</li> </ul>
------------------------	--



**Examples**

```
## Not run:
# Calculate distances from reference point
ref_distances <- calculate_cumulative_distances(coords, ndim=2, reference_row=1)

# Calculate all pairwise distances
all_distances <- calculate_cumulative_distances(coords, ndim=2, reference_row=FALSE)

## End(Not run)
```

---

calculate\_diagnostics *Calculate Adaptive Monte Carlo Sampling Diagnostics*

---

**Description**

Calculates standard Adaptive Monte Carlo Sampling diagnostics including R-hat (potential scale reduction) and effective sample size for multiple chains. Can be used with any iterative sampling or optimization procedure that produces chain-like output.

**Usage**

```
calculate_diagnostics(chain_files, mutual_size = 500)
```

**Arguments**

chain_files	Character vector of paths to CSV files containing chains
mutual_size	Integer number of samples to use from end of each chain

**Value**

List containing:

rhat	R-hat statistic for each parameter
ess	Effective sample size for each parameter

**Examples**

```
## Not run:
chain_files <- c("chain1.csv", "chain2.csv", "chain3.csv")
diag <- calculate_diagnostics(chain_files, mutual_size = 1000)
print(diag) # Shows R-hat and ESS
plot(diag) # Creates density plots
print(diag$rhat) # Should be close to 1
print(diag$ess) # Should be large enough (>400) for reliable inference

## End(Not run)
```

---

`calculate_prediction_interval`
*Calculate prediction interval for distance estimates*


---

### Description

Computes prediction intervals for the estimated distances based on residual variation between true and predicted values.

### Usage

```
calculate_prediction_interval(
  distance_matrix,
  p_dist_mat,
  confidence_level = 0.95
)
```

### Arguments

<code>distance_matrix</code>	Matrix of true distances
<code>p_dist_mat</code>	Matrix of predicted distances
<code>confidence_level</code>	Confidence level for interval (default: 0.95)

### Value

Numeric margin of error for prediction interval

---

`calculate_procrustes_difference`
*Calculate Procrustes Difference Between Maps*


---

### Description

Computes the quantitative difference between two maps using Procrustes analysis. The difference is calculated as the sum of squared differences after optimal rotation and scaling.

### Usage

```
calculate_procrustes_difference(map1, map2)
```

### Arguments

<code>map1</code>	Data frame with coordinates from first map (must have X, X.1 columns)
<code>map2</code>	Data frame with coordinates from second map (must have X, X.1 columns)

### Value

Numeric sum of squared differences after Procrustes transformation

## Examples

```
## Not run:
map1 <- read.csv("map1_coords.csv")
map2 <- read.csv("map2_coords.csv")
diff <- calculate_procrustes_difference(map1, map2)

## End(Not run)
```

---

calculate\_procrustes\_significance

*Calculate Statistical Significance Between Maps Using Procrustes Analysis*

---

## Description

Performs Procrustes analysis between two maps and calculates statistical significance of their differences using permutation tests. Handles common data cleaning steps like removing missing values and ensuring comparable point sets.

## Usage

```
calculate_procrustes_significance(map1, map2)
```

## Arguments

map1	Data frame with coordinates from first map (must have X, X.1 columns)
map2	Data frame with coordinates from second map (must have X, X.1 columns)

## Value

Numeric p-value from Procrustes permutation test

## Examples

```
## Not run:
map1 <- read.csv("map1_coords.csv")
map2 <- read.csv("map2_coords.csv")
p_val <- calculate_procrustes_significance(map1, map2)

## End(Not run)
```

---

`calculate_weighted_marginals`
*Calculate Weighted Marginal Distributions*


---

### Description

Calculates marginal distributions for each parameter with weights derived from log-likelihoods. Uses parallel processing for efficiency.

### Usage

```
calculate_weighted_marginals(samples)
```

### Arguments

<code>samples</code>	Data frame containing: - <code>log_N</code> , <code>log_k0</code> , <code>log_cooling_rate</code> , <code>log_c_repulsion</code> : Parameter columns - <code>NLL</code> : Negative log-likelihood column
----------------------	--

### Details

Uses kernel density estimation weighted by normalized likelihoods. Parallelizes computation across parameter dimensions using `mclapply`.

### Value

Named list of marginal distributions, each containing:

<code>x</code>	Vector of parameter values
<code>y</code>	Vector of density estimates

---

`check_gaussian_convergence`
*Check Multivariate Gaussian Convergence*


---

### Description

Assesses convergence of multivariate samples by monitoring changes in mean vector and covariance matrix over a sliding window. Useful for checking stability of parameter distributions in optimization or sampling.

### Usage

```
check_gaussian_convergence(data, window_size = 300, tolerance = 0.01)
```

### Arguments

<code>data</code>	Matrix or data frame of samples where columns are parameters
<code>window_size</code>	Integer size of sliding window for statistics
<code>tolerance</code>	Numeric convergence threshold for relative changes

**Value**

List containing:

converged	Logical indicating if convergence achieved
mean_converged	Logical for mean convergence
cov_converged	Logical for covariance convergence
final_mean	Vector of final mean values
final_cov	Final covariance matrix
mean_history	Matrix of mean values over iterations
cov_changes	Vector of covariance changes

**Examples**

```
## Not run:
data <- read.csv("chain_data.csv")
conv_results <- check_gaussian_convergence(data)
print(conv_results) # Shows summary
plot(conv_results) # Creates convergence plots

## End(Not run)
```

---

check_job_status	<i>Check Status of Submitted Job</i>
------------------	--------------------------------------

---

**Description**

Check Status of Submitted Job

**Usage**

```
check_job_status(job_id)
```

**Arguments**

job_id	Character. SLURM job ID
--------	-------------------------

**Value**

Character job status or NA if not found

---

`clean_data`*Clean Data by Removing MAD-based Outliers*

---

## Description

Removes outliers from numeric data using the Median Absolute Deviation method. Outliers are replaced with NA values. This function is particularly useful for cleaning parameter tables where each column may contain outliers.

## Usage

```
clean_data(x, k = 3, take_log = FALSE)
```

## Arguments

<code>x</code>	Numeric vector to clean
<code>k</code>	Numeric threshold for outlier detection (default: 3)
<code>take_log</code>	Logical. Whether to log transform data before outlier detection (default: FALSE)

## Value

Numeric vector with outliers replaced by NA

## See Also

[detect\\_outliers\\_mad](#) for the underlying outlier detection

## Examples

```
# Clean parameter values
params <- c(0.01, 0.012, 0.011, 0.1, 0.009, 0.011, 0.15)
clean_params <- clean_data(params)

# Clean multiple parameter columns
param_table <- data.frame(
  k0 = runif(100),
  cooling_rate = runif(100),
  c_repulsion = runif(100)
)
clean_table <- as.data.frame(lapply(param_table, clean_data))
```

---

color_palettes	<i>Color Palettes</i>
----------------	-----------------------

---

**Description**

Predefined color palettes optimized for visualization

**Usage**

c25

c25\_claud

c25\_old

c25\_older

**Format**

An object of class character of length 20.

An object of class character of length 24.

An object of class character of length 25.

An object of class character of length 25.

---

coordinates_to_matrix	<i>Convert coordinates to distance matrix</i>
-----------------------	---

---

**Description**

Calculates pairwise Euclidean distances between points in coordinate space

**Usage**

coordinates\_to\_matrix(positions)

**Arguments**

positions      Matrix of coordinates where rows are points and columns are dimensions

**Value**

Matrix of pairwise distances between points

---

copy\_reproduction\_examples

*Copy Reproduction Examples to Working Directory*


---

**Description**

Copies all reproduction examples, including data files and supporting materials, to a specified directory.

**Usage**

```
copy_reproduction_examples(dest_dir = file.path(getwd(), "examples"))
```

**Arguments**

dest_dir	Character. Destination directory (default: "reproduction_examples" in current working directory)
----------	--

**Value**

Invisibly returns the path to the destination directory

---

create\_and\_optimize\_RACMACS\_map

*Create and Optimize RACMACS Map*


---

**Description**

Creates and optimizes an antigenic map using RACMACS and keeps the best optimization. This function wraps RACMACS functionality to provide a simplified interface for map creation and optimization.

**Usage**

```
create_and_optimize_RACMACS_map(
  titer_table,
  dim = 2,
  optimization_number = 400,
  scenario_name,
  num_cores = 1
)
```

**Arguments**

titer_table	Matrix or data frame of titer measurements
dim	Integer number of dimensions for the map (default: 2)
optimization_number	Integer number of optimization runs (default: 400)
scenario_name	Character string for output file naming
num_cores	Integer number of cores to use for optimization (default: 1)



**Value**

RACMACS map object containing optimized coordinates

**Examples**

```
## Not run:
# Create and optimize map from titer data
map <- create_and_optimize_RACMACS_map(titer_table)

# Create map with specific settings
map <- create_and_optimize_RACMACS_map(
  titer_table,
  dim = 3,
  optimization_number = 1000,
  scenario_name = "example_map"
)

## End(Not run)
```

---

create\_cv\_folds

---

*Create Cross-validation Folds for Distance Matrix*


---

**Description**

Creates k-fold cross-validation splits of a distance matrix while maintaining symmetry. Each fold has a training matrix with some values masked for validation.

**Usage**

```
create_cv_folds(
  truth_matrix,
  no_noise_truth = NULL,
  n_folds = 10,
  random_seed = NULL
)
```

**Arguments**

truth_matrix	Matrix of true distances
no_noise_truth	Optional matrix of noise-free distances. If provided, used as truth.
n_folds	Integer number of folds to create
random_seed	Integer random seed for reproducibility

**Value**

List of lists, each containing:

truth	Truth matrix for this fold
train	Training matrix with masked validation entries

**Examples**

```
## Not run:
# Create 5-fold CV splits
folds <- create_cv_folds(dist_matrix, n_folds = 5, random_seed = 123)

## End(Not run)
```

---

create\_diagnostic\_plots

*Create Diagnostic Plots for Multiple Chains*

---

**Description**

Creates trace and density plots for multiple Adaptive Monte Carlo Sampling or optimization chains to assess convergence and mixing. Displays parameter trajectories and distributions across chains.

**Usage**

```
create_diagnostic_plots(
  chain_files,
  mutual_size = 2000,
  output_file = "diagnostic_plots.png",
  output_dir = NULL,
  save_plot = TRUE,
  width = 3000,
  height = 3000,
  res = 300
)
```

**Arguments**

chain_files	Character vector of paths to CSV files containing chain data
mutual_size	Integer number of samples to use from end of each chain
output_file	Character path for saving plot
output_dir	Character. Directory for output files. If NULL, uses current directory
save_plot	Logical. Whether to save plots to files. Default: TRUE
width, height, res	Plot dimensions and resolution for saving

**Value**

Invisible NULL, saves plot to file

**Examples**

```
## Not run:
chain_files <- c("chain1.csv", "chain2.csv", "chain3.csv")
create_diagnostic_plots(chain_files, mutual_size = 2000,
  output_file = "chain_diagnostics.png")

## End(Not run)
```

---

create_slurm_script	Create SLURM Job Script
---------------------	-------------------------

---

## Description

Creates a SLURM batch script with specified parameters and resource requests.

## Usage

```
create_slurm_script(  
  job_name,  
  script_path,  
  args,  
  num_cores,  
  output_file,  
  error_file,  
  time = "8:00:00",  
  memory = "4G",  
  partition = "rohani_p",  
  r_module = "R/4.4.1-foss-2022b",  
  working_dir = NULL,  
  extra_sbatch_args = NULL  
)
```

## Arguments

job_name	Name of the job
script_path	Path to R script to execute
args	Vector of command line arguments
num_cores	Number of CPU cores to request
output_file	Path for job output file
error_file	Path for job error file
time	Time limit (default: "8:00:00")
memory	Memory request (default: "14G")
partition	SLURM partition (default: "rohani_p")
r_module	Character. R module to load (default: "R/4.4.1-foss-2022b")
working_dir	Working directory (default: NULL)
extra_sbatch_args	Additional SBATCH arguments (default: NULL)

## Value

Path to created script file

---

create_topolow_map	<i>Main TopoLow algorithm implementation</i>
--------------------	--

---

## Description

TopoLow (Topological Optimization for Low-Dimensional Mapping) optimizes point positions in n-dimensional space to match a target distance matrix. The algorithm uses a physics-inspired approach with spring and repulsive forces to find optimal point configurations while handling missing and thresholded measurements.

## Usage

```
create_topolow_map(
  distance_matrix,
  ndim,
  mapping_max_iter,
  k0,
  cooling_rate,
  c_repulsion,
  relative_epsilon = 1e-04,
  convergence_counter = 5,
  initial_positions = NULL,
  write_positions_to_csv = TRUE,
  verbose = FALSE
)
```

## Arguments

distance_matrix	Matrix. Square, symmetric distance matrix. Can contain NA values for missing measurements and character strings with < or > prefixes for thresholded measurements.
ndim	Integer. Number of dimensions for the embedding space.
mapping_max_iter	Integer. Maximum number of map optimization iterations.
k0	Numeric. Initial spring constant controlling spring forces.
cooling_rate	Numeric. Rate of spring constant decay per iteration ( $0 < \text{cooling\_rate} < 1$ ).
c_repulsion	Numeric. Repulsion constant controlling repulsive forces.
relative_epsilon	Numeric. Convergence threshold for relative change in error. Default is 1e-4.
convergence_counter	Integer. Number of iterations below threshold before declaring convergence. Default is 5.
initial_positions	Matrix or NULL. Optional starting coordinates. If NULL, random initialization is used. Matrix should have $\text{nrow} = \text{nrow}(\text{distance\_matrix})$ and $\text{ncol} = \text{ndim}$ .
write_positions_to_csv	Logical. Whether to save point positions to CSV file. Default is TRUE.
verbose	Logical. Whether to print progress messages. Default is TRUE.

## Details

The algorithm iteratively updates point positions using:

- Spring forces between points with measured distances
- Repulsive forces between points without measurements
- Modified forces for thresholded measurements (< or >)
- Adaptive spring constant that decays over iterations
- Convergence monitoring based on relative error change

Valid parameter ranges and constraints:

- `ndim`: Positive integer, typically 2-20.
- `k0`: Initial spring constant, positive numeric > 0. Typical range: 0.1-30 Controls initial force strength
- `cooling_rate`: Spring and repulsion decay rate, numeric between 0 and 1. Typical range: 0.0001-0.1 Controls how quickly spring forces weaken
- `c_repulsion`: Repulsion constant, positive numeric > 0. Typical range: 0.00001-0.1 Controls strength of repulsive forces
- `relative_epsilon`: Positive numeric, typically 1e-9 to 1e-3 Smaller values require more iterations but give higher precision
- `convergence_counter`: Positive integer, typically 5-20 Higher values do not necessarily lead to a better convergence

## Value

A list with class "topolow" containing:

- `positions`: Matrix of optimized point coordinates
- `est_distances`: Matrix of distances in the optimized configuration
- `mae`: Mean absolute error between target and optimized distances
- `iter`: Number of iterations performed
- `parameters`: List of input parameters used
- `convergence`: List with convergence status and final error

## Examples

```
# Create a simple distance matrix
dist_mat <- matrix(c(0, 2, 3, 2, 0, 4, 3, 4, 0), nrow=3)

# Run TopoLow in 2D
result <- create_topolow_map(dist_mat, ndim=2, mapping_max_iter=1000,
                             k0=1.0, cooling_rate=0.001, c_repulsion=0.1)

# Plot results
plot(result$positions)
```

---

dist\_to\_titer\_table      *Convert Distance Matrix to Titer Panel Format*

---

### Description

Converts a distance matrix to a titer panel format, handling threshold measurements and logarithmic transformations common in antigenic cartography. The function identifies reference points (typically antisera) and challenge points (typically antigens) based on row/column name prefixes.

### Usage

```
dist_to_titer_table(input_matrix, base = exp(1), tens = 1)
```

### Arguments

input_matrix	Matrix of distances, with row/column names prefixed with "V/" for antigens and "S/" for sera
base	Numeric. Base for logarithmic transformation. Default exp(1). For HI Assay 2
tens	Numeric. Scaling factor for final titers. Default 1. For HI Assay 10

### Details

The function:

1. Identifies antigen and serum entries from matrix row/column names
2. Creates titer table from antigen-serum pairs
3. Handles threshold indicators (< and >) in distance values
4. Applies appropriate transformations to convert distances to titers

Transformation steps:

1. Extract numeric values from thresholded measurements
2. Convert distances to titers via logarithmic transformation
3. Apply scaling factor
4. Reapply threshold indicators to transformed values

### Value

A matrix of titers with:

- Rows corresponding to antigen strains (without "V/" prefix)
- Columns corresponding to antisera (without "S/" prefix)
- Values as character strings including threshold indicators where applicable
- NA values replaced with "\*"

**Examples**

```
## Not run:
# Create sample distance matrix
dist_mat <- matrix(c(0, 2, ">3", 2, 0, 4, "3", 4, 0), nrow=3)
rownames(dist_mat) <- c("V/strain1", "V/strain2", "S/serum1")
colnames(dist_mat) <- c("V/strain1", "V/strain2", "S/serum1")

# Convert to titer panel
titer_panel <- dist_to_titer_table(dist_mat)

## End(Not run)
```

---

error\_calculator\_comparison

*Calculate comprehensive error metrics between predicted and true distances*

---

**Description**

Computes various error metrics including in-sample and out-of-sample errors, and Completeness statistics for model evaluation.

**Usage**

```
error_calculator_comparison(p_dist_mat, truth_matrix, input_matrix)
```

**Arguments**

p_dist_mat	Matrix of predicted distances
truth_matrix	Matrix of true distances
input_matrix	Matrix of input distances (may contain NAs and is used to find the NAs' pattern)

**Details**

Input requirements and constraints:

- Matrices must have matching dimensions
- Row and column names must be consistent between matrices
- NAs are allowed and handled appropriately
- Threshold indicators (< or >) in input matrix are processed correctly

**Value**

List containing:

report_df	Data frame with error metrics per point
Completeness	Numeric Completeness statistic

---

example_positions	<i>Example Antigenic Mapping Data</i>
-------------------	---------------------------------------

---

### Description

HI titers of Influenza antigens and antisera published in Smith et al., 2004 were used to find the antigenic relationships and coordinates of the antigens. It can be used for mapping. The data captures how different influenza virus strains (antigens) react with antisera from infected individuals.

### Usage

```
example_positions
```

### Format

A data frame with 285 rows and 11 variables:

**V1** First dimension coordinate from 5D mapping

**V2** Second dimension coordinate from 5D mapping

**V3** Third dimension coordinate from 5D mapping

**V4** Fourth dimension coordinate from 5D mapping

**V5** Fifth dimension coordinate from 5D mapping

**name** Strain identifier

**antigen** Logical; TRUE if point represents an antigen

**antiserum** Logical; TRUE if point represents an antiserum

**cluster** Factor indicating antigenic cluster assignment (A/H3N2 1968-2003)

**color** Color assignment for visualization

**year** Year of strain isolation

### Source

Arhami and Rohani 2025 [doi:](#)

---

find_mode	<i>Find Mode of Density Distribution</i>
-----------	--

---

### Description

Calculates the mode (maximum point) of a kernel density estimate.

### Usage

```
find_mode(density)
```



**Arguments**

density      List containing density estimate with components:  
                  **x** Vector of values  
                  **y** Vector of density estimates

**Value**

Numeric value of the mode

---

generate\_complex\_data    *Generate Complex High-Dimensional Data for Testing*

---

**Description**

Generates synthetic high-dimensional data with clusters and trends for testing dimensionality reduction methods. Creates data with specified properties:

- Multiple clusters along a trend line
- Variable density regions
- Controllable noise levels
- Optional visualization

The function generates cluster centers along a trend line, adds points around those centers with specified spread, and incorporates random noise to create high and low density areas. The data is useful for testing dimensionality reduction and visualization methods.

**Usage**

```
generate_complex_data(
  n_points = 500,
  n_dim = 10,
  n_clusters = 4,
  cluster_spread = 1,
  fig_name = NA
)
```

**Arguments**

n\_points      Integer number of points to generate  
 n\_dim          Integer number of dimensions  
 n\_clusters    Integer number of clusters  
 cluster\_spread   Numeric controlling cluster variance  
 fig\_name       Character path to save visualization (optional)

**Value**

Data frame with generated coordinates in n\_dim dimensions. Column names are "Dim1" through "DimN" where N is n\_dim.

## Examples

```
## Not run:
# Generate basic dataset
data <- generate_complex_data(n_points = 500, n_dim = 10,
                             n_clusters = 4, cluster_spread = 1)

# Generate and visualize dataset
data <- generate_complex_data(n_points = 500, n_dim = 10,
                             n_clusters = 4, cluster_spread = 1,
                             fig_name = "cluster_viz.png")

## End(Not run)
```

---

generate\_synthetic\_datasets

*Generate Synthetic Distance Matrices with Missing Data*

---

## Description

Creates synthetic distance matrices with controlled levels of missingness and noise for testing and validating mapping algorithms. Generates multiple datasets with different dimensionalities and missingness patterns.

## Usage

```
generate_synthetic_datasets(
  n_dims_list,
  seeds,
  n_points,
  missingness_levels = list(S = 0.67, M = 0.77, L = 0.87),
  output_dir = NULL,
  prefix = "sim",
  save_plots = FALSE
)
```

## Arguments

n_dims_list	Numeric vector of dimensions to generate data for
seeds	Integer vector of random seeds (same length as n_dims_list)
n_points	Integer number of points to generate
missingness_levels	Named list of missingness percentages (default: list(S=0.67, M=0.77, L=0.87))
output_dir	Character path to directory for saving outputs (optional)
prefix	Character string to prefix output files (optional)
save_plots	Logical whether to save network visualization plots

**Value**

List containing:

matrices	List of generated distance matrices
panels	List of generated assay panels
metadata	Data frame with generation parameters

**Examples**

```
## Not run:
# Generate datasets with different dimensions
results <- generate_synthetic_datasets(
  n_dims_list = c(2, 5, 10),
  seeds = c(123, 456, 789),
  n_points = 250,
  output_dir = "sim_data"
)

# Custom missingness levels
results <- generate_synthetic_datasets(
  n_dims_list = c(2, 5),
  seeds = c(123, 456),
  n_points = 200,
  missingness_levels = list(low=0.5, high=0.8)
)

## End(Not run)
```

---

generate\_unique\_string

*Generate unique string identifiers with year suffix*

---

**Description**

Generate unique string identifiers with year suffix

**Usage**

```
generate_unique_string(n, length = 8, lower_bound = 1, upper_bound = 20)
```

**Arguments**

n	Number of strings to generate
length	Length of random part of string (default: 8)
lower_bound	Lower bound for year suffix (default: 1)
upper_bound	Upper bound for year suffix (default: 20)

**Value**

Character vector of unique strings with year suffixes

---

ggsave	<i>Save ggplot with white background</i>
--------	--

---

### Description

Wrapper around `ggplot2::ggsave` that ensures white background. This function masks `ggplot2::ggsave`.

### Usage

```
ggsave(..., bg = "white")
```

### Arguments

...	Other arguments passed on to the graphics device function, as specified by device.
bg	Background colour. If NULL, uses the <code>plot.background</code> fill value from the plot theme.

---

h3n2_data	<i>H3N2 Influenza HI Assay Data from Smith et al. 2004</i>
-----------	--

---

### Description

Hemagglutination inhibition (HI) assay data for influenza A/H3N2 viruses spanning 35 years of evolution.

### Usage

```
h3n2_data
```

### Format

A data frame with the following variables:

<b>virusStrain</b>	Character. Virus strain identifier
<b>serumStrain</b>	Character. Antiserum strain identifier
<b>titer</b>	Numeric. HI assay titer value
<b>virusYear</b>	Numeric. Year virus was isolated
<b>serumYear</b>	Numeric. Year serum was collected
<b>cluster</b>	Factor. Antigenic cluster assignment
<b>color</b>	Character. Color code for visualization

### Source

Smith et al. (2004) Science, 305(5682), 371-376.

---

hiv_titers	<i>HIV Neutralization Assay Data</i>
------------	--------------------------------------

---

**Description**

IC50 neutralization measurements between HIV viruses and antibodies.

**Usage**

hiv\_titers

**Format**

A data frame with the following variables:

**Antibody** Character. Antibody identifier

**Virus** Character. Virus strain identifier

**IC50** Numeric. IC50 neutralization value

**Source**

Los Alamos HIV Database (<https://www.hiv.lanl.gov/>)

---

hiv_viruses	<i>HIV Virus Metadata</i>
-------------	---------------------------

---

**Description**

Reference information for HIV virus strains used in neutralization assays.

**Usage**

hiv\_viruses

**Format**

A data frame with the following variables:

**Virus.name** Character. Virus strain identifier

**Country** Character. Country of origin

**Subtype** Character. HIV subtype

**Year** Numeric. Year of isolation

**Source**

Los Alamos HIV Database (<https://www.hiv.lanl.gov/>)

---

`increase_na_percentage`*Increase Missing Values in a Matrix*

---

## Description

Strategically introduces NA values into a distance matrix while maintaining symmetry. New NA values are added preferentially farther from the diagonal to simulate real-world measurement patterns where distant pairs are more likely to be unmeasured.

## Usage

```
increase_na_percentage(mat, target_na_percentage)
```

## Arguments

<code>mat</code>	Matrix to modify
<code>target_na_percentage</code>	Numeric between 0 and 1 specifying desired proportion of NAs

## Details

The function:

1. Calculates needed additional NAs to reach target percentage
2. Creates probability matrix favoring off-diagonal elements
3. Randomly selects positions weighted by distance from diagonal
4. Maintains matrix symmetry by mirroring NAs

## Value

Matrix with increased NA values, maintaining symmetry

## Examples

```
## Not run:  
# Create sample distance matrix  
dist_mat <- matrix(runif(100), 10, 10)  
dist_mat[lower.tri(dist_mat)] <- t(dist_mat)[lower.tri(dist_mat)]  
diag(dist_mat) <- 0  
  
# Increase NAs to 70%  
sparse_mat <- increase_na_percentage(dist_mat, 0.7)  
  
## End(Not run)
```

---

initial\_parameter\_optimization

*Run Parameter Optimization Via Latin Hypercube Sampling*


---

## Description

Performs parameter optimization using Latin Hypercube Sampling (LHS) combined with k-fold cross-validation. Parameters are sampled from specified ranges using maximin LHS design to ensure good coverage of parameter space. Each parameter set is evaluated using k-fold cross-validation to assess prediction accuracy. To calculate one NLL per set of parameters, the function uses a pooled errors approach which combine all validation errors into one set, then calculate a single NLL. This approach has two main advantages: 1- It treats all validation errors equally, respecting the underlying error distribution assumption 2- It properly accounts for the total number of validation points

## Usage

```
initial_parameter_optimization(
  distance_matrix,
  mapping_max_iter = 1000,
  relative_epsilon,
  convergence_counter,
  scenario_name,
  N_min,
  N_max,
  k0_min,
  k0_max,
  c_repulsion_min,
  c_repulsion_max,
  cooling_rate_min,
  cooling_rate_max,
  num_samples = 20,
  max_cores = NULL,
  folds = 20,
  verbose = FALSE,
  write_files = FALSE,
  output_dir = NULL,
  time = "8:00:00",
  memory = "3G",
  use_slurm = FALSE,
  cider = FALSE
)
```

## Arguments

distance\_matrix

Matrix or data frame. Input distance matrix. Must be square and symmetric. Can contain NA values for missing measurements.

mapping\_max\_iter

Integer. Maximum number of optimization iterations.

relative_epsilon	Numeric. Convergence threshold for relative change in error.
convergence_counter	Integer. Number of iterations below threshold before declaring convergence.
scenario_name	Character. Name for output files and job identification.
N_min, N_max	Integer. Range for number of dimensions parameter.
k0_min, k0_max	Numeric. Range for initial spring constant parameter.
c_repulsion_min, c_repulsion_max	Numeric. Range for repulsion constant parameter.
cooling_rate_min, cooling_rate_max	Numeric. Range for spring decay parameter.
num_samples	Integer. Number of LHS samples to generate (default: 20).
max_cores	Integer. Maximum number of cores to use for parallel processing. If NULL, uses all available cores minus 1 (default: NULL).
folds	Integer. Number of cross-validation folds. Default: 20.
verbose	Logical. Whether to print progress messages. Default: FALSE.
write_files	Logical. Whether to save results to CSV. Default: FALSE. Only set TRUE on SLURM
output_dir	Character. Directory where output and temporary files will be saved. If NULL, uses current working directory. Directory will be created if it doesn't exist.
time	Character. Walltime for SLURM jobs in HH:MM:SS format. Default: "8:00:00".
memory	Character. Memory allocation for SLURM jobs. Default: "3G".
use_slurm	Logical. Whether to submit jobs via SLURM. Default: FALSE.
cider	Logical. Whether to use cider queue in SLURM. Default: FALSE.

## Details

The function performs these steps:

1. Generates LHS samples in parameter space
2. Creates k-fold splits of input data
3. For each parameter set and fold:
  - Trains model on training set
  - Evaluates on validation set
  - Calculates MAE and negative log likelihood
4. Can run computation locally or distribute via SLURM

Parameters ranges are transformed to log scale where appropriate to handle different scales effectively.

## Value

If write\_files=FALSE, returns a data frame with columns:

N	Number of dimensions used
k0	Initial spring constant
cooling_rate	Spring decay rate



c_repulsion	Repulsion constant
Holdout_MAE	Mean absolute error on validation sets
NLL	Negative log likelihood

If write\_files=TRUE, results are saved to CSV files in the format: {scenario\_name}\_model\_parameters.csv

### See Also

[create\\_topolow\\_map](#) for the core optimization algorithm

### Examples

```
## Not run:
# Generate sample distance matrix
dist_mat <- matrix(runif(100), 10, 10)
dist_mat[lower.tri(dist_mat)] <- t(dist_mat)[lower.tri(dist_mat)]
diag(dist_mat) <- 0

# Run local optimization with 50 samples
results <- initial_parameter_optimization(
  distance_matrix = dist_mat,
  mapping_max_iter = 1000,
  relative_epsilon = 1e-4,
  convergence_counter = 10,
  scenario_name = "test_opt",
  N_min = 2, N_max = 10,
  k0_min = 1, k0_max = 30,
  c_repulsion_min = 0.00001, c_repulsion_max = 0.2,
  cooling_rate_min = 0.00001, cooling_rate_max = 0.2,
  num_samples = 50,
  max_cores = 4 # Limit to 4 cores
)

# Run with SLURM using 100 samples
initial_parameter_optimization(
  distance_matrix = dist_mat,
  mapping_max_iter = 1000,
  scenario_name = "slurm_opt",
  N_min = 2, N_max = 10,
  num_samples = 100,
  use_slurm = TRUE
)

## End(Not run)
```

---

log\_transform\_parameters

*Log Transform Parameter Samples*

---

### Description

Reads samples from a CSV file and log transforms specific parameters (N, k0, cooling\_rate, c\_repulsion) if they exist in the data. Handles validation and error checking.

**Usage**

```
log_transform_parameters(samples_file, output_file = NULL)
```

**Arguments**

samples_file	Character. Path to CSV file containing samples
output_file	Character. Optional path for saving transformed data. If NULL, overwrites input file

**Value**

Data frame with log-transformed parameters

**Examples**

```
## Not run:
# Transform and save to new file
log_transform_parameters("input_samples.csv", "transformed_samples.csv")

# Transform and overwrite original
log_transform_parameters("samples.csv")

## End(Not run)
```

---

long\_to\_matrix

---

*Convert Long Format Data to Distance Matrix*


---

**Description**

Converts a dataset from long format to a symmetric distance matrix. The function handles antigenic cartography data where measurements may exist between antigens and antisera points. Row and column names can be optionally sorted by a time variable.

**Usage**

```
long_to_matrix(
  data,
  chnames,
  chorder = NULL,
  rnames,
  rorder = NULL,
  values_column,
  rc = FALSE,
  sort = FALSE
)
```

**Arguments**

data	Data frame in long format
chnames	Character. Name of column holding the challenge point names.
chorder	Character. Optional name of column for challenge point ordering.
rnames	Character. Name of column holding reference point names.
rorder	Character. Optional name of column for reference point ordering.
values_column	Character. Name of column containing distance/difference values. It should be from the nature of "distance" (e.g., antigenic distance or IC50), not "similarity" (e.g., HI Titer.)
rc	Logical. If TRUE, reference points are treated as a subset of challenge points. If FALSE, they are treated as distinct sets. Default is FALSE.
sort	Logical. Whether to sort rows/columns by chorder/rorder. Default FALSE.

**Details**

The function expects data in long format with at least three columns:

- A column for challenge point names
- A column for reference point names
- A column containing the distance/difference values

Optionally, ordering columns can be provided to sort the output matrix. The 'rc' parameter determines how to handle shared names between references and challenges.

**Value**

A symmetric matrix of distances with row and column names corresponding to the unique points in the data.

**Examples**

```
## Not run:
data <- data.frame(
  antigen = c("A", "B", "A"),
  serum = c("X", "X", "Y"),
  distance = c(2.5, 1.8, 3.0),
  year = c(2000, 2001, 2000)
)

# Basic conversion
mat <- long_to_matrix(data,
  chnames = "antigen",
  rnames = "serum",
  values_column = "distance")

# With sorting by year
mat_sorted <- long_to_matrix(data,
  chnames = "antigen",
  chorder = "year",
  rnames = "serum",
  rorder = "year",
  values_column = "distance",
```

```

                                sort = TRUE)

## End(Not run)

```

---

make_interactive	<i>Create Interactive Plot</i>
------------------	--------------------------------

---

## Description

Converts a static ggplot visualization to an interactive plotly visualization with customizable tooltips and interactive features.

## Usage

```
make_interactive(plot, tooltip_vars = NULL)
```

## Arguments

plot	ggplot object to convert
tooltip_vars	Vector of variable names to include in tooltips

## Details

The function enhances static plots by adding:

- Hover tooltips with data values
- Zoom capabilities
- Pan capabilities
- Click interactions
- Double-click to reset

If tooltip\_vars is NULL, the function attempts to automatically determine relevant variables from the plot's mapping.

## Value

plotly object with interactive features

## Examples

```

## Not run:
# Create sample data and plot
data <- data.frame(
  V1 = rnorm(100),
  V2 = rnorm(100),
  antigen = rep(c(0,1), 50),
  antiserum = rep(c(1,0), 50),
  year = rep(2000:2009, each=10),
  cluster = rep(1:5, each=20)
)

```

```

# Create temporal plot
p1 <- plot_temporal_mapping(data, ndim=2)

# Make interactive with default tooltips
p1_interactive <- make_interactive(p1)

# Create cluster plot with custom tooltips
p2 <- plot_cluster_mapping(data, ndim=2)
p2_interactive <- make_interactive(p2,
  tooltip_vars = c("cluster", "year", "antigen")
)

## End(Not run)

```

---

new\_aesthetic\_config    *Plot Aesthetic Configuration Class*

---

## Description

S3 class for configuring plot visual aesthetics including points, colors, labels and text elements.

## Usage

```

new_aesthetic_config(
  point_size = 3.5,
  point_alpha = 0.8,
  point_shapes = c(antigen = 16, antiserum = 0),
  color_palette = c25,
  gradient_colors = list(low = "blue", high = "red"),
  show_labels = FALSE,
  show_title = FALSE,
  label_size = 3,
  title_size = 14,
  subtitle_size = 12,
  axis_title_size = 12,
  axis_text_size = 10,
  legend_text_size = 10,
  legend_title_size = 12,
  show_legend = TRUE,
  legend_position = "right",
  arrow_head_size = 0.2,
  arrow_alpha = 0.6
)

```

## Arguments

point_size	Base point size
point_alpha	Point transparency
point_shapes	Named vector of shapes for different point types
color_palette	Color palette name or custom palette

gradient_colors	List with low and high colors for gradients
show_labels	Whether to show point labels
show_title	Whether to show plot title (default: FALSE)
label_size	Label text size
title_size	Title text size
subtitle_size	Subtitle text size
axis_title_size	Axis title text size
axis_text_size	Axis text size
legend_text_size	Legend text size
legend_title_size	Legend title text size
show_legend	Whether to show the legend
legend_position	Legend position ("none", "right", "left", "top", "bottom")
arrow_head_size	Size of the arrow head for velocity arrows (in cm)
arrow_alpha	Transparency of arrows (0 = invisible, 1 = fully opaque)

**Value**

An aesthetic\_config object

---

new\_annotation\_config *Plot Annotation Configuration Class*

---

**Description**

S3 class for configuring point annotations in plots, including labels, connecting lines, and visual properties.

**Usage**

```
new_annotation_config(
  notable_points = NULL,
  size = 4.9,
  color = "black",
  alpha = 0.9,
  fontface = "plain",
  box = FALSE,
  segment_size = 0.3,
  segment_alpha = 0.6,
  min_segment_length = 0,
  max_overlaps = Inf,
  outline_size = 0.4
)
```

**Arguments**

notable_points	Character vector of notable points to highlight
size	Numeric. Size of annotations for notable points
color	Character. Color of annotations for notable points
alpha	Numeric. Alpha transparency of annotations
fontface	Character. Font face of annotations ("plain", "bold", "italic", etc.)
box	Logical. Whether to draw a box around annotations
segment_size	Numeric. Size of segments connecting annotations to points
segment_alpha	Numeric. Alpha transparency of connecting segments
min_segment_length	Numeric. Minimum length of connecting segments
max_overlaps	Numeric. Maximum number of overlaps allowed for annotations
outline_size	Numeric. Size of the outline for annotations

**Value**

An annotation\_config object

---

new\_dim\_reduction\_config

*Dimension Reduction Configuration Class*

---

**Description**

S3 class for configuring dimension reduction parameters including method selection and algorithm-specific parameters.

**Usage**

```
new_dim_reduction_config(
  method = "pca",
  n_components = 2,
  scale = TRUE,
  center = TRUE,
  pca_params = list(tol = sqrt(.Machine$double.eps), rank. = NULL),
  umap_params = list(n_neighbors = 15, min_dist = 0.1, metric = "euclidean", n_epochs =
    200),
  tsne_params = list(perplexity = 30, mapping_max_iter = 1000, theta = 0.5),
  compute_loadings = FALSE,
  random_state = NULL
)
```

**Arguments**

method	Dimension reduction method ("pca", "umap", "tsne")
n_components	Number of components to compute
scale	Scale the data before reduction
center	Center the data before reduction
pca_params	List of PCA-specific parameters
umap_params	List of UMAP-specific parameters
tsne_params	List of t-SNE-specific parameters
compute_loadings	Compute and return loadings
random_state	Random seed for reproducibility

**Value**

A dim\_reduction\_config object

---

new_layout_config	<i>Plot Layout Configuration Class</i>
-------------------	--

---

**Description**

S3 class for configuring plot layout including dimensions, margins, grids and coordinate systems.

**Usage**

```
new_layout_config(
  width = 8,
  height = 8,
  dpi = 300,
  aspect_ratio = 1,
  show_grid = TRUE,
  grid_type = "major",
  grid_color = "grey80",
  grid_linetype = "dashed",
  show_axis = TRUE,
  axis_lines = TRUE,
  plot_margin = margin(1, 1, 1, 1, "cm"),
  coord_type = "fixed",
  background_color = "white",
  panel_background_color = "white",
  panel_border = TRUE,
  panel_border_color = "black",
  save_format = "png",
  reverse_x = 1,
  reverse_y = 1,
  x_limits = NULL,
  y_limits = NULL,
  arrow_plot_threshold = 0.1
)
```



**Arguments**

width	Plot width in inches
height	Plot height in inches
dpi	Plot resolution
aspect_ratio	Plot aspect ratio
show_grid	Show plot grid
grid_type	Grid type ("none", "major", "minor", "both")
grid_color	Grid color
grid_linetype	Grid line type
show_axis	Show axes
axis_lines	Show axis lines
plot_margin	Plot margins in cm
coord_type	Coordinate type ("fixed", "equal", "flip", "polar")
background_color	Plot background color
panel_background_color	Panel background color
panel_border	Show panel border
panel_border_color	Panel border color
save_format	Plot save format ("png", "pdf", "svg", "eps")
reverse_x	Numeric multiplier for x-axis direction (1 or -1)
reverse_y	Numeric multiplier for y-axis direction (1 or -1)
x_limits	Numeric vector of length 2 specifying c(min, max) for x-axis. If NULL, limits are set automatically.
y_limits	Numeric vector of length 2 specifying c(min, max) for y-axis. If NULL, limits are set automatically.
arrow_plot_threshold	Threshold for velocity arrows to be drawn in the same antigenic distance unit (default: 0.10)

**Value**

A layout\_config object

---

only_virus_vs_as	<i>Filter matrix to only virus vs antiserum distances</i>
------------------	---

---

**Description**

Filter matrix to only virus vs antiserum distances

**Usage**

```
only_virus_vs_as(dist_matrix, selected_names)
```

**Arguments**

dist\_matrix      Distance matrix  
 selected\_names   Names of selected reference points

**Value**

Filtered distance matrix

---

parameter\_sensitivity\_analysis  
*Parameter Sensitivity Analysis*

---

**Description**

Analyzes the sensitivity of model performance (MAE) to changes in a parameter. Uses binning to identify the minimum MAE across parameter ranges and calculates thresholds for acceptable parameter values.

**Usage**

```
parameter_sensitivity_analysis(  
  param,  
  samples,  
  bins = 30,  
  mae_col = "Holdout_MAE",  
  threshold_pct = 5,  
  min_samples = 1  
)
```

**Arguments**

param              Character name of parameter to analyze  
 samples            Data frame containing parameter samples and performance metrics  
 bins                Integer number of bins for parameter range (default: 40)  
 mae\_col            Character name of column containing MAE values (default: "Holdout\_MAE")  
 threshold\_pct      Numeric percentage above minimum for threshold calculation (default: 5)  
 min\_samples        Integer minimum number of samples required in a bin (default: 1)

**Details**

The function performs these steps:

1. Cleans the input data using MAD-based outlier detection
2. Bins the parameter values into equal-width bins
3. Calculates the minimum MAE within each bin. Analogous to "poorman's likelihood" approach, minimum MAE within each bin is an empirical estimate of the performance surface at this parameter value when other parameters are at their optimal values.
4. Identifies a threshold of acceptable performance (default: Topolow min. +5% MAE)
5. Returns an object for visualization and further analysis

**Value**

Object of class "parameter\_sensitivity" containing:

param_values	Vector of parameter bin midpoints
min_mae	Vector of minimum MAE values per bin
param_name	Name of analyzed parameter
threshold	Threshold value (default: Topolow min. +5%)
min_value	Minimum MAE value across all bins
sample_counts	Number of samples per bin

---

plot.parameter\_sensitivity

*Plot Method for Parameter Sensitivity Analysis*


---

**Description**

Creates a visualization of parameter sensitivity showing minimum MAE values across parameter ranges with threshold indicators.

**Usage**

```
## S3 method for class 'parameter_sensitivity'
plot(
  x,
  width = 3.5,
  height = 3.5,
  save_plot = TRUE,
  output_dir = NULL,
  y_limit_factor = NULL,
  ...
)
```

**Arguments**

x	A parameter_sensitivity object
width	Numeric width of output plot in inches (default: 3.5)
height	Numeric height of output plot in inches (default: 3.5)
save_plot	Logical. Whether to save plot to file. Default: TRUE
output_dir	Character. Directory for output files. If NULL, uses current directory
y_limit_factor	Numeric. Factor to set the upper y-axis limit as a percentage above the threshold value (e.g., 1.10 for 10% above). Default: NULL (automatic scaling)
...	Additional arguments passed to plot

**Value**

A ggplot object

---

plot.profile\_likelihood

*Plot Method for Profile Likelihood Objects*


---

### Description

Creates a visualization of profile likelihood for a parameter showing maximum likelihood estimates and confidence intervals. Supports mathematical notation for parameter names and configurable output settings.

Confidence interval is found using the likelihood ratio test:  $LR(\theta_{ij}) = -2[\log L_{max}(\theta_{ij}) - \log L_{max}(\hat{\theta})]$  where  $\hat{\theta}$  is the maximum likelihood estimate for all parameters. The 95% confidence interval is:  $\{\theta_{ij} : LR(\theta_{ij}) \leq \chi^2_{1,0.05} = 3.84\}$

### Usage

```
## S3 method for class 'profile_likelihood'
plot(
  x,
  LL_max,
  width = 3.5,
  height = 3.5,
  save_plot = TRUE,
  output_dir = NULL,
  ...
)
```

### Arguments

x	A profile_likelihood object
LL_max	Numeric maximum log-likelihood value
width	Numeric width of output plot in inches (default: 3.5)
height	Numeric height of output plot in inches (default: 3.5)
save_plot	Logical. Whether to save plot to file. Default: TRUE
output_dir	Character. Directory for output files. If NULL, uses current directory
...	Additional arguments passed to plot

### Value

A ggplot object

### Examples

```
## Not run:
# Calculate profile likelihood
pl_result <- profile_likelihood("log_N", mcmc_samples)

# Plot with maximum likelihood from samples
LL_max <- max(-samples$NLL)
plot(pl_result, LL_max, width = 4, height = 3)

## End(Not run)
```

---

plot.topolow\_amcs\_diagnostics

*Plot Method for Adaptive Monte Carlo Sampling Diagnostics*


---

### Description

Creates trace and density plots for multiple chains to assess convergence and mixing.

### Usage

```
## S3 method for class 'topolow_amcs_diagnostics'
plot(
  x,
  output_file = "mc_diagnostics.png",
  width = 3000,
  height = 3000,
  res = 300,
  ...
)
```

### Arguments

x	A topolow_amcs_diagnostics object
output_file	Character path for saving plot
width, height, res	Plot dimensions and resolution
...	Additional arguments passed to plot functions

### Value

Invisible NULL, saves plot to file

---

plot.topolow\_convergence

*Plot Method for Convergence Diagnostics*


---

### Description

Creates visualization of convergence diagnostics from Monte Carlo sampling, including parameter mean trajectories and covariance matrix stability over iterations. Helps assess whether parameter estimation has converged to stable distributions.

### Usage

```
## S3 method for class 'topolow_convergence'
plot(x, param_names = NULL, ...)
```

**Arguments**

x	A topolow_convergence object from check_gaussian_convergence().
param_names	Optional character vector of parameter names to use in plot titles. If NULL (default), uses the param_names from the topolow_convergence object.
...	Additional arguments passed to underlying plot functions (currently not used).

**Details**

The function generates two types of plots:

1. Parameter mean plots: Shows how the mean value for each parameter changes over iterations. Stabilization of these plots indicates convergence of parameter distributions.
2. Covariance change plot: Shows relative changes in the covariance matrix using the Frobenius norm (also called Hilbert-Schmidt norm), which is defined as the square root of the sum of the absolute squares of all matrix elements:  $\sqrt{\sum |a_{ij}|^2}$ . A decreasing trend approaching zero indicates stable relationships between parameters.

**Value**

A grid of plots showing convergence metrics.

**See Also**

[check\\_gaussian\\_convergence](#) for generating the convergence object

**Examples**

```
## Not run:
# Example with simulated data
chain_data <- data.frame(
  log_N = rnorm(1000, mean = 1.5, sd = 0.1),
  log_k0 = rnorm(1000, mean = -0.5, sd = 0.2)
)

# Check convergence
results <- check_gaussian_convergence(chain_data)

# Plot diagnostics
plot(results)

# With custom parameter names
plot(results, param_names = c("Dimensions (log)", "Spring constant (log)"))

## End(Not run)
```

---

plot_3d_mapping	Create 3D Visualization
-----------------	-------------------------

---

## Description

Creates an interactive or static 3D visualization using rgl. Supports both temporal and cluster-based coloring schemes with configurable point appearances and viewing options.

## Usage

```
plot_3d_mapping(
  df,
  ndim,
  dim_config = new_dim_reduction_config(),
  aesthetic_config = new_aesthetic_config(),
  layout_config = new_layout_config(),
  interactive = TRUE,
  output_dir = NULL
)
```

## Arguments

df	Data frame containing: - V1, V2, ... Vn: Coordinate columns - antigen: Binary indicator for antigen points - antiserum: Binary indicator for antiserum points - cluster: (Optional) Factor or integer cluster assignments - year: (Optional) Numeric year values for temporal coloring
ndim	Number of dimensions in input coordinates (must be $\geq 3$ )
dim_config	Dimension reduction configuration object
aesthetic_config	Aesthetic configuration object
layout_config	Layout configuration object
interactive	Logical; whether to create an interactive plot
output_dir	Character. Directory for output files. If NULL, uses current directory

## Details

The function supports two main visualization modes:

1. Interactive mode: Creates a manipulatable 3D plot window
2. Static mode: Generates a static image from a fixed viewpoint

Color schemes are automatically selected based on available data:

- If cluster data is present: Uses discrete colors per cluster
- If year data is present: Uses continuous color gradient
- Otherwise: Uses default point colors

For data with more than 3 dimensions, dimension reduction is applied first.

Note: This function requires the rgl package and OpenGL support. If rgl is not available, the function will return a 2D plot with a message explaining how to enable 3D visualization.

**Value**

Invisibly returns rgl scene ID for further manipulation if rgl is available, or a 2D ggplot object as a fallback.

**See Also**

[plot\\_temporal\\_mapping](#) for 2D temporal visualization [plot\\_cluster\\_mapping](#) for 2D cluster visualization [make\\_interactive](#) for converting 2D plots to interactive versions

**Examples**

```
## Not run:
# Create sample data
set.seed(123)
data <- data.frame(
  V1 = rnorm(100),
  V2 = rnorm(100),
  V3 = rnorm(100),
  V4 = rnorm(100),
  antigen = rep(c(0,1), 50),
  antiserum = rep(c(1,0), 50),
  cluster = rep(1:5, each=20),
  year = rep(2000:2009, each=10)
)

# Basic interactive plot
plot_3d_mapping(data, ndim=4)

# Custom configuration for temporal visualization
aesthetic_config <- new_aesthetic_config(
  point_size = 5,
  point_alpha = 0.8,
  gradient_colors = list(
    low = "blue",
    high = "red"
  )
)

layout_config <- new_layout_config(
  width = 12,
  height = 12,
  background_color = "black",
  show_axis = TRUE
)

# Create customized static plot
plot_3d_mapping(data, ndim=4,
  aesthetic_config = aesthetic_config,
  layout_config = layout_config,
  interactive = FALSE
)

# Dimension reduction with UMAP
dim_config <- new_dim_reduction_config(
  method = "umap",
  n_components = 3,
```



```

    umap_params = list(
      n_neighbors = 20,
      min_dist = 0.2
    )
  )

  plot_3d_mapping(data, ndim=4,
    dim_config = dim_config,
    interactive = TRUE
  )

  ## End(Not run)

```

---

plot\_cluster\_mapping    *Create Clustered Mapping Plots*

---

## Description

Creates a visualization of points colored by cluster assignment using dimension reduction, with optional antigenic velocity arrows. Points are colored by cluster with different shapes for antigens and antisera.

## Usage

```

plot_cluster_mapping(
  df_coords,
  ndim,
  dim_config = new_dim_reduction_config(),
  aesthetic_config = new_aesthetic_config(),
  layout_config = new_layout_config(),
  annotation_config = new_annotation_config(),
  output_dir = NULL,
  show_shape_legend = TRUE,
  cluster_legend_title = "Cluster",
  draw_arrows = FALSE,
  annotate_arrows = TRUE,
  phylo_tree = NULL,
  sigma_t = NULL,
  sigma_x = NULL,
  clade_node_depth = NULL,
  show_one_arrow_per_cluster = FALSE,
  cluster_legend_order = NULL
)

```

## Arguments

df_coords	Data frame containing: - V1, V2, ... Vn: Coordinate columns - antigen: Binary indicator for antigen points - antiserum: Binary indicator for antiserum points - cluster: Factor or integer cluster assignments
ndim	Number of dimensions in input coordinates
dim_config	Dimension reduction configuration object specifying method and parameters

aesthetic_config	Aesthetic configuration object controlling plot appearance
layout_config	Layout configuration object controlling plot dimensions and style. Use <code>x_limits</code> and <code>y_limits</code> in <code>layout_config</code> to set axis limits.
annotation_config	Annotation configuration object for labeling notable points
output_dir	Character. Directory for output files. If NULL, uses current directory
show_shape_legend	Logical. Whether to show the shape legend (default: TRUE)
cluster_legend_title	Character. Custom title for the cluster legend (default: "Cluster")
draw_arrows	logical; if TRUE, compute and draw antigenic drift vectors
annotate_arrows	logical; if TRUE, show names of the points having arrows
phylo_tree	Optional; phylo object in Newick format. Does not need to be rooted. If provided, used to compute antigenic velocity arrows.
sigma_t	Optional; numeric; bandwidth for the Gaussian kernel discounting on time in years or the time unit of the data. If NULL, uses Silverman's rule of thumb.
sigma_x	Optional; numeric; bandwidth for the Gaussian kernel discounting on antigenic distance in antigenic units. If NULL, uses Silverman's rule of thumb.
clade_node_depth	Optional; integer; number of levels of parent nodes to define clades. Antigens from different clades will be excluded from the calculation antigenic velocity arrows. (Default: Automatically calculated mode of leaf-to-backbone distance of the tree)
show_one_arrow_per_cluster	Shows only the largest antigenic velocity arrow in each cluster
cluster_legend_order	in case you prefer a certain order for clusters in the legend, provide a list with that order here; e.g., <code>c("cluster 2", "cluster 1")</code>

## Details

The function performs these steps:

1. Validates input data structure and types
2. Applies dimension reduction if `ndim > 2`
3. Creates visualization with cluster-based coloring
4. Applies specified aesthetic and layout configurations
5. Applies custom axis limits if specified in `layout_config`

Different shapes distinguish between antigens and antisera points, while color represents cluster assignment. The color palette can be customized through the `aesthetic_config`.

## Value

ggplot object containing the cluster mapping visualization

**See Also**

[plot\\_temporal\\_mapping](#) for temporal visualization [plot\\_3d\\_mapping](#) for 3D visualization [plot\\_combined](#) for creating multiple visualizations [new\\_dim\\_reduction\\_config](#) for dimension reduction options [new\\_aesthetic\\_config](#) for aesthetic options [new\\_layout\\_config](#) for layout options [new\\_annotation\\_config](#) for annotation options

**Examples**

```
## Not run:
# Basic usage with default configurations
data <- data.frame(
  V1 = rnorm(100),
  V2 = rnorm(100),
  V3 = rnorm(100),
  antigen = rep(c(0,1), 50),
  antiserum = rep(c(1,0), 50),
  cluster = rep(1:5, each=20)
)
p1 <- plot_cluster_mapping(data, ndim=3)

# Custom configurations with specific color palette and axis limits
aesthetic_config <- new_aesthetic_config(
  point_size = 4,
  point_alpha = 0.7,
  color_palette = c("red", "blue", "green", "purple", "orange"),
  show_labels = TRUE,
  label_size = 3
)

layout_config <- new_layout_config(
  width = 10,
  height = 8,
  coord_type = "fixed",
  show_grid = TRUE,
  grid_type = "major",
  x_limits = c(-10, 10),
  y_limits = c(-8, 8)
)

p2 <- plot_cluster_mapping(
  data,
  ndim = 3,
  aesthetic_config = aesthetic_config,
  layout_config = layout_config
)

## End(Not run)
```

## Description

Creates multiple coordinated visualizations of the same data using different methods and arrangements. Supports combining temporal, cluster, and 3D visualizations in flexible layouts.

## Usage

```
plot_combined(
  df_coords,
  ndim,
  plot_types = c("temporal", "cluster"),
  dim_config = new_dim_reduction_config(),
  aesthetic_config = new_aesthetic_config(),
  layout_config = new_layout_config(),
  arrange = "grid",
  output_dir = NULL
)
```

## Arguments

<code>df_coords</code>	Data frame containing: - V1, V2, ... Vn: Coordinate columns - antigen: Binary indicator for antigen points - antiserum: Binary indicator for antiserum points - cluster: (Optional) Factor or integer cluster assignments - year: (Optional) Numeric year values for temporal coloring
<code>ndim</code>	Number of dimensions in input coordinates
<code>plot_types</code>	Vector of plot types to create ("temporal", "cluster", "3d")
<code>dim_config</code>	Dimension reduction configuration object
<code>aesthetic_config</code>	Aesthetic configuration object
<code>layout_config</code>	Layout configuration object
<code>arrange</code>	How to arrange multiple plots ("grid", "vertical", "horizontal")
<code>output_dir</code>	Character. Directory for output files. If NULL, uses current directory

## Details

This function provides a high-level interface for creating multiple coordinated views of the same data. It supports:

Plot Types:

- temporal: Time-based color gradients
- cluster: Cluster-based discrete colors
- 3d: Three-dimensional interactive or static views (requires rgl package)

Arrangement Options:

- grid: Automatic square-like arrangement
- vertical: Plots stacked vertically
- horizontal: Plots arranged horizontally

All plots share consistent:

- Color schemes

- Point styles
- Axis scales
- Theme elements

Note: If "3d" is specified but the rgl package is not available, the function will skip the 3D plot and display a message.

## Value

Combined plot object (grid arrangement of plots)

## See Also

[plot\\_temporal\\_mapping](#) for individual temporal plots [plot\\_cluster\\_mapping](#) for individual cluster plots [plot\\_3d\\_mapping](#) for individual 3D plots [make\\_interactive](#) for creating interactive versions [save\\_plot](#) for saving plots to files

## Examples

```
## Not run:
# Create sample data
set.seed(123)
data <- data.frame(
  V1 = rnorm(100),
  V2 = rnorm(100),
  V3 = rnorm(100),
  V4 = rnorm(100),
  antigen = rep(c(0,1), 50),
  antiserum = rep(c(1,0), 50),
  cluster = rep(1:5, each=20),
  year = rep(2000:2009, each=10)
)

# Basic combined plot
p1 <- plot_combined(data, ndim=4,
  plot_types = c("temporal", "cluster")
)

# Advanced configuration
dim_config <- new_dim_reduction_config(
  method = "umap",
  n_components = 2,
  scale = TRUE,
  umap_params = list(
    n_neighbors = 15,
    min_dist = 0.1
  )
)

aesthetic_config <- new_aesthetic_config(
  point_size = 3,
  point_alpha = 0.7,
  point_shapes = c(antigen = 17, antiserum = 1),
  gradient_colors = list(
    low = "navy",
    high = "red"
  )
)
```

```

    ),
    show_labels = TRUE,
    label_size = 3
  )

  layout_config <- new_layout_config(
    width = 12,
    height = 8,
    aspect_ratio = 1,
    show_grid = TRUE,
    grid_type = "major",
    background_color = "white",
    panel_border = TRUE
  )

  # Create comprehensive visualization
  p2 <- plot_combined(data, ndim=4,
    plot_types = c("temporal", "cluster", "3d"),
    dim_config = dim_config,
    aesthetic_config = aesthetic_config,
    layout_config = layout_config,
    arrange = "grid"
  )

  # Save combined plot
  save_plot(p2, "combined_visualization.pdf")

  # Create interactive versions
  p3 <- plot_combined(data, ndim=4,
    plot_types = c("temporal", "cluster"),
    arrange = "horizontal"
  )

  p3_interactive <- make_interactive(p3,
    tooltip_vars = c("year", "cluster", "antigen")
  )

  # Example with different layouts
  # Vertical arrangement
  p4 <- plot_combined(data, ndim=4,
    plot_types = c("temporal", "cluster", "3d"),
    arrange = "vertical"
  )

  # Horizontal arrangement with temporal and cluster only
  p5 <- plot_combined(data, ndim=4,
    plot_types = c("temporal", "cluster"),
    arrange = "horizontal"
  )

  # Grid arrangement with custom layout
  layout_config$width <- 15
  layout_config$height <- 15
  p6 <- plot_combined(data, ndim=4,
    plot_types = c("temporal", "cluster", "3d"),
    layout_config = layout_config,
    arrange = "grid"
  )

```

```

)

# Example workflow for publication-quality figures
# 1. Create base visualization
p7 <- plot_combined(data, ndim=4,
  plot_types = c("temporal", "cluster")
)

# 2. Customize for publication
layout_config <- new_layout_config(
  width = 8,
  height = 6,
  dpi = 600,
  save_format = "pdf",
  background_color = "white",
  panel_border = TRUE,
  grid_type = "major"
)

# 3. Save high-resolution version
save_plot(p7, "publication_figure.pdf", layout_config)

## End(Not run)

```

---

plot\_distance\_heatmap *Plot Distance Matrix Heatmap*

---

## Description

Creates heatmap visualization of distance matrix showing patterns and structure in the measurements.

## Usage

```

plot_distance_heatmap(
  heatmap_data,
  scenario_name,
  aesthetic_config = new_aesthetic_config(),
  layout_config = new_layout_config()
)

```

## Arguments

heatmap_data	List output from prepare_heatmap_data()
scenario_name	Character string for output file naming
aesthetic_config	Plot aesthetic configuration object
layout_config	Plot layout configuration object

**Value**

A ggplot object containing:

- Heatmap visualization of the distance matrix
- Color gradient representing distance values
- Title showing matrix completeness percentage

**Examples**

```
## Not run:
# Basic heatmap
hmap_data <- prepare_heatmap_data(dist_mat)
p <- plot_distance_heatmap(hmap_data, "scenario1")

# Heatmap with clustering
hmap_data <- prepare_heatmap_data(dist_mat, cluster_rows = TRUE)
p2 <- plot_distance_heatmap(hmap_data, "scenario1")

# Custom configuration
aesthetic_config <- new_aesthetic_config(
  gradient_colors = list(low = "navy", high = "red")
)
p3 <- plot_distance_heatmap(hmap_data, "scenario1",
  aesthetic_config = aesthetic_config)

## End(Not run)
```

---

plot\_network\_structure

*Plot Network Structure Analysis*

---

**Description**

Creates visualization of distance matrix network structure showing data availability patterns and connectivity.

**Usage**

```
plot_network_structure(
  network_results,
  scenario_name,
  aesthetic_config = new_aesthetic_config(),
  layout_config = new_layout_config()
)
```

**Arguments**

network_results	List output from analyze_network_structure()
scenario_name	Character string for output file naming
aesthetic_config	Plot aesthetic configuration object
layout_config	Plot layout configuration object



**Value**

ggplot object

**Examples**

```
## Not run:
net_analysis <- analyze_network_structure(dist_mat)
p <- plot_network_structure(net_analysis, "scenario1")

## End(Not run)
```

---

plot\_temporal\_mapping *Create Temporal Mapping Plot*

---

**Description**

Creates a visualization of points colored by time (year) using dimension reduction, with optional antigenic velocity arrows. Points are colored on a gradient scale based on their temporal values, with different shapes for antigens and antisera.

**Usage**

```
plot_temporal_mapping(
  df_coords,
  ndim,
  dim_config = new_dim_reduction_config(),
  aesthetic_config = new_aesthetic_config(),
  layout_config = new_layout_config(),
  annotation_config = new_annotation_config(),
  output_dir = NULL,
  show_shape_legend = TRUE,
  cluster_legend_title = "Cluster",
  draw_arrows = FALSE,
  annotate_arrows = TRUE,
  phylo_tree = NULL,
  sigma_t = NULL,
  sigma_x = NULL,
  clade_node_depth = NULL
)
```

**Arguments**

df_coords	Data frame containing: - V1, V2, ... Vn: Coordinate columns - antigen: Binary indicator for antigen points - antiserum: Binary indicator for antiserum points - year: Numeric year values for temporal coloring
ndim	Number of dimensions in input coordinates
dim_config	Dimension reduction configuration object specifying method and parameters
aesthetic_config	Aesthetic configuration object controlling plot appearance

<code>layout_config</code>	Layout configuration object controlling plot dimensions and style. Use <code>x_limits</code> and <code>y_limits</code> in <code>layout_config</code> to set axis limits.
<code>annotation_config</code>	Annotation configuration object for labeling notable points
<code>output_dir</code>	Character. Directory for output files. If NULL, uses current directory
<code>show_shape_legend</code>	Logical. Whether to show the shape legend (default: TRUE)
<code>cluster_legend_title</code>	Character. Title for the cluster legend (default: "Cluster")
<code>draw_arrows</code>	logical; if TRUE, compute and draw antigenic drift vectors
<code>annotate_arrows</code>	logical; if TRUE, show names of the points having arrows
<code>phylo_tree</code>	Optional; phylo object in Newick format. Does not need to be rooted. If provided, used to compute antigenic velocity arrows.
<code>sigma_t</code>	Optional; numeric; bandwidth for the Gaussian kernel discounting on time in years or the time unit of the data. If NULL, uses Silverman's rule of thumb.
<code>sigma_x</code>	Optional; numeric; bandwidth for the Gaussian kernel discounting on antigenic distance in antigenic units. If NULL, uses Silverman's rule of thumb.
<code>clade_node_depth</code>	Optional; integer; number of levels of parent nodes to define clades. Antigens from different clades will be excluded from the calculation antigenic velocity arrows. (Default: Automatically calculated mode of leaf-to-backbone distance of the tree)

## Details

The function performs these steps:

1. Validates input data structure and types
2. Applies dimension reduction if `ndim > 2`
3. Creates visualization with temporal color gradient
4. Applies specified aesthetic and layout configurations
5. Applies custom axis limits if specified in `layout_config`

Different shapes distinguish between antigens and antisera points, while color represents temporal progression.

## Value

ggplot object containing the temporal mapping visualization

## See Also

[plot\\_cluster\\_mapping](#) for cluster-based visualization [plot\\_3d\\_mapping](#) for 3D visualization [plot\\_combined](#) for creating multiple visualizations [new\\_dim\\_reduction\\_config](#) for dimension reduction options [new\\_aesthetic\\_config](#) for aesthetic options [new\\_layout\\_config](#) for layout options [new\\_annotation\\_config](#) for annotation options

**Examples**

```
## Not run:
# Basic usage with default configurations
data <- data.frame(
  V1 = rnorm(100),
  V2 = rnorm(100),
  V3 = rnorm(100),
  antigen = rep(c(0,1), 50),
  antiserum = rep(c(1,0), 50),
  year = rep(2000:2009, each=10)
)
# Default axis limits
p1 <- plot_temporal_mapping(data, ndim=3)

# Custom axis limits via layout configuration
layout_config <- new_layout_config(
  x_limits = c(-10, 10),
  y_limits = c(-8, 8)
)
p2 <- plot_temporal_mapping(data, ndim=3,
  layout_config=layout_config)

## End(Not run)
```

---

```
prepare_heatmap_data    Generate Distance Matrix Heatmap Data
```

---

**Description**

Prepares distance matrix data for heatmap visualization by handling missing values and calculating relevant statistics.

**Usage**

```
prepare_heatmap_data(
  distance_matrix,
  cluster_rows = FALSE,
  cluster_cols = FALSE
)
```

**Arguments**

distance_matrix	Square symmetric matrix of distances
cluster_rows	Logical; whether to cluster rows
cluster_cols	Logical; whether to cluster columns

**Value**

List containing:

matrix_data	Processed matrix for visualization
row_order	Optional row ordering from clustering
col_order	Optional column ordering from clustering
stats	List of matrix statistics

**Examples**

```
## Not run:
heatmap_data <- prepare_heatmap_data(dist_mat)
print(heatmap_data$stats$completeness)

## End(Not run)
```

---

```
print.parameter_sensitivity
```

*Print Method for Parameter Sensitivity Objects*

---

**Description**

Print Method for Parameter Sensitivity Objects

**Usage**

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

**Arguments**

x	A parameter_sensitivity object
...	Additional arguments passed to print

---

```
print.profile_likelihood
```

*Print Method for Profile Likelihood Objects*

---

**Description**

Print Method for Profile Likelihood Objects

**Usage**

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

**Arguments**

x	Profile likelihood object
...	Additional arguments passed to print

---

print.topolow	<i>Print method for topolow objects</i>
---------------	---

---

**Description**

Provides a concise display of key optimization results including dimensions, iterations, error metrics and convergence status.

**Usage**

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

**Arguments**

x	A topolow object returned by create_topolow_map()
...	Additional arguments passed to print (not used)

**Examples**

```
dist_mat <- matrix(c(0, 2, 3, 2, 0, 4, 3, 4, 0), nrow=3)
result <- create_topolow_map(dist_mat, ndim=2, mapping_max_iter=100, k0=1.0, cooling_rate=0.001, c_repulsion=
print(result)
```

---

print.topolow_amcs_diagnostics	<i>Print Method for Adaptive Monte Carlo Sampling Diagnostics</i>
--------------------------------	---

---

**Description**

Print Method for Adaptive Monte Carlo Sampling Diagnostics

**Usage**

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

**Arguments**

x	A topolow_amcs_diagnostics object
...	Additional arguments passed to print

---

```
print.topolow_convergence
```

*Print Method for Convergence Diagnostics*

---

### Description

Print Method for Convergence Diagnostics

### Usage

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

### Arguments

x	A topolow_convergence object
...	Additional arguments passed to print

---

```
process_antigenic_data
```

*Process Raw Antigenic Assay Data*

---

### Description

Processes raw antigenic assay data from CSV files into standardized long and matrix formats. Handles both titer data (which needs conversion to distances) and direct distance measurements like IC50. Preserves threshold indicators (<, >) and handles repeated measurements by averaging.

### Usage

```
process_antigenic_data(
  file_path,
  antigen_col,
  serum_col,
  value_col,
  is_titer = TRUE,
  metadata_cols = NULL,
  id_prefix = FALSE,
  base = NULL,
  scale_factor = 10
)
```

### Arguments

file_path	Character. Path to CSV file containing raw data.
antigen_col	Character. Name of column containing virus/antigen identifiers.
serum_col	Character. Name of column containing serum/antibody identifiers.
value_col	Character. Name of column containing measurements (titers or distances).

is_titer	Logical. Whether values are titers (TRUE) or distances like IC50 (FALSE).
metadata_cols	Character vector. Names of additional columns to preserve.
id_prefix	Logical. Whether to prefix IDs with V/ and S/ (default: TRUE).
base	Numeric. Base for logarithm transformation (default: 2 for titers, e for IC50).
scale_factor	Numeric. Scale factor for titers (default: 10).

## Details

The function handles these key steps:

1. Reads and validates input data
2. Transforms values to log scale
3. Converts titers to distances if needed
4. Averages repeated measurements
5. Creates standardized long format
6. Creates distance matrix
7. Preserves metadata and threshold indicators
8. Preserves virusYear and serumYear columns if present

Input requirements and constraints:

- CSV file must contain required columns
- Column names must match specified parameters in the function input
- Values can include threshold indicators (< or >)
- Metadata columns must exist if specified
- Allowed Year-related column names are "virusYear" and "serumYear"

## Value

List containing:

long	Data frame in long format with standardized columns
matrix	Distance matrix

## Examples

```
## Not run:
# Process titer data (e.g., HI assay)
results <- process_antigenic_data(
  "smith2004.csv",
  antigen_col = "virusStrain",
  serum_col = "serumStrain",
  value_col = "titer",
  is_titer = TRUE,
  metadata_cols = c("cluster", "color")
)

# Process IC50 data
results <- process_antigenic_data(
  "hiv_assays.csv",
  antigen_col = "Virus",
```

```

    serum_col = "Antibody",
    value_col = "IC50",
    is_titer = FALSE
)

## End(Not run)

```

---

```
process_antigenic_data_notransform
```

*Process Raw Antigenic Assay Data without transformations*

---

## Description

Processes raw antigenic assay data from CSV files into standardized long and matrix formats. Handles both titer data (which needs conversion to distances) and direct distance measurements like IC50. Preserves threshold indicators (<, >) and handles repeated measurements by averaging.

## Usage

```

process_antigenic_data_notransform(
  file_path,
  antigen_col,
  serum_col,
  value_col,
  is_titer = TRUE,
  metadata_cols = NULL,
  id_prefix = FALSE,
  base = NULL,
  scale_factor = 10
)

```

## Arguments

file_path	Character. Path to CSV file containing raw data.
antigen_col	Character. Name of column containing virus/antigen identifiers.
serum_col	Character. Name of column containing serum/antibody identifiers.
value_col	Character. Name of column containing measurements (titers or distances).
is_titer	Logical. Whether values are titers (TRUE) or distances like IC50 (FALSE).
metadata_cols	Character vector. Names of additional columns to preserve.
id_prefix	Logical. Whether to prefix IDs with V/ and S/ (default: TRUE).
base	Numeric. Base for logarithm transformation (default: 2 for titers, e for IC50).
scale_factor	Numeric. Scale factor for titers (default: 10).



## Details

The function handles these key steps:

1. Reads and validates input data
2. Transforms values to log scale
3. Converts titers to distances if needed
4. Averages repeated measurements
5. Creates standardized long format
6. Creates distance matrix
7. Preserves metadata and threshold indicators
8. Preserves virusYear and serumYear columns if present

Input requirements and constraints:

- CSV file must contain required columns
- Column names must match specified parameters in the function input
- Values can include threshold indicators (< or >)
- Metadata columns must exist if specified
- Allowed Year-related column names are "virusYear" and "serumYear"

## Value

List containing:

long	Data frame in long format with standardized columns
matrix	Distance matrix

## Examples

```
## Not run:
# Process titer data (e.g., HI assay)
results <- process_antigenic_data(
  "smith2004.csv",
  antigen_col = "virusStrain",
  serum_col = "serumStrain",
  value_col = "titer",
  is_titer = TRUE,
  metadata_cols = c("cluster", "color")
)

# Process IC50 data
results <- process_antigenic_data(
  "hiv_assays.csv",
  antigen_col = "Virus",
  serum_col = "Antibody",
  value_col = "IC50",
  is_titer = FALSE
)

## End(Not run)
```

---

profile_likelihood	<i>Profile Likelihood Analysis</i>
--------------------	------------------------------------

---

### Description

Calculates profile likelihood for a parameter by evaluating conditional maximum likelihood across a grid of parameter values. Uses local sample windowing to estimate conditional likelihoods. This implementation is not a classical profile likelihood calculation, but rather an "empirical profile likelihood" which estimates the profile likelihood at each point based on the many observations previously sampled in Monte Carlo simulations.

### Usage

```
profile_likelihood(
  param,
  samples,
  grid_size = 40,
  bandwidth_factor = 0.05,
  start_factor = 0.5,
  end_factor = 1.5,
  min_samples = 5
)
```

### Arguments

param	Character name of parameter to analyze
samples	Data frame containing parameter samples and log-likelihoods
grid_size	Integer number of grid points (default: 48)
bandwidth_factor	Numeric factor for local sample window (default: 0.03)
start_factor, end_factor	Numeric range multipliers for parameter grid (default: 0.5, 1.2)
min_samples	Integer minimum samples required for reliable estimate (default: 10)

### Details

For each value in the parameter grid, the function:

1. Identifies nearby samples using bandwidth window
2. Calculates conditional maximum likelihood from these samples
3. Tracks sample counts to assess estimate reliability
4. Handles boundary conditions and sparse regions

### Value

Object of class "profile\_likelihood" containing:

param	Vector of parameter values
ll	Vector of log-likelihood values

param_name	Name of analyzed parameter
bandwidth	Bandwidth used for local windows
sample_counts	Number of samples per estimate

**See Also**

[plot.profile\\_likelihood](#) for visualization

**Examples**

```
## Not run:
# Calculate profile likelihood for parameter "log_N"
pl <- profile_likelihood("log_N", mcmc_samples,
                        grid_size = 60,
                        bandwidth_factor = 0.02)

# Plot results
plot(pl)

## End(Not run)
```

---

prune\_distance\_network

*Prune Distance Data for Network Quality*


---

**Description**

Iteratively removes viruses and antibodies with insufficient connections to create a well-connected network subset. The pruning continues until all remaining points have at least the specified minimum number of connections.

**Usage**

```
prune_distance_network(
  data,
  virus_col,
  antibody_col,
  min_connections,
  iterations = 100
)
```

**Arguments**

data	Data frame in long format containing: - Column for viruses/antigens - Column for antibodies/antisera - Distance measurements (can contain NAs) - Optional metadata columns
virus_col	Character name of virus/antigen column
antibody_col	Character name of antibody/antiserum column
min_connections	Integer minimum required connections per point
iterations	Integer maximum pruning iterations (default 100)

**Value**

List containing:

pruned_data	Data frame of pruned measurements
stats	List of pruning statistics including: <ul style="list-style-type: none"> <li>• original_points: Number of points before pruning</li> <li>• remaining_points: Number of points after pruning</li> <li>• iterations: Number of pruning iterations performed</li> <li>• min_connections: Minimum connections in final set</li> </ul>

**Examples**

```
## Not run:
# Basic pruning keeping points with at least 10 connections
pruned <- prune_distance_network(hiv_data,
                                virus_col = "Virus",
                                antibody_col = "Antibody",
                                min_connections = 10)

# Check pruning statistics
print(pruned$stats)

## End(Not run)
```

---

prune\_distance\_network\_temporal

*Prune Distance Data for Network Quality with Temporal Coverage*


---

**Description**

Prunes network data while maintaining temporal coverage by keeping the most well-connected points in each year. For each year, retains points with at least min\_connections, but if this leaves too few points, keeps the top min\_per\_year most-connected points regardless of their connection count.

**Usage**

```
prune_distance_network_temporal(
  data,
  virus_col,
  antibody_col,
  year_col,
  min_connections,
  min_per_year = 1,
  iterations = 100
)
```

**Arguments**

data	Data frame in long format containing: - Column for viruses/antigens - Column for antibodies/antisera - Distance measurements (can contain NAs) - Column for years
virus_col	Character name of virus/antigen column
antibody_col	Character name of antibody/antiserum column
year_col	Character name of year column
min_connections	Target minimum connections (soft threshold)
min_per_year	Integer minimum points to keep per year (default: 1)
iterations	Integer maximum pruning iterations (default 100)

**Value**

List containing:

pruned_data	Data frame of pruned measurements
stats	List of pruning statistics including: <ul style="list-style-type: none"> <li>• original_points: Number of points before pruning</li> <li>• remaining_points: Number of points after pruning</li> <li>• min_connections: Target connection threshold used</li> <li>• years_coverage: Points per year in final set</li> </ul>

**Examples**

```
## Not run:
pruned <- prune_distance_network_temporal(
  data = hiv_results$long,
  virus_col = "Virus",
  antibody_col = "Antibody",
  year_col = "virusYear",
  min_connections = 10,
  min_per_year = 1
)

## End(Not run)
```

---

prune\_distance\_network\_topn

*Prune Distance Network by Keeping Top N Points Per Year*


---

**Description**

Prunes network data by keeping the top N most-connected viruses and antibodies for each year. If a year has fewer than min\_per\_year points, keeps all points for that year sorted by their connection counts.

**Usage**

```
prune_distance_network_topn(
  data,
  virus_col,
  antibody_col,
  year_col,
  top_n,
  min_per_year = 1
)
```

**Arguments**

<code>data</code>	Data frame in long format containing: - Column for viruses/antigens - Column for antibodies/antisera - Distance measurements (can contain NAs) - Column for years
<code>virus_col</code>	Character name of virus/antigen column
<code>antibody_col</code>	Character name of antibody/antiserum column
<code>year_col</code>	Character name of year column
<code>top_n</code>	Integer number of top viruses and antibodies to keep per year
<code>min_per_year</code>	Integer minimum total points to keep per year (default: 1)

**Value**

List containing:

<code>pruned_data</code>	Data frame of pruned measurements
<code>stats</code>	List of pruning statistics including: <ul style="list-style-type: none"> <li>• <code>original_points</code>: Number of points before pruning</li> <li>• <code>remaining_points</code>: Number of points after pruning</li> <li>• <code>top_n</code>: Number of top points requested per category</li> <li>• <code>years_coverage</code>: Points per year in final set</li> </ul>

**Examples**

```
## Not run:
pruned <- prune_distance_network_topn(
  data = hiv_results$long,
  virus_col = "Virus",
  antibody_col = "Antibody",
  year_col = "virusYear",
  top_n = 5,
  min_per_year = 1
)

## End(Not run)
```

---

run\_adaptive\_sampling *Run Adaptive Monte Carlo Sampling*


---

## Description

Performs adaptive Monte Carlo sampling to explore parameter space, either locally or distributed via SLURM. Samples are drawn adaptively based on previous evaluations to focus sampling in high-likelihood regions. Results from all jobs accumulate in a single output file.

## Usage

```
run_adaptive_sampling(
    initial_samples_file,
    scenario_name,
    distance_matrix,
    num_parallel_jobs = 5,
    max_cores = NULL,
    num_samples = 10,
    mapping_max_iter = 1000,
    relative_epsilon = 1e-04,
    folds = 20,
    time = "8:00:00",
    memory = "10G",
    output_dir = NULL,
    use_slurm = FALSE,
    cider = FALSE,
    verbose = FALSE
)
```

## Arguments

initial_samples_file	Character. Path to CSV file containing initial samples. Must contain columns: log_N, log_k0, log_cooling_rate, log_c_repulsion, NLL
scenario_name	Character. Name for output files.
distance_matrix	Matrix. Distance matrix of the input data.
num_parallel_jobs	Integer. Number of parallel jobs (cores on local machine or SLURM jobs).
max_cores	Integer. Maximum number of cores to use for parallel processing. If NULL, uses all available cores minus 1 (default: NULL).
num_samples	Integer. Number of new samples to be added to the CSV file containing initial samples through Adaptive Monte Carlo sampling (default: 10).
mapping_max_iter	Integer. Maximum iterations per map optimization.
relative_epsilon	Numeric. Convergence threshold.
folds	Integer. Number of CV folds (default: 10).
time	Character. Walltime for SLURM jobs in HH:MM:SS format. Default: "8:00:00".

memory	Character. Memory allocation for SLURM jobs. Default: "10G".
output_dir	Character. Directory for output files. If NULL, uses current directory.
use_slurm	Logical. Whether to use SLURM (default: FALSE).
cider	Logical. Whether to use cider queue (default: FALSE).
verbose	Logical. Whether to print progress messages. Default: FALSE.

**Value**

NULL. Results are written to: model\_parameters/{scenario\_name}\_model\_parameters.csv

---

save_plot	<i>Save Plot to File</i>
-----------	--------------------------

---

**Description**

Saves a plot (ggplot or rgl scene) to file with specified configuration. Supports multiple output formats and configurable dimensions.

**Usage**

```
save_plot(
  plot,
  filename,
  layout_config = new_layout_config(),
  output_dir = NULL
)
```

**Arguments**

plot	ggplot or rgl scene object to save
filename	Output filename (with or without extension)
layout_config	Layout configuration object controlling output parameters
output_dir	Character. Directory for output files. If NULL, uses current directory

**Details**

Supported file formats:

- PNG: Best for web and general use
- PDF: Best for publication quality vector graphics
- SVG: Best for web vector graphics
- EPS: Best for publication quality vector graphics

The function will:

1. Auto-detect plot type (ggplot or rgl)
2. Use appropriate saving method
3. Apply layout configuration settings
4. Add file extension if not provided



**Value**

Invisible NULL

**Examples**

```
## Not run:
# Create sample plot
data <- data.frame(
  V1 = rnorm(100),
  V2 = rnorm(100),
  antigen = rep(c(0,1), 50),
  antiserum = rep(c(1,0), 50),
  year = rep(2000:2009, each=10)
)
p <- plot_temporal_mapping(data, ndim=2)

# Basic save
save_plot(p, "temporal_plot.png")

# Save with custom layout
layout_config <- new_layout_config(
  width = 12,
  height = 8,
  dpi = 600,
  save_format = "pdf"
)

save_plot(p, "high_res_plot", layout_config)

# Save 3D plot
p3d <- plot_3d_mapping(data, ndim=3, interactive=FALSE)
save_plot(p3d, "3d_plot.png", layout_config)

## End(Not run)
```

---

scatterplot\_fitted\_vs\_true

*Plot Fitted vs True Distances*


---

**Description**

Creates diagnostic plots comparing fitted distances from a model against true distances. Generates both a scatter plot with prediction intervals and a residuals plot.

**Usage**

```
scatterplot_fitted_vs_true(
  distance_matrix,
  p_dist_mat,
  scenario_name = NA,
  ndim = NA,
  save_plot = TRUE,
```

```

    output_dir = NULL,
    confidence_level = 0.95
  )

```

### Arguments

distance_matrix	Matrix of true distances
p_dist_mat	Matrix of predicted/fitted distances
scenario_name	Character string for output file naming
ndim	Integer number of dimensions used in the model
save_plot	Logical. Whether to save plots to files. Default: TRUE
output_dir	Character. Directory for output files. If NULL, uses current directory
confidence_level	Numeric confidence level for prediction intervals (default: 0.95)

### Value

Invisibly returns NULL, creates two plot files:

- {scenario\_name}prediction\_scatter\_dim{ndim}.png
- {scenario\_name}residuals\_vs\_fitted\_dim{ndim}.png

### Examples

```

## Not run:
# Create scatter and residual plots
scatterplot_fitted_vs_true(truth_matrix, predicted_matrix,
                           scenario_name = "example",
                           ndim = 5)

## End(Not run)

```

---

submit\_job

*Submit Job to SLURM or Run Locally*


---

### Description

Submits a job to SLURM if available, otherwise runs locally. Provides consistent interface for both execution modes.

### Usage

```
submit_job(script_file, use_slurm = TRUE, cider = FALSE)
```

### Arguments

script_file	Path to script file
use_slurm	Logical; whether to use SLURM if available
cider	Logical; whether to use cider_qos queue

**Value**

Exit status code (invisible)

---

summary.topolow

*Summary method for topolow objects*


---

**Description**

Provides a detailed summary of the optimization results including parameters, convergence and performance metrics.

**Usage**

```
## S3 method for class 'topolow'
summary(object, ...)
```

**Arguments**

object            A topolow object returned by create\_topolow\_map()  
 ...              Additional arguments passed to summary (not used)

**Examples**

```
dist_mat <- matrix(c(0, 2, 3, 2, 0, 4, 3, 4, 0), nrow=3)
result <- create_topolow_map(dist_mat, ndim=2, mapping_max_iter=100, k0=1.0, cooling_rate=0.001, c_repulsion=
summary(result)
```

---

symmetric\_to\_nonsymmetric\_matrix

*Convert distance matrix to assay panel format*


---

**Description**

Convert distance matrix to assay panel format

**Usage**

```
symmetric_to_nonsymmetric_matrix(dist_matrix, selected_names)
```

**Arguments**

dist\_matrix      Distance matrix  
 selected\_names   Names of reference points

**Value**

Matrix in assay panel format

---

unweighted_kde	<i>Unweighted Kernel Density Estimation</i>
----------------	---

---

**Description**

Standard kernel density estimation for univariate data with various bandwidth selection rules.

**Usage**

```
unweighted_kde(x, n = 512, from = min(x), to = max(x), bw = "nrd0")
```

**Arguments**

x	Numeric vector of samples
n	Integer number of evaluation points
from, to	Numeric range for evaluation points
bw	Bandwidth selection ("nrd0", "nrd", "ucv", "bcv", "sj" or numeric)

**Value**

List containing:

x	Vector of evaluation points
y	Vector of density estimates
bw	Selected bandwidth

---

weighted_kde	<i>Weighted Kernel Density Estimation</i>
--------------	---

---

**Description**

Performs weighted kernel density estimation for univariate data. Useful for analyzing parameter distributions with importance weights.

**Usage**

```
weighted_kde(x, weights, n = 512, from = min(x), to = max(x))
```

**Arguments**

x	Numeric vector of samples
weights	Numeric vector of weights
n	Integer number of evaluation points
from, to	Numeric range for evaluation points

**Value**

List containing:

x	Vector of evaluation points
y	Vector of density estimates

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