

Package: TemporalModelR (via r-universe)

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Type Package

Title Temporally Explicit Species Distribution Modelling

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Description Increases the ease of implementing a temporally-explicit modeling methodology when building ecological niche and species distribution models. Provides functions to assist with three major steps of temporally-explicit models: (i) preprocessing species and environmental data and generating suitable background or pseudoabsence data, (ii) building a niche model and generating temporally-explicit predictions from that model, and (iii) model postprocessing to explore spatiotemporal trends in model predictions. Methodological and theoretical foundations are described in Ingenloff and Peterson (2021) <doi:10.1111/2041-210X.13564>, Franklin (2010, ISBN:9780521700023), Peterson et al. (2011, ISBN:9780691136882), Blonder (2018) <doi:10.1111/ecog.03187>, Senay et al. (2013) <doi:10.1371/journal.pone.0071218>, and Li and Zhang (2024) <doi:10.48550/arXiv.2404.05933>.

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<https://cjhughes926.github.io/TemporalModelR/>

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Contents

analyze_temporal_patterns	3
analyze_trends_by_spatial_unit	5
build_temporal_gam	7
build_temporal_glm	10
build_temporal_hv	13
build_temporal_rf	15
extdata	18
generate_absences	19
generate_spatiotemporal_predictions	23
plot_model_assessment	26
raster_align	28
scale_rasters	29
spatiotemporal_partition	31
spatiotemporal_rarefaction	35
summarize_raster_outputs	37
temporally_explicit_extraction	39
tmr_absences	41
tmr_absences_annual	42
tmr_absences_user	42
tmr_glm	43
tmr_glm_annual	43
tmr_partition	44
tmr_partition_annual	44
tmr_partition_small	45
tmr_predictions	45
tmr_predictions_annual	46
Index	47

analyze_temporal_patterns

Analyze Temporal Patterns in Binary Raster Time Series

Description

Postprocessing function that applies changepoint detection methods to identify temporal trends in habitat suitability across consecutive predictions. Classifies pixels as stable, increasing in quality, or decreasing in quality, and identifies time periods of significant change.

Usage

```
analyze_temporal_patterns(
  binary_stack,
  summary_raster,
  time_steps,
  fastcpd_params = list(),
  output_dir = NULL,
  n_tiles_x = 1,
  n_tiles_y = 1,
  alpha = 0.05,
  spatial_autocorrelation = TRUE,
  verbose = TRUE,
  estimate_time = TRUE,
  overwrite = FALSE
)
```

Arguments

binary_stack	RasterStack, RasterBrick, or character. Stack of binary raster layers across time, or path to directory containing binary rasters. Typically from summarize_raster_outputs .
summary_raster	RasterLayer. Per-pixel proportion of time periods where a pixel is suitable. From summarize_raster_outputs .
time_steps	Integer vector. Time labels corresponding to raster layers (same length as number of layers).
fastcpd_params	List. Named list of parameters passed to fastcpd changepoint detection function. Default is empty list. Supports parameterization from fastcpd_binomial .
output_dir	Character. Optional. Output directory for pattern rasters. When NULL (default), rasters are written to temporary files and not saved persistently. Provide a path to write named output files to disk.
n_tiles_x	Integer. Number of tiles in the x direction for tiled processing. Default is 1. Increase to reduce peak memory use for large rasters and prevent crashes.
n_tiles_y	Integer. Number of tiles in the y direction for tiled processing. Default is 1. Increase to reduce peak memory use for large rasters and prevent crashes.
alpha	Numeric. Significance level for changepoint detection. Default is 0.05.

spatial_autocorrelation	Logical. If TRUE (default), includes a neighbor variable in the changepoint analysis to account for spatial autocorrelation.
verbose	Logical. If TRUE (default), prints progress messages during processing.
estimate_time	Logical. If TRUE (default), estimates runtime from a sample of pixels before full processing begins. If FALSE, proceeds directly to processing without a time estimate.
overwrite	Logical. If TRUE, overwrites existing output files. If FALSE (default), existing files are skipped.

Details

Applies changepoint detection using `fastcpd` to identify significant temporal shifts in spatial suitability. Accounts for spatial and temporal autocorrelation when `spatial_autocorrelation = TRUE`. The `fastcpd_params` list allows customization of the changepoint detection algorithm, and is passed through to `fastcpd.binomial` (e.g. `list(cost_adjustment = "BIC", trim = 0.025)`).

Pattern classifications enable identification of expanding, contracting, or stable g-space distributions over time or site level assessments of directional change in suitability.

Classification assumes consecutive rasters. Time periods shorter than ~15 time steps may be too short to classify increases or decreases.

Value

Invisibly returns a list containing:

- `pattern`: `SpatRaster` classifying pixels as integer values 1-6, corresponding to "Never Suitable", "Always Suitable", "No Pattern", "Increasing Suitability", "Decreasing Suitability", or "Fluctuating".
- `time_decrease`: `SpatRaster` showing the time step of first significant decrease for pixels classified as decreasing.
- `time_increase`: `SpatRaster` showing the time step of first significant increase for pixels classified as increasing.

See Also

Postprocessing: [summarize_raster_outputs](#)

External: [fastcpd](#)

Examples

```
con_file <- system.file("extdata/binary/consensus_stack.tif",
  package = "TemporalModelR")

frq_file <- system.file("extdata/binary/frequency_raster.tif",
  package = "TemporalModelR")

binary_stack <- terra::rast(con_file)
```

```
summary_raster <- terra::rast(frq_file)

time_steps <- expand.grid(
  year      = 1:15,
  season    = "Spring",
  stringsAsFactors = FALSE
)

analyze_temporal_patterns(
  binary_stack      = binary_stack,
  summary_raster    = summary_raster,
  time_steps        = time_steps,
  output_dir        = tempdir(),
  spatial_autocorrelation = FALSE,
  overwrite         = TRUE,
  estimate_time     = FALSE,
  verbose           = FALSE
)
```

analyze_trends_by_spatial_unit

Summarize Temporal Patterns and Trends by Spatial Unit

Description

Aggregates temporal pattern classifications and change metrics across user-defined spatial units (e.g., states, counties, watersheds). Returns summary tables and optionally generates simple visualizations.

Usage

```
analyze_trends_by_spatial_unit(shapefile_path, name_field, binary_stack = NULL,
                               pattern_raster = NULL, time_decrease_raster = NULL,
                               time_increase_raster = NULL, time_steps = NULL,
                               output_dir = NULL, overwrite = FALSE,
                               create_plot = TRUE, pie_scale = 0.15,
                               verbose = TRUE)
```

Arguments

shapefile_path Character, sf object, or sfc object. Path to a shapefile or directory containing one, an sf object, or an sfc geometry. Shapefiles spatial units will be used as the units for the data summary.

name_field Character. Attribute field to use as spatial unit labels.

binary_stack SpatRaster or character. Optional stack of binary prediction rasters across time. Required for per-unit habitat summaries and time series plots.

<code>pattern_raster</code>	SpatRaster or character. Optional pattern classification raster from analyze_temporal_patterns . Required for pattern composition summaries and scatterpie map.
<code>time_decrease_raster</code>	SpatRaster or character. Optional raster of first decrease time step from analyze_temporal_patterns .
<code>time_increase_raster</code>	SpatRaster or character. Optional raster of first increase time step from analyze_temporal_patterns .
<code>time_steps</code>	Vector. Time labels for layers in <code>binary_stack</code> . Required when <code>binary_stack</code> or change rasters are provided.
<code>output_dir</code>	Character or NULL. Directory for CSV outputs and plots. If NULL, results are returned in memory only and no files are written. Default is NULL.
<code>overwrite</code>	Logical. If TRUE, recomputes and overwrites existing CSVs. Default is FALSE.
<code>create_plot</code>	Logical. If TRUE (default), generates and saves plots.
<code>pie_scale</code>	Numeric in (0, 1]. Largest pie's radius as a fraction of the smaller map dimension. Default is 0.15, meaning the biggest pie spans roughly 30% of the smaller map dimension (radius = 15%, so diameter = 30%). Smaller pies scale so their area is proportional to the unit's pixel count. The fraction is converted internally to coordinate units, so this argument works identically across CRSes (degrees, meters, etc.) without manual rescaling.
<code>verbose</code>	Logical. If TRUE (default), prints progress messages during processing. Includes details on raster extraction and per-spatial-unit summaries.

Details

Summarizes results from modeling and post-processing at the scale of specific spatial blocks to allow for a nuanced look at spatiotemporal patterns.

Value

Invisibly returns a list containing:

- `overall_summary`: Pattern composition per spatial unit (present when `pattern_raster` is supplied).
- `timestep_summary`: Suitable pixel counts per unit per time step (present when `binary_stack` is supplied).
- `change_by_timestep`: Gain and loss pixel counts per unit per time step (present when both change rasters are supplied).
- `plots`: Named list of recorded plot objects (present when `create_plot = TRUE`).

See Also

Post-processing: [summarize_raster_outputs](#), [analyze_temporal_patterns](#)

Examples

```

con_file <- system.file("extdata/binary/consensus_stack.tif",
                        package = "TemporalModelR")

binary_stack <- terra::rast(con_file)

study_crs <- sf::st_crs(binary_stack)

zones_sf <- rbind(
  sf::st_sf(ZONE = "West",
            geometry = sf::st_sfc(sf::st_polygon(list(
              matrix(c(0, 0, 1500, 1500, 0,
                    0, 1500, 1500, 0, 0), ncol = 2)
            )), crs = study_crs)),
  sf::st_sf(ZONE = "East",
            geometry = sf::st_sfc(sf::st_polygon(list(
              matrix(c(1500, 1500, 3000, 3000, 1500,
                    0, 1500, 1500, 0, 0), ncol = 2)
            )), crs = study_crs))
)

time_steps <- expand.grid(
  year      = 1:15,
  season    = "Spring",
  stringsAsFactors = FALSE
)

analyze_trends_by_spatial_unit(
  shapefile_path = zones_sf,
  name_field     = "ZONE",
  binary_stack   = binary_stack,
  time_steps     = time_steps,
  create_plot    = FALSE,
  verbose        = FALSE
)

```

build_temporal_gam *Build Temporal GAM Models Across Cross-Validation Folds*

Description

Modeling function that constructs binomial generalized additive models (GAMs) for each cross-validation fold using presence and pseudoabsence data. Each model reserves one fold as testing data and uses the remaining folds as training data. The user supplies the model formula directly using standard **mgcv** formula syntax, including smooth terms such as `s()`, `te()`, and `ti()`. Supports automatic or manual probability thresholding for converting continuous predictions to binary suitability classifications necessary for downstream analyses. The returned object follows the same structure as `build_temporal_glm`, `build_temporal_hv`, and `build_temporal_rf`, and is accepted directly by `generate_spatiotemporal_predictions`.

Usage

```
build_temporal_gam(partition_result, pseudoabsence_result, model_formula,
  link = "logit", gam_params = list(method = "REML"),
  threshold_method = "tss",
  output_dir = file.path(tempdir(), "GAM_Models"),
  create_plot = TRUE, plot_palette = "Dark 2",
  overwrite = FALSE, time_cols = NULL, verbose = TRUE)
```

Arguments

- partition_result** List or character. Output from [spatiotemporal_partition](#) or path to an .rds file containing that output.
- pseudoabsence_result** List or character. Output from [generate_absences](#) or path to an .rds file containing that output.
- model_formula** Formula or character. The right-hand side of the model formula supplied as either a formula object or a character string. The response variable (presence) is always added automatically on the left-hand side, so only the right-hand side needs to be provided. Both of the following are accepted and equivalent:
- $\sim s(\text{Var1}) + s(\text{Var2}) + \text{Var3}$
 - $\sim s(\text{Var1}) + s(\text{Var2}) + \text{Var3}$
- Standard **mgecv** formula syntax applies. Smooth terms are specified with `s()` for univariate smooths, `te()` for tensor product smooths of two or more variables, and `ti()` for tensor product interaction terms. Parametric terms can be included alongside smooth terms using `+`. The basis type and dimension can be controlled via arguments to `s()`, e.g. `s(Var1, k = 5, bs = "tp")`. All predictor names referenced in the formula must be present as columns in both the presence and pseudoabsence data.
- link** Character. The link function for the binomial GAM. One of "logit" (default), "probit", "cloglog", or "cauchit". See [binomial](#) for details on each link function.
- gam_params** Named list. Additional arguments passed to [gam](#), such as method for the smoothing parameter estimation method (e.g. "REML") or select for additional shrinkage. Default is `list(method = "REML")`.
- threshold_method** Character or numeric. Method used to convert continuous predicted probabilities to binary suitability. Accepted values:
- "prevalence": Sets threshold equal to the prevalence (proportion of presences) in the training data for that fold.
 - "tss": Selects the threshold that maximizes the True Skill Statistic (sensitivity + specificity - 1) on the training data. Default.
 - A numeric value between 0 and 1 (e.g. 0.4): Uses that value as a fixed threshold for all folds directly.
- output_dir** Character. Directory to write output files including saved model objects and plots. Default is `file.path(tempdir(), "GAM_Models")`.

create_plot	Logical. If TRUE, generates per-fold response curve plots and a combined ROC curve summary. Default is TRUE.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see hcl.pals) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".
overwrite	Logical. If TRUE, overwrites existing saved model files. If FALSE, loads existing files when available. Default is FALSE.
time_cols	Character. Name of the column(s) containing year or time step values in the occurrence data. Must match time_cols used in spatiotemporal_partition . Default is NULL.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-fold training summaries and file-saved messages. The completion summary and metrics table are always printed regardless of this setting.

Details

GAMs are fit using [gam](#) from the **mgcv** package with `family = binomial(link = link)`. Smooth terms default to thin plate regression splines (`bs = "tp"`) with the basis dimension `k` chosen automatically by **mgcv** unless specified in the formula. Smoothing parameters are estimated by REML by default.

The returned object is recognized by [generate_spatiotemporal_predictions](#), which uses the `model_type` field to use the correct prediction and evaluation logic.

Value

A list with class "TemporalGAM" containing:

- `models`: Named list of fitted `gam` objects, one per fold.
- `thresholds`: Named numeric vector of probability thresholds used for binary classification, one per fold.
- `threshold_method`: Character string recording the thresholding method used.
- `model_formula`: The formula object as passed to the fitting function.
- `link`: Character string recording the link function used.
- `model_vars`: Character vector of predictor names extracted from the formula right-hand side.
- `fold_training_data`: Named list of training data frames used to fit each fold model, retained for downstream prediction.
- `fold_test_metrics`: Data frame of held-out test fold metrics per fold: Threshold, AUC, TSS, Kappa, Sensitivity, and Specificity. Also written to `Fold_Test_Metrics.csv` in `output_dir`.
- `output_dir`: Path to the output directory.
- `model_type`: Character string "gam", used by [generate_spatiotemporal_predictions](#).
- `plots`: Named list of recorded plot objects when `create_plot = TRUE`. Plots can be replayed with `grDevices::replayPlot()`.

See Also

Preprocessing: [spatiotemporal_partition](#), [generate_absences](#)

Modeling: [build_temporal_glm](#), [build_temporal_rf](#), [build_temporal_hv](#), [generate_spatiotemporal_predictions](#)

External: [gam](#), [s](#)

Examples

```
data(tmr_partition, package = "TemporalModelR")

data(tmr_absences, package = "TemporalModelR")

build_temporal_gam(
  partition_result      = tmr_partition,
  pseudoabsence_result = tmr_absences,
  model_formula         = ~ s(elevation) + s(forest_cover) + s(prseas),
  threshold_method     = "tss",
  output_dir           = tempdir(),
  create_plot          = FALSE,
  time_cols            = c("year", "season"),
  verbose              = FALSE
)
```

build_temporal_glm *Build Temporal GLM Models Across Cross-Validation Folds*

Description

Modeling function that constructs binomial generalized linear models (GLMs) for each cross-validation fold using presence and pseudoabsence data. Each model reserves one fold as testing data and uses the remaining folds as training data. The user supplies the model formula directly, giving full control over predictor terms, polynomials, and interactions. The link function can be set to logit, probit, complementary log-log, or cauchit. Supports automatic or manual probability thresholding for converting continuous predictions to binary suitability classifications necessary for downstream analyses. The returned object follows the same structure as [build_temporal_hv](#), [build_temporal_gam](#), and [build_temporal_rf](#), and is accepted directly by [generate_spatiotemporal_predictions](#).

Usage

```
build_temporal_glm(partition_result, pseudoabsence_result, model_formula,
  link = "logit", threshold_method = "tss",
  output_dir = file.path(tempdir(), "GLM_Models"),
  create_plot = TRUE, plot_palette = "Dark 2", overwrite = FALSE,
  time_cols = NULL, verbose = TRUE)
```

Arguments

partition_result	List or character. Output from spatiotemporal_partition or path to an .rds file containing that output.
pseudoabsence_result	List or character. Output from generate_absences or path to an .rds file containing that output.
model_formula	Formula or character. The right-hand side of the model formula supplied as either a formula object or a character string. The response variable (presence) is always added automatically on the left-hand side, so only the right-hand side needs to be provided. Both of the following are accepted and equivalent: <ul style="list-style-type: none"> • $\sim \text{Var1} + \text{Var2} + \text{I}(\text{Var1}^2)$ • <code>"~ Var1 + Var2 + I(Var1^2)"</code> Standard R formula syntax applies: + for additive terms, * for main effects plus interaction, : for interaction only, I() for arithmetic transformations, poly() for orthogonal polynomials, log(), sqrt(), and any other base R function that can appear in a formula. All predictor names referenced in the formula must be present as columns in both the presence and pseudoabsence data.
link	Character. The link function for the binomial GLM. One of "logit" (default), "probit", "cloglog", or "cauchit". See binomial for details on each link function.
threshold_method	Character or numeric. Method used to convert continuous predicted probabilities to binary suitability. Accepted values: <ul style="list-style-type: none"> • "prevalence": Sets threshold equal to the prevalence (proportion of presences) in the training data for that fold. • "tss": Selects the threshold that maximizes the True Skill Statistic (sensitivity + specificity - 1) on the training data. Default. • A numeric value between 0 and 1 (e.g. 0.4): Uses that value as a fixed threshold for all folds directly.
output_dir	Character. Directory to write output files including saved model objects and plots. Default is <code>file.path(tempdir(), "GLM_Models")</code> .
create_plot	Logical. If TRUE, generates per-fold response curve plots and a combined ROC curve summary. Default is TRUE.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see hcl.pals) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".
overwrite	Logical. If TRUE, overwrites existing saved model files. If FALSE, loads existing files when available. Default is FALSE.
time_cols	Character. Name of the column(s) containing year or time step values in the occurrence data. Must match time_cols used in spatiotemporal_partition . Default is NULL.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-fold training summaries and file-saved messages. The completion summary and metrics table are always printed regardless of this setting.

Details

The `model_formula` argument accepts any standard R formula right-hand side. The response (presence) is prepended automatically. All R formula operators are valid, including `I()`, `poly()`, `log()`, `sqrt()`, `:`, and `*`. Variable names must match column names in the data exactly. Predictor names for response curve plots are extracted via `all.vars()`, which correctly unwraps terms such as `I(Var1^2)` to the base variable `Var1`.

All models are fit as `stats::glm(..., family = binomial(link = link))`. Predicted values are always probabilities on the 0-1 scale.

The returned object is recognized by [generate_spatiotemporal_predictions](#), which uses the `model_type` field to use the correct prediction and evaluation logic.

Value

A list with class "TemporalGLM" containing:

- `models`: Named list of fitted `glm` objects, one per fold.
- `thresholds`: Named numeric vector of probability thresholds used for binary classification, one per fold.
- `threshold_method`: Character string recording the thresholding method used.
- `model_formula`: The formula object as passed to the fitting function.
- `link`: Character string recording the link function used.
- `model_vars`: Character vector of predictor names extracted from the formula right-hand side.
- `fold_training_data`: Named list of training data frames used to fit each fold model, retained for downstream prediction.
- `fold_test_metrics`: Data frame of held-out test fold metrics per fold: Threshold, AUC, TSS, Kappa, Sensitivity, and Specificity. Also written to `Fold_Test_Metrics.csv` in `output_dir`.
- `output_dir`: Path to the output directory.
- `model_type`: Character string "glm", used by [generate_spatiotemporal_predictions](#).
- `plots`: Named list of recorded plot objects when `create_plot = TRUE`. Plots can be replayed with `grDevices::replayPlot()`.

See Also

Preprocessing: [spatiotemporal_partition](#), [generate_absences](#)

Modeling: [build_temporal_gam](#), [build_temporal_rf](#), [build_temporal_hv](#), [generate_spatiotemporal_predictions](#)

Examples

```
data(tmr_partition, package = "TemporalModelR")
```

```
data(tmr_absences, package = "TemporalModelR")
```

```
build_temporal_glm(
  partition_result = tmr_partition,
```

```

pseudoabsence_result = tmr_absences,
model_formula         = ~ elevation + forest_cover + prseas,
threshold_method      = "tss",
output_dir            = tempdir(),
create_plot           = FALSE,
time_cols             = c("year", "season"),
verbose               = FALSE
)

```

build_temporal_hv *Build Temporal Hypervolume Models Across Cross-Validation Folds*

Description

Modeling function that constructs hypervolume models for each cross-validation fold using either Gaussian kernel density estimation or one-class SVM. Each hypervolume reserves one fold as testing data and uses the remaining folds as training data. The returned object follows the same structure as [build_temporal_glm](#), [build_temporal_gam](#), and [build_temporal_rf](#), and is accepted directly by [generate_spatiotemporal_predictions](#).

Usage

```

build_temporal_hv(partition_result, model_vars, method,
                  hypervolume_params = list(),
                  output_dir = file.path(tempdir(), "Hypervolume_Models"),
                  create_plot = TRUE, overwrite = FALSE,
                  plot_palette = "Dark 2", verbose = TRUE)

```

Arguments

partition_result	List or character. Output from spatiotemporal_partition or path to an .rds file containing that output.
model_vars	Character vector. Names of predictor columns to use in hypervolume construction. All variables must be present as columns in the occurrence data produced by temporally_explicit_extraction .
method	Character. Hypervolume method. One of "gaussian" for Gaussian kernel density estimation or "svm" for one-class support vector machine. Required.
hypervolume_params	Named list. Additional parameters passed to hypervolume_gaussian or hypervolume_svm . For Gaussian models, valid keys are kde.bandwidth, quantile.requested, quantile.requested.type, chunk.size, verbose, and samples.per.point. For SVM models, valid keys are svm.nu, svm.gamma, chunk.size, verbose, and samples.per.point. Default is an empty list, which uses the built-in defaults.
output_dir	Character. Directory to write output files including saved hypervolume objects and plots. Default is file.path(tempdir(), "Hypervolume_Models").

create_plot	Logical. If TRUE, generates pairplot visualisations of each fold's hypervolume and a combined comparison plot. Default is TRUE.
overwrite	Logical. If TRUE, overwrites existing saved hypervolume files. If FALSE, loads existing files when available. Default is FALSE.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see hcl.pals) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-fold hypervolume construction progress, volume summaries, and overlap statistics.

Details

For N folds, constructs N hypervolumes where each fold reserves one group of points for testing and uses the remaining N-1 groups for training. Pairwise overlap statistics quantify similarity between hypervolumes across folds, with low overlap indicating that the environmental space sampled differs substantially across folds.

Hypervolume objects are saved as a combined `.rds` file in `output_dir`. If the file already exists and `overwrite = FALSE`, the saved file is loaded rather than re-fitting.

The returned object is accepted directly by [generate_spatiotemporal_predictions](#), which uses the `model_type` field to dispatch hypervolume-specific projection logic via [hypervolume_project](#).

Value

A list with class "TemporalHypervolume" containing:

- `models`: Named list of fitted Hypervolume objects, one per fold, named `fold1`, `fold2`, etc. This naming convention matches the other `build_temporal_*`(`)` functions and is required by [generate_spatiotemporal_predictions](#).
- `volumes`: Named numeric vector of hypervolume sizes (units depend on the number of dimensions and bandwidth).
- `overlaps`: Named list of pairwise percent volume overlaps between all fold combinations.
- `method`: Character string recording the method used.
- `model_vars`: Character vector of predictor names used.
- `fold_training_data`: Named list of training data frames used to fit each fold model, retained for consistency with the other model types and for downstream use.
- `fold_test_metrics`: Data frame of E-space inclusion metrics computed on the held-out test points for each fold. Columns: `fold`, `n_test`, `volume`, `tp`, `fn`, `sensitivity`, `Sensitivity`. Printed as a summary table at the end of model building.
- `output_dir`: Path to the output directory.
- `model_type`: Character string "hypervolume", used by [generate_spatiotemporal_predictions](#).
- `plots`: List of recorded plot objects (if `create_plot = TRUE`). Plots can be replayed with `grDevices::replayPlot()`.

See Also

Preprocessing: [spatiotemporal_partition](#)

Modeling: [build_temporal_glm](#), [build_temporal_gam](#), [build_temporal_rf](#), [generate_spatiotemporal_predictions](#)

External: [hypervolume_gaussian](#), [hypervolume_svm](#)

Examples

```
data(tmr_partition_small, package = "TemporalModelR")

build_temporal_hv(
  partition_result = tmr_partition_small,
  model_vars      = c("elevation", "forest_cover"),
  method          = "svm",
  output_dir      = tempdir(),
  create_plot     = FALSE,
  verbose         = FALSE
)
```

build_temporal_rf *Build Temporal Random Forest Models Across Cross-Validation Folds*

Description

Modeling function that constructs Random Forest classification models for each cross-validation fold using presence and pseudoabsence data. Each model reserves one fold as testing data and uses the remaining folds as training data. The user specifies predictors as a character vector. Predicted probabilities of presence are extracted from the out-of-bag or in-bag vote fractions and thresholded to produce binary suitability classifications. Variable importance is recorded for each fold. The returned object follows the same structure as [build_temporal_glm](#), [build_temporal_gam](#), and [build_temporal_hv](#), and is accepted directly by [generate_spatiotemporal_predictions](#).

Usage

```
build_temporal_rf(partition_result, pseudoabsence_result, model_vars,
                  rf_params = list(), threshold_method = "tss",
                  output_dir = file.path(tempdir(), "RF_Models"),
                  create_plot = TRUE, plot_palette = "Dark 2",
                  overwrite = FALSE, time_cols = NULL, verbose = TRUE)
```

Arguments

partition_result
List or character. Output from [spatiotemporal_partition](#) or path to an .rds file containing that output.

pseudoabsence_result
List or character. Output from [generate_absences](#) or path to an .rds file containing that output.

model_vars	Character vector. Names of predictor columns to include in the Random Forest. All variables must be present as columns in both the presence and pseudoabsence data.
rf_params	Named list. Additional arguments passed to <code>randomForest</code> , such as <code>ntree</code> (number of trees, default 500), <code>mtry</code> (number of variables tried at each split, default <code>floor(sqrt(length(model_vars)))</code>), and <code>nodesize</code> (minimum node size, default 1 for classification). Default is an empty list, which uses randomForest defaults.
threshold_method	Character or numeric. Method used to convert continuous predicted probabilities to binary suitability. Accepted values: <ul style="list-style-type: none"> • "prevalence": Sets threshold equal to the prevalence (proportion of presences) in the training data for that fold. • "tss": Selects the threshold that maximizes the True Skill Statistic (sensitivity + specificity - 1) on the training data. Default. • A numeric value between 0 and 1 (e.g. 0.4): Uses that value as a fixed threshold for all folds directly.
output_dir	Character. Directory to write output files including saved model objects and plots. Default is <code>file.path(tempdir(), "RF_Models")</code> .
create_plot	Logical. If TRUE, generates a per-fold variable importance plot, partial dependence curves for each predictor, and a combined ROC curve summary. Default is TRUE.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see <code>hcl.pals</code>) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".
overwrite	Logical. If TRUE, overwrites existing saved model files. If FALSE, loads existing files when available. Default is FALSE.
time_cols	Character. Name of the column(s) containing year or time step values in the occurrence data. Must match <code>time_cols</code> used in <code>spatiotemporal_partition</code> . Default is NULL.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-fold training summaries and file-saved messages.

Details

Random Forests are fit using `randomForest` from the **randomForest** package. The response is treated as a factor (0/1) so the model runs in classification mode, which produces class vote fractions used as predicted probabilities. Importance is computed with `importance = TRUE` and `type = 1` (mean decrease in accuracy).

Predicted probabilities are the vote fraction for class 1 from `predict(..., type = "prob")[, "1"]`. These are used for threshold selection and ROC curve construction.

Diagnostic plots include: a variable importance bar chart (mean decrease in accuracy across folds), partial dependence curves for each predictor showing the marginal effect of each variable while averaging over all others (with rug marks for presences and pseudoabsences), and a combined ROC curve panel.

The returned object is recognized by [generate_spatiotemporal_predictions](#), which uses the `model_type` field to use the correct prediction and evaluation logic.

Value

A list with class "TemporalRF" containing:

- `models`: Named list of fitted randomForest objects, one per fold.
- `thresholds`: Named numeric vector of probability thresholds used for binary classification, one per fold.
- `threshold_method`: Character string recording the thresholding method used.
- `model_vars`: Character vector of predictor names used.
- `variable_importance`: Named list of importance data frames, one per fold, with mean decrease in accuracy for each predictor.
- `fold_training_data`: Named list of training data frames used to fit each fold model, retained for downstream prediction.
- `fold_test_metrics`: Data frame of held-out test fold metrics per fold: Threshold, AUC, TSS, Kappa, Sensitivity, and Specificity. Also written to `Fold_Test_Metrics.csv` in `output_dir`.
- `output_dir`: Path to the output directory.
- `model_type`: Character string "rf", used by [generate_spatiotemporal_predictions](#).
- `plots`: Named list of recorded plot objects when `create_plot = TRUE`. Plots can be replayed with `grDevices::replayPlot()`.

See Also

Preprocessing: [spatiotemporal_partition](#), [generate_absences](#)

Modeling: [build_temporal_glm](#), [build_temporal_gam](#), [build_temporal_hv](#), [generate_spatiotemporal_predictions](#)

External: [randomForest](#)

Examples

```
data(tmr_partition, package = "TemporalModelR")
```

```
data(tmr_absences, package = "TemporalModelR")
```

```
build_temporal_rf(
  partition_result      = tmr_partition,
  pseudoabsence_result = tmr_absences,
  model_vars            = c("elevation", "forest_cover", "prseas"),
  rf_params             = list(ntree = 100),
  threshold_method     = "tss",
  output_dir           = tempdir(),
  create_plot          = FALSE,
  time_cols            = c("year", "season"),
  verbose              = FALSE
)
```

 extdata

Bundled rasters, point files, and prediction outputs

Description

Several non-R objects ship in `inst/extdata/` for use in function examples and the package vignette. They cannot be portably serialized as `.rda` files, so they are stored as GeoTIFF and CSV files and loaded via [system.file](#).

Details

`extdata/rasters_raw/` Raw synthetic environmental rasters before alignment. Includes `elevation.tif`, `forest_cover_1.tif` through `forest_cover_15.tif`, `pr_ann_1.tif` through `pr_ann_15.tif`, and `prseas_<year>_<season>.tif` for each of 15 years and 4 seasons (60 files).

`extdata/rasters_aligned/` Same rasters after [raster_align](#) has reprojected and masked them to the reference grid.

`extdata/rasters_scaled/` Aligned rasters z-scored using the scaling parameters from the seasonal extraction. Used by examples and modeling functions that work with the seasonal predictor set.

`extdata/rasters_scaled_annual/` Aligned rasters z-scored using the scaling parameters from the annual extraction. Used by examples and modeling functions that work with the annual predictor set (`pr_ann` instead of `prseas`).

`extdata/points/synthetic_occurrence_points.csv` The raw synthetic presence dataset: 150 points with `x`, `y`, `year`, `season`, and `pres = 1`.

`extdata/points/synthetic_occurrence_points.shp` Same points as a shapefile.

`extdata/points/synthetic_user_presences.csv` A second-species presence dataset for demonstrating `method = "user_data"` in [generate_absences](#). Points were derived from buffer-constrained environmental pseudoabsences of the primary species and reformatted as presences (`pres = 1`). Same column structure as `synthetic_occurrence_points.csv` (`x`, `y`, `year`, `season`, `pres`).

`extdata/points/extracted_seasonal_*.csv` Outputs from [temporally_explicit_extraction](#) using the seasonal predictor set: `_Raw_Values.csv`, `_Scaled_Values.csv`, and `_Scaling_Parameters.csv`.

`extdata/points/extracted_annual_*.csv` Same outputs but using the annual predictor set.

`extdata/predictions/` Per-timestep fold-vote rasters from the seasonal workflow's [generate_spatiotemporal_predictions](#) call. Fifteen files (`Prediction_<year>_Spring.tif`) suitable for direct input to [summarize_raster_outputs](#).

`extdata/binary/consensus_stack.tif` Multi-layer GeoTIFF of binary suitable/unsuitable rasters produced by [summarize_raster_outputs](#) with `consensus = 3`. Fifteen layers, one per year, ordered 1 through 15.

`extdata/binary/frequency_raster.tif` Companion single-layer raster giving the proportion of years each pixel was classified as suitable.

`extdata/precomputed/` Precomputed prediction outputs read directly by the modeling vignettes (V3a-V3d) so that [generate_spatiotemporal_predictions](#) does not need to be rerun at vignette build time. One subdirectory per model type (`glm/`, `gam/`, `rf/`, `hv/`), each containing

preds.rds and a pred_tifs/ folder. preds.rds is the list returned by [generate_spatiotemporal_predictions](#) for that model (\$timestep_metrics, \$overall_summary, \$prediction_files, and \$model_type), with \$prediction_files reduced to bare file names rather than absolute build-time paths. pred_tifs/ holds the 60 per-timestep fold-vote rasters (Prediction_<year>_<season>.tif, 15 years x 4 seasons) projected from that model. The vignettes load preds.rds and rebuild \$prediction_files from pred_tifs/ via [system.file](#).

Example load patterns:

```
### Aligned raster directory
aln_dir <- system.file("extdata/rasters_aligned",
                      package = "TemporalModelR")

### Consensus stack (multi-layer)
binary_stack <- terra::rast(system.file(
  "extdata/binary/consensus_stack.tif", package = "TemporalModelR"
))

### Frequency raster
frequency_rast <- terra::rast(system.file(
  "extdata/binary/frequency_raster.tif", package = "TemporalModelR"
))

### Per-timestep prediction directory
pred_dir <- system.file("extdata/predictions",
                      package = "TemporalModelR")

### Precomputed GLM prediction object and its rasters
glm_preds <- readRDS(system.file(
  "extdata/precomputed/glm/preds.rds", package = "TemporalModelR"
))
glm_pred_files <- list.files(
  system.file("extdata/precomputed/glm/pred_tifs",
             package = "TemporalModelR"),
  pattern = "\.tif$", full.names = TRUE
)
```

generate_absences

Generate Temporally Explicit Pseudoabsence Points

Description

Generates pseudoabsence or background points for each fold produced by [spatiotemporal_partition](#), distributed across time steps proportionally to the number of presence points in each time step within each fold. Three generation methods are supported: random sampling within the study area, buffer-constrained sampling around presence points, and environmentally biased sampling that targets areas outside the known environmental tolerance of the species. Additionally, this function can

be used to process user defined absences to work with downflow operations. This may be any list of points for which a user wants to count as 'absences' in downflow operations, including negative occupancy surveys, or alternatively surveys for similar species which may act as pseudoabsences for the presence of the species of interest.

Usage

```
generate_absences(partition_result, reference_shapefile_path, raster_dir,
                  variable_patterns, method = "random", ratio = 1,
                  buffer_distance = NULL, env_percentile = 0.05,
                  time_cols = NULL, pseudoabsence_times = NULL,
                  min_points_per_timestep = 1, user_absence_data = NULL,
                  xcol = NULL, ycol = NULL, points_crs = NULL,
                  create_plot = TRUE, plot_by_fold = FALSE,
                  plot_palette = "Dark 2", output_file = NULL,
                  verbose = TRUE)
```

Arguments

partition_result	List or character. Output from spatiotemporal_partition or path to an .rds file containing that output.
reference_shapefile_path	Character or sf object. Path to a polygon file or an sf polygon object defining the study area.
raster_dir	Character. Directory containing environmental raster files (.tif), typically the output of raster_align or scale_rasters . File names must follow the patterns supplied in variable_patterns, with any time placeholder substituted for the corresponding value from time_cols. Required for all methods.
variable_patterns	Named character vector mapping clean variable names to raster filename patterns. For time-varying variables include the time placeholder in the pattern (e.g. "forest_cover" = "forest_cover_YEAR"); for static variables omit it (e.g. "elevation" = "elevation"). Time placeholders must match entries in time_cols.
method	Character. Pseudoabsence generation method. One of "random", "buffer", "environmental", or "user_data". Default is "random". When "user_data" is specified, user_absence_data is used as the source of absence locations instead of generating them. ratio, buffer_distance, env_percentile, and pseudoabsence_times are ignored. raster_dir and variable_patterns are required for all methods, including "user_data", for temporally-matched environmental extraction at the absence points.
ratio	Numeric. Number of pseudoabsence points to generate per presence point. Default is 1. Values of 2, 10, 50, etc. are accepted. Points are always distributed proportionally across time steps within each fold. Set to 0 to disable proportional allocation and use a fixed number of points per time step instead, in which case min_points_per_timestep must be greater than 0. ratio and min_points_per_timestep cannot both be 0.

buffer_distance	Numeric. Distance in the units of the CRS (typically meters for projected CRS) within which pseudoabsence points are sampled. Required when method = "buffer". When method = "environmental", supplying a value automatically applies a spatial buffer constraint before environmental profiling, following the three-step approach of Senay et al. (2013). If NULL for the environmental method, no spatial constraint is applied. Default is NULL.
env_percentile	Numeric between 0 and 1. Quantile threshold used to define the boundary of the known environmental tolerance when method = "environmental". Environmental cells within this quantile range across all variables are excluded from pseudoabsence sampling. Default is 0.05 (5th to 95th percentile envelope).
time_cols	Character or character vector. Name of the column(s) containing the time step values. Must match time_cols used in spatiotemporal_partition and the time placeholders used in variable_patterns . Default is NULL.
pseudoabsence_times	Vector. Optional vector of specific time step values (for the first time column) at which to generate pseudoabsences. When NULL (default), all time steps present in the occurrence data are used.
min_points_per_timestep	Integer. Minimum number of pseudoabsence points to generate per time step per fold. Default is 1. When ratio = 0, this value sets the exact (fixed) number of points generated per time step per fold, independent of the number of presence points. ratio and min_points_per_timestep cannot both be 0.
user_absence_data	Character, sf object, sfc object, Spatial object, or data frame. Path to occurrence data (.csv, .shp, .geojson, .gpkg) or a spatial object to be processed as absence data for downstream operations. Required when method = "user_data". Should be preprocessed with spatiotemporal_rarefaction in the same formatting as presence data if not already thinned.
xcol	Character. Name of the x-coordinate column in user_absence_data. Required when when method = "environmental" and user_absence_data is a CSV file or data frame.
ycol	Character. Name of the y-coordinate column in user_absence_data. Required when when method = "environmental" and user_absence_data is a CSV file or data frame.
points_crs	Character or CRS object. CRS of the user_absence_data. Required when when method = "environmental" and user_absence_data is a CSV file or data frame.
create_plot	Logical. If TRUE (default), generates diagnostic plots showing the spatial and temporal distribution of generated pseudoabsence points alongside presence points.
plot_by_fold	Logical. If TRUE, generates one map per fold. If FALSE (default), generates a single combined map.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see hcl.pals) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".

output_file	Character. Optional path to save the result as an .rds file. The parent directory will be created if it does not exist. Default is NULL.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-fold and per-time-step pseudoabsence counts.

Details

Generates sets of background data based on user-specified methodology that can be used as pseudoabsence data for the purposes of training presence/absence models.

The four generation methods differ in how the absence locations are obtained:

- **Random:** Points are sampled uniformly at random from the full study area, excluding a negligible buffer around presence locations to prevent exact overlap.
- **Buffer:** Points are sampled within buffers of radius `buffer_distance` drawn around all fold presences, clipped to the reference shapefile boundary.
- **Environmental:** Raster cells whose values fall outside the species tolerance envelope in at least one variable are identified as candidates. K-means clustering then selects a spatially representative subset. If `buffer_distance` is supplied the environmental filtering is applied only within that buffered region, implementing the full three-step approach of Senay et al. (2013).
- **User data:** Absence locations are taken directly from `user_absence_data` to be used when user has a predefined set of absence points. Points are assigned to folds by spatial join against the partition fold boundaries, with unmatched points routed to temporal folds by time value. Environmental values are then extracted at the supplied locations using the same time-matched logic as the generated methods.

Value

Invisibly returns a list containing:

- `pseudoabsences`: An sf object of all generated pseudoabsence points with columns `fold`, `temporal_block`, `presence` (always 0), the time column(s) if provided, and extracted environmental variable values matched to each point's time step.
- `plots`: A named list of recorded plot objects when `create_plot = TRUE`. Contains `temporal_distribution` and either `spatial_combined` or one `spatial_fold_N` entry per fold. Plots can be replayed with `grDevices::replayPlot()`.
- `summary`: A data frame summarising points generated per fold with columns `fold`, `n_presences`, `n_pseudoabsences`, and `ratio_achieved`.

References

Senay SD, Worner SP, Ikeda T (2013) Novel Three-Step Pseudo-Absence Selection Technique for Improved Species Distribution Modeling. PLoS ONE 8(8): e71218.

See Also

Preprocessing: [spatiotemporal_partition](#), [temporally_explicit_extraction](#)

Modeling: [build_temporal_hv](#), [build_temporal_glm](#), [build_temporal_gam](#), [build_temporal_rf](#)

Examples

```

data(tmr_partition_small, package = "TemporalModelR")

scl_dir  <- system.file("extdata/rasters_scaled",
                       package = "TemporalModelR")

ref_file <- system.file("extdata/rasters_raw/elevation.tif",
                       package = "TemporalModelR")

study_crs <- sf::st_crs(terra::rast(ref_file))

study_area_sf <- sf::st_as_sf(sf::st_as_sfc(
  sf::st_bbox(c(xmin = 0, xmax = 3000, ymin = 0, ymax = 1500),
              crs = study_crs)
))

generate_absences(
  partition_result      = tmr_partition_small,
  reference_shapefile_path = study_area_sf,
  raster_dir           = scl_dir,
  variable_patterns    = c(
    "elevation" = "elevation",
    "forest_cover" = "forest_cover_YEAR"
  ),
  method               = "random",
  ratio                = 1,
  time_cols            = c("year"),
  create_plot          = FALSE,
  verbose              = FALSE
)

```

generate_spatiotemporal_predictions

Generate Spatiotemporal Predictions from Temporal Models

Description

Generates temporally explicit habitat suitability predictions by projecting fitted models onto environmental raster stacks matching each time period. Accepts output from any of the four TemporalModelR modeling functions. Produces per-time-step assessment metrics showing how predictions and test point coverage vary over time.

Usage

```

generate_spatiotemporal_predictions(partition_result, model_result,
                                   pseudoabsence_result = NULL, raster_dir,
                                   variable_patterns, time_cols, time_steps,
                                   output_dir = file.path(tempdir(), "Predictions"),
                                   overwrite = FALSE,
                                   verbose = TRUE)

```

Arguments

partition_result	List or character. Output from <code>spatiotemporal_partition</code> or path to an <code>.rds</code> file containing that output.
model_result	List or character. Output from any of <code>build_temporal_hv</code> , <code>build_temporal_glm</code> , <code>build_temporal_gam</code> , or <code>build_temporal_rf</code> , or a path to an <code>.rds</code> file. Model type is detected automatically from the <code>model_type</code> field.
pseudoabsence_result	List, character, or NULL. Optional. Output from <code>generate_absences</code> or path to an <code>.rds</code> file. When supplied for presence/absence models (GLM, GAM, RF), the held-out pseudoabsence test points for each fold are filtered to the current time step and used alongside presence test points to compute per-timestep TN, FP, Specificity, and TSS. These columns are added to the timestep metrics table when pseudoabsences are available. Ignored for hypervolume models. Default is NULL.
raster_dir	Character. Directory containing environmental raster files (<code>.tif</code>), typically the output of <code>raster_align</code> or <code>scale_rasters</code> . File names must follow the patterns supplied in <code>variable_patterns</code> , with any time placeholder substituted for the corresponding value from <code>time_cols</code> .
variable_patterns	Named character vector mapping clean variable names to raster filename patterns. For time-varying variables include the time placeholder in the pattern (e.g. <code>"forest_cover" = "forest_cover_YEAR"</code>); for static variables omit it (e.g. <code>"elevation" = "elevation"</code>). Time placeholders must match entries in <code>time_cols</code> .
time_cols	Character. Name of the column(s) containing year or time step values in the occurrence data. Must match <code>time_cols</code> used in <code>spatiotemporal_partition</code> and the time placeholders used in <code>variable_patterns</code> .
time_steps	Vector, data frame, or matrix of time periods for which to generate predictions.
output_dir	Character. Directory to write prediction rasters and the assessment metrics CSV. Default is <code>file.path(tempdir(), "Predictions")</code> .
overwrite	Logical. If TRUE, overwrites existing output files. If FALSE (default), existing files are skipped.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-time-step prediction progress.

Details

G-space predictions are produced as rasters for each time-step and fold of an input model.

Per-timestep metrics are computed per fold per time step by extracting raster predictions at the held-out presence points that fall within that time step. `Pct_Suitable` records the proportion of the study area predicted suitable. `Sensitivity` shows how consistently test points are captured. CBP (cumulative binomial probability) tests whether the observed number of correctly predicted test points is better than expected by random placement: under the null, each point has `Pct_Suitable` probability of falling in suitable area, so `dbinom(TP, N_Test_Pts, Pct_Suitable)` gives the probability of observing exactly TP correct by chance. Small values indicate predictions are better than random.

Value

Invisibly returns a list containing:

- `timestep_metrics`: data frame of per-fold per-time-step metrics. Columns always present: Fold, the time column(s), Pct_Suitable, N_Pres, TP, FN, Sensitivity, CBP. When `pseudoabsence_result` is supplied for parametric models, additionally: N_Abs, TN, FP, Specificity, TSS. Saved as `Timestep_Assessment_Metrics.csv`.
- `overall_summary`: data frame of pooled metrics per fold. Columns: Fold, N_Timesteps, Mean_Pct_Suitable, Total_TP, Total_FN, Overall_Sensitivity, Overall_CBP. When pseudoabsences available: additionally Total_TN, Total_FP, Overall_Specificity, Overall_TSS.
- `prediction_files`: character vector of paths to saved prediction rasters.
- `model_type`: character string recording the model type used.

See Also

Preprocessing: [scale_rasters](#), [spatiotemporal_partition](#)

Modeling: [build_temporal_hv](#), [build_temporal_glm](#), [build_temporal_gam](#), [build_temporal_rf](#)

Post-processing: [summarize_raster_outputs](#), [plot_model_assessment](#)

Examples

```
data(tmr_partition, package = "TemporalModelR")

data(tmr_glm,      package = "TemporalModelR")

data(tmr_absences, package = "TemporalModelR")

scl_dir  <- system.file("extdata/rasters_scaled",
                       package = "TemporalModelR")

time_steps <- expand.grid(
  year      = 1:15,
  season    = "Spring",
  stringsAsFactors = FALSE
)

generate_spatiotemporal_predictions(
  partition_result = tmr_partition,
  model_result     = tmr_glm,
  pseudoabsence_result = tmr_absences,
  raster_dir       = scl_dir,
  variable_patterns = c(
    "elevation" = "elevation",
    "forest_cover" = "forest_cover_YEAR",
    "prseas" = "prseas_YEAR_SEASON"
  ),
  time_cols      = c("year", "season"),
  time_steps     = time_steps,
  output_dir     = tempdir(),
  overwrite      = TRUE,
```

```

    verbose          = FALSE
  )

```

plot_model_assessment *Visualize Model Assessment Metrics Across Time*

Description

Generates diagnostic plots from the per-timestep assessment table produced by [generate_spatiotemporal_predictions](#), optionally overlaying overall reference values from the model result object.

Usage

```

plot_model_assessment(predictions, time_column,
                      secondary_time_mode = "combine", model_result = NULL,
                      cbp_threshold = 0.05, plot_palette = "Dark 2",
                      verbose = TRUE)

```

Arguments

predictions	List returned by generate_spatiotemporal_predictions , or a named list with at least a <code>timestep_metrics</code> element. The <code>timestep_metrics</code> element may also be a path to a <code>Timestep_Assessment_Metrics.csv</code> file produced by generate_spatiotemporal_predictions .
time_column	Character. Name of the primary time column in <code>timestep_metrics</code> to use as the x axis (e.g. "year"). When predictions span multiple time columns (e.g. "year" and "season"), provide all relevant column names as a character vector and control how secondary columns are handled via <code>secondary_time_mode</code> .
secondary_time_mode	Character. How to handle secondary time columns when <code>time_column</code> has length > 1. One of: <ul style="list-style-type: none"> "combine" (default): secondary time values are appended to the primary value to form a single ordered x-axis label (e.g. 1_Spring, 1_Summer, 2_Spring, ...). "facet": a separate plot is produced for each unique combination of secondary time values, with the primary time column as the x axis on every panel.
model_result	List or character. Optional. Output from a <code>build_temporal_*()</code> function or path to its <code>.rds</code> file. When supplied, overall sensitivity and specificity from <code>model_result\$fold_test_metrics</code> are added as per-fold reference lines. Default is NULL.
cbp_threshold	Numeric. Significance threshold for CBP. Default is 0.05.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see hcl.pals) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".
verbose	Logical. If TRUE (default), prints progress messages during processing.

Details

Plots per-fold and per-timestep diagnostic plots for data produced by [generate_spatiotemporal_predictions](#). These quick visuals can be used by users to assess model performance and significance and decide if the model's performance warrants further interpretation of the results through post-processing analyses.

Value

Invisibly returns a named list containing:

- `pct_suitable`: Recorded plot of proportion of study area predicted suitable per time step.
- `sensitivity`: Recorded plot of per-timestep sensitivity.
- `specificity`: Recorded plot of per-timestep specificity (only present when pseudoabsence data were used).
- `cbp`: Recorded plot of cumulative binomial probability per time step on a log scale.
- `tp_fn`: Recorded plot of true positives and false negatives per time step.
- `tn_fp`: Recorded plot of true negatives and false positives per time step (only present when pseudoabsence data were used).
- `timestep_summary`: Data frame of per-time-step cross-fold mean and SD for each metric.
- `overall_summary`: Data frame from `predictions$overall_summary`, when present.

See Also

Preprocessing: [spatiotemporal_partition](#), [generate_absences](#)

Modeling: [build_temporal_glm](#), [build_temporal_gam](#), [build_temporal_rf](#), [build_temporal_hv](#),

Post-processing: [generate_spatiotemporal_predictions](#), [summarize_raster_outputs](#)

Examples

```
data(tmr_predictions, package = "TemporalModelR")

plot_model_assessment(
  predictions      = tmr_predictions,
  time_column      = c("year", "season"),
  secondary_time_mode = "combine",
  verbose          = FALSE
)
```

raster_align

*Align and Standardize Raster Files to a Reference Raster***Description**

Preprocessing function that aligns a batch of raster files to a specified reference raster by performing reprojection, resampling, and masking operations. Ensures all rasters share identical CRS, resolution, and spatial extent for later analyses.

Usage

```
raster_align(input_dir, output_dir, reference_raster,
             output_suffix = "_Masked_Updated", pattern = ".*\\.tif$",
             resample_method = "bilinear",
             overwrite = FALSE, verbose = TRUE)
```

Arguments

input_dir	Character. Directory containing the input raster files.
output_dir	Character. Directory where processed rasters will be saved.
reference_raster	Character, SpatRaster, or RasterLayer. File path or raster object used as the alignment reference.
output_suffix	Character. Suffix appended to output filenames. Default is "_Masked_Updated". Output files are named <original_name><output_suffix>.tif.
pattern	Character. Regular expression used to match raster files within input_dir. Default is ".*\\.tif\$".
resample_method	Character. Resampling method passed to <code>resample</code> . Default is "bilinear", which is appropriate for continuous variables. Use "near" for categorical rasters (e.g. land cover classes) to avoid interpolating between class codes. Other accepted values include "cubic" and "lanczos".
overwrite	Logical. If TRUE, overwrites existing output files. If FALSE (default), existing files are skipped.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes file counts, overwrite mode, per-file progress, and a completion summary.

Details

For each raster in `input_dir` matching `pattern`, the function:

1. Reprojects to the CRS of the reference raster
2. Resamples to match the reference resolution using `resample_method`
3. Masks values outside the reference raster's non-NA extent
4. Saves the result as a GeoTIFF to `output_dir`

This preprocessing step ensures spatial alignment before applying other downstream analyses such as [temporally_explicit_extraction](#) or [scale_rasters](#).

Value

Invisibly returns a list containing:

- `output_files`: Character vector of file paths written to `output_dir`.
- `n_processed`: Integer. Number of rasters successfully processed in this call (excludes skipped files when `overwrite = FALSE`).

See Also

Preprocessing: [scale_rasters](#), [temporally_explicit_extraction](#)

Examples

```
raw_dir <- system.file("extdata/rasters_raw", package = "TemporalModelR")
ref      <- file.path(raw_dir, "elevation.tif")
out_dir  <- file.path(tempdir(), "aligned")

raster_align(
  input_dir      = raw_dir,
  output_dir     = out_dir,
  reference_raster = ref,
  overwrite      = TRUE,
  verbose        = FALSE
)
```

scale_rasters

Scale Environmental Rasters Using Species Occurrence Data

Description

Preprocessing function that standardizes raster files using precomputed mean and standard deviation values from species occurrence data. Supports both temporally static and dynamic rasters.

Usage

```
scale_rasters(input_dir, output_dir, scaling_params_file,
              variable_patterns, time_cols = NULL, output_suffix = "_Scaled",
              overwrite = FALSE, verbose = TRUE)
```

Arguments

input_dir	Character. Directory containing aligned input .tif raster files, typically the output of raster_align .
output_dir	Character. Directory where scaled rasters will be saved.
scaling_params_file	Character. Path to CSV file with columns: variable, mean, sd. Typically generated by temporally_explicit_extraction .
variable_patterns	Named character vector mapping clean variable names to raster filename patterns. For time-varying variables include the time placeholder in the pattern (e.g. "forest_cover" = "forest_cover_YEAR"); for static variables omit it (e.g. "elevation" = "elevation"). Time placeholders must match entries in time_cols.
time_cols	Character vector of time placeholders for dynamic variables. Default is NULL.
output_suffix	Character. Suffix to append to output raster filenames. Default is "_Scaled".
overwrite	Logical. If TRUE, overwrites existing output files. If FALSE (default), existing files are skipped.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes per-variable scaling progress.

Details

Applies scaling to rasters via z-score transformation: $(\text{value} - \text{mean}) / \text{sd}$ as is calculated during [temporally_explicit_extraction](#). Scaled rasters are written to output_dir.

Scaled rasters should use the same scaling parameters derived from species occurrence data to ensure consistent standardization between training data and prediction layers.

Value

Invisibly returns a list containing:

- n_scaled: Integer. Total number of variables successfully scaled (static plus dynamic).
- output_dir: Character. Path to the directory containing scaled rasters.

See Also

Preprocessing: [temporally_explicit_extraction](#), [raster_align](#)

Examples

```
aln_dir      <- system.file("extdata/rasters_aligned",
                           package = "TemporalModelR")

params_file <- system.file(
  "extdata/points/extracted_seasonal_Scaling_Parameters.csv",
  package = "TemporalModelR"
)
```

```

out_dir <- file.path(tempdir(), "scaled")

scale_rasters(
  input_dir      = aln_dir,
  output_dir     = out_dir,
  scaling_params_file = params_file,
  variable_patterns = c(
    "elevation" = "elevation",
    "forest_cover" = "forest_cover_YEAR",
    "prseas" = "prseas_YEAR_SEASON"
  ),
  time_cols      = c("year", "season"),
  overwrite      = TRUE,
  verbose        = FALSE
)

```

spatiotemporal_partition

Spatiotemporal Cross-Validation Partitioning

Description

Preprocesses species occurrence data by partitioning it into spatially and temporally structured folds for cross-validation. Supports creation of spatial-only folds, temporal-only folds, and random folds.

Usage

```

spatiotemporal_partition(reference_shapefile_path, points_file_path,
  time_cols = NULL, xcol = NULL, ycol = NULL,
  points_crs = NULL, n_spatial_folds = 0,
  n_temporal_folds = 0, n_balanced_folds = 0,
  n_random_folds = 0, single_fold = FALSE,
  max_imbalance = 0.05, max_attempts = 10,
  create_plot = TRUE, plot_palette = "Dark 2",
  output_file = NULL, verbose = TRUE)

```

Arguments

reference_shapefile_path	Character or sf object. Path to a polygon file or an sf polygon object defining the study area.
points_file_path	Character, sf object, sfc object, Spatial object, or data frame. Path to occurrence data (.csv, .shp, .geojson, .gpkg) or a spatial object.
time_cols	Character. Name of a single column containing temporal values (e.g. year). Used to define temporal blocks. Required when using temporal folds. Must be a single column name; does not support more than one time column unlike other

functions in this package. Compound time representations (e.g. year + season) should be encoded into a single ordered numeric column before partitioning, or only one (e.g. year) should be used.

xcol	Character. Name of the x-coordinate column. Required when <code>points_file_path</code> is a CSV file or data frame.
ycol	Character. Name of the y-coordinate column. Required when <code>points_file_path</code> is a CSV file or data frame.
points_crs	Character or CRS object. CRS of the input points. Required when <code>points_file_path</code> is a CSV file or data frame.
n_spatial_folds	Integer. Number of spatially explicit folds. Ignored when using random folds. Default is 0.
n_temporal_folds	Integer. Number of temporally explicit folds. When used alone (with <code>n_spatial_folds</code> = 0), creates temporal-only folds where each fold spans the full study area but covers a distinct slice of the time series. When combined with <code>n_spatial_folds</code> , creates a spatiotemporal design. Ignored when using random folds. Default is 0.
n_balanced_folds	Integer. Reserved for future use. Default is 0 (disabled).
n_random_folds	Integer. Number of random folds with no spatial or temporal structure. Overrides all other fold parameters. Default is 0.
single_fold	Logical. If TRUE, bypasses all partitioning and assigns all points to a single fold (fold 1). In this mode all points are used for both training and testing, producing a single model trained on the full dataset. All downstream functions accept the result identically to a standard multi-fold partition. Overrides all fold count parameters. Default is FALSE.
max_imbalance	Numeric. Maximum allowed fold size imbalance as a proportion between 0 and 1. Default is 0.05.
max_attempts	Integer. Maximum number of partitioning attempts for spatiotemporal and balanced modes. Each attempt re-runs the spatial block construction; the attempt with the lowest imbalance is returned. Ignored for random and spatial-only modes. Default is 10.
create_plot	Logical. If TRUE (default), generates diagnostic plots showing fold distributions.
plot_palette	Character. Name of an HCL or RColorBrewer palette used to color folds in diagnostic plots. Accepts any HCL palette name (see hcl.pals) or, if RColorBrewer is installed, any Brewer palette name. Default is "Dark 2".
output_file	Character. Optional path to save the result as an <code>.rds</code> file. The parent directory will be created if it does not exist. Default is NULL.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes the partition mode, fold structure, per-fold point counts, and file-save confirmation.

Details

Works better with smaller numbers of folds and may have difficulties creating even folds for large numbers of groups or where sample sizes are very small.

The function partitions data into folds using one of five modes:

- **Single fold:** All points are assigned to fold 1 and used for both training and testing. This produces a single model trained on the full dataset with no held-out validation. Useful when sample sizes are too small for cross-validation, or as a final production model step after cross-validation has already established model quality. Set `single_fold = TRUE`. All downstream functions accept the result identically to standard multi-fold output.
- **Random:** Points are assigned to folds by random shuffling with no spatial or temporal structure. Each fold is a simple random sample of the full dataset, intended as a naive baseline that makes no attempt to reduce spatial or temporal autocorrelation between training and test sets. Use `n_random_folds`.
- **Spatial-only:** The study area is divided into k contiguous spatial regions using a recursive k-d tree bisection algorithm. At each step the point set is split along its longest spatial axis, recursively halving until the target number of folds is reached. A centroid reassignment pass then refines boundaries to improve balance. Each region becomes one fold, so training always occurs on data from geographically distinct areas relative to the test fold. No temporal separation is imposed, meaning that points from any time period may appear in any fold. Use `n_spatial_folds` alone.
- **Temporal-only:** Each fold covers the full spatial extent of the study area but is restricted to a distinct, non-overlapping slice of the time series. The global time series is divided into `n_temporal_folds` equal intervals using quantile-based breaks, and all points within each interval form one fold. This design tests model transferability across time while retaining full spatial coverage in every fold. Use `n_temporal_folds` alone (with `n_spatial_folds = 0`). Requires `time_cols`.
- **Spatiotemporal:** Folds are assigned using the same recursive k-d tree bisection as spatial-only mode, operating on the full point set to produce spatially contiguous groups. The resulting groups are then split into a spatial pool (`n_spatial_folds` folds drawn from geographically distinct regions) and a temporal pool (`n_temporal_folds` folds each restricted to a distinct slice of the time series but spanning the full study area). Together the two pools assess both geographic and temporal transferability in a single cross-validation design. Use `n_spatial_folds` and `n_temporal_folds` together. Requires `time_cols`.

Fold assignment uses a recursive k-d tree bisection algorithm that splits points along their longest spatial axis at each step, followed by a centroid reassignment pass to improve boundary regularity and point-count balance. Voronoi tessellation on fold centroids is used only for visualisation of the resulting spatial boundaries. For temporal mode, temporal blocks are defined by dividing the global time series into equal intervals using quantile-based breaks. For spatiotemporal mode, the typical spatial assignment is done, but with one larger spatial block made with enough points to represent all of the temporal folds, then the temporal blocking is applied to those points.

Partitioned datasets are suitable for cross-validation in modeling workflows, ensuring spatial and/or temporal independence between folds.

Value

Invisibly returns a list containing:

- `folds`: Data frame of fold assignments with a `fold` column identifying each point's cross-validation fold.
- `points_sf`: sf object of occurrence points with assigned folds.
- `voronoi_folds`: sf object of Voronoi polygons representing the spatial fold boundaries. NULL for random folds, temporal-only folds, and single-fold mode.
- `summary`: Data frame of partitioning summary statistics.
- `plots`: Named list of recorded plot objects when `create_plot = TRUE`. Empty list in single-fold mode.

See Also

Preprocessing: [spatiotemporal_rarefaction](#), [temporally_explicit_extraction](#), [generate_absences](#)

Modeling: [build_temporal_hv](#), [build_temporal_glm](#), [build_temporal_gam](#), [build_temporal_rf](#)

Examples

```
pts_file <- system.file(
  "extdata/points/extracted_seasonal_Scaled_Values.csv",
  package = "TemporalModelR"
)

ref_file <- system.file("extdata/rasters_raw/elevation.tif",
  package = "TemporalModelR")

study_crs <- sf::st_crs(terra::rast(ref_file))

study_area_sf <- sf::st_as_sf(sf::st_as_sfc(
  sf::st_bbox(c(xmin = 0, xmax = 3000, ymin = 0, ymax = 1500),
    crs = study_crs)
))

spatiotemporal_partition(
  reference_shapefile_path = study_area_sf,
  points_file_path        = pts_file,
  xcol                    = "x",
  ycol                    = "y",
  points_crs              = study_crs,
  time_cols               = "year",
  n_spatial_folds        = 2,
  n_temporal_folds        = 2,
  create_plot             = FALSE,
  verbose                  = FALSE
)
```

spatiotemporal_rarefaction

Spatiotemporal Rarefaction of Species Occurrence Data

Description

Preprocessing function that rarefies species occurrence data to one point per raster pixel, optionally accounting for temporal components. Reduces sampling bias and spatial autocorrelation in occurrence datasets.

Usage

```
spatiotemporal_rarefaction(points_sp, output_dir, reference_raster,
                           time_cols = NULL, xcol = NULL, ycol = NULL,
                           points_crs = NULL, output_prefix = "Pts_Database",
                           verbose = TRUE)
```

Arguments

points_sp	Input point data. Accepts an sf object, data frame, SpatialPointsDataFrame, or file path to a .csv, .shp, .geojson, or .gpkg file.
output_dir	Character. Directory where output CSV files will be saved.
reference_raster	Character, SpatRaster, or RasterLayer. Raster used to define pixel boundaries for rarefaction. Accepts a file path, RasterLayer, or SpatRaster.
time_cols	Character vector. Column names in points_sp defining temporal grouping for spatiotemporal rarefaction. When NULL (default), only spatial rarefaction is performed.
xcol	Character. Name of the x-coordinate column. Required when points_sp is a CSV file or data frame.
ycol	Character. Name of the y-coordinate column. Required when points_sp is a CSV file or data frame.
points_crs	Character or CRS object. CRS of the input points. Required when points_sp is a CSV file or data frame.
output_prefix	Character. Prefix for output file names. Default is "Pts_Database". Output files are named <output_prefix>_OnePerPix.csv and, when time_cols are provided, <output_prefix>_OnePerPixPerTimeStep.csv.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes file loading, missing-data removal counts, rarefaction summaries, and a final comparison of spatial vs spatiotemporal point counts.

Details

The function assigns each point to a raster pixel using the resolution and extent of `reference_raster`, then performs:

- Spatial rarefaction: retains one point per pixel, written to `<output_prefix>_OnePerPix.csv`.
- Spatiotemporal rarefaction (when `time_cols` are provided): retains one point per pixel per unique combination of time column values, written to `<output_prefix>_OnePerPixPerTimeStep.csv`.

Output CSV files are suitable as direct input to [temporally_explicit_extraction](#).

Value

Invisibly returns a list containing:

- `input_points`: Integer. Number of input points after CRS alignment and removal of rows with missing time column values.
- `spatial_points`: Integer. Number of points retained after spatial-only rarefaction (one per pixel).
- `spatiotemporal_points`: Integer. Number of points retained after spatiotemporal rarefaction (one per pixel per time combination). NA when `time_cols` is not provided.
- `time_cols_used`: Character vector of time columns used. NULL when `time_cols` is not provided.
- `spatial_table`: Data frame of spatially rarefied points with columns `pixel_id`, `X`, `Y`, and any `time_cols`.
- `spatiotemporal_table`: Data frame of spatiotemporally rarefied points with columns `pixel_id`, `X`, `Y`, and `time_cols`. NULL when `time_cols` is not provided.
- `files_created`: Named list of file paths written. Always contains `$spatial`; additionally contains `$spatiotemporal` when `time_cols` are provided.

See Also

Preprocessing: [temporally_explicit_extraction](#), [spatiotemporal_partition](#)

Examples

```
pts_file <- system.file(
  "extdata/points/synthetic_occurrence_points.csv",
  package = "TemporalModelR"
)

ref_file <- system.file("extdata/rasters_raw/elevation.tif",
  package = "TemporalModelR")

out_dir <- file.path(tempdir(), "rarefied")

spatiotemporal_rarefaction(
  points_sp      = pts_file,
  output_dir     = out_dir,
  reference_raster = ref_file,
```

```

time_cols      = c("year", "season"),
xcol           = "x",
ycol           = "y",
points_crs     = terra::crs(terra::rast(ref_file)),
verbose        = FALSE
)

```

summarize_raster_outputs

Summarize Prediction Rasters into Consensus Outputs

Description

Post-processing function that synthesizes per-time-step fold-vote rasters (output from [generate_spatiotemporal_predictions](#)) into binary consensus predictions and a temporal frequency summary. Each input raster contains integer vote counts per pixel the number of cross-validation folds that classified that pixel as suitable. The consensus threshold controls how many folds must agree for a pixel to be classified as suitable in the output binary rasters.

Usage

```

summarize_raster_outputs(predictions_dir, output_dir = NULL,
                          consensus = 1, file_pattern = "Prediction_.*\\.tif$",
                          overwrite = FALSE, verbose = TRUE)

```

Arguments

predictions_dir	Character. Directory containing prediction raster files, typically the output_dir used in generate_spatiotemporal_predictions .
output_dir	Character. Directory for output files. Defaults to predictions_dir if NULL.
consensus	Integer. Minimum number of folds that must agree on suitability for a pixel to be classified as suitable in the binary output. For example, consensus = 1 marks any pixel suitable if at least one fold predicts it suitable; consensus = 4 requires at least four folds to agree. Must be between 1 and the maximum vote count in the rasters (number of folds). Default is 1.
file_pattern	Character. Regular expression to match prediction raster files. Default is "Prediction_.*\\.tif\$".
overwrite	Logical. If TRUE, overwrites existing output files. If FALSE (default), existing files are skipped.
verbose	Logical. If TRUE (default), prints progress messages during processing.

Details

Input rasters are fold-vote-count rasters produced by [generate_spatiotemporal_predictions](#), where each pixel value is the number of cross-validation fold models that predicted suitability at that location for that time step. The consensus threshold is applied as: `binary = as.integer(vote_count >= consensus)`.

The frequency raster (proportion of time steps suitable under the chosen consensus) serves as input to [analyze_temporal_patterns](#) for identifying long-term trends in suitability.

Value

Invisibly returns a list containing:

- `consensus_stack`: SpatRaster stack of per-time-step binary consensus rasters (one layer per input file).
- `frequency_raster`: SpatRaster showing the proportion of time steps during which each pixel met the consensus threshold. Values range from 0 (never suitable) to 1 (always suitable).
- `consensus`: the consensus threshold used.
- `n_timesteps`: number of time steps processed.
- `consensus_dir`: path to the directory containing per-time-step binary consensus rasters.
- `frequency_file`: path to the written frequency raster file.

See Also

Upstream: [generate_spatiotemporal_predictions](#)

Downstream: [analyze_temporal_patterns](#)

Examples

```
pred_dir <- system.file("extdata/predictions",
                        package = "TemporalModelR")

summarize_raster_outputs(
  predictions_dir = pred_dir,
  output_dir      = tempdir(),
  consensus       = 3,
  overwrite       = TRUE,
  verbose         = FALSE
)
```

temporally_explicit_extraction

Extract Time-Aligned Environmental Values at Species Occurrences

Description

Preprocessing function that extracts raster values to species occurrence records based on temporal components. Matches environmental layers to occurrence timestamps and optionally computes scaling parameters for standardization.

Usage

```
temporally_explicit_extraction(points_sp, raster_dir, variable_patterns,
                              time_cols, xcol = NULL, ycol = NULL,
                              points_crs = NULL, output_dir,
                              output_prefix = "temp_explicit_df",
                              save_raw = TRUE, save_scaled = TRUE,
                              save_scaling_params = TRUE,
                              verbose = TRUE)
```

Arguments

points_sp	sf object, SpatialPointsDataFrame, file path to .csv/.shp/.geojson/.gpkg, or data frame with coordinate columns.
raster_dir	Character. Directory containing environmental raster files (.tif), typically the output of <code>raster_align</code> . File names must follow the patterns supplied in <code>variable_patterns</code> , with any time placeholder substituted for the corresponding value from <code>time_cols</code> .
variable_patterns	Named character vector mapping clean variable names to raster filename patterns. For time-varying variables include the time placeholder in the pattern (e.g. "forest_cover" = "forest_cover_YEAR"); for static variables omit it (e.g. "elevation" = "elevation"). Time placeholders must match entries in <code>time_cols</code> .
time_cols	Character vector of time column names present in the point data (e.g., c("YEAR"), c("YEAR", "MONTH")).
xcol	Character. Name of the x-coordinate column. Required when <code>points_sp</code> is a CSV file or data frame.
ycol	Character. Name of the y-coordinate column. Required when <code>points_sp</code> is a CSV file or data frame.
points_crs	Character or CRS object. CRS of the input points. Required when <code>points_sp</code> is a CSV file or data frame.
output_dir	Character. Directory to write output files.
output_prefix	Character. Prefix for output filenames. Default is "temp_explicit_df".
save_raw	Logical. If TRUE (default), writes raw extracted values CSV. If FALSE, skips raw values output.

save_scaled	Logical. If TRUE (default), writes z-scaled values CSV. If FALSE, skips scaled values output.
save_scaling_params	Logical. If TRUE (default), writes CSV of per-variable means and standard deviations. If FALSE, skips scaling parameters output.
verbose	Logical. If TRUE (default), prints progress messages during processing. Includes file loading, extraction progress, and file-save confirmation.

Details

Extracts raster values to species occurrence records based on matched temporal components. Matches environmental layers to occurrence timestamps and optionally computes scaling parameters for standardization.

Output CSV files are written to `output_dir` containing raw values, scaled values, and scaling parameters.

Scaling parameters (mean and standard deviation) are optionally computed across all occurrence records for each variable. These parameters should be used with [scale_rasters](#) to standardize prediction layers.

Value

Invisibly returns a list containing:

- `raw_values`: Data frame of raw extracted values at each occurrence record (when `save_raw = TRUE`; NULL otherwise).
- `scaled_values`: Data frame of z-scaled extracted values (when `save_scaled = TRUE`; NULL otherwise).
- `scaling_params`: Data frame of per-variable means and standard deviations used for scaling (when `save_scaling_params = TRUE`; NULL otherwise). Pass this to [scale_rasters](#).
- `files_created`: Named list of file paths written, with elements `raw`, `scaled`, and `scaling_params` (each NULL when the corresponding save flag is FALSE).

See Also

Preprocessing: [spatiotemporal_rarefaction](#), [scale_rasters](#), [spatiotemporal_partition](#)

Examples

```
pts_file <- system.file(
  "extdata/points/synthetic_occurrence_points.csv",
  package = "TemporalModelR"
)

aln_dir <- system.file("extdata/rasters_aligned",
  package = "TemporalModelR")

ref_file <- system.file("extdata/rasters_raw/elevation.tif",
  package = "TemporalModelR")
```

```

out_dir <- file.path(tempdir(), "extracted")

temporally_explicit_extraction(
  points_sp      = pts_file,
  raster_dir     = aln_dir,
  variable_patterns = c(
    "elevation"   = "elevation",
    "forest_cover" = "forest_cover_YEAR",
    "prseas"      = "prseas_YEAR_SEASON"
  ),
  time_cols      = c("year", "season"),
  xcol           = "x",
  ycol           = "y",
  points_crs     = terra::crs(terra::rast(ref_file)),
  output_dir     = out_dir,
  save_raw       = TRUE,
  save_scaled    = FALSE,
  save_scaling_params = TRUE,
  verbose        = FALSE
)

```

tmr_absences

Pre-built pseudoabsence result (seasonal workflow)

Description

Output from [generate_absences](#) using the buffer method with a 300 m buffer (3 pixels at the synthetic landscape's 100 m resolution) and a 2:1 pseudoabsence-to-presence ratio. Pseudoabsences are stratified by fold from `tmr_partition` and have `forest_cover`, `prseas`, and `elevation` extracted at each location's year-season combination. Loaded with `data(tmr_absences)`.

Usage

```
tmr_absences
```

Format

A list as returned by [generate_absences](#), containing `$pseudoabsences` (an sf object with attached predictor columns), `$plots`, and `$summary`.

tmr_absences_annual *Pre-built pseudoabsence result (annual workflow)*

Description

Annual variant of tmr_absences. Buffer method with 300 m buffer and 2:1 ratio, generated against tmr_partition_annual with the annual predictor set (forest_cover, pr_ann, elevation). Loaded with data(tmr_absences_annual).

Usage

tmr_absences_annual

Format

A list as returned by [generate_absences](#).

tmr_absences_user *Pre-built user_data pseudoabsences (seasonal workflow)*

Description

Output of [generate_absences](#) run with method = "user_data" against tmr_partition, using inst/extdata/points/synthetic_user_presences.csv as the supplied absence locations. The CSV contains occurrence-formatted points for a 'related species' to that data of interest to be used as a proxy for survey effort for the species of interest, serving as an alternative method for generating pseudoabsences.

Usage

tmr_absences_user

Format

A list as returned by [generate_absences](#), containing \$pseudoabsences (an sf object with attached predictor columns), \$plots, and \$summary.

tmr_glm	<i>Pre-built GLM result (seasonal workflow)</i>
---------	---

Description

Output from `build_temporal_glm` fit to `tmr_partition` and `tmr_absences` with the formula `~ forest_cover + prseas + elevation`, a logit link, and TSS-based threshold selection. One model per fold. Loaded with `data(tmr_glm)`.

Usage

```
tmr_glm
```

Format

A list of class "TemporalGLM" as returned by `build_temporal_glm`, containing `$models`, `$thresholds`, `$threshold_method`, `$model_formula`, `$link`, `$model_vars`, `$fold_training_data`, `$fold_test_metrics`, `$output_dir`, `$model_type`, and `$plots`.

tmr_glm_annual	<i>Pre-built GLM result (annual workflow)</i>
----------------	---

Description

Annual variant of `tmr_glm`. Fit with the formula `~ forest_cover + pr_ann + elevation`, a logit link, and TSS-based threshold selection. One model per fold. Loaded with `data(tmr_glm_annual)`.

Usage

```
tmr_glm_annual
```

Format

A list of class "TemporalGLM".

tmr_partition	<i>Pre-built spatiotemporal partition (seasonal workflow)</i>
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Description

Output from [spatiotemporal_partition](#) run on the synthetic occurrence dataset bundled in `inst/extdata/`. Built with `n_spatial_folds = 2` and `n_temporal_folds = 2`, producing four cross-validation folds (2 spatial + 2 temporal). Points span 15 years and the seasons Spring, Summer, and Autumn on a 15 x 30 cell study area (3000 m x 1500 m, 100 m pixels) in a custom synthetic local CRS. Predictors attached to each point are `forest_cover`, `prseas` (seasonal precipitation), and `elevation`, all z-scored. Loaded with `data(tmr_partition)`.

Usage

```
tmr_partition
```

Format

A list as returned by [spatiotemporal_partition](#), containing `$folds`, `$points_sf`, `$voronoi_blocks`, `$voronoi_folds`, `$summary`, and `$plots`.

tmr_partition_annual	<i>Pre-built spatiotemporal partition (annual workflow)</i>
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Description

Annual variant of `tmr_partition`. Built from points rarefied with `time_cols = "year"` only (one point per pixel per year) and extracted against annual predictors. Predictors attached to each point are `forest_cover`, `pr_ann` (annual precipitation), and `elevation`, all z-scored. Uses `n_spatial_folds = 2` and `n_temporal_folds = 2` for four folds. Loaded with `data(tmr_partition_annual)`.

Usage

```
tmr_partition_annual
```

Format

A list as returned by [spatiotemporal_partition](#).

tmr_partition_small *Pre-built spatiotemporal partition, small version (seasonal workflow)*

Description

A subsampled version of [tmr_partition](#) retaining approximately half the points per fold, for use in examples and tests where runtime is a concern. Built by sampling $\text{ceiling}(n / 2)$ rows from each fold of `tmr_partition$points_sf`. Loaded with `data(tmr_partition_small)`.

Usage

```
tmr_partition_small
```

Format

A list with the same structure as [tmr_partition](#), containing `$folds`, `$points_sf`, `$voronoi_blocks`, `$voronoi_folds`, `$summary`, and `$plots`.

See Also

[tmr_partition](#)

tmr_predictions *Pre-built spatiotemporal predictions (seasonal workflow)*

Description

Output from [generate_spatiotemporal_predictions](#) projecting `tmr_glm` across 15 years for the Spring season only (one prediction layer per year-season combination, 15 total). Loaded with `data(tmr_predictions)`.

Usage

```
tmr_predictions
```

Format

A list as returned by [generate_spatiotemporal_predictions](#), containing `$timestep_metrics`, `$overall_summary`, `$prediction_files`, and `$model_type`.

Details

Note that `$prediction_files` stores the absolute paths used at build time. To work with the per-timestep rasters on a user machine, regenerate them via [generate_spatiotemporal_predictions](#) or use the bundled prediction set in `inst/extdata/predictions/`.

tmr_predictions_annual

Pre-built spatiotemporal predictions (annual workflow)

Description

Annual variant of tmr_predictions. Projects tmr_glm_annual across 15 years on a single (year-only) time axis. Loaded with data(tmr_predictions_annual).

Usage

```
tmr_predictions_annual
```

Format

A list as returned by [generate_spatiotemporal_predictions](#).

Index

* datasets

- tmr_absences, 41
 - tmr_absences_annual, 42
 - tmr_absences_user, 42
 - tmr_glm, 43
 - tmr_glm_annual, 43
 - tmr_partition, 44
 - tmr_partition_annual, 44
 - tmr_partition_small, 45
 - tmr_predictions, 45
 - tmr_predictions_annual, 46
- analyze_temporal_patterns, 3, 6, 38
- analyze_trends_by_spatial_unit, 5
- binomial, 8, 11
- build_temporal_gam, 7, 10, 12, 13, 15, 17, 22, 24, 25, 27, 34
- build_temporal_glm, 7, 10, 10, 13, 15, 17, 22, 24, 25, 27, 34, 43
- build_temporal_hv, 7, 10, 12, 13, 15, 17, 22, 24, 25, 27, 34
- build_temporal_rf, 7, 10, 12, 13, 15, 15, 22, 24, 25, 27, 34
- extdata, 18
- fastcpd, 4
- fastcpd.binomial, 4
- fastcpd_binomial, 3
- gam, 8–10
- generate_absences, 8, 10–12, 15, 17, 18, 19, 24, 27, 34, 41, 42
- generate_spatiotemporal_predictions, 7, 9, 10, 12–15, 17–19, 23, 26, 27, 37, 38, 45, 46
- hcl.pals, 9, 11, 14, 16, 21, 26, 32
- hypervolume_gaussian, 13, 15
- hypervolume_project, 14
- hypervolume_svm, 13, 15
- plot_model_assessment, 25, 26
- randomForest, 16, 17
- raster_align, 18, 20, 24, 28, 30, 39
- resample, 28
- s, 10
- scale_rasters, 20, 24, 25, 29, 29, 40
- spatiotemporal_partition, 8–13, 15–17, 19–22, 24, 25, 27, 31, 36, 40, 44
- spatiotemporal_rarefaction, 21, 34, 35, 40
- summarize_raster_outputs, 3, 4, 6, 18, 25, 27, 37
- system.file, 18, 19
- temporally_explicit_extraction, 13, 18, 22, 29, 30, 34, 36, 39
- tmr_absences, 41
- tmr_absences_annual, 42
- tmr_absences_user, 42
- tmr_glm, 43
- tmr_glm_annual, 43
- tmr_partition, 42, 44, 45
- tmr_partition_annual, 44
- tmr_partition_small, 45
- tmr_predictions, 45
- tmr_predictions_annual, 46