Package: ct (via r-universe)

October 31, 2026

Type Package

Title Camera Trap Data Management and Multi-Method Ecological Analysis

Version 0.5.0

Date 2026-10-20

Imports activity (>= 1.3.4), dplyr (>= 1.1.4), camtrapdp, cli (>= 3.6.3), Distance (>= 2.0.0), ggplot2 (>= 3.5.2), lubridate, magrittr (>= 2.0.3), methods, nloptr, overlap (>= 0.3.9), rlang (>= 1.1.5), sbd (>= 0.1.0), tibble, tidyr (>= 1.3.1), tidyselect, Rcpp (>= 1.0.8)

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Description Tools for the complete camera trap data workflow in wildlife monitoring and ecological research. Reads and edits media metadata, filters independent detections, and standardises records for analysis. Measures diel activity and overlap (Ridout and Linkie (2009) <doi:10.1198/jabes.2009.08038>), directed short-term association between species with an encounter-response model (Hawkes (1971) <doi:10.1093/biomet/58.1.83>), seasonal shifts in activity, spatial coverage of detections, and species diversity. Estimates density or abundance of unmarked populations with several methods, including the random encounter model, camera trap distance sampling, time-to-event, space-to-event, instantaneous sampling, and the random encounter and staying-time model (see Rowcliffe et al. (2008) <doi:10.1111/j.1365-2664.2008.01473.x>, Howe et al. (2017) <doi:10.1111/2041-210X.12790>, Moeller et al. (2018) <doi:10.1002/ecs2.2331>, and Nakashima et al. (2018) <doi:10.1111/1365-2664.13059>).

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Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

Suggests assertr, iNEXT (>= 3.0.2), httr2, glmmTMB, kableExtra (>= 1.4.0), knitr (>= 1.50), leaflet (>= 2.2.2), lme4, MASS, MCMCvis, msm, nimble, coda, progress, rmarkdown, sf, shiny (>= 1.10.0), terra, testthat (>= 3.0.0), vegan (>= 2.6-6.1), xml2

Config/testthat/edition 3

URL https://stangandaho.github.io/ct/

BugReports https://github.com/stangandaho/ct/issues

Depends R (>= 3.5)

Config/Needs/website rmarkdown

LinkingTo Rcpp

Config/pak/sysreqs
libabsl-dev cmake libgdal-dev gdal-bin libgeos-dev make libicu-dev libjq-dev libuv1-dev libxml2-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev libnode-dev libx11-dev

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

Date/Publication 2026-10-31 17:46:32 UTC

RemoteUrl https://github.com/stangandaho/ct

RemoteRef HEAD

RemoteSha 046e3849fe576e884a6ae00c3a340f20c17d3071

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`ACBR` *Camera trap dataset from Agbogon Community Biological Reserve (ACBR), Benin*

Description

A curated camera trap dataset from the Agonve Community Wetland Reserve in West Africa, adapted from Gandaho et al. (2026). The dataset contains wildlife camera trap observations and associated deployment metadata.

Format

A named list with two tibbles:

`acbr_data` Camera trap observations.

`deployment` Deployment metadata.

Details

The object is provided as a named list with two elements:

`acbr_data` A tibble containing camera trap observations.

Variables include:

`image` Image file name.

`deployment` Deployment identifier.

`cam` Camera station identifier.

`model` Camera model (`RD1003L` or `TC302445`).

`dates` Observation date.

`times` Observation time.

`species` Recorded species name.

`count` Number of individuals detected.

`datetime` Combined date-time in POSIX format.

`deployment` A tibble containing deployment-level metadata.

Variables include:

`deployment` Deployment identifier.
`cam` Camera station identifier.
`model` Camera model.
`start` Deployment start date-time.
`end` Deployment end date-time.
`radius` Camera detection radius (meters).
`angle` Camera detection angle (degrees).
`area` Estimated detection area (square meters).

The deployment table was reconstructed from the observation data using the first and last timestamps recorded for each deployment.

References

Gandaho, S. M., Agossou, H., Madokoun, D. L., Hounnouvi, E. F. K., Oussoukpevi, S. J. K., Akpona, H. A., Thompson, L., & Djagoun, C. A. M. S. (2026). Habitat loss and species diel ecology in a West African community wetland reserve. Zenodo. doi:10.5281/zenodo.19662320

Examples

```
data(ACBR)

# Access observation data
head(ACBR$acbr_data)

# Access deployment metadata
head(ACBR$deployment)
```

`ct_alpha_diversity` *Alpha diversity index*

Description

Calculate index diversity within a particular area or ecosystem; usually expressed by the number of species (i.e., species richness) in that ecosystem.

Usage

```
ct_alpha_diversity(
  data,
  to_community = TRUE,
  index = "shannon",
  site_column,
  species_column,
  size_column = NULL,
  margin = 1
)
```

Arguments

`data`	A data frame containing species observation data.
`to_community`	Logical; if `TRUE`, the function first transforms `data` into a community matrix format where sites are rows and species are columns before computing indices. Default is `TRUE`.
`index`	A character vector specifying the diversity index to calculate. Accepted values are `"shannon"`, `"simpson"`, `"invsimpson"`, `"evenness"`, and `"pielou"`. Multiple indices can be computed simultaneously by providing a vector.
`site_column`	The column name in `data` that represents the site or location where species were recorded.
`species_column`	The column(s) in `data` representing species or taxa. This can be a single column name, a range of column indices (e.g., `2:5`), or a selection helper (e.g., `dplyr::starts_with("sp_")`).
`size_column`	(Optional) The column in `data` containing the count or abundance of individuals per species. If `NULL`, the function assumes each row represents one individual.
`margin`	An integer specifying whether diversity calculations should be performed by row (`margin = 1`) or by column (`margin = 2`). Default is `1` (row-wise).

Details

Simpson diversity index

Simpson (1949) introduced a diversity index that quantifies the likelihood of two randomly chosen individuals belonging to the same species. This probability increases as diversity decreases; in a scenario with no diversity (only one species), the probability reaches 1. Simpson's Index is computed using the following formula:

$$D = \sum_{i=1}^{S} \left(\frac{n_i}{N}\right)^2$$

where n_i is the number of individuals in species *i*, N = total number of individuals of all species, and $\frac{n_i}{N} = pi$ (proportion of individuals of species *i*), and S = species richness. The value of Simpson's *D* ranges from 0 to 1, with 0 representing infinite diversity and 1 representing no diversity, so the larger the value of D, the lower the diversity. For this reason, Simpson's index is often as its complement (*1-D*). Simpson's Dominance Index is the inverse of the Simpson's Index $(1/D)$.

Shannon-Weiner Diversity Index

Shannon-Weiner Diversity Index is a measure of diversity that takes into account both species richness and evenness, introduced by Claude Shannon in 1948. Commonly referred to as Shannon's Diversity Index, it is based on the concept of uncertainty. For instance, in a community with very low diversity, there is a high level of certainty (or low uncertainty) about the identity of a randomly selected organism. Conversely, in a highly diverse community, the uncertainty increases, making it harder to predict which species a randomly chosen organism will belong to (low certainty or high uncertainty).

$$H = -\sum_{i=1}^{S} p_i * \ln p_i$$

where p_i = proportion of individuals of species *i*, and *ln* is the natural logarithm, and S = species richness. The value of H ranges from 0 to Hmax. Hmax is different for each community and depends on species richness. (Note: Shannon-Weiner is often denoted H').

Pielou or Evenness diversity index

Species evenness refers to the relative abundance of each species within an environment. For example, if there are 40 foxes and 1000 dogs, the community is uneven because one species dominates. However, if there are 40 foxes and 42 dogs, the community is much more even, as the species are more balanced in number. The degree of evenness in a community can be quantified using Pielou's evenness index (Pielou, 1966):

$$J = \frac{H}{H_{\max}}$$

The value of J ranges from 0 to 1. Higher values indicate higher levels of evenness. At maximum evenness, J = 1. J and D can be used as measures of species dominance (the opposite of diversity) in a community. Low J indicates that 1 or few species dominate the community.

Value

A tibble with diversity index values for each site. The first column corresponds to `site_column`, followed by one or more columns containing the computed diversity indices, depending on the values specified in the `index` argument.

References

Pielou, E.C. (1966). The measurement of diversity in different types of biological collections. Journal of Theoretical Biology, 13, pp. 131-144. doi:10.1016/00225193(66)900130.

Simpson, E.H. (1949). Measurement of diversity. Nature, 163, pp. 688. doi:10.1038/163688a0

Shannon, C.E. (1948). A mathematical theory of communication. The Bell System Technical Journal, 27, pp. 379-423.doi:10.1002/j.15387305.1948.tb01338.x

Examples

```
data(penessoulou)
cam_data <- penessoulou %>%
  dplyr::filter(project == "Last")

# Transform data to community format and compute diversity indices
alpha1 <- cam_data %>%
  ct_alpha_diversity(
    to_community = TRUE,
    size_column = number,
    site_column = camera,
    species_column = species,
    index = c("shannon", "evenness", "invsimpson")
  )

# Alternative method using a manually transformed community matrix
alpha2 <- cam_data %>%
  ct_to_community(site_column = camera, species_column = species,
```

```
                  size_column = number, values_fill = 0) %>%
  ct_alpha_diversity(
    to_community = FALSE,
    site_column = camera,
    species_column = 2:11,
    index = c("shannon", "evenness", "invsimpson")
  )
alpha2
# Compare results
all(alpha1 == alpha2) # TRUE
```

`ct_availability` *Temporal availability adjustment*

Description

Calculates availability correction factors by accounting for temporal variation in animal activity patterns and camera deployment effort. The availability rate represents the proportion of time animals are available for detection (Rowcliffe, et al., 2014; Howe et al., 2017) given their activity patterns and camera sampling effort.

Usage

```
ct_availability(
  times,
  format = NULL,
  sample = c("data", "model"),
  n_bootstrap = 1000,
  cam_daily_effort = 24,
  ...
)
```

Arguments

`times`	Vector of detection times, either in radians (0 - $2 * pi$) or formatted times (see `format` parameter).
`format`	Time format string (e.g., "%H:%M:%S", "%H:%M") if times need conversion to radians. Set to NULL if times are already in radians.
`sample`	Character string defining sampling method for bootstrapping errors (see details).
`n_bootstrap`	Number of bootstrap iterations to perform. Ignored if sample=="none"
`cam_daily_effort`	Daily operational hours of cameras (default = 24 for continuous operation).
`...`	Arguments passed on to `ct_fit_activity` `weights` A numeric vector of weights for each dat value.

`bandwidth` Numeric value for kernel bandwidth. If NULL, calculated internally.

`adjustment` Numeric bandwidth adjustment multiplier.

`bounds` A two-element vector defining radian bounds at which to truncate.

`show` Logical whether or not to show a progress bar while bootstrapping.

Value

A list containing data frame with:

- `rate`: Estimated availability rate (0-1)
- `SE`: Standard error of the availability rate

References

Howe, E. J., Buckland, S. T., Després-Einspenner, M. L., & Kühl, H. S. (2017). Distance sampling with camera traps. Methods in Ecology and Evolution, 8(11), 1558-1565. doi:10.1111/2041-210X.12790

Rowcliffe, J. M., Kays, R., Kranstauber, B., Carbone, C., & Jansen, P. A. (2014). Quantifying levels of animal activity using camera trap data. Methods in Ecology and Evolution, 5(11), 1170-1179. doi:10.1111/2041210X.12278

See Also

`ct_fit_activity()`

Examples

```
# Example with times already in radians
radian_times <- c(1.2, 3.4, 5.1, 0.5, 2.8)
ct_availability(radian_times, sample = "data")

# Example with formatted times
time_strings <- c("06:30", "18:15", "12:00", "23:45")
ct_availability(time_strings, sample = "data", format = "%H:%M")

# With bootstrap resampling
ct_availability(radian_times, sample = "data", n_bootstrap = 100)
```

---

ct_boot_ci *Bootstrap confidence intervals*

Description

Confidence interval calculation from bootstrap samples.

Usage

```
ct_boot_ci(t0, bt, conf = 0.95)
```

Arguments

t0	the statistic estimated from the original sample, usually the output from ct_overlap_estimates()
bt	a vector of bootstrap statistics, usually the output from ct_boot_estimates()
conf	a (single!) confidence interval to estimate.

Value

A numeric matrix of confidence limits, as returned by overlap::bootCI(). Each row corresponds to one of the estimators supplied in t0 and the two columns give the lower and upper bounds of the confidence interval at the requested level (conf).

---

ct_bootstrap *Generate bootstrap estimates of overlap*

Description

The function takes two sets of times of observations and calculates bootstrap estimates of the chosen estimator of overlap. Alternatively, bootstrap estimates can be calculated in a 2-stage process: (1) create a matrix of bootstrap samples for each data set, using ct_resample(); (2) pass these matrices to ct_boot_estimates() to obtain the bootstrap estimates.

A vector of bootstrap estimates can then be used to produce confidence intervals with ct_boot_ci().

Usage

```
ct_bootstrap(
  A,
  B,
  nb,
  smooth = TRUE,
  kmax = 3,
  adjust = NA,
  n_grid = 128,
  type = c("Dhat1", "Dhat4", "Dhat5"),
  cores = 1
)

ct_resample(x, nb, smooth = TRUE, kmax = 3, adjust = 1, n_grid = 512)

ct_boot_estimates(
  Amat,
  Bmat,
  kmax = 3,
```

```
  adjust = c(0.8, 1, 4),
  n_grid = 128,
  type = c("all", "Dhat1", "Dhat4", "Dhat5"),
  cores = 1
)
```

Arguments

A	A numeric vector of time-of-day observations (in radians, 0 to 2π) for species A.
B	A numeric vector of time-of-day observations (in radians, 0 to 2π) for species B.
nb	the number of bootstrap samples required
smooth	if TRUE, smoothed bootstrap samples are produced.
kmax	An integer indicating the maximum number of modes allowed in the activity pattern. Default is 3.
adjust	A numeric value to adjust the bandwidth of the kernel density estimation. Default is 1.
n_grid	An integer specifying the number of grid points for density estimation. Default is 128.
type	the name of the estimator to use, or "all" to produce all three estimates. See ct_overlap_estimates() for recommendations on which to use.
cores	the number of cores to use for parallel processing. If NA, all but one of the available cores will used. Parallel processing may take longer than serial processing if the bootstrap runs quickly.
x	a numeric vector of time-of-capture data in *radians*, ie. on $[0, 2\pi]$ scale
Amat, Bmat	matrices of resampled data for each species produced by resample; see Value below.

Value

The function ct_bootstrap() returns a vector of bootstrap estimates. If estimation fails for a bootstrap sample, the corresponding value will be NA.

The function ct_resample() returns a numeric matrix with each column corresponding to a bootstrap sample. Times are in radians. It may return a matrix of NAs if smooth = TRUE and bandwidth estimation fails.

The Function ct_boot_estimates() with type = "all" returns a numeric matrix with three columns, one for each estimator of overlap, otherwise a vector of bootstrap estimates.

Author(s)

Mike Meredith, Martin Ridout.

References

Ridout & Linkie (2009) Estimating overlap of daily activity patterns from camera trap data. Journal of Agricultural, Biological, and Environmental Statistics 14:322-337

See Also

ct_boot_ci()

Examples

```
# Generate random data for two species
set.seed(42)
species_A <- runif(100, 1.2, 2 * pi)
species_B <- runif(100, 0.23, 2 * pi)

est <- ct_overlap_estimates(species_A, species_B, type="Dhat4")

boots <- ct_bootstrap(species_A, species_B, 100, type="Dhat4", cores=1)
mean(boots)
hist(boots)
ct_boot_ci(est, boots)

# alternatively:
species_A_gen <- ct_resample(species_A, 100)
species_B_gen <- ct_resample(species_B, 100)
boots <- ct_boot_estimates(species_A_gen, species_B_gen, type="Dhat4", cores=1)
mean(boots)
```

---

ct_camera_day *Calculate daily camera trap captures*

Description

Aggregates camera trap data into daily capture summaries.

Usage

```
ct_camera_day(
  data,
  deployment_data = NULL,
  deployment_column,
  datetime_column,
  species_column,
  size_column,
  format,
  start_column = NULL,
  end_column = NULL,
  deployment_format = format,
  time_zone = ""
)
```

Arguments

`data`	A data frame containing camera trap observation data.
`deployment_data`	A data frame containing camera trap deployment records.
`deployment_column`	The column name (unquoted or as a string) that uniquely identifies the deployment (e.g., camera ID).
`datetime_column`	Column in `data` containing observation timestamps. Can be supplied as a bare name, quoted string, or column position.
`species_column`	The column in the data frame representing species identifiers. Can be specified as a string or unquoted column name.
`size_column`	(Optional) The column representing the size or abundance of the species at each site. If not provided, counts of species occurrences are calculated.
`format`	Character string specifying the datetime format for parsing `datetime_column`.
`start_column`	The column name (unquoted or as a string) indicating deployment start datetime.
`end_column`	The column name (unquoted or as a string) indicating deployment end datetime.
`deployment_format`	Character string specifying the datetime format for parsing `start_column` and `end_column`. Defaults to the same format as `format`.
`time_zone`	The time zone used to parse the datetime columns. Default is `""` (i.e., system time zone).

Value

A tibble with the following columns:

- `deployment_column` (camera/location identifier)
- `date` (Date of observation)
- `species_column` (species name)
- `size_column` (daily count, `0` if no observations)
- `sampling_unit` (unique identifier for location x date combination)

See Also

`ct_inext()`, `ct_get_effort()`

Examples

```
# Example observation data
obs <- data.frame(
  species = c("Deer", "Deer", "Fox", "Deer"),
  count = c(2, 1, 1, 3),
  datetime = c("2023-06-01 08:12:00", "2023-06-01 15:30:00",
               "2023-06-01 21:10:00", "2023-06-02 06:45:00"),
  location_id = c("Cam1", "Cam1", "Cam1", "Cam1"),
```

```
  stringsAsFactors = FALSE
)

# Example deployment data
dep <- data.frame(
  location_id = c("Cam1"),
  deploy_start = "2023-06-01 00:00:00",
  deploy_end = "2023-06-03 23:59:59",
  stringsAsFactors = FALSE
)

ct_camera_day(
  data = obs,
  deployment_data = dep,
  datetime_column = "datetime",
  species_column = "species",
  size_column = "count",
  deployment_column = "location_id",
  format = "%Y-%m-%d %H:%M:%S",
  start_column = "deploy_start",
  end_column = "deploy_end"
)
```

`ct_camtrap_animal_distance` *Estimate distance from camera trap to animal*

Description

Calculates the radial distance between a camera trap and an animal detected in an image using geometric principles and reference markers.

Usage

```
ct_camtrap_animal_distance(fov, forward_distance, ref_halfwidth, animal_offset)
```

Arguments

`fov`	Numeric. The camera's horizontal field of view in degrees. Common values range from 30° to 60° depending on camera model.
`forward_distance`	Numeric. The forward distance (in meters) from the camera to the animal along the central axis, estimated using reference markers visible in the image.
`ref_halfwidth`	Numeric. The measured half-width of the camera's field of view in the image at distance `forward_distance`, in any unit (e.g., cm, pixels). This is typically measured with a ruler on the photo or using image analysis software.
`animal_offset`	Numeric. The measured horizontal offset of the animal from the central vertical line in the image, in the same units as `ref_halfwidth`.

Value

Numeric. The estimated radial distance (in meters) from the camera to the animal.

Examples

```
distance <- ct_camtrap_animal_distance(
  fov = 35,
  forward_distance = 7.5,
  ref_halfwidth = 12,
  animal_offset = 3
)
```

---

ct_check_location *Interactive camera trap location adjustment*

Description

This function launches a shiny application that allows to visualize and manually adjust the geographic coordinates of camera trap locations.

Usage

```
ct_check_location(
  data,
  longitude,
  latitude,
  location_name,
  coord_system = c("geographic", "projected"),
  crs,
  new_data_name
)
```

Arguments

`data`	A data frame containing the camera trap data to be processed.
`longitude`	Column name for longitude in the dataset.
`latitude`	Column name for latitude in the dataset.
`location_name`	Column name that identifies each camera-trap location.
`coord_system`	A string specifying the coordinate system of the input data. Choices are `"geographic"` for longitude and latitude, or `"projected"` for projected coordinates.
`crs`	An integer representing the coordinate reference system (CRS) in EPSG format. Required when `coord_system = "projected"`.
`new_data_name`	A string specifying the name of the new dataset with updated coordinates to be created in the calling environment.

Value

A shiny application object (see shiny::shinyApp()). It is called for its side effect: when run interactively it displays the map and allows manual coordinate adjustments, and the modified dataset is assigned in the calling environment under the name provided in new_data_name.

Examples

```
# Example dataset
camera_traps <- tibble::tibble(
  trap_id = c("Trap1", "Trap2", "Trap3"),
  lon = c(36.8, 36.9, 37.0),
  lat = c(-1.4, -1.5, -1.6)
)

# The function launches an interactive Shiny app, so it is only run in an
# interactive session.
if (interactive()) {
  # Launch the application
  ct_check_location(
    data = camera_traps,
    longitude = "lon",
    latitude = "lat",
    location_name = "trap_id",
    coord_system = "geographic",
    new_data_name = "updated_camera_traps"
  )
  # After adjustments, the updated dataset will be available in the calling
  # environment as `updated_camera_traps`.
}
```

---

ct_check_name *Check species name and retrieve Taxonomic Serial Number (TSN) from ITIS*

Description

This function queries the **Integrated Taxonomic Information System (ITIS)** to find taxonomic details for a given species name. It can search using either a **scientific name** or a **common name** and return relevant taxonomic information, including the TSN.

Usage

```
ct_check_name(
  species_name,
  search_type = c("common_name", "scientific_name"),
  ask = FALSE
)
```

Arguments

species_name	A character string specifying the species name to search for. Only a **single name** is allowed.
search_type	A character string specifying the type of search. Options: • "scientific_name": Search by scientific name. • "common_name": Search by common name.
ask	A logical value (TRUE or FALSE). If TRUE, allows interactive selection when multiple matches are found.

Details

- If the necessary packages (httr2, xml2) are not installed, the function prompts the user to install them.
- If multiple results are found and ask = TRUE, the user is prompted to select the correct match.
- If no exact match is found, all results are displayed for manual selection.

Value

A tibble containing taxonomic details:

- search: The original species name queried.
- tsn: The **Taxonomic Serial Number** (TSN) from ITIS.
- common_name: The common name of the species (if available).
- scientific_name: The scientific name of the species.
- author: The author who classified the species.
- itis_url: A direct link to the species report on ITIS.
- taxon_status: The taxonomic status of the species.

See Also

https://www.itis.gov/

Examples

```
# Search for a species by scientific name
ct_check_name("Panthera leo", search_type = "scientific_name")

# Search by common name with interactive selection
ct_check_name("Lion", search_type = "common_name")
```

`ct_chi2_select` *Select best detection function model by Chi-squared Goodness-of-fit*

Description

Compares detection function models with different key functions using the ratio of the chi-squared statistic to its degrees of freedom. This method selects the best model among different key functions after the best adjustment term model is chosen for each key function.

Usage

```
ct_chi2_select(models)
```

Arguments

`models`	A list of fitted detection function models (objects returned by `Distance::ds()` or `ct_fit_ds()`).

Details

If only one model is supplied, the function returns the chi-squared goodness-of-fit ratio for that model and issues a warning that model selection cannot be performed. For multiple models, each must have a unique key function. This step is designed to be applied after selecting the best model within each key function family using QAIC (see `ct_QAIC()`). The model with the smallest chi-squared/df ratio is typically preferred.

Value

A tibble with one row per model containing:

- `key`: The key function of the model.
- `model`: The model name.
- `criteria`: The chi-squared goodness-of-fit statistic divided by its degrees of freedom, i.e. χ^2/df. Lower values indicate better fit.

References

Howe, E. J., Buckland, S. T., Després-Einspenner, M., & Kühl, H. S. (2019). Model selection with overdispersed distance sampling data. **Methods in Ecology and Evolution**, 10(1), 38-47. doi:10.1111/2041210X.13082

Examples

```
library(Distance)
library(dplyr)

data("duiker")
duiker_data <- duikers$DaytimeDistances %>%
```

```
  dplyr::slice_sample(prop = .3) # sample 30% of rows
truncation <- list(left = 2, right = 15) # Keep only distance between 2-15 m

# fit hazard-rate key models
w3_hr0 <- ds(duiker_data, transect = "point", key = "hr", adjustment = NULL,
             truncation = truncation)
w3_hr1 <- ds(duiker_data, transect = "point", key = "hr", adjustment = "cos",
             order = 2, truncation = truncation)
w3_hr2 <- ds(duiker_data, transect = "point", key = "hr", adjustment = "cos",
             order = c(2, 4), truncation = truncation)
# fit half-normal key models
w3_hn0 <- ds(duiker_data, transect = "point", key = "hn", adjustment = NULL,
             truncation = truncation)
w3_hn1 <- ds(duiker_data, transect = "point", key = "hn", adjustment = "cos",
             order = 2, truncation = truncation)
w3_hn2 <- ds(duiker_data, transect = "point", key = "hn", adjustment = "cos",
             order = c(2, 4), truncation = truncation)
# fit uniform key models
w3_u0 <- ds(duiker_data, transect = "point", key = "unif", adjustment = NULL,
            truncation = truncation)
w3_u1 <- ds(duiker_data, transect = "point", key = "unif", adjustment = "cos",
            order = 2, truncation = truncation)
w3_u2 <- ds(duiker_data, transect = "point", key = "unif", adjustment = "cos",
            order = c(2, 4), truncation = truncation)

# Create model list
model_list <- list(w3_hn0, w3_hn1, w3_hn2,
                   w3_hr0, w3_hr1, w3_hr2,
                   w3_u0, w3_u1, w3_u2)

# Compute model QAICs
ct_QAIC(list(w3_hr0, w3_hr1, w3_hr2)) # All key functions must be the same
ct_QAIC(list(w3_hn0, w3_hn1, w3_hn2)) # All key functions must be the same

# Compute Chi-squared Goodness-of-fit
ct_chi2_select(list(w3_hn0, w3_hr0, w3_u0)) # All key functions must be different
ct_chi2_select(list(w3_hn2, w3_hr1, w3_u0)) # All key functions must be different

# Two-step model selection
ct_select_model(model_list)
```

`ct_ci` *Calculate confidence interval*

Description

Calculates the confidence interval for the mean of a numeric vector using the t-distribution.

Usage

```
ct_ci(x, alpha = 0.05, side = "all")
```

Arguments

x	A numeric vector of data values.
alpha	Significance level for the confidence interval. Default is 0.05 (for 95% confidence).
side	A character string indicating the type of interval: **"all"** Two-sided confidence interval (default). **"left"** One-sided lower bound. **"right"** One-sided upper bound.

Value

A numeric vector containing the confidence interval bounds:

- If `side = "all"`, returns a vector of length 2: `c(lower, upper)`.
- If `side = "left"` or `"right"`, returns a single numeric value.

Examples

```
x <- c(10, 12, 11, 14, 13, 15)
ct_ci(x)
ct_ci(x, alpha = 0.01)
ct_ci(x, side = "left")
```

---

ct_clone_dir *Clone directory structure*

Description

Clones the directory structure from a source directory (`from`) to a destination directory (`to`). This function replicates the folder hierarchy and subdirectories, but does not copy files, making it useful for setting up empty directory templates when organizing camera trap data.

Usage

```
ct_clone_dir(from, to, recursive = TRUE)
```

Arguments

from	Character. The path to the source directory whose structure will be cloned. Must exist and be a directory.
to	Character. The path to the destination directory where the structure will be cloned. Must exist and be a directory.
recursive	Logical. Should the directory structure be cloned recursively, including all subdirectories? Default is `TRUE`.

Value

Invisibly returns NULL. The function is called for its side-effect of creating directories.

Examples

```
# Create a temporary directory structure
src <- tempfile("source_dir")
dir.create(src)
dir.create(file.path(src, "site1"))
dir.create(file.path(src, "site1", "cameraA"))
dir.create(file.path(src, "site2"))

# Create destination directory
dst <- tempfile("destination_dir")
dir.create(dst)

# Clone the directory structure
ct_clone_dir(from = src, to = dst)

# Check that structure was cloned
list.files(dst, recursive = TRUE)

# Clean up
unlink(c(src, dst), recursive = TRUE)
```

---

ct_convert_unit *Convert values between different units*

Description

Convert a numeric value from one unit to another. It supports **area**, **distance (length)**, and **angle** units.

Usage

```
ct_convert_unit(x, from, to, show_units = FALSE)
```

Arguments

x	Numeric. Value(s) to convert.
from	Character. The unit to convert from. Can be any synonym e.g. "meter", "m", "metre", "feet", "°", "um" (i.e μm), etc.
to	Character. The unit to convert to. Can also be any synonym.
show_units	Logical. If TRUE, returns the full table of supported units and their synonyms instead of performing a conversion.

Value

A numeric vector of converted values.

See Also

`units_table()` for supported units and synonyms.

Examples

```
# Distance
ct_convert_unit(1000, "m", "km")
ct_convert_unit(1, "mile", "m")
ct_convert_unit(12, "inches", "ft")

# Area
ct_convert_unit(1, "acre", "m2")
ct_convert_unit(2, "km2", "hectare")

# Angle
ct_convert_unit(180, "deg", "rad")
ct_convert_unit(pi, "rad", "deg")
```

---

ct_correct_datetime *Correct camera trap datetime records*

Description

This function corrects datetime stamps in camera trap data using a reference correction table. It applies time adjustments based on known timing errors for each camera deployment.

Usage

```
ct_correct_datetime(
  data,
  datetime,
  deployment,
  corrector,
  format = NULL,
  time_zone = "UTC"
)
```

Arguments

`data`	A data.frame or tibble containing camera trap records with datetime information that needs correction.
`datetime`	Column name (unquoted) in `data` containing the datetime values to be corrected. Can be character or POSIXct format.

`deployment` Column name (unquoted) in both `data` and `corrector` that identifies unique camera deployments (e.g., camera ID, site name, or deployment identifier).

`corrector` A data.frame containing correction information with columns:

- deployment column matching the deployment parameter
- `sign` - character indicating correction direction ("+" or "-")
- `datetimes` - correct date-time of the first (earliest) record of the deployment
- `end_datetimes` - optional; correct date-time of the last (latest) record of the deployment. When present and not missing, the correction drifts linearly between the first and the last record.

`format` Optional datetime format specification. Can be:

- `NULL` (default) - attempts multiple common formats
- Single format string - used for both `data` and `corrector` datetimes
- Vector of 2 format strings - first for data, second for corrector

`time_zone` Time zone used to parse the datetimes in `data` and `corrector`. Defaults to `"UTC"`, which has no daylight saving time and so keeps camera wall-clock times unchanged. Any time zone name accepted by `as.POSIXct()` can be used, for example `Sys.timezone()` for the computer's time zone when the deployment does not span a daylight-saving change.

Details

Two kinds of clock error are handled. A constant offset (a camera set to the wrong date or time) is corrected from the true datetime of the first record of each deployment. Clock drift (a camera that gains or loses time during the deployment) is corrected when the true datetime of the last record is also supplied: the correction then changes linearly with time, from the offset at the first record to the offset at the last record.

Camera clocks do not change for daylight saving time. Datetimes are therefore parsed in the time zone given by `time_zone`, which defaults to `"UTC"` (no daylight saving), so that recorded wall-clock times are kept as they are and no record is shifted or lost at a daylight saving change.

Value

A data.frame with the original data plus additional columns:

- `corrected_datetime` - corrected datetime as POSIXct
- `correction_applied` - sign of correction applied
- `time_offset_seconds` - magnitude of correction in seconds (varies between records when drift is corrected)
- `corrector_reference` - reference datetime used for correction

Examples

```
# Load camera trap data
library(dplyr)
data(penessoulou)
```

```
camtrap_data <- penessoulou %>%
  dplyr::filter(project == "Last")

# Create correction table
# CAMERA 1 was running slow (+), CAMERA 2 was running fast (-)
crtor <- data.frame(
  camera = c("CAMERA 1", "CAMERA 2"),
  sign = c("+", "-"),
  datetimes = c("2025-03-14 8:17:00", "2024-11-14 10:02:03")
)

# Apply datetime corrections
ct_correct_datetime(
  data = camtrap_data,
  datetime = datetimes,
  deployment = camera,
  corrector = crtor
) %>%
  dplyr::select(datetimes,
                corrected_datetime,
                time_offset_seconds) %>%
  dplyr::slice_head(n = 10)

# Clock drift: CAMERA 1 also lost 90 s over the deployment, so the true time
# of its last record is 90 s later than the constant offset gives
crtor_drift <- crtor
crtor_drift$end_datetimes <- c("2025-04-16 01:16:15", NA)

ct_correct_datetime(
  data = camtrap_data,
  datetime = datetimes,
  deployment = camera,
  corrector = crtor_drift
) %>%
  dplyr::filter(camera == "CAMERA 1") %>%
  dplyr::select(datetimes, corrected_datetime, time_offset_seconds) %>%
  dplyr::slice_tail(n = 5)
```

`ct_create_hs` *Create or add hierarchical subject (hs) values in image metadata*

Description

Adds hierarchical subject metadata to image files. Hierarchical subjects follow a parent|child structure, allowing for organized taxonomic or categorical classification of images.

Usage

```
ct_create_hs(
  path,
  value = NULL,
  overwrite = FALSE,
  recursive = FALSE,
  intern = TRUE,
  quiet = TRUE,
  ...
)
```

Arguments

path	A character string specifying the full path to an image file or directory. If a directory is provided, hierarchical subjects will be added to all supported image files in that directory.
value	A named character vector specifying hierarchical subjects to add. Names represent parent categories, values represent child categories. **Simple format:** `c("Species" = "Vulture", "Location" = "Africa")` creates "Species|Vulture" and "Location|Africa". **Multiple values format:** `c("Species" = "Mammal, Bird", "Count" = "2, 3")` creates "Species|Mammal", "Species|Bird", "Count|2", and "Count|3". All parents must have equal number of comma-separated values.
overwrite	Logical. If `TRUE`, replaces existing hierarchical subjects. If `FALSE` (default), adds to existing subjects. Default: `FALSE`.
recursive	Logical. If `TRUE` and `path` is a directory, searches for images recursively in subdirectories. Default: `FALSE`.
intern	Logical. If `TRUE`, returns output as a character vector. Default: `TRUE`.
quiet	Logical. If `TRUE`, suppresses command output. Default: `TRUE`.
...	Additional arguments passed to `system2()`.

Details

Two input formats are supported:

1. Simple format: One child per parent, e.g., `c("Species" = "Vulture")`
2. Multiple values format: Multiple children per parent using comma-separated values, e.g., `c("Species" = "Mammal, Bird, Reptile")`. When using this format, all parents must have the same number of comma-separated values.

The function validates that all values have parent categories (names) and preserves existing hierarchical subjects unless `overwrite = TRUE`. Duplicate parent|child combinations are automatically removed.

When processing directories, the function applies hierarchical subjects to all supported image files found. Use `recursive = TRUE` to include subdirectories.

When using comma-separated values, the function splits each value string and creates separate hierarchical subjects for each position across all parents.

Value

Invisibly returns TRUE on success. Called primarily for side effects (modifying image metadata).

See Also

- ct_get_hs() to retrieve hierarchical subjects
- ct_remove_hs() to remove hierarchical subjects
- ct_read_metadata() to read image metadata

Examples

```
## Not run:
# Path to example image
image_path <- file.path(system.file("img", package = "ct"), "large.jpeg")

# Simple format: single child per parent
ct_create_hs(path = image_path, value = c("Species" = "Vulture"))
ct_get_hs(path = image_path) # Returns: "Species|Vulture"

# Simple format: multiple parents, one child each
ct_create_hs(
  path = image_path,
  value = c("Species" = "Vulture",
            "Location" = "Africa",
            "Status" = "Endangered")
)
ct_get_hs(path = image_path, into_tibble = TRUE)

# Multiple values format: recording multiple observations
ct_create_hs(
  path = image_path,
  value = c(
    "Species" = "Gyps_africanus, Kobus_kob",
    "Sex" = "Male, Female",
    "Count" = "3, 2"
  ),
  overwrite = TRUE
)
ct_get_hs(path = image_path)

# Parse Hierarchical Subject to tibble
ct_get_hs(path = image_path, into_tibble = TRUE)

# Overwrite existing hierarchical subjects
ct_create_hs(
  path = image_path,
  value = c("Species" = "Eagle"),
  overwrite = TRUE
)

## End(Not run)
```

`ct_describe_df` *Descriptive statistic on dataset*

Description

This function provides a summary of a dataset, including both numeric and non-numeric variables. For numeric variables, it calculates basic descriptive statistics such as minimum, maximum, median, mean, and count of non-missing values. Additionally, users can pass custom functions via the `fn` argument to compute additional statistics for numeric variables. For non-numeric variables, it provides frequency counts and proportions for each unique value.

Usage

```
ct_describe_df(data, ..., fn = NULL, by_group = TRUE)
```

Arguments

`data`	A data frame containing the dataset to be summarized.
`...`	(Optional) Columns to include in the summary. If no column is specified, all columns in the data will be included.
`fn`	A list of functions to apply to numeric variables. Each function must accept `x` as a vector of numeric values and return a single value or a named vector. Additional arguments for these functions can be specified as a list. For example: `fn = list('sum' = list(na.rm = TRUE), 'sd')`.
`by_group`	Logical, default `TRUE`. When `TRUE` and both categorical and numeric variables are selected, each numeric variable is summarised within the groups defined by the categorical variable(s). When `FALSE`, numeric and categorical variables are summarised independently and stacked into a single table. If only one variable type is present, `by_group` has no effect.

Value

A tibble whose shape depends on `by_group`.

With `by_group = TRUE` (and at least one categorical and one numeric variable), the data are grouped by the selected categorical variable(s) and each numeric variable is summarised within every group. The result has one row per numeric variable and group combination, with columns:

`Variable` Name of the numeric variable being summarised.

grouping column(s) One column per selected categorical variable, each holding the group value.

`N` Number of non-missing values of `Variable` in the group.

`Min`, `Max`, `Median`, `Mean` Descriptive statistics of `Variable` within the group.

`CI Left`, `CI Right` Lower and upper bounds of the 95% t-based confidence interval for the group mean (see `ct_ci()`).

With by_group = FALSE (also used as a fallback when only numeric or only categorical variables are selected), numeric and categorical summaries are stacked into one tibble with one row per numeric variable and one row per distinct value of each categorical variable; columns that do not apply to a row are NA:

Variable Name of the summarised column.

Group For a categorical variable, the distinct value described; NA for numeric variables.

Prop For a categorical variable, the percentage of its non-missing records falling in Group; NA for numeric variables.

N Non-missing count: values for a numeric variable, or records in Group for a categorical variable.

Min, Max, Median, Mean Numeric statistics; NA for categorical variables.

CI Left, CI Right 95% t-based confidence interval bounds for the mean (see ct_ci()); NA for categorical variables.

In both modes, supplying fn appends one extra column per named function, holding that statistic for each numeric variable (or group).

See Also

parse_list_fn

Examples

```
df <- data.frame(x = c(1:3, NA),
                 y = c(3:4, NA, NA),
                 z = c("A", "A", "B", "A"))

# Numeric variables summarised within each group of the categorical variable
ct_describe_df(df, y, x, z)

# Summarise every variable independently
ct_describe_df(df, y, x, z, by_group = FALSE)

# Add custom statistics for the numeric variables
ct_describe_df(df, y, x, z,
               fn = list('sum' = list(na.rm = TRUE), 'sd' = list(na.rm = TRUE)))
```

---

ct_dissimilarity *Calculate dissimilarity between communities*

Description

The function computes dissimilarity indices that are useful for or popular with community ecologists. All indices use quantitative data, although they would be named by the corresponding binary index, but you can calculate the binary index using an appropriate argument. If you do not find your favourite index here, you can see if it can be implemented using designdist. Gower, Bray-Curtis,

Jaccard and Kulczynski indices are good in detecting underlying ecological gradients (Faith et al. 1987). Morisita, Horn-Morisita, Binomial, Cao and Chao indices should be able to handle different sample sizes (Wolda 1981, Krebs 1999, Anderson & Millar 2004), and Mountford (1962) and Raup-Crick indices for presence-absence data should be able to handle unknown (and variable) sample sizes. Most of these indices are discussed by Krebs (1999) and Legendre & Legendre (2012), and their properties further compared by Wolda (1981) and Legendre & De Caceres (2012). Aitchison (1986) distance is equivalent to Euclidean distance between CLR-transformed samples ("clr") and deals with positive compositional data. Robust Aitchison distance by Martino et al. (2019) uses robust CLR ("rlcr"), making it applicable to non-negative data including zeroes (unlike the standard Aitchison).

Usage

```
ct_dissimilarity(
  data,
  to_community = FALSE,
  site_column,
  species_column,
  size_column = NULL,
  method = "bray",
  binary = FALSE,
  diag = FALSE,
  upper = FALSE,
  na.rm = FALSE,
  ...
)
```

Arguments

data	A data frame or matrix containing the species abundance data. The rows represent sites (or samples), and the columns represent species. The data can be in raw or transformed format (if to_community = TRUE).
to_community	A logical indicating whether the input data should be transformed into community data (site in row and species in column). Default is FALSE.
site_column	The name of the column representing the site/sample identifiers (only used if to_community = TRUE).
species_column	The name of the column representing species identifiers (only used if to_community = TRUE).
size_column	The name of the column representing size or abundance counts of each species at each site (optional, used if to_community = TRUE).
method	A character string indicating the distance measure to use for calculating beta diversity. The available methods are: "manhattan", "euclidean", "canberra", "bray", "kulczynski", "gower", "morisita", "horn", "mountford", "jaccard", "raup", "binomial", "chao", "altGower", "cao", "mahalanobis", "clark", "chisq", "chord", "hellinger", "aitchison", "robust.aitchison". The default is "bray".
binary	A logical indicating whether to transform the data to presence/absence (binary data) before calculating dissimilarities. Default is FALSE.

`diag`	A logical indicating whether to include the diagonal in the output dissimilarity matrix. Default is `FALSE` (diagonal values are omitted).
`upper`	A logical indicating whether to return only the upper triangular part of the dissimilarity matrix. Default is `FALSE`.
`na.rm`	A logical indicating whether to remove `NA` values from the data before calculating dissimilarities. Default is `FALSE`. If `FALSE`, an error is raised if there are any missing values in the data.
`...`	Additional arguments passed to other functions, such as transformation functions for data scaling or standardization.

Details

Jaccard (`"jaccard"`), Mountford (`"mountford"`), Raup–Crick (`"raup"`), Binomial and Chao indices are discussed later in this section. The function also finds indices for presence/ absence data by setting `binary = TRUE`. The following overview gives first the quantitative version, where x_{ij} x_{ik} refer to the quantity on species (column) i and sites (rows) j and k. In binary versions A and B are the numbers of species on compared sites, and J is the number of species that occur on both compared sites similarly as in `designdist` (many indices produce identical binary versions):

`euclidean` $d_{jk} = \sqrt{\sum_i (x_{ij} - x_{ik})^2}$
binary: $\sqrt{A + B - 2J}$

`manhattan` $d_{jk} = \sum_i |x_{ij} - x_{ik}|$
binary: $A + B - 2J$

`gower` $d_{jk} = (1/M) \sum_i \frac{|x_{ij} - x_{ik}|}{\max x_i - \min x_i}$
binary: $(A + B - 2J)/M$
where M is the number of columns (excluding missing values)

`altGower` $d_{jk} = (1/NZ) \sum_i |x_{ij} - x_{ik}|$
where NZ is the number of non-zero columns excluding double-zeros (Anderson et al. 2006).
binary: $\frac{A+B-2J}{A+B-J}$

`canberra` $d_{jk} = \frac{1}{NZ} \sum_i \frac{|x_{ij} - x_{ik}|}{|x_{ij}| + |x_{ik}|}$
where NZ is the number of non-zero entries.
binary: $\frac{A+B-2J}{A+B-J}$

`clark` $d_{jk} = \sqrt{\frac{1}{NZ} \sum_i (\frac{x_{ij} - x_{ik}}{x_{ij} + x_{ik}})^2}$
where NZ is the number of non-zero entries.
binary: $\frac{A+B-2J}{A+B-J}$

`bray` $d_{jk} = \frac{\sum_i |x_{ij} - x_{ik}|}{\sum_i (x_{ij} + x_{ik})}$
binary: $\frac{A+B-2J}{A+B}$

`kulczynski` $d_{jk} = 1 - 0.5(\frac{\sum_i \min(x_{ij}, x_{ik})}{\sum_i x_{ij}} + \frac{\sum_i \min(x_{ij}, x_{ik})}{\sum_i x_{ik}})$
binary: $1 - (J/A + J/B)/2$

`morisita` $d_{jk} = 1 - \frac{2 \sum_i x_{ij} x_{ik}}{(\lambda_j + \lambda_k) \sum_i x_{ij} \sum_i x_{ik}}$, where
$\lambda_j = \frac{\sum_i x_{ij}(x_{ij} - 1)}{\sum_i x_{ij} \sum_i (x_{ij} - 1)}$
binary: cannot be calculated

`horn` Like `morisita`, but $\lambda_j = \sum_i x_{ij}^2 / (\sum_i x_{ij})^2$
binary: $\frac{A+B-2J}{A+B}$

`binomial` $d_{jk} = \sum_i [x_{ij} \log(\frac{x_{ij}}{n_i}) + x_{ik} \log(\frac{x_{ik}}{n_i}) - n_i \log(\frac{1}{2})]/n_i$,

where $n_i = x_{ij} + x_{ik}$

binary: $\log(2) \times (A + B - 2J)$

`cao` $d_{jk} = \frac{1}{S}\sum_i \log\left(\frac{n_i}{2}\right) - (x_{ij}\log(x_{ik}) + x_{ik}\log(x_{ij}))/n_i$,
where S is the number of species in compared sites and $n_i = x_{ij} + x_{ik}$

Jaccard index is computed as $2B/(1 + B)$, where B is Bray–Curtis dissimilarity.

Binomial index is derived from Binomial deviance under null hypothesis that the two compared communities are equal. It should be able to handle variable sample sizes. The index does not have a fixed upper limit, but can vary among sites with no shared species. For further discussion, see Anderson & Millar (2004).

Cao index or CYd index (Cao et al. 1997) was suggested as a minimally biased index for high beta diversity and variable sampling intensity. Cao index does not have a fixed upper limit, but can vary among sites with no shared species. The index is intended for count (integer) data, and it is undefined for zero abundances; these are replaced with arbitrary value 0.1 following Cao et al. (1997). Cao et al. (1997) used $\log_{10}$, but the current function uses natural logarithms so that the values are approximately 2.30 times higher than with 10-based logarithms. Anderson & Thompson (2004) give an alternative formulation of Cao index to highlight its relationship with Binomial index (above).

Mountford index is defined as $M = 1/\alpha$ where α is the parameter of Fisher's logseries assuming that the compared communities are samples from the same community (cf. `fisherfit`, `fisher.alpha`). The index M is found as the positive root of equation $\exp(aM) + \exp(bM) = 1 + \exp[(a + b - j)M]$, where j is the number of species occurring in both communities, and a and b are the number of species in each separate community (so the index uses presence–absence information). Mountford index is usually misrepresented in the literature: indeed Mountford (1962) suggested an approximation to be used as starting value in iterations, but the proper index is defined as the root of the equation above. The function `vegdist` solves M with the Newton method. Please note that if either a or b are equal to j, one of the communities could be a subset of other, and the dissimilarity is 0 meaning that non-identical objects may be regarded as similar and the index is non-metric. The Mountford index is in the range $0 \ldots \log(2)$.

Raup–Crick dissimilarity (`method = "raup"`) is a probabilistic index based on presence/absence data. It is defined as $1 - prob(j)$, or based on the probability of observing at least j species in shared in compared communities. The current function uses analytic result from hypergeometric distribution (`phyper`) to find the probabilities. This probability (and the index) is dependent on the number of species missing in both sites, and adding all-zero species to the data or removing missing species from the data will influence the index. The probability (and the index) may be almost zero or almost one for a wide range of parameter values. The index is nonmetric: two communities with no shared species may have a dissimilarity slightly below one, and two identical communities may have dissimilarity slightly above zero. The index uses equal occurrence probabilities for all species, but Raup and Crick originally suggested that sampling probabilities should be proportional to species frequencies (Chase et al. 2011). A simulation approach with unequal species sampling probabilities is implemented in `raupcrick` function following Chase et al. (2011). The index can be also used for transposed data to give a probabilistic dissimilarity index of species co-occurrence (identical to Veech 2013).

Chao index tries to take into account the number of unseen species pairs, similarly as in `method = "chao"` in `specpool`. Function `vegdist` implements a Jaccard, index defined as $1 - \frac{U \times V}{U+V-U \times V}$; other types can be defined with function `chaodist`. In Chao equation, $U = C_j/N_j + (N_k - 1)/N_k \times a_1/(2a_2) \times S_j/N_j$, and V is similar except for site index k. C_j is the total number of individuals

in the species of site j that are shared with site k, N_j is the total number of individuals at site j, a_1 (and a_2) are the number of species occurring in site j that have only one (or two) individuals in site k, and S_j is the total number of individuals in the species present at site j that occur with only one individual in site k (Chao et al. 2005).

Morisita index can be only used with genuine count data (integers). It is based on the idea of resampling without replacement in finite samples and should not be used with presence/absence data, and gives meaningless results if compared sampling units (rows) have largest integer 1. Its Horn–Morisita variant is able to handle any abundance data, and should be used if data are unsuitable for Morisita.

Mahalanobis distances are Euclidean distances of a matrix where columns are centred, have unit variance, and are uncorrelated. The index is not commonly used for community data, but it is sometimes used for environmental variables. The calculation is based on transforming data matrix and then using Euclidean distances following Mardia et al. (1979). The Mahalanobis transformation usually fails when the number of columns is larger than the number of rows (sampling units). When the transformation fails, the distances are nearly constant except for small numeric noise. Users must check that the returned Mahalanobis distances are meaningful.

Euclidean and Manhattan dissimilarities are not good in gradient separation without proper standardization but are still included for comparison and special needs.

Chi-square distances (`"chisq"`) are Euclidean distances of Chi-square transformed data (see `decostand`). This is the internal standardization used in correspondence analysis (`cca`, `decorana`). Weighted principal coordinates analysis of these distances with row sums as weights is equal to correspondence analysis (see the Example in `wcmdscale`). Chi-square distance is intended for non-negative data, such as typical community data. However, it can be calculated as long as all margin sums are positive, but warning is issued on negative data entries.

Chord distances (`"chord"`) are Euclidean distance of a matrix where rows are standardized to unit norm (their sums of squares are 1) using `decostand`. Geometrically this standardization moves row points to a surface of multidimensional unit sphere, and distances are the chords across the hypersphere. Hellinger distances (`"hellinger"`) are related to Chord distances, but data are standardized to unit total (row sums are 1) using `decostand`, and then square root transformed. These distances have upper limit of $\sqrt{2}$.

Bray–Curtis and Jaccard indices are rank-order similar, and some other indices become identical or rank-order similar after some standardizations, especially with presence/absence transformation of equalizing site totals with `decostand`. Jaccard index is metric, and probably should be preferred instead of the default Bray-Curtis which is semimetric.

Aitchison distance (1986) and robust Aitchison distance (Martino et al. 2019) are metrics that deal with compositional data. Aitchison distance has been said to outperform Jensen-Shannon divergence and Bray-Curtis dissimilarity, due to a better stability to subsetting and aggregation, and it being a proper distance (Aitchison et al., 2000).

The naming conventions vary. The one adopted here is traditional rather than truthful to priority. The function finds either quantitative or binary variants of the indices under the same name, which correctly may refer only to one of these alternatives For instance, the Bray index is known also as Steinhaus, Czekanowski and Sørensen index. The quantitative version of Jaccard should probably called Ružička index. The abbreviation `"horn"` for the Horn–Morisita index is misleading, since there is a separate Horn index. The abbreviation will be changed if that index is implemented in `vegan`.

Value

A distance matrix (of class `dist`) containing the pairwise dissimilarities between sites. The dissimilarities are calculated according to the chosen distance metric, and various attributes (e.g., method, size, labels) are attached to the result.

Note

The function is an alternative to `dist` adding some ecologically meaningful indices. Both methods should produce similar types of objects which can be interchanged in any method accepting either. Manhattan and Euclidean dissimilarities should be identical in both methods. Canberra index is divided by the number of variables in `vegdist`, but not in `dist`. So these differ by a constant multiplier, and the alternative in `vegdist` is in range (0,1). Function `daisy` (package **cluster**) provides alternative implementation of Gower index that also can handle mixed data of numeric and class variables. There are two versions of Gower distance (`"gower"`, `"altGower"`) which differ in scaling: `"gower"` divides all distances by the number of observations (rows) and scales each column to unit range, but `"altGower"` omits double-zeros and divides by the number of pairs with at least one above-zero value, and does not scale columns (Anderson et al. 2006). You can use `decostand` to add range standardization to `"altGower"` (see Examples). Gower (1971) suggested omitting double zeros for presences, but it is often taken as the general feature of the Gower distances. See Examples for implementing the Anderson et al. (2006) variant of the Gower index.

Most dissimilarity indices in `vegdist` are designed for community data, and they will give misleading values if there are negative data entries. The results may also be misleading or `NA` or `NaN` if there are empty sites. In principle, you cannot study species composition without species and you should remove empty sites from community data.

Author(s)

Jari Oksanen, with contributions from Tyler Smith (Gower index), Michael Bedward (Raup–Crick index), and Leo Lahti (Aitchison and robust Aitchison distance).

References

This function adapts the dissimilarity methods of **vegan**. See `vegdist` for the methods and their original references. Oksanen, J. et al. vegan: Community Ecology Package. `https://CRAN.R-project.org/package=vegan`

`ct_dp_example` *Read the Camtrap DP example dataset*

Description

Reads the Camtrap DP example dataset. This dataset is maintained and versioned with the Camtrap DP standard.

Usage

```
ct_dp_example()
```

Value

Camera Trap Data Package object.

`ct_dp_filter` *Filter camera trap data package*

Description

Subsets observations in camera trap data package, retaining all rows that satisfy the conditions.

Usage

```
ct_dp_filter(package, table = c("observations", "deployments", "media"), ...)
```

Arguments

`package`	Camera trap data package object, as returned by ct_read_dp().
`table`	Character indicating the table to read - one "observations", "deployments", or "media"
`...`	Filtering conditions, see dplyr::filter()

Value

A Camera Trap Data Package object of the same class as `package`, with the selected `table` subset to the rows satisfying the conditions in `....` Related tables are updated so the package stays internally consistent (see `camtrapdp::filter_observations()`).

Examples

```
dp <- ct_dp_example()
ct_dp_filter(package = dp, table = "observation",
scientificName == "Vulpes vulpes", observationLevel == "event"
)

ct_dp_filter(package = dp, table = "deployments",
             latitude > 51.0, longitude > 5.0)


ct_dp_filter(package = dp, table = "media",
             captureMethod == "activityDetection", filePublic == FALSE
)
```

ct_dp_read *Read camera trap data package*

Description

Reads Camera Trap Data Package (Camtrap DP) dataset into memory.

Usage

```
ct_dp_read(file)
```

Arguments

file	Path or URL to a datapackage.json file.

Value

A Camera Trap Data Package object.

Taxonomic information

Camtrap DP metadata has a taxonomic property that can contain extra information for each scientificName found in observations. Such information can include higher taxonomy (family, order, etc.) and vernacular names in multiple languages.

The read_camtrapdp() function **will automatically include this taxonomic information in observations**, as extra columns starting with taxon.. It will then update the taxonomic scope in the metadata to the unique taxa() found in the data.

Events

Observations can contain classifications at two levels:

- **Media-based** observations (observationLevel = "media") are based on a single media file and are directly linked to it via mediaID.
- **Event-based** observations (observationLevel = "event") are based on an event, defined as a combination of eventID, eventStart and eventEnd. This event can consist of one or more media files, but is not directly linked to these.

The read_camtrapdp() function **will automatically assign** eventIDs **to media**, using media.deploymentID = observations.deploymentID and observations.eventStart <= media.timestamp <= observations.eventEnd. Note that this can result in media being linked to multiple events (and thus being duplicated), for example when events and sub-events were defined.

Examples

```
file <- "https://raw.githubusercontent.com/tdwg/camtrap-dp/1.0/example/datapackage.json"
dp <- ct_dp_read(file)
```

`ct_dp_table` *Get core tables*

Description

Acess table like observations, deployement, and media from data package.

Usage

```
ct_dp_table(
  package,
  table = c("observations", "deployments", "media", "events", "taxa")
)
```

Arguments

`package`	Camera trap data package object, as returned by ct_read_dp().
`table`	Character indicating the table to read - one "observations", "deployments", or "media"

Value

A tibble of table specified

Examples

```
dp <- ct_dp_example()
ct_dp_table(dp, "deployments")
```

`ct_dp_version` *Get Camtrap DP version Extracts the version number used by a Camera Trap Data Package object. This version number indicates what version of the* R*hrefhttps://camtrap-dp.tdwg.orgCamtrap DP standard was used.*

Description

Get Camtrap DP version Extracts the version number used by a Camera Trap Data Package object. This version number indicates what version of the Camtrap DP standard was used.

Usage

```
ct_dp_version(package)
```

Arguments

package	Camera trap data package object, as returned by ct_read_dp().

Details

The version number is derived as follows:

1. The `version` attribute, if defined.
2. A version number contained in `x$profile`, which is expected to contain the URL to the used Camtrap DP standard.
3. `x$profile` in its entirety (can be `NULL`).

Value

A Camera Trap Data Package object.

Examples

```
dp <- ct_dp_example()
ct_dp_version(dp)
```

---

ct_exiftool_call *Call ExifTool*

Description

Execute ExifTool with specified arguments

Usage

```
ct_exiftool_call(
  path = NULL,
  args = NULL,
  quiet = TRUE,
  intern = TRUE,
  exiftool_path = NULL
)
```

Arguments

path	Files or directories to process
args	Character vector of arguments to pass to ExifTool
quiet	Suppress ExifTool output messages
intern	Capture and return output as character vector
exiftool_path	Path to ExifTool executable (auto-detected if NULL)

Value

If intern=TRUE, returns output as character vector. Otherwise returns exit status.

`ct_find_break` *Detect time gaps in a datetime series*

Description

Identifies breaks in a sequence of datetime observations based on a specified time threshold.

Usage

```
ct_find_break(
  data,
  datetime_column,
  format,
  threshold = 10,
  time_unit = "hours"
)
```

Arguments

`data`	A data frame containing the datetime column.
`datetime_column`	The datetime column.
`format`	Optional. A character string specifying the datetime format, passed to `as.POSIXlt`.
`threshold`	A numeric value indicating the minimum gap to be considered a break (default is 10).
`time_unit`	The unit for the threshold. Supported values include "secs", "mins", "hours", "days", and "weeks".

Value

A tibble with columns `start`, `end`, and `duration` showing the start and end of each break and its length.

Examples

```
library(dplyr)
data(penessoulou)

pene <- penessoulou %>%
  dplyr::filter(project == "Last")


set_cam <- pene %>%
  dplyr::filter(camera == "CAMERA 3")
```

```
ct_find_break(data = pene, datetime_column = "datetimes",
threshold = 5, time_unit = "days")
```

`ct_fit_activity` *Fit activity model to time-of-day data*

Description

Fits kernel density to radian time-of-day data and estimates activity level from this distribution. Optionally: 1. bootstraps the distribution, in which case SEs and confidence limits are also stored for activity level and PDF; 2. weights the distribution; 3. truncates the distribution at given times.

Usage

```
ct_fit_activity(
  time_of_day,
  weights = NULL,
  n_bootstrap = 1000,
  bandwidth = NULL,
  adjustment = 1,
  sample = c("none", "data", "model"),
  bounds = NULL,
  show = TRUE
)
```

Arguments

`time_of_day`	A numeric vector of radian time-of-day data
`weights`	A numeric vector of weights for each dat value.
`n_bootstrap`	Number of bootstrap iterations to perform. Ignored if sample=="none"
`bandwidth`	Numeric value for kernel bandwidth. If NULL, calculated internally.
`adjustment`	Numeric bandwidth adjustment multiplier.
`sample`	Character string defining sampling method for bootstrapping errors (see details).
`bounds`	A two-element vector defining radian bounds at which to truncate.
`show`	Logical whether or not to show a progress bar while bootstrapping.

Details

When no `bounds` are given (default), a circular kernel distribution is fitted using `dvmkern`. Otherwise, a normal kernel distribution is used, truncated at the values of `bounds`, using `density2`.

The bandwidth adjustment multiplier `adj` is provided to allow exploration of the effect of adjusting the internally calculated bandwidth on accuracy of activity level estimates.

The alternative bootstrapping methods defined by `sample` are:

- "none": no bootstrapping
- "data": sample from the data
- "model": sample from the fitted probability density distribution

It's generally better to sample from the data, but sampling from the fitted distribution can sometimes provide more sensible confidence intervals when the number of observations is very small.

Value

A list

Examples

```
data("ctdp")
observations <- ctdp$data$observations %>%
  dplyr::filter(scientificName == "Vulpes vulpes") %>%
  # Add time of day
  ct_to_radian(times = timestamp)


fit_act <- ct_fit_activity(time_of_day = observations$time_radian,
                           sample = "model", n_bootstrap = 100)

# Access activity level estimation
fit_act$activity
```

---

ct_fit_detmodel *Fit animal detection*

Description

Fits a detection function (either point or line transect) to model detection radius or angle.

Usage

```
ct_fit_detmodel(
  formula,
  data,
  newdata = NULL,
  unit = c("m", "km", "cm", "degree", "radian"),
  ...
)
```

Arguments

formula	A formula specifying the response (e.g., radius ~ 1 or angle ~ covariate).
data	A data frame containing detection observations.
newdata	Optional new data frame with covariate values for prediction.
unit	Unit of the detection variable. One of "m", "km", "cm" for distance, or "degree", "radian" for angle.
...	Additional arguments passed to Distance::ds().

Value

a list with elements:

- ddf a detection function model object.
- dht abundance/density information (if survey region data was supplied, else NULL)

See Also

ct_fit_rem(), ct_fit_speedmodel(), ct_fit_activity()

Examples

```
data("ctdp")
observations <- ctdp$data$observations %>%
  dplyr::filter(scientificName == "Vulpes vulpes")


ct_fit_detmodel(radius ~ 1, data = observations)


# For angle
ct_fit_detmodel(angle ~ 1, data = observations)
```

---

ct_fit_distribution *Fit a count distribution by maximum likelihood*

Description

Fits a Poisson, negative binomial, or binomial distribution to a vector of counts and returns the parameter estimates together with the log-likelihood, AIC and BIC.

Usage

```
ct_fit_distribution(count, distribution)
```

Arguments

count	Numeric vector of non-negative counts. For distribution = "binomial" it must contain only 0 and 1.
distribution	One of "poisson", "nbinomial" or "binomial".

Value

A one-row tibble with the fitted parameter(s), their standard error(s), the log-likelihood, AIC, BIC and sample size.

See Also

ct_plot_calendar()

Examples

```
set.seed(1)
ct_fit_distribution(stats::rpois(100, 3), "poisson")
ct_fit_distribution(stats::rnbinom(100, size = 1, mu = 4), "nbinomial")
```

---

ct_fit_ds *Fit detection functions and estimate density/abundance*

Description

ct_fit_ds fits detection functions to camera trap distance sampling data and estimates animal density or abundance using bootstrap variance estimation. Supports both single model fitting and automated model selection procedures.

Usage

```
ct_fit_ds(
  data,
  estimate = c("density", "abundance"),
  cutpoints = NULL,
  truncation = set_truncation(data = data, cutpoints = cutpoints),
  formula = ~1,
  key = c("hn", "hr", "unif"),
  adjustment = c("cos", "herm", "poly"),
  nadj = NULL,
  order = NULL,
  select_model = FALSE,
 model_params = list(key = list("hn", "hr", "unif"), adjustment = list("cos", "herm",
    "poly"), nadj = list(0, 1, 2), order = NULL),
  availability,
  n_bootstrap = 100,
```

```
  n_cores = 1,
  fast_bootstrap = TRUE,
  seed = NULL,
  ...
)
```

Arguments

data	A data frame containing distance sampling observations. Must include following columns: • distance: the midpoint (m) of the assigned distance interval between animal and camera • object: a unique identifier for each observation • Sample.Label: identifier for the sample (transect id) • Effort: number of a given second (e.g 0.25, 2, or 3) time steps the camera operated (i.e. temporal effort) • Region.Label: label for a given stratum • Area: area of the strata in km^2 • fraction: fraction of a full circle covered (field of view/360) Other columns could be used as covariate. Note that in the simplest case (one area surveyed only once) there is only one Region.Label and a single corresponding Area duplicated for each observation.
estimate	Character string specifying the parameter to estimate. Either "density" (animals per km^2) or "abundance" (total number of animals). Default is "density".
cutpoints	if the data are binned, this vector gives the cutpoints of the bins. Supplying a distance column in your data and specifying cutpoints is the recommended approach for all standard binned analyses. Ensure that the first element is 0 (or the left truncation distance) and the last is the distance to the end of the furthest bin. (Default NULL, no binning.) Provide distbegin and distend columns in your data only when your cutpoints are not constant across all your data, e.g. planes flying at differing altitudes then do not specify the cutpoints argument.
truncation	either truncation distance (numeric, e.g. 5) or percentage (as a string, e.g. "15%","15"). Can be supplied as a list with elements left and right if left truncation is required (e.g. list(left=1,right=20) or list(left="1%",right="15%") or even list(left="1",right="15%")). By default for exact distances the maximum observed distance is used as the right truncation. When the data is binned, the right truncation is the largest bin end point. Default left truncation is set to zero.
formula	formula for the scale parameter. For a CDS analysis leave this as its default ~1.
key	key function to use; "hn" gives half-normal (default), "hr" gives hazard-rate and "unif" gives uniform. Note that if uniform key is used, covariates cannot be included in the model.
adjustment	adjustment terms to use; "cos" gives cosine (default), "herm" gives Hermite polynomial and "poly" gives simple polynomial. A value of NULL indicates that no adjustments are to be fitted.

nadj — the number of adjustment terms to fit. In the absence of covariates in the formula, the default value (NULL) will select via AIC (using a sequential forward selection algorithm) up to max.adjustment adjustments (unless order is specified). When covariates are present in the model formula, the default value of NULL results in no adjustment terms being fitted in the model. A non-negative integer value will cause the specified number of adjustments to be fitted. Supplying an integer value will allow the use of adjustment terms in addition to specifying covariates in the model. The order of adjustment terms used will depend on the keyand adjustment. For key="unif", adjustments of order 1, 2, 3, ... are fitted when adjustment = "cos" and order 2, 4, 6, ... otherwise. For key="hn" or "hr" adjustments of order 2, 3, 4, ... are fitted when adjustment = "cos" and order 4, 6, 8, ... otherwise. See Buckland et al. (2001) p. 47 for details.

order — order of adjustment terms to fit. The default value (NULL) results in ds choosing the orders to use - see nadj. Otherwise a scalar positive integer value can be used to fit a single adjustment term of the specified order, and a vector of positive integers to fit multiple adjustment terms of the specified orders. For simple and Hermite polynomial adjustments, only even orders are allowed. The number of adjustment terms specified here must match nadj (or nadj can be the default NULL value).

select_model — Logical. If TRUE, performs automated model selection using the procedure in Howe et al. (2019). If FALSE (default), fits a single model with specified parameters. When TRUE, model_param defines the candidate model set.

model_params — Named list defining candidate models for selection when select_model = TRUE. Elements can include:

- key - List of key functions to test
- adjustment - List of adjustment types
- nadj - List of adjustment term numbers
- order - List vector of adjustment orders (must match nadj)

availability — A list containing availability rate corrections (output from ct_availability()). Must include elements availability rate (0-1) and/or standard error of availability rate

n_bootstrap — Integer. Number of bootstrap replicates for variance estimation of density/abundance. Default is 100. Larger values provide more precise confidence intervals but increase computation time.

n_cores — Integer. Number of CPU cores to use for parallel bootstrap computation. Default is 1. Used only when the bootstrap is run by Distance::bootdht().

fast_bootstrap — Logical. If TRUE (default), and the selected detection function is intercept-only (half-normal, hazard-rate or uniform key, with optional cosine or simple polynomial adjustments) fitted to binned distances in a single stratum, each replicate is refitted from its distance-bin counts instead of the full data set. This gives the same likelihood, detection probability and density as Distance::bootdht() (resampling camera stations) and is several hundred times faster. Each refit starts from the full-data estimates and from the key function fitted alone, and keeps the higher likelihood. Other models, or fast_bootstrap = FALSE, use Distance::bootdht().

seed — Optional integer. If supplied, the random-number generator is seeded with this value immediately before bootstrapping, making the resampling reproducible. If NULL (default), the current RNG state is used and results vary between runs. Note that a single fixed seed can occasionally land on a resample that is slow to fit; leave it NULL unless you specifically need reproducible bootstrap draws.

... — Arguments passed on to Distance::ds

scale the scale by which the distances in the adjustment terms are divided. Defaults to "width", scaling by the truncation distance. If the key is uniform only "width" will be used. The other option is "scale": the scale parameter of the detection

dht_group should density abundance estimates consider all groups to be size 1 (abundance of groups) dht_group=TRUE or should the abundance of individuals (group size is taken into account), dht_group=FALSE. Default is FALSE (abundance of individuals is calculated).

monotonicity should the detection function be constrained for monotonicity weakly ("weak"), strictly ("strict") or not at all ("none" or FALSE). See Monotonicity, below. (Default "strict"). By default it is on for models without covariates in the detection function, off when covariates are present.

method optimization method to use (any method usable by optim or optimx). Defaults to "nlminb".

mono_method optimization method to use when monotonicity is enforced. Can be either slsqp or solnp. Defaults to slsqp.

initial_values a list of named starting values, see mrds_opt. Only allowed when AIC term selection is not used.

max_adjustments maximum number of adjustments to try (default 5) only used when order=NULL.

er_method encounter rate variance calculation: default = 2 gives the method of Innes et al. (2002), using expected counts in the encounter rate. Setting to 1 gives observed counts (which matches Distance for Windows) and 0 uses negative binomial variance (only useful in the rare situation where study area = surveyed area). See dht.se for more details, noting this er_method argument corresponds to the varflag element of the options argument in dht.se.

dht_se should uncertainty be calculated when using dht? Safe to leave as TRUE, used in bootdht.

optimizer By default this is set to 'both'. In this case the R optimizer will be used and if present the MCDS optimizer will also be used. The result with the best likelihood value will be selected. To run only a specified optimizer set this value to either 'R' or 'MCDS'. See mcds_dot_exe for setup instructions.

winebin If you are trying to use our MCDS.exe optimizer on a non-windows system then you may need to specify the winebin. Please see mcds_dot_exe for more details.

Value

A named list containing: A list containing:

- QAIC: (only if select_model = TRUE) QAIC comparison table.
- Chi2: (only if select_model = TRUE) Chi-squared goodness-of-fit comparison.
- best_model: The best fitted detection function model selected.
- rho: Estimated effective detection radius (in meters).
- density or abundance: A tibble with density or abundance estimates containing: median, mean, se: standard error, lcl: lower confidence limit, ucl: upper confidence limit

Truncation

The right truncation point is by default set to be largest observed distance or bin end point. This is a default will not be appropriate for all data and can often be the cause of model convergence failures. It is recommended that one plots a histogram of the observed distances prior to model fitting so as to get a feel for an appropriate truncation distance. (Similar arguments go for left truncation, if appropriate). Buckland et al. (2001) provide guidelines on truncation.

When specified as a percentage, the largest right and smallest left percent distances are discarded. Percentages cannot be supplied when using binned data.

For left truncation, there are two options: (1) fit a detection function to the truncated data as is (this is what happens when you set left). This does not assume that g(x)=1 at the truncation point. (2) manually remove data with distances less than the left truncation distance – effectively move the centre line out to be the truncation distance (this needs to be done before calling ds). This then assumes that detection is certain at the left truncation distance. The former strategy has a weaker assumption, but will give higher variance as the detection function close to the line has no data to tell it where to fit – it will be relying on the data from after the left truncation point and the assumed shape of the detection function. The latter is most appropriate in the case of aerial surveys, where some area under the plane is not visible to the observers, but their probability of detection is certain at the smallest distance.

Monotonicity

When adjustment terms are used, it is possible for the detection function to not always decrease with increasing distance. This is unrealistic and can lead to bias. To avoid this, the detection function can be constrained for monotonicity (and is by default for detection functions without covariates).

Monotonicity constraints are supported in a similar way to that described in Buckland et al. (2001). 20 equally spaced points over the range of the detection function (left to right truncation) are evaluated at each round of the optimisation and the function is constrained to be either always less than it's value at zero ("weak") or such that each value is less than or equal to the previous point (monotonically decreasing; "strict"). See also check.mono.

Even with no monotonicity constraints, checks are still made that the detection function is monotonic, see check.mono.

Data format

One can supply data only to simply fit a detection function. However, if abundance/density estimates are necessary further information is required. Either the region_table, sample_table and obs_table data.frames can be supplied or all data can be supplied as a "flat file" in the data argument. In this format each row in data has additional information that would ordinarily be in the other tables. This usually means that there are additional columns named: Sample.Label, Region.Label, Effort and Area for each observation. See flatfile for an example.

Clusters/groups

Note that if the data contains a column named `size`, cluster size will be estimated and density/abundance will be based on a clustered analysis of the data. Setting this column to be `NULL` will perform a non-clustered analysis (for example if "`size`" means something else in your dataset).

References

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Howe, E. J., Buckland, S. T., Després-Einspenner, M., & Kühl, H. S. (2017). Distance sampling with camera traps. Methods in Ecology and Evolution, 8(11), 1558-1565. doi:10.1111/2041-210X.12790

Howe, E. J., Buckland, S. T., Després-Einspenner, M., & Kühl, H. S. (2019). Model selection with overdispersed distance sampling data. Methods in Ecology and Evolution, 10(1), 38-47. doi:10.1111/2041210X.13082

Rowcliffe, J. M., Kays, R., Kranstauber, B., Carbone, C., & Jansen, P. A. (2014). Quantifying levels of animal activity using camera trap data. Methods in Ecology and Evolution, 5(11), 1170-1179. doi:10.1111/2041210X.12278

See Also

`ct_availability()`, `ct_select_model()`, `ct_QAIC()`, `ct_chi2_select()`

Examples

```
## Not run:
data("duikers")

# Calculates animal availability adjustment factor
trigger_events <- duikers$VideoStartTimesFullDays
avail <- ct_availability(times = trigger_events$time,
                         format = "%H:%M", n_bootstrap = 100)

# Estimate density, building multiple models
flat_data <- duikers$DaytimeDistances %>%
  dplyr::rename(fraction = multiplier) %>%
  dplyr::slice_sample(prop = .2) # sample 20% of rows

duiker_density <- ct_fit_ds(data = flat_data,
                            estimate = "density",
                            select_model = TRUE,
                            model_params = list(key = list("hn", "hr"),
                                                adjustment = list("cos"),
                                                nadj = list(2, 3),
                                                order = NULL),
                            availability = avail,
                            truncation = list(left = 2, right = 15),
                            n_bootstrap = 2,
                            cutpoints = c(seq(2, 8, 1), 10, 12, 15)
)
```

```
# View density
duiker_density$density

## End(Not run)
```

`ct_fit_encounter_response` *Fit a conditional encounter-response model for camera-trap events*

Description

Estimates whether encounters of a response species become more or less likely in the minutes to hours after encounters of a trigger species at the same camera. Unlike a diel overlap coefficient – which only compares two species' marginal activity curves – this is a directed, time-lagged association: it contrasts the response encounter rate in successive windows after a trigger with that camera's expected rate at the same time of day and month. It quantifies association, not causation.

Usage

```
ct_fit_encounter_response(
  data,
  deployment,
  trigger,
  response,
  species_column,
  cam_column,
  datetime_column,
  start_column,
  end_column,
  interval = 15 * 60,
  lag_breaks = c(0, 30 * 60, 2 * 3600, 6 * 3600),
  independence = 2 * 60,
  engine = c("glm", "glmm"),
  n_boot = NULL,
  interval_sensitivity = NULL,
  seed = NULL
)
```

Arguments

`data`	A data frame with one row per camera-trap record (the observation data).
`deployment`	A data frame of actual camera deployment intervals. It must contain the camera ID, start, and end columns. Intervals for the same camera may not overlap.
`trigger`	Character scalar naming the species whose event initiates a response window.
`response`	Character scalar naming the species whose encounter rate is modelled.

`species_column` Unquoted column in `data` giving the species name.

`cam_column` Unquoted column giving the camera ID. This column must be present, with the same name, in both `data` and `deployment` so that records can be matched to their deployment intervals.

`datetime_column` Unquoted column in `data` giving the event date-time.

`start_column, end_column` Unquoted columns in `deployment` giving the deployment interval start and end date-times respectively.

`interval` Width of analysis intervals in seconds. It must not exceed the narrowest response-lag window.

`lag_breaks` Numeric vector of lag boundaries in seconds. The default estimates associations for 0–30 minutes, 30 minutes–2 hours, and 2–6 hours after a trigger. Time after the final boundary is the reference.

`independence` Minimum number of seconds between retained records of the same species at the same camera. Defaults to 2 minutes; set to `0` to retain every record. See Details for why this default is smaller than the value used for activity-level estimation.

`engine` Fitting engine. `"glm"` (default) fits a camera-stratified quasi-Poisson GLM with camera fixed effects and a camera-block bootstrap. `"glmm"` fits a Poisson/negative-binomial mixed model with camera (and, where present, deployment) random intercepts, using **glmmTMB** if installed and otherwise **lme4**.

`n_boot` Number of camera-block bootstrap replicates used for percentile confidence intervals. If `NULL` (default) it is set to 199 for `engine = "glm"` and to 0 for `engine = "glmm"`. Set to `0` to return model-based intervals only.

`interval_sensitivity` Optional numeric vector of alternative `interval` widths (seconds). When supplied, the lag-specific rate ratios are refitted at each width and returned in `$sensitivity`, so the reader can judge how far the conclusion depends on the binning choice. Each value must not exceed the narrowest lag window.

`seed` Optional integer seed for the bootstrap.

Details

What is being approximated. The quantity of interest – "does an encounter of species A raise or lower the short-term encounter intensity of species B?" – is formally a *mutually exciting (Hawkes-type) point process*. Fitting such a process directly is data-hungry and fragile with sparse camera-trap detections, so this function uses a transparent discrete-time approximation: camera uptime is sliced into short intervals, the number of response detections per interval is modelled as a count, and time-since-last-trigger is entered as a step function (`lag_breaks`). Because it is an approximation, the interval width matters – always inspect `interval_sensitivity` before interpreting an effect.

How confounders are handled. Camera uptime enters as an offset so unequal effort is accounted for; circular (harmonic) terms hold the shared diel activity curve constant; a month factor absorbs broad seasonal variation; and each camera contributes only *within-camera* temporal contrasts, so time-invariant differences in habitat, placement and baseline abundance are differenced out. With

`engine = "glm"` cameras are fixed effects; with `engine = "glmm"` they are random intercepts (partial pooling), which is more efficient with many sparse cameras and avoids the incidental-parameter problem of many fixed effects.

Inference. Successive intervals at one camera are serially correlated and response detections cluster in time. A quasi-Poisson dispersion correction rescales for overdispersion but *not* for this autocorrelation, so model-based intervals from `engine = "glm"` are optimistic. The default inference is therefore a **camera-block bootstrap** (`n_boot`), which resamples whole cameras and so respects within-camera dependence; treat those intervals as the primary uncertainty. With `engine = "glmm"` the camera random effect already propagates between-camera variance, so the bootstrap is skipped.

The dominant limitation – shared transient drivers. The controls above remove *stable* and *diel/seasonal* confounding, but they cannot remove *episodic* shared drivers: a fruiting tree, a waterhole, a prey pulse, moonlight or a weather front can draw both species independently within the same hours and manufacture an apparent "response" with no behavioural interaction whatsoever. Detection is also a thinned, imperfect observation of presence, so a shift in detection rate need not reflect a shift in true site use. For these reasons the result is an *association conditional on the fitted baseline*, never evidence of a direct behavioural or causal effect. Corroborate with randomization or simulation checks, and never treat deployments reconstructed from first/last detections as camera uptime.

Independence filtering. `independence` collapses repeat detections of the same species at the same camera that fall within a short window – these are usually one animal lingering in front of the sensor, i.e. one biological event. Note the tension with this model: unlike activity-level estimation (where 30 min is conventional), a long filter here would erase exactly the rapid successive detections that a short-term response would produce. The default is therefore deliberately small (2 minutes): long enough to merge a single pass into one event, short enough to preserve genuine reactivity in the first lag window. Set `independence = 0` to keep every record.

Value

An object of class `ct_encounter_response` containing the fitted model, lag-specific rate ratios, analysis-interval data, an optional bin-width sensitivity table, and settings. A rate ratio below one indicates fewer response encounters than expected after a trigger, conditional on the fitted baseline terms.

References

Hawkes, A. G. (1971). Spectra of some self-exciting and mutually exciting point processes. *Biometrika*, 58(1), 83–90. doi:10.1093/biomet/58.1.83

Ridout, M. S., & Linkie, M. (2009). Estimating overlap of daily activity patterns from camera trap data. *Journal of Agricultural, Biological, and Environmental Statistics*, 14(3), 322–337. doi:10.1198/jabes.2009.08038

Examples

```
## Not run:
data(ACBR)
fit <- ct_fit_encounter_response(
  data = ACBR$acbr_data,
  deployment = ACBR$deployment,
```

```
  trigger = "Cercopithecus mona", response = "Tragelaphus spekii",
  species_column = species, cam_column = cam, datetime_column = datetime,
  start_column = start, end_column = end
)
summary(fit)

# Random-effects engine plus a bin-width sensitivity check
fit_glmm <- ct_fit_encounter_response(
  data = ACBR$acbr_data,
  deployment = ACBR$deployment,
  trigger = "Cercopithecus mona", response = "Tragelaphus spekii",
  species_column = species, cam_column = cam, datetime_column = datetime,
  start_column = start, end_column = end,
  engine = "glmm",
  interval_sensitivity = c(5 * 60, 10 * 60, 30 * 60)
)
fit_glmm$sensitivity

## End(Not run)
```

`ct_fit_ise` *Estimate abundance from Instantaneous Sampling (ISE) Data*

Description

Estimate abundance from camera trap data using Instantaneous Sampling / point counts.

Usage

```
ct_fit_ise(
  data,
  deployment_data,
  sampling_frequency,
  sampling_length,
  study_area,
  study_start = NULL,
  study_end = NULL,
  quiet = FALSE
)
```

Arguments

`data`	A tibble of camera trap detections. Must contain columns `cam`, `datetime`, and `count`.
`deployment_data`	A tibble of camera deployments. Must contain columns `cam`, `start`, `end`, and `area`.

`sampling_frequency`
: Numeric. The number of seconds between the start of each sampling occasion.

`sampling_length`
: Numeric. The number of seconds to sample at each sampling occasion.

`study_area`
: Numeric. The size of the total study area in the same units as the camera viewshed area.

`study_start`
: POSIXct. The start of the study. Defaults to the minimum start time in `deployment_data`.

`study_end`
: POSIXct. The end of the study. Defaults to the maximum end time in `deployment_data`.

`quiet`
: Logical. Suppress status messages? Defaults to FALSE.

Value

A data.frame with the estimated abundance (`N`), its standard error (`SE`), and confidence intervals.

References

Moeller, A. K. and P. M. Lukacs. 2021. spaceNtime: an R package for estimating abundance of unmarked animals using camera-trap photographs. Mammalian Biology. doi:10.1007/s42991021-001818

Moeller, A. K., P. M. Lukacs, and J. Horne. 2018. Three novel methods to estimate abundance of unmarked animals using remote cameras. Ecosphere 9(8): e02331. doi:10.1002/ecs2.2331

See Also

`ct_fit_tte()`, `ct_fit_ste()`

Examples

```
data <- dplyr::tibble(
  cam = c(1, 1, 2, 2, 2),
  datetime = as.POSIXct(
    c(
      "2026-01-02 12:00:00",
      "2026-01-03 13:12:00",
      "2026-01-02 12:00:00",
      "2026-01-02 14:00:00",
      "2026-01-03 16:53:42"
    ),
    tz = "Africa/Lagos"
  ),
  count = c(1, 0, 2, 1, 2)
)
deployment_data <- dplyr::tibble(
  cam = c(1, 2, 2, 2),
  start = as.POSIXct(
    c(
      "2025-12-01 15:00:00",
      "2025-12-08 00:00:00",
      "2026-01-01 00:00:00",
      "2026-01-02 00:00:00"
```

```
    ),
    tz = "Africa/Lagos"
  ),
  end = as.POSIXct(
    c(
      "2026-01-05 00:00:00",
      "2025-12-19 03:30:00",
      "2026-01-01 05:00:00",
      "2026-01-05 00:00:00"
    ),
    tz = "Africa/Lagos"
  ),
  area = c(300, 200, 200, 450)
)
ct_fit_ise(data, deployment_data,
       sampling_frequency = 3600,
       sampling_length = 10,
       study_area = 1e6)
```

---

ct_fit_rem *Fit Random Encounter Model (REM)*

Description

Fits a random encounter model using observed data and trap rate information. Automatically estimates detection radius, detection angle, animal speed, and activity pattern models if not provided.

Usage

```
ct_fit_rem(
  data,
  traprate_data,
  radius_model = NULL,
  angle_model = NULL,
  speed_model = NULL,
  activity_model = NULL,
  strata = NULL,
  time_of_day,
  n_bootstrap = 1000
)
```

Arguments

data	A data frame of observations, including distance, angle, speed, and time-of-day (in radians).
traprate_data	A data frame created by ct_traprate_data().
radius_model	Optional. A detection function model for radius (distance) fitted using ct_fit_detmodel().

angle_model	Optional. A detection function model for angle fitted using ct_fit_detmodel().
speed_model	Optional. A model for movement speed fitted using ct_fit_speedmodel().
activity_model	Optional. An activity model fitted with activity::fitact().
strata	Optional. A data frame of stratification information with columns stratumID and area.
time_of_day	The column name (unquoted or as a string) representing time-of-day in radians.
n_bootstrap	Number of bootstrap replicates for uncertainty estimation. Default is 1000.

Value

A data frame with columns:

- parameters: Model parameter name
- estimate: Estimated value
- se: Standard error
- cv: Coefficient of variation
- lower_ci: Lower bound of 95% confidence interval
- upper_ci: Upper bound of 95% confidence interval

See Also

ct_fit_speedmodel(), ct_fit_detmodel(), ct_fit_activity()

Examples

```
data("ctdp")
deployments <- ctdp$data$deployments
observations <- ctdp$data$observations %>%
  dplyr::filter(scientificName == "Vulpes vulpes") %>%
  # Add time of day
  dplyr::mutate(time_of_day = ct_to_radian(times = timestamp))

# Prepare trap rate data
trap_rate <- ct_traprate_data(observation_data = observations,
                              deployment_data = deployments,
                              deployment_column = deploymentID,
                              datetime_column = timestamp,
                              start = start, end = 'end'
)


# Fit REM
ct_fit_rem(data = observations,
           traprate_data = trap_rate,
           time_of_day = time_of_day)
```

ct_fit_rest *Fit the Random Encounter and Staying Time (REST / RAD-REST) model*

Description

Estimates animal density from camera-trap data **without individual recognition** using the Random Encounter and Staying Time (REST) model of Nakashima, Fukasawa & Samejima (2018) and its RAD-REST extension (Nakashima et al. 2026). Parameters are estimated in a Bayesian framework by MCMC sampling with **nimble**.

Usage

```
ct_fit_rest(
  stay_data,
  station_data,
  activity_data,
  species,
  focal_area,
  model = c("REST", "RAD-REST"),
  stay_formula = Stay ~ 1,
  density_formula = ~1,
  passes_formula = ~1,
  stay_random_effect = NULL,
  stay_distribution = c("lognormal", "gamma", "weibull", "exponential"),
  activity_method = c("kernel", "mixture"),
  bandwidth_adjust = 1,
  mixture_components = 10,
  compare_models = FALSE,
  iterations = 5000,
  burnin = 1000,
  thin = 2,
  chains = 3,
  cores = 3,
  quiet = FALSE
)
```

Arguments

stay_data	Staying-time data, e.g. the output of ct_rest_stay(), with columns Station, Species, Stay (seconds) and Cens (1 = censored, 0 = fully observed).
station_data	Per-station encounter and effort data, e.g. the output of ct_rest_effort(). For model = "REST" it must contain Station, Species, Effort (days) and Y (passes). For model = "RAD-REST" it must instead contain N (videos) and the y_0, y_1, ... pass-count columns.
activity_data	Detection times in radians, e.g. the output of ct_rest_activity(), with columns Species and time.

species	Single species name to analyse (must appear in the data).
focal_area	Focal-area size in square metres. Either a single number (the same area at every camera) or the name of a column in station_data giving a camera-specific focal area per station.
model	Either "REST" or "RAD-REST".
stay_formula	Model formula for staying time. The left-hand side names the staying-time column, e.g. Stay ~ 1 or Stay ~ 1 + habitat.
density_formula	One-sided formula for density covariates, e.g. ~ 1 or ~ habitat. Density is latent, so the left-hand side is omitted.
passes_formula	One-sided formula for the number of passes. Used only when model = "RAD-REST"; ignored otherwise.
stay_random_effect	Optional column in stay_data giving a random effect on staying time. Default NULL (no random effect).
stay_distribution	Distribution for staying time: one of "lognormal", "gamma", "weibull" or "exponential". Ideally chosen with ct_rest_select_stay().
activity_method	How to estimate the activity proportion: "kernel" (fixed kernel density) or "mixture" (Bayesian von Mises mixture).
bandwidth_adjust	Bandwidth multiplier for activity_method = "kernel".
mixture_components	Maximum number of von Mises components for activity_method = "mixture".
compare_models	If TRUE, fit every combination of the density covariates and rank them by WAIC. If FALSE, fit only density_formula.
iterations, burnin, thin, chains, cores	MCMC settings: total iterations per chain, burn-in length, thinning interval, number of chains and CPU cores for parallel sampling.
quiet	If TRUE, suppress progress messages.

Details

The idea behind REST:

A camera watches a small *focal area* of known size in front of the lens. If we know (i) how often animals pass through that area, (ii) how long they stay in it on average, and (iii) the fraction of the day they are active, density follows from a simple flow argument. Intuitively, the expected number of detected passes is

$$E[Y] = D \times S \times T \times p_{act}/\bar{t}$$

where D is density, S the focal-area size, T the survey duration, p_{act} the activity proportion and $\bar{t}$ the mean staying time. Re-arranging gives the density estimator $D = Y\,\bar{t}/(S\,T\,p_{act})$. ct_fit_rest() fits every piece of this equation jointly so that uncertainty propagates into the density estimate.

Three sub-models are combined:

- **Staying time** (`stay_data`): a survival model. Animals still in the focal area when the video ends are *right-censored*; the chosen `stay_distribution` (lognormal/gamma/weibull/exponential) handles this.
- **Encounters** (`station_data`): the number of passes `Y` per station is modelled as negative-binomial (REST), or, for RAD-REST, the number of videos showing 0,1,2,... passes is modelled with a Dirichlet-multinomial so that miscounting of passes is accounted for.
- **Activity** (`activity_data`): the active fraction of the day, estimated either by kernel density (Rowcliffe et al. 2014) or a Bayesian von Mises mixture (Nakashima et al. 2026).

Value

An object of class `ct_rest` (a list) with:

`waic` A tibble ranking the candidate density models by WAIC.

`summary` A tibble of posterior summaries for density (individuals per km^2), mean staying time and, for RAD-REST, the mean number of passes.

`samples` A `coda::mcmc.list` of posterior draws for the best model.

`activity_curve` (mixture only) the estimated activity density curve.

References

Nakashima, Y., Fukasawa, K. & Samejima, H. (2018) Estimating animal density without individual recognition using information derived from camera traps. *Journal of Applied Ecology*, 55, 735-744.

Nakashima, Y. et al. (2026) Reducing data-processing effort in camera-trap density estimation: extending the REST model. *Methods in Ecology and Evolution*.

See Also

`ct_rest_stay()`, `ct_rest_effort()`, `ct_rest_activity()`, `ct_rest_select_stay()`

Examples

```
data(rest_detection)
data(rest_station)

# 1. Build the three inputs from raw detections (these steps run quickly)
stay <- ct_rest_stay(rest_detection, rest_station)
stations <- ct_rest_passes(rest_detection, rest_station, model = "REST")
stations <- ct_rest_effort(rest_detection, stations)
activity <- ct_rest_activity(rest_detection)

## Not run:
# 2. Fit REST for the focal species (requires the 'nimble' package)
fit <- ct_fit_rest(
  stay_data = stay,
  station_data  = stations,
  activity_data = activity,
  species = "Red duiker",
  focal_area = 3.0, # focal-area size in m^2
  model = "REST",
```

```
  stay_distribution = "lognormal",
  iterations = 3000, burnin = 1000, chains = 2, cores = 2
)
fit
fit$summary   # density (individuals per km^2) and mean staying time

# RAD-REST instead: use pass-classified station data
stations_rad <- ct_rest_effort(
  detection_data = rest_detection,
  station_data = ct_rest_passes(rest_detection, rest_station, model = "RAD-REST")
)

fit_rad <- ct_fit_rest(
  stay_data = stay,
  station_data  = stations_rad,
  activity_data = activity,
  species = "Red duiker",
  focal_area = 3.0,
  model = "RAD-REST"
)

## End(Not run)
```

`ct_fit_speedmodel` *Fit animal speed model*

Description

Fits a statistical model to estimate average movement speed of animals. Used in the REM density estimation.

Usage

```
ct_fit_speedmodel(
  formula = speed ~ 1,
  data,
  newdata = NULL,
  distance_unit = c("m", "km", "cm"),
  time_unit = c("second", "minute", "hour", "day"),
  ...
)
```

Arguments

`formula`	A formula indicating how speed should be modeled (e.g., `speed ~ 1`).
`data`	A data frame containing speed observations.
`newdata`	Optional new data to use for prediction.

distance_unit	Unit of distance. One of "m", "km", "cm".
time_unit	Unit of time. One of "second", "minute", "hour", "day".
...	Additional arguments passed to sbd::sbm().

Value

An object of class sbm, with an additional unit attribute indicating the speed unit.

See Also

ct_fit_rem(), ct_fit_detmodel(), ct_fit_activity()

Examples

```
data("ctdp")
observations <- ctdp$data$observations %>%
  dplyr::filter(scientificName == "Vulpes vulpes")

ct_fit_speedmodel(speed ~ 1, data = observations)
```

---

ct_fit_ste *Estimate abundance from Space-To-Event (STE) Data*

Description

Estimate abundance from camera trap data using the Space-To-Event (STE) model.

Usage

```
ct_fit_ste(
  data,
  deployment_data,
  sampling_frequency,
  sampling_length,
  study_area,
  study_start = NULL,
  study_end = NULL,
  quiet = FALSE
)
```

Arguments

data	A tibble of camera trap detections. Must contain columns cam, datetime, and count.
deployment_data	A tibble of camera deployments. Must contain columns cam, start, end, and area.

`sampling_frequency`
: Numeric. The number of seconds between the start of each sampling occasion.

`sampling_length`
: Numeric. The number of seconds to sample at each sampling occasion.

`study_area`
: Numeric. The size of the total study area in the same units as the camera viewshed area.

`study_start`
: POSIXct. The start of the study. Defaults to the minimum start time in `deployment_data`.

`study_end`
: POSIXct. The end of the study. Defaults to the maximum end time in `deployment_data`.

`quiet`
: Logical. Suppress status messages? Defaults to FALSE.

Value

A data.frame with the estimated abundance (`N`), its standard error (`SE`), and confidence intervals.

References

Moeller, A. K. and P. M. Lukacs. 2021. spaceNtime: an R package for estimating abundance of unmarked animals using camera-trap photographs. Mammalian Biology. doi:10.1007/s42991021-001818

Moeller, A. K., P. M. Lukacs, and J. Horne. 2018. Three novel methods to estimate abundance of unmarked animals using remote cameras. Ecosphere 9(8): e02331. doi:10.1002/ecs2.2331

See Also

`ct_fit_ise()`, `ct_fit_tte()`

Examples

```
data <- dplyr::tibble(
  cam = c(1,1,2,2,2),
  datetime = as.POSIXct(c("2026-01-02 12:00:00",
                          "2026-01-03 13:12:00",
                          "2026-01-02 12:00:00",
                          "2026-01-02 14:00:00",
                          "2026-01-03 16:53:42"),
                        tz = "Africa/Lagos"),
  count = c(1, 0, 2, 1, 2)
)
deployment_data <- dplyr::tibble(
  cam = c(1, 2, 2, 2),
  start = as.POSIXct(c("2025-12-01 15:00:00",
                       "2025-12-08 00:00:00",
                       "2026-01-01 00:00:00",
                       "2026-01-02 00:00:00"),
                     tz = "Africa/Lagos"),
  end = as.POSIXct(c("2026-01-05 00:00:00",
                     "2025-12-19 03:30:00",
                     "2026-01-01 05:00:00",
                     "2026-01-05 00:00:00"),
                   tz = "Africa/Lagos"),
```

```
  area = c(300, 200, 200, 450)
)
ct_fit_ste(data,
       deployment_data,
       sampling_frequency = 3600,
       sampling_length = 10,
       study_area = 1e6)
```

`ct_fit_tte` *Estimate abundance from Time-To-Event (TTE) Data*

Description

Estimate abundance from camera trap data using the Time-To-Event (TTE) model.

Usage

```
ct_fit_tte(
  data,
  deployment_data,
  viewshed_transit_time,
  periods_per_occasion,
  time_between_occasions,
  study_area,
  study_start = NULL,
  study_end = NULL,
  quiet = FALSE
)
```

Arguments

`data` A tibble of camera trap detections. Must contain columns `cam`, `datetime`, and `count`.

`deployment_data`
A tibble of camera deployments. Must contain columns `cam`, `start`, `end`, and `area`.

`viewshed_transit_time`
Numeric. This is equal to the mean amount of time (in seconds) required for an animal to cross the average viewshed of a camera. It can be calculated in different ways depending on available information.

For an animal with a movement speed of 30 m/hr passing through camera viewsheds of 300 m^2, 400 m^2, and 380 m^2, the sampling period can be approximated as:

$$\frac{\sqrt{\frac{1}{n}\sum_{i=1}^{n} A_i}}{30/3600}$$

where A_i represents the camera viewshed areas (in m^2) and n is the number of cameras. The denominator is the animal speed converted from meters/hour to meters/second.

`periods_per_occasion`
: Numeric. Number of TTE sampling periods per sampling occasion.

`time_between_occasions`
: Numeric. Length of time between sampling occasions (in seconds), allowing animals to re-randomize.

`study_area`
: Numeric. The size of the total study area in the same units as the camera viewshed area.

`study_start`
: POSIXct. The start of the study. Defaults to the minimum start time in `deployment_data`.

`study_end`
: POSIXct. The end of the study. Defaults to the maximum end time in `deployment_data`.

`quiet`
: Logical. Suppress status messages? Defaults to FALSE.

Value

A data.frame with the estimated abundance (`N`), its standard error (`SE`), and confidence intervals.

References

Moeller, A. K. and P. M. Lukacs. 2021. spaceNtime: an R package for estimating abundance of unmarked animals using camera-trap photographs. Mammalian Biology. doi:10.1007/s42991021-001818

Moeller, A. K., P. M. Lukacs, and J. Horne. 2018. Three novel methods to estimate abundance of unmarked animals using remote cameras. Ecosphere 9(8): e02331. doi:10.1002/ecs2.2331

See Also

`ct_fit_ste()`, `ct_fit_ise()`

Examples

```
data <- dplyr::tibble(
  cam = c(1, 1, 2, 2, 2),
  datetime = as.POSIXct(
    c(
      "2026-01-02 12:00:00",
      "2026-01-03 13:12:00",
      "2026-01-02 12:00:00",
      "2026-01-02 14:00:00",
      "2026-01-03 16:53:42"
    ),
    tz = "Africa/Lagos"
  ),
  count = c(1, 0, 2, 1, 2)
)
deployment_data <- dplyr::tibble(
  cam = c(1, 2, 2, 2),
  start = as.POSIXct(
```

```
      c(
        "2025-12-01 15:00:00",
        "2025-12-08 00:00:00",
        "2026-01-01 00:00:00",
        "2026-01-02 00:00:00"
      ),
      tz = "Africa/Lagos"
    ),
    end = as.POSIXct(
      c(
        "2026-01-05 00:00:00",
        "2025-12-19 03:30:00",
        "2026-01-01 05:00:00",
        "2026-01-05 00:00:00"
      ),
      tz = "Africa/Lagos"
    ),
    area = c(300, 200, 200, 450)
  )
  ct_fit_tte(data,
         deployment_data,
         viewshed_transit_time = sqrt(mean(deployment_data$area))/(30/3600),
         periods_per_occasion = 24,
         time_between_occasions = 2 * 3600,
         study_area = 1e6)
```

`ct_get_effort` *Calculate camera trap deployment effort*

Description

Computes the monitoring effort (e.g., in days) for each camera deployment based on start and end timestamps.

Usage

```
ct_get_effort(
  deployment_data,
  start_column,
  end_column,
  deployment_column,
  format = "%Y-%m-%d %H:%M:%OS",
  time_zone = "",
  time_unit = "days"
)
```

Arguments

deployment_data	A data frame containing camera trap deployment records.
start_column	The column name (unquoted or as a string) indicating deployment start datetime.
end_column	The column name (unquoted or as a string) indicating deployment end datetime.
deployment_column	The column name (unquoted or as a string) that uniquely identifies the deployment (e.g., camera ID).
format	A character string specifying the format of the datetime columns. Default is "%Y-%m-%d %H:%M:%OS".
time_zone	The time zone used to parse the datetime columns. Default is "" (i.e., system time zone).
time_unit	The unit in which to compute the effort duration. Can be "secs", "mins", "hours", "days", or "weeks". Default is "days".

Value

A data frame with columns:

- deployment_column: Deployment identifier
- effort: Numeric value of monitoring effort
- effort_unit: The time unit used

See Also

ct_traprate_data()

Examples

```
data("ctdp")
deployments <- ctdp$data$deployments
ct_get_effort(deployment_data = deployments,
              deployment_column = deploymentID,
              start_column = start,
              end_column = end)
```

---

ct_get_hs *Retrieve hierarchical subject (hs) values from image metadata*

Description

Extracts hierarchical subject metadata from image files using ExifTool. Hierarchical subjects follow a parent|child structure (e.g., "Species|Vulture") and are commonly used for taxonomic or categorical image classification.

Usage

```
ct_get_hs(path, hs_delimitor = "|", into_tibble = FALSE)
```

Arguments

path	A character string specifying the full path to the image file. Must be a valid file path to an image with EXIF metadata support.
hs_delimitor	The character delimiting hierarchy levels in image metadata tags in field "HierarchicalSubject"
into_tibble	Logical. Parse hierarchical subjects into tibble.

Value

A character vector or tibble of unique hierarchical subjects if they exist, otherwise NULL. Each element represents one hierarchical subject in "parent|child" format.

See Also

- ct_create_hs() to add hierarchical subjects
- ct_remove_hs() to remove hierarchical subjects
- ct_read_metadata() to read image metadata

Examples

```
## Not run:
# Path to example image
image_path <- file.path(system.file("img", package = "ct"), "large.jpeg")

# Retrieve hierarchical subjects (returns NULL if none exist)
hs <- ct_get_hs(path = image_path)
print(hs)

# After adding hierarchical subjects
ct_create_hs(path = image_path, value = c("Species" = "Vulture"))
ct_get_hs(path = image_path)  # Returns: "Species|Vulture"

# Multiple hierarchical subjects
ct_create_hs(
  path = image_path,
  value = c("Species" = "Eagle", "Location" = "Mountains")
)
ct_get_hs(path = image_path)  # Returns vector with both subjects

## End(Not run)
```

`ct_independence` *Evaluate independent detections*

Description

Filters camera trap data to ensure temporal independence between detections, removing consecutive entry of the same species at the same location within a specified time window.

Usage

```
ct_independence(
  data = NULL,
  species_column,
  site_column,
  datetime,
  format,
  threshold = 30 * 60
)
```

Arguments

`data`	A `data.frame`, `tbl_df`, or `tbl` containing the event data. This should include a column with datetime values. If `NULL`, the function will use the `datetime` argument instead of the `data` argument.
`species_column`	An optional column name specifying the species grouping. If provided, independence will be assessed separately within each species group.
`site_column`	An optional column name specifying the site/camera grouping. If provided, independence will be assessed separately within each site group.
`datetime`	A `character` string specifying the name of the column in `data` that contains the datetime values. This argument is required if `data` is provided.
`format`	A `character` string defining the format used to parse the datetime values in the `datetime` column.
`threshold`	A `numeric` value representing the time difference threshold (in seconds) to determine whether events are independent. Events are considered independent if the time difference between them is greater than or equal to this threshold. The default is 30 minutes (1800 seconds).

Details

Following Ridout & Linkie (2009), consecutive photos of the same species at the same location within 30 minutes are considered non-independent and removed.

The approach mirrors the methodology applied by Linkie & Ridout (2011) for Sumatran tiger-prey interactions study and Ahmad et al. (2024) to calculate activity levels where such filtering is essential for:

- Avoiding autocorrelation in activity pattern data

- Ensuring each record represents an independent observation
- Creating a random sample from the underlying activity distribution

The filtered data can then be used to estimate probability density functions of daily activity patterns, assuming animals are equally detectable during their active periods.

Value

- If `data` is provided and `only` is `TRUE`, a tibble of events identified as independent.
- If `data` is provided and `only` is `FALSE`, a tibble of the original data with additional columns indicating the `independent` status and `deltatime` differences (in second).
- If `data` is not provided, a tibble of the `deltatime` values with `independent` status.

References

Ridout, M.S., & Linkie, M. (2009). Estimating overlap of daily activity patterns from camera trap data. Journal of Agricultural, Biological, and Environmental Statistics, 14(3), 322-337. doi:10.1198/jabes.2009.08038

Linkie, M., & Ridout, M.S. (2011). Assessing tiger-prey interactions in Sumatran rainforests. Journal of Zoology, 284(3), 224-229.doi:10.1111/j.14697998.2011.00801.x

Ahmad, F., Mori, T., Rehan, M., Bosso, L., & Kabir, M. (2024). Applying a Random Encounter Model to Estimate the Asiatic Black Bear (Ursus thibetanus) Density from Camera Traps in the Hindu Raj Mountains, Pakistan. Biology, 13(5), 341. doi:10.3390/biology13050341

Examples

```
library(dplyr)
data(penessoulou)

# Load example dataset
cam_data <- penessoulou %>%
  dplyr::filter(project == "Last")

# Independence without considering species
indep1 <- cam_data %>%
  ct_independence(data = ., datetime = datetimes, format = "%Y-%m-%d %H:%M:%S")

sprintf("Independent observations: %s", nrow(indep1))

# Independence considering species
indep2 <- cam_data %>%
  ct_independence(data = ., datetime = datetimes,
                  format = "%Y-%m-%d %H:%M:%S",
                  species_column = "species")

sprintf("Independent observations: %s", nrow(indep2))

# Use a standalone vector of datetime values
dtime <- cam_data$datetimes
ct_independence(datetime = dtime, format = "%Y-%m-%d %H:%M:%S")
```

`ct_inext` *Interpolation and extrapolation of Hill number*

Description

Computes incidence-based species diversity estimates (Hill numbers) from camera trap data. This is a wrapper around iNEXT package (Chao et al., 2014; Hsieh, Ma, & Chao, 2016).

Usage

```
ct_inext(
  data,
  species_column,
  site_column,
  size_column,
  strata_column = NULL,
  diversity_order = 0,
  sample_size = NULL,
  endpoint = NULL,
  knots = 40,
  n_bootstrap = 100
)
```

Arguments

`data`	A data frame, preferably the output of `ct_camera_day()`.
`species_column`	The column in the data frame representing species identifiers. Can be specified as a string or unquoted column name.
`site_column`	The column in the data frame representing site identifiers. Can be specified as a string or unquoted column name.
`size_column`	(Optional) The column representing the size or abundance of the species at each site. If not provided, counts of species occurrences are calculated.
`strata_column`	Optional column name for a grouping variable (e.g. habitat, treatment). If provided, estimates are computed separately for each stratum.
`diversity_order`	Numeric specifying the order of diversity (q) for Hill numbers. Common values: • `0` = species richness, • `1` = Shannon diversity (exponential of Shannon entropy), • `2` = Simpson diversity (inverse of Simpson index). Defaults to `0`.
`sample_size`	Optional numeric vector specifying sample sizes for interpolation/extrapolation.
`endpoint`	Optional numeric specifying the maximum sample size for extrapolation. If NULL, endpoint is the double of the current sample size
`knots`	Integer specifying the number of equally spaced knots for rarefaction/extrapolation. Default is `40`.
`n_bootstrap`	Number of bootstrap replications for estimating confidence intervals. Default is `100`.

Details

This function converts the input data into an **incidence-frequency vector**. The first element of the vector is the number of sampling units, followed by species frequencies. If `strata_column` is provided, the conversion is done separately for each stratum.

Value

A list containing:

- `DataInfo`: Summary statistics of input data.
- `iNextEst`: Rarefaction/extrapolation results for specified diversity order.
- `AsyEst`: Asymptotic diversity estimates.

References

Chao, A., Gotelli, N. J., Hsieh, T. C., Sander, E. L., Ma, K. H., Colwell, R. K., & Ellison, A. M. (2014). Rarefaction and extrapolation with Hill numbers: a framework for sampling and estimation in species diversity studies. Ecological Monographs, 84, 45-67. doi:10.1890/130133.1

Hsieh, T. C., Ma, K. H., & Chao, A. (2016). iNEXT: an R package for rarefaction and extrapolation of species diversity (Hill numbers). Methods in Ecology and Evolution, 7(12), 1451-1456. doi:10.1111/2041210X.12613

See Also

`ct_camera_day()` for preparing sampling data (camera-day).

Examples

```
if (requireNamespace("iNEXT", quietly = TRUE)) {
## Import example data
data(penessoulou)
camdata1 <- penessoulou %>%
  dplyr::filter(project == "Last") %>%
  dplyr::mutate(site = "pene") %>%
  # remove consecutive entry of the same species at the same location within 60s
  ct_independence(species_column = species,
                  site_column = camera,
                  datetime = datetimes,
                  threshold = 60, format = "%Y-%m-%d %H:%M:%S"
                  )
head(camdata1)

# Prepare sampling data (camera-day)
camday <- ct_camera_day(
  data = camdata1,
  deployment_column = camera,
  datetime_column = datetime,
  species_column = species,
  size_column = number
)
```

```
# RAREFACTION/EXTRAPOLATION
int_ext <- ct_inext(data = camday,
                    diversity_order = c(0, 1, 2),
                    species_column = species,
                    site_column = sampling_unit,
                    size_column = number,
                    n_bootstrap = 50)
int_ext

# plot with curves colored by order
ct_plot_inext(int_ext, type = 1, color_var = "Order.q")

# plot with curves faceted by order
ct_plot_inext(int_ext, type = 1, facet_var = "Order.q")
 }
```

`ct_install_exiftool` *Install ExifTool, downloading (by default) the current version*

Description

Install the current version of ExifTool

Usage

```
ct_install_exiftool(
  install_location = NULL,
  win_exe = NULL,
  local_exiftool = NULL,
  quiet = FALSE
)
```

Arguments

`install_location`	Path to the directory into which ExifTool should be installed. If `NULL` (the default), installation will be into the package's per-user data directory, i.e. the path returned by `tools::R_user_dir("ct", "data")`.
`win_exe`	Logical, only used on Windows machines. Should we install the standalone ExifTool Windows executable or the ExifTool Perl library? (The latter relies, for its execution, on an existing installation of Perl being present on the user's machine.) If set to `NULL` (the default), the function installs the Windows executable on Windows machines and the Perl library on other operating systems.
`local_exiftool`	If installing ExifTool from a local "*.zip" or ".tar.gz", supply the path to that file as a character string. With default value, `NULL`, the function downloads ExifTool from https://exiftool.org and then installs it.
`quiet`	Logical. Should function should be chatty?

Value

Called for its side effect

`ct_overlap_estimates` *Estimates of coefficient of overlapping*

Description

Estimates of coefficient of overlapping

Usage

```
ct_overlap_estimates(
  A,
  B,
  kmax = 3,
  adjust = c(0.8, 1, 4),
  n_grid = 128,
  type = c("all", "Dhat1", "Dhat4", "Dhat5")
)
```

Arguments

`A`	A numeric vector of time-of-day observations (in radians, 0 to 2π) for species A.
`B`	A numeric vector of time-of-day observations (in radians, 0 to 2π) for species B.
`kmax`	An integer indicating the maximum number of modes allowed in the activity pattern. Default is 3.
`adjust`	A numeric value to adjust the bandwidth of the kernel density estimation. Default is 1.
`n_grid`	An integer specifying the number of grid points for density estimation. Default is 128.
`type`	the name of the estimator to use: Dhat4 is recommended if both samples are larger than 50, otherwise use Dhat1. See Details. The default is "all" for compatibility with older versions.

Details

See `overlapTrue` for the meaning of coefficient of overlapping, Δ.

These estimators of Δ use kernel density estimates fitted to the data to approximate the true density functions *f(t)* and *g(t)*. Schmid & Schmidt (2006) propose five estimators of overlap:

Dhat1 is calculated from vectors of densities estimated at T equally-spaced times, t, between 0 and 2π:

$$\hat{\Delta}_1 = \frac{2\pi}{T}\sum_{i=1}^{T}\min\{\hat{f}(t_i), \hat{g}(t_i)\}$$

For circular distributions, Dhat2 is equivalent to Dhat1, and Dhat3 is inapplicable.

Dhat4 and Dhat5 use vectors of densities estimated at the times of the observations of the species, *x* and *y*:

$$\hat{\Delta}_4 = \frac{1}{2}\left(\frac{1}{n}\sum_{i=1}^{n}\min\left\{1, \frac{\hat{g}(x_i)}{\hat{f}(x_i)}\right\} + \frac{1}{m}\sum_{j=1}^{m}\min\left\{1, \frac{\hat{f}(y_j)}{\hat{g}(y_j)}\right\}\right)$$

$$\hat{\Delta}_5 = \frac{1}{n}\sum_{i=1}^{n} I\left\{\hat{f}(x_i) < \hat{g}(x_i)\right\} + \frac{1}{m}\sum_{j=1}^{m} I\left\{\hat{g}(y_j) \le \hat{f}(y_j)\right\}$$

where *n, m* are the sample sizes and *I* is the indicator function (1 if the condition is true, 0 otherwise).

Dhat5 simply checks which curve is higher at each point; even tiny changes in the data can result in large, discontinuous changes in Dhat5, and it can take values > 1. Don't use Dhat5.

Comparing curves at times of actual observations works well if there are enough observations of each species. Simulations show that Dhat4 is best when the smallest sample has at least 50 observations. Dhat1 compares curves at `n.grid` equally spaced points, and is best for small samples.

Value

A named numeric vector of overlap coefficient estimates. When `type = "all"` it has three elements, `Dhat1`, `Dhat4` and `Dhat5`; otherwise it has a single element named after the requested estimator. Each value lies between 0 (no overlap) and 1 (identical activity distributions).

Examples

```
set.seed(42)
species_A <- runif(100, 1.2, 2 * pi)
species_B <- runif(100, 0.23, 2 * pi)
ct_overlap_estimates(species_A, species_B)
ct_overlap_estimates(species_A, species_B, type = "Dhat4")
```

`ct_overlap_matrix` *Estimate overlap coefficients for multiple species*

Description

This function calculates pairwise overlap coefficients for activity patterns of multiple species using their time data, and optionally bootstrap confidence intervals for every pair.

Usage

```
ct_overlap_matrix(
  data,
  species_column,
  time_column,
  convert_time = FALSE,
  format = "%H:%M:%S",
  fill_na = NULL,
  n_boot = 0,
  conf = 0.95,
  ci_method = c("auto", "norm", "norm0", "basic", "basic0", "perc"),
  cores = 1,
  ...
)
```

Arguments

data	A data.frame or tibble containing species and time information.
species_column	A column in data indicating species names.
time_column	A column in data containing time data (either as radians or in a time format to be converted).
convert_time	Logical. If TRUE, the time data will be converted to radians using the ct_to_radian function.
format	A character string specifying the time format (e.g., "%H:%M:%S") if ct_to_radian() is TRUE. Defaults to "%H:%M:%S".
fill_na	Optional. A numeric value used to fill NA values in the overlap coefficient matrix. Defaults to NULL (does not fill NA values).
n_boot	Integer. Number of bootstrap samples used to derive a confidence interval for each species pair. When n_boot <= 1 (the default, 0) no bootstrap is run and a single coefficient matrix is returned, preserving the original behaviour. When n_boot > 1, a list of matrices is returned (see Value).
conf	Numeric scalar in (0, 1). Confidence level for the bootstrap interval. Defaults to 0.95.
ci_method	Character. How to choose the confidence-interval type returned by overlap::bootCI() for each pair. "auto" (default) selects, per pair, between the two interval types appropriate for the uncorrected estimate reported in the matrix: "norm0" when the bootstrap estimates are approximately normal (Shapiro-Wilk p >= 0.05) and the skew-robust "basic0" otherwise. Alternatively, force a single type for all pairs with one of "norm", "norm0", "basic", "basic0" or "perc".
cores	Integer. Number of cores passed to ct_bootstrap(). Defaults to 1.
...	Additional arguments passed to overlap::overlapEst()‘ for overlap estimation.

Details

The function calculates pairwise overlap coefficients for all species in the dataset. The overlap coefficients are estimated using the `overlap` package:

- For species pairs with sample sizes of at least 50 observations each, the `Dhat4` estimator is used.
- For smaller sample sizes, the `Dhat1` estimator is used (Schmid & Schmidt, 2006).

When `n_boot > 1`, each pair is bootstrapped with the same estimator used for its point estimate, and a confidence interval is obtained through `ct_boot_ci()`. Because the coefficient stored in the matrix is the uncorrected estimate, the `"auto"` selection restricts itself to the interval types, namely `"norm0"` and `"basic0"`; the choice between them is made per pair from a normality check on the bootstrap estimates. Pairs for which the bootstrap or interval cannot be computed receive `NA`.

Value

If `n_boot <= 1`, a square numeric matrix of pairwise overlap coefficients, where rows and columns represent species (the original return value).

If `n_boot > 1`, a named list of matrices:

`estimate` the square numeric matrix of overlap coefficients;

`ci` a character matrix whose cells give the confidence interval as `"[lower ; upper]"`;

`ci_method` a character matrix recording which `ct_boot_ci()` interval type was used for each cell if ci_method is `"auto"`;

References

Schmid & Schmidt (2006) Nonparametric estimation of the coefficient of overlapping - theory and empirical application, Computational Statistics and Data Analysis, 50:1583-1596.

See Also

`overlap::overlapEst()` for overlap coefficient estimation; `ct_bootstrap()` and `ct_boot_ci()` for the bootstrap machinery.

Examples

```
# Example dataset
data <- data.frame(
  species = c("SpeciesA", "SpeciesA", "SpeciesB", "SpeciesB"),
  time = c("10:30:00", "11:45:00", "22:15:00", "23:30:00")
)

# Calculate overlap coefficients with time conversion
overlap_matrix <- ct_overlap_matrix(
  data = data,
  species_column = species,
  time_column = time,
  convert_time = TRUE,
  format = "%H:%M:%S"
```

```
)


# With bootstrap confidence intervals (returns a list of matrices)
overlap_ci <- ct_overlap_matrix(
  data = data,
  species_column = species,
  time_column = time,
  convert_time = TRUE,
  n_boot = 99,
  conf = 0.95
)
overlap_ci$estimate
overlap_ci$ci
overlap_ci$ci_method
```

`ct_plot_calendar` *Plot a calendar heatmap of daily camera trap activity*

Description

Visualises a year of camera-trap records as a calendar heatmap. Tiles are shaded by the number of records per day, or by the summed value of a chosen column. A count distribution can optionally be fitted to the daily values and used for the shading.

Usage

```
ct_plot_calendar(
  data,
  datetime,
  format = NULL,
  size_column = NULL,
  only_month = NULL,
  fit_distribution = FALSE,
  abbreviate_month_name = FALSE,
  month_name = NULL,
  day_name = NULL,
  number_of_column = 4,
  low = NULL,
  high = NULL,
  palette = NULL,
  na_value = "grey95",
  show_day_number = TRUE,
  title = NULL
)
```

Arguments

data	A data frame of records, one row per detection.
datetime	Column holding the date or date-time of each record.
format	Optional date format(s) passed to as.Date() via tryFormats. If NULL (default), a set of common date and date-time formats is tried.
size_column	Optional column whose values are summed per day, for example the number of individuals recorded in each detection. If omitted, the number of records (detections) per day is used instead.
only_month	Optional integer vector of month numbers (1 to 12) to keep, for example 3:5. Records outside these months are dropped and only those month panels are drawn. Default NULL (the whole year).
fit_distribution	Logical. If TRUE, a count distribution is fitted to the records per day over the displayed period (days with no record count as zeros) with ct_fit_distribution(), and the fitted distribution is reported in the plot subtitle. Tiles are then shaded by the fitted density, that is the probability of each day's count under the model. The calendar therefore becomes a typicality map, not an activity map: the brightest tiles are the most probable days under the fitted distribution, which for zero-heavy camera-trap data are usually the days with no detection, while busier days carry rarer counts and appear darker. See Details. Default FALSE.
abbreviate_month_name	Logical. Use three-letter month names. Ignored when month_name is supplied. Default FALSE.
month_name	Optional length-12 character vector of month labels, for localisation. Defaults to the English month names.
day_name	Optional length-7 character vector of weekday labels, Monday first. Defaults to c("Mon", "Tue", "Wed", "Thu", "Fri", "Sat", "Sun").
number_of_column	Number of month panels per row. Default 4.
low, high	Optional start and end colours for a two-colour gradient fill. When both are supplied they override palette.
palette	Optional fill palette. Either a single viridis option letter (for example "C"), or a vector of two or more colours for a custom gradient. Default NULL (viridis option C).
na_value	Fill colour for days with no records. Default "grey95".
show_day_number	Logical. Print the day number inside each tile. Default TRUE.
title	Optional plot title. Generated automatically when NULL.

Details

With fit_distribution = FALSE the calendar is an activity map: tiles are shaded by the records per day (or the summed size_column), so busier days are brighter.

With `fit_distribution = TRUE` the calendar is instead a typicality map. A single distribution is fitted to the whole displayed period, and each tile is shaded by the fitted probability of that day's count. Because most days have no detection, the count of zero is the most probable value, so empty days receive the highest density and the brightest colour, while the rarer busy days appear darker. The map highlights how typical or unusual each day is under the model, rather than how much activity occurred. Use `fit_distribution = FALSE` if you want activity intensity instead.

Value

A ggplot2::ggplot object.

See Also

`ct_fit_distribution()`, `ct_plot_camtrap_activity()`

Examples

```
library(dplyr)
data(ACBR)

# The calendar covers one year at a time, so keep a single year.
d2024 <- ACBR$acbr_data %>%
  # Filter to independent (10min separated) detections
  ct_independence(species_column = species,
                  datetime = datetime,
                  format = "%Y-%m-%d %H:%M:%S",
                  threshold = 10*60
  ) %>%
  # Select data for 2025 year
  filter(lubridate::year(datetime) == 2025)

ct_plot_calendar(d2024, datetime = datetime,
                 size_column = count,
                 low = "gray", high = "red"
)
#'
```

`ct_plot_camtrap_activity` *Plot camera trap activity over time*

Description

Visualizes the activity history of camera trap deployments to show periods of data capture. It also optionally highlights periods of inactivity (break/gap).

Usage

```
ct_plot_camtrap_activity(
  data,
  deployment_column,
  datetime_column,
  threshold = 5,
  time_unit = "days",
  format = NULL,
 activity_style = list(linewidth = 0.8, color = "steelblue", alpha = 0.7, linetype = 1,
    label = "Active period"),
 break_style = list(linewidth = 0.8, color = "#c90026", alpha = 0.9, linetype = 1, label
    = "Break period"),
  show_gaps = TRUE,
  ylabel_format = "%Y-%m-%d",
  ybreak = paste(nrow(data)%/%10, time_unit),
  legend_title = "Activity"
)
```

Arguments

data	A data frame containing the datetime column.
deployment_column	Column name (unquoted) that identifies the deployment or camera ID.
datetime_column	The datetime column.
threshold	A numeric value indicating the minimum gap to be considered a break (default is 10).
time_unit	The unit for the threshold. Supported values include "secs", "mins", "hours", "days", and "weeks".
format	Optional. A character string specifying the datetime format, passed to `as.POSIXlt`.
activity_style	A list controlling the appearance of active periods. Can include: • `linewidth`: Line width (default 0.8) • `color`: Color of activity bars (default `"steelblue"`) • `alpha`: Transparency (default 0.7) • `linetype`: Line type (default 1) • `label`: Legend label for active periods (default `"Active period"`)
break_style	A list controlling the appearance of gaps/inactive periods. Can include: • `linewidth`: Line width (default 0.8) • `color`: Color of gap bars (default `"#c90026"`) • `alpha`: Transparency (default 0.9) • `linetype`: Line type (default 1) • `label`: Legend label for break periods (default `"Break period"`)
show_gaps	Logical. If `TRUE` (default), shows vertical bars for detected gaps in deployment activity.

ylabel_format	Character. Format for y-axis date-time labels. Default is "%Y-%m-%d".
ybreak	Character. Spacing for y-axis breaks, e.g., "1 days" or "12 hours". Default is based on time_unit.
legend_title	Character. Title of the colour legend that distinguishes active periods from breaks (default "Activity").

Value

A ggplot2 object showing periods of activity (and optionally gaps) for each deployment. Active periods and breaks are mapped to colour, so a legend is drawn (blue for active periods, red for breaks by default). Because the return value is a standard ggplot object, it can be customised further with the usual + syntax (for example + ggplot2::labs() or + ggplot2::theme()).

Examples

```
# Load example data and filter for one project phase
data(penessoulou)

camtrap_data <- penessoulou %>%
  dplyr::filter(project == "Last")

# Plot with default styles (a legend distinguishes active periods from breaks)
ct_plot_camtrap_activity(
  data = camtrap_data,
  deployment_column = camera,
  datetime_column = datetimes,
  threshold = 7,
  time_unit = "days"
)

# Customise the colours, the legend labels and the legend title
ct_plot_camtrap_activity(
  data = camtrap_data,
  deployment_column = camera,
  datetime_column = "datetimes",
  threshold = 15,
  time_unit = "days",
  ybreak = "3 days",
  activity_style = list(linewidth = 1.1, color = "gray10", label = "Recording"),
  break_style = list(color = "orange", label = "Gap"),
  legend_title = "Camera status"
)

# The result is a ggplot, so it can be extended with the usual + syntax
ct_plot_camtrap_activity(
  data = camtrap_data,
  deployment_column = camera,
  datetime_column = datetimes,
  threshold = 7,
  time_unit = "days"
) +
```

```
  ggplot2::labs(title = "Camera activity") +
  ggplot2::theme(legend.position = "bottom")
```

`ct_plot_density` *Plot species' activity patterns*

Description

This function visualizes species' activity patterns based on time-of-day data. It uses kernel density estimation to estimate activity density.

Usage

```
ct_plot_density(
  time_of_day,
  xscale = 24,
  xcenter = c("noon", "midnight"),
  n_grid = 128,
  kmax = 3,
  adjust = 1,
  rug = FALSE,
  line_type = 2,
  line_color = "gray10",
  line_width = 1,
  rug_lentgh = 0.018,
  rug_color = "gray30",
  extend = "lightgrey",
  extend_alpha = 0.8,
  ...
)
```

Arguments

`time_of_day`	A numeric vector of time-of-day observations (in radians, 0 to 2π).
`xscale`	A numeric value to scale the x-axis. Default is 24 for representing time in hours.
`xcenter`	A string indicating the center of the x-axis. Options are `"noon"` (default) or `"midnight"`.
`n_grid`	An integer specifying the number of grid points for density estimation. Default is 128.
`kmax`	An integer indicating the maximum number of modes allowed in the activity pattern. Default is 3.
`adjust`	A numeric value to adjust the bandwidth of the kernel density estimation. Default is 1.
`rug`	A logical value indicating whether to include a rug plot of the observations. Default is `FALSE`.

line_type	A numeric specifying the line types. Default is 2.
line_color	A string specifying the colors of the density lines. Default is "gray10".
line_width	A numeric value specifying the line width. Default is 1.
rug_lentgh	A numeric value specifying the length of the rug ticks. Default is 0.018 (in normalized plot coordinates).
rug_color	A string specifying the color of the rug ticks. Default is "gray30".
extend	A string specifying the color of the extended area beyond the activity period. Default is "lightgrey".
extend_alpha	A numeric value (0 to 1) for the transparency of the extended area. Default is 0.8.
...	Additional arguments passed to the geom_rug function.

Value

A ggplot object representing the activity density curves of the species.

Examples

```
# Generate random data for two species
set.seed(42)
A <- runif(100, 0, 2 * pi)

# Plot overlap with default settings
ct_plot_density(A)
# Customize plot with specific colors and line types
ct_plot_density(A, line_color = "gray10", line_width = 0.8,
                xcenter = "midnight", rug = TRUE,
                rug_color = 'red', extend_alpha = 0)
```

---

ct_plot_inext *Plot diversity interploation and extrapolation*

Description

plot sample-size-based and coverage-based rarefaction/extrapolation curves along with a bridging sample completeness curve

Usage

```
ct_plot_inext(
  inext_object,
  type = 1,
  se = TRUE,
```

```
  facet_var = "None",
  color_var = "Assemblage",
  grey = FALSE
)
```

Arguments

inext_object	an object as outputed by `ct_inext()`
type	three types of plots: • `type = 1`: sample-size-based rarefaction/extrapolation curve • `type = 2`: sample completeness curve • `type = 3`: coverage-based rarefaction/extrapolation curve
se	a logical variable to display confidence interval around the estimated sampling curve.
facet_var	create a separate plot for each value of a specified variable: • `facet_var = "None"`: no separation • `facet_var = "Order.q"`: a separate plot for each diversity order • `facet_var = "Assemblage"`: a separate plot for each assemblage • `facet_var = "Both"`: a separate plot for each combination of order x assemblage
color_var	create curves in different colors for values of a specified variable: • `color_var = "None"`: all curves are in the same color • `color_var = "Order.q"`: use different colors for diversity orders • `color_var = "Assemblage"`: use different colors for sites • `color_var = "Both"`: use different colors for combinations of order x assemblage
grey	a logical variable to display grey and white ggplot2 theme

Value

a ggplot2 object

Examples

```
if (requireNamespace("iNEXT", quietly = TRUE)) {
## Import example data
data(penessoulou)
camdata1 <- penessoulou %>%
  dplyr::filter(project == "Last") %>%
  dplyr::mutate(site = "pene") %>%
  # remove consecutive entry of the same species at the same location within 60s
  ct_independence(species_column = species,
                  site_column = camera,
                  datetime = datetimes,
                  threshold = 60, format = "%Y-%m-%d %H:%M:%S"
                  )
```

```
head(camdata1)

# Prepare sampling data (camera-day)
camday <- ct_camera_day(
  data = camdata1,
  deployment_column = camera,
  datetime_column = datetime,
  species_column = species,
  size_column = number
)

# RAREFACTION/EXTRAPOLATION
int_ext <- ct_inext(data = camday,
                    diversity_order = c(0, 1, 2),
                    species_column = species,
                    site_column = sampling_unit,
                    size_column = number,
                    n_bootstrap = 50)
int_ext

# plot with curves colored by order
ct_plot_inext(int_ext, type = 1, color_var = "Order.q")

# plot with curves faceted by order
ct_plot_inext(int_ext, type = 1, facet_var = "Order.q")
 }
```

`ct_plot_overlap` *Plot overlap between two species' activity patterns*

Description

This function visualizes the temporal overlap between two species' activity patterns based on time-of-day data. It uses kernel density estimation to estimate activity densities and highlights areas of overlap between the two species.

Usage

```
ct_plot_overlap(
  A,
  B,
  xscale = 24,
  xcenter = c("noon", "midnight"),
  n_grid = 128,
  kmax = 3,
  adjust = 1,
  rug = FALSE,
  overlap_color = "gray40",
```

```
  overlap_alpha = 0.8,
  line_type = c(1, 2),
  line_color = c("gray10", "gray0"),
  line_width = c(1, 1),
  species_names = c("Species A", "Species B"),
  legend_title = "Species",
  overlap_only = FALSE,
  extend = "lightgrey",
  extend_alpha = 0.8,
  rug_length = 0.018,
  rug_color = NULL,
  ...
)
```

Arguments

A	A numeric vector of time-of-day observations (in radians, 0 to 2π) for species A.
B	A numeric vector of time-of-day observations (in radians, 0 to 2π) for species B.
xscale	A numeric value to scale the x-axis. Default is 24 for representing time in hours.
xcenter	A string indicating the center of the x-axis. Options are "noon" (default) or "midnight".
n_grid	An integer specifying the number of grid points for density estimation. Default is 128.
kmax	An integer indicating the maximum number of modes allowed in the activity pattern. Default is 3.
adjust	A numeric value to adjust the bandwidth of the kernel density estimation. Default is 1.
rug	A logical value indicating whether to add a rug of the observations along the x-axis. Default is FALSE.
overlap_color	A string specifying the color of the overlap area. Default is "gray40".
overlap_alpha	A numeric value (0 to 1) for the transparency of the overlap area. Default is 0.8.
line_type	A vector of integers specifying the line types for species A and B density lines. Default is c(1, 2).
line_color	A vector of strings specifying the colors of the density lines for species A and B. Default is c("gray10", "gray0").
line_width	A vector of numeric values specifying the line widths for species A and B density lines. Default is c(1, 1).
species_names	A character vector of length two giving the legend labels for species A and B.
legend_title	A character string giving the density-line legend title.
overlap_only	A logical value indicating whether to plot only the overlap region without individual density lines. Default is FALSE.

extend	A string specifying the color of the extended area beyond the activity period. Default is "lightgrey".
extend_alpha	A numeric value (0 to 1) for the transparency of the extended area. Default is 0.8.
rug_length	A numeric value giving the length of the rug ticks, in normalized plot coordinates. Default is 0.018.
rug_color	Colour of the rug ticks. Default NULL draws each species' ticks in its line_color. A single colour is used for both species, and two colours are matched to species A and B.
...	Additional arguments passed to ggplot2::geom_rug(). The former argument name rug_lentgh is still accepted for rug_length.

Value

A ggplot object representing the activity density curves and overlap between the two species. If overlap_only = TRUE, only the overlap region is displayed.

Examples

```
# Generate random data for two species
set.seed(42)
species_A <- runif(100, 0, 2 * pi)
species_B <- runif(100, 0, 2 * pi)

# Plot overlap with default settings
ct_plot_overlap(A = species_A, B = species_B)


# Customize plot with specific colors and line types
ct_plot_overlap(A = species_A, B = species_B, overlap_color = "blue",
line_color = c("red", "green"))

# Add rug ticks coloured by species
ct_plot_overlap(A = species_A, B = species_B, rug = TRUE,
line_color = c("darkorange", "steelblue"))
```

---

ct_plot_overlap_coef *Plot overlap coefficient matrix*

Description

Visualizes an overlap coefficient matrix.

Usage

```
ct_plot_overlap_coef(
  data,
  side = c("lower", "upper"),
  show = c("shape", "value"),
  shape_type = 21,
  shape_size = 0.5,
  text_size = 6,
  text_font = NA,
  excludes = NULL,
  color_scale = "gray3",
  ...
)
```

Arguments

data	A square matrix (e.g ct_overlap_matrix() output) representing overlap coefficients to be visualized.
side	A character string indicating which triangle of the matrix to display. Options are "lower" (default) or "upper".
show	A character string specifying whether to display "shape" (default) or "value" in the plot.
shape_type	Numeric value specifying the type of shape to use in the plot. Defaults to 21 (circle).
shape_size	Numeric value controlling the stroke size of the shapes. Defaults to 0.5.
text_size	Numeric value specifying the size of the text when show = "value". Defaults to 6.
text_font	Character string specifying the font family to use for text labels. Defaults to NA.
excludes	A vector of numeric values to exclude from the plot. Defaults to NULL.
color_scale	A character string or vector of colors to define the gradient color scale. Defaults to "gray3".
...	Additional arguments passed to the guide_colorbar function.

Value

A ggplot object representing the overlap coefficient matrix visualization.

Examples

```
library(ggplot2)
# Example overlap coefficient matrix
overlap_matrix <- matrix(c(1, 0.8, 0.7, 0.8, 1, 0.9, 0.7, 0.9, 1), ncol = 3)
colnames(overlap_matrix) <- rownames(overlap_matrix) <- c("A", "B", "C")

# Plot lower triangle with shapes
ct_plot_overlap_coef(overlap_matrix, side = "lower", show = "shape")
```

```
# Plot upper triangle with values
ct_plot_overlap_coef(overlap_matrix, side = "upper", show = "value")
```

`ct_plot_rose_diagram` *Plot a 24-hour rose diagram of daily activity*

Description

This function generates a rose diagram (circular bar plot) to visualize daily activity patterns over a 24-hour period. Each bar represents either the absolute or relative frequency of observations within hourly intervals. The plot also includes a segment indicating the mean activity time, and an optional segment showing the 95% confidence interval of the activity period.

Usage

```
ct_plot_rose_diagram(
  data = NULL,
  times,
  frequencies = "absolute",
  hide_lebels = FALSE,
  label_position = NULL,
  label_style = list(),
  time_range = 1,
  ci_segment = TRUE,
  mean_segment = TRUE,
  ring = TRUE,
  color = "gray20",
  fill = color,
  ci_style = list(),
  mean_style = list(),
  start = -0.12,
  width = NULL
)
```

Arguments

`data`	A data frame containing the time values. If `NULL`, `times` must be provided as a vector.
`times`	A numeric vector of time values (in radians) or a column name from `data`.
`frequencies`	Character. Use `"absolute"` to show counts or `"relative"` to show percentages. Default is `"absolute"`.
`hide_lebels`	Logical. If `TRUE`, frequency value labels on top of bars are hidden. Default is `FALSE`.
`label_position`	Numeric. Controls vertical position of the frequency value labels (if shown).

label_style	A list of styles for labels. Accepts color, size, and family.
time_range	Numeric. Width of the time bins in hours. Default is 1 (hourly bins).
ci_segment	Logical or numeric. If TRUE, a segment representing the 95% confidence interval is added. If numeric, this value sets the length of the CI ticks. Default is TRUE.
mean_segment	Logical. If TRUE, a segment representing the mean time is added. Default is TRUE.
ring	Logical or numeric vector. If TRUE, a default ring range is set. If a numeric vector of length 2 is provided, sets custom inner and outer limits of the radial axis.
color	Color of the bar border and segments. Default is "gray20".
fill	Fill color of the bars. Default is the same as color.
ci_style	A list of styles for the confidence interval segment. Accepts color, linetype, and linewidth.
mean_style	A list of styles for the mean segment. Accepts color, linetype, and linewidth.
start	Numeric. The angle (in radians) where the polar plot starts. Default is -0.12.
width	Numeric. Width of each bar. Default is NULL, which uses the default width from geom_col().

Value

A ggplot object representing the rose diagram.

Examples

```
set.seed(129)
library(dplyr)
library(ggplot2)

rf <- runif(123, 0, max = 6)

ct_plot_rose_diagram(data = NULL,
                     times = rf,
                     frequencies = "relative",
                     label_style = list(size = 4, color = 'red'),
                     label_position = 11,
                     time_range = 1,
                     mean_segment = TRUE,
                     ci_segment = 1,
                     ring = c(-5, 12),
                     color = 'gray20',
                     mean_style = list(linetype = 1, linewidth = .5, color = 'red'),
                     ci_style = list(linetype = 1, linewidth = .5, color = 'black')
)
```

`ct_QAIC` *Compute QAIC for a set of detection function models*

Description

Calculates the quasi-Akaike Information Criterion (QAIC) for one or more detection function models within the same key function family. If multiple models are provided, all must have the same key function. This function is typically used as the first step of a two-step model selection approach (Howe et al., 2019).

Usage

```
ct_QAIC(models, chat = NULL, k = 2)
```

Arguments

`models`	A list of fitted detection function models (objects returned by `Distance::ds()` or `ct_fit_ds()`).
`chat`	Optional numeric value of overdispersion ($\hat{c}$). If not provided, it is estimated from the most parameterised model in each key function set.
`k`	Numeric. The penalty term used in QAIC (default is 2).

Details

If only one model is supplied and `chat` is not provided, the function estimates $\hat{c}$ using the provided model and issues a warning that model selection cannot be performed. For multiple models, All models must use the same key function.

QAIC is calculated as:

$$QAIC = -2 \times \log(L)/\hat{c} + 2k$$

where L is the likelihood, $\hat{c}$ is the estimated overdispersion, and k is the number of parameters.

Value

A tibble with one row per model containing:

- `model`: The model name
- `df`: The degrees of freedom for the model.
- `QAIC`: The computed QAIC value.

References

Howe, E. J., Buckland, S. T., Després-Einspenner, M., & Kühl, H. S. (2019). Model selection with overdispersed distance sampling data. **Methods in Ecology and Evolution**, 10(1), 38-47. doi:10.1111/2041210X.13082

Examples

```
library(Distance)
library(dplyr)

data("duiker")
duiker_data <- duikers$DaytimeDistances %>%
  dplyr::slice_sample(prop = .3) # sample 30% of rows
truncation <- list(left = 2, right = 15) # Keep only distance between 2-15 m

# fit hazard-rate key models
w3_hr0 <- ds(duiker_data, transect = "point", key = "hr", adjustment = NULL,
             truncation = truncation)
w3_hr1 <- ds(duiker_data, transect = "point", key = "hr", adjustment = "cos",
             order = 2, truncation = truncation)
w3_hr2 <- ds(duiker_data, transect = "point", key = "hr", adjustment = "cos",
             order = c(2, 4), truncation = truncation)
# fit half-normal key models
w3_hn0 <- ds(duiker_data, transect = "point", key = "hn", adjustment = NULL,
             truncation = truncation)
w3_hn1 <- ds(duiker_data, transect = "point", key = "hn", adjustment = "cos",
             order = 2, truncation = truncation)
w3_hn2 <- ds(duiker_data, transect = "point", key = "hn", adjustment = "cos",
             order = c(2, 4), truncation = truncation)
# fit uniform key models
w3_u0 <- ds(duiker_data, transect = "point", key = "unif", adjustment = NULL,
            truncation = truncation)
w3_u1 <- ds(duiker_data, transect = "point", key = "unif", adjustment = "cos",
            order = 2, truncation = truncation)
w3_u2 <- ds(duiker_data, transect = "point", key = "unif", adjustment = "cos",
            order = c(2, 4), truncation = truncation)

# Create model list
model_list <- list(w3_hn0, w3_hn1, w3_hn2,
                   w3_hr0, w3_hr1, w3_hr2,
                   w3_u0, w3_u1, w3_u2)

# Compute model QAICs
ct_QAIC(list(w3_hr0, w3_hr1, w3_hr2)) # All key functions must be the same
ct_QAIC(list(w3_hn0, w3_hn1, w3_hn2)) # All key functions must be the same

# Compute Chi-squared Goodness-of-fit
ct_chi2_select(list(w3_hn0, w3_hr0, w3_u0)) # All key functions must be different
ct_chi2_select(list(w3_hn2, w3_hr1, w3_u0)) # All key functions must be different

# Two-step model selection
ct_select_model(model_list)
```

`ct_read` *Read a delimited file into a tibble*

Description

The ct_read function reads a delimited text file. It automatically detects the delimiter if not specified and provides an easy-to-use interface for importing data with additional customization options.

Usage

```
ct_read(file_path, header = TRUE, sep, ...)
```

Arguments

file_path	A string specifying the path to the file to be read.
header	A logical value indicating whether the file contains a header row. Defaults to TRUE.
sep	The field separator character. If not provided, the function automatically detects the separator.
...	Additional arguments passed to the read.table function for fine-tuned control over file reading.

Value

A tibble containing the data from the specified file.

---

ct_read_metadata *Read Image Metadata*

Description

Extracts metadata from image files using ExifTool and returns the results as a tibble.

Usage

```
ct_read_metadata(
  path,
  tags = NULL,
  recursive = FALSE,
  parse_hs = FALSE,
  args = NULL,
  exiftool_path = NULL
)
```

Arguments

path	Character vector of image file paths or a directory path.
tags	Character vector of tag names to extract. Use: • NULL or "all" to extract all tags • "standard" to extract a predefined, commonly used set of tags • a character vector of tag names to extract specific fields
recursive	Logical. If TRUE, searches directories recursively. Default is FALSE.
parse_hs	Logical. If TRUE, parses the HierarchicalSubject field into separate columns where each parent category becomes a column name. Default is FALSE.
args	Character vector of additional arguments passed directly to ExifTool (e.g., "-fast").
exiftool_path	Character. Path to the ExifTool executable. If NULL, the function attempts to auto-detect it.

Details

By default, all available tags are returned. You can limit the output to a predefined set of tags or provide a custom list of tag names.

This function calls ExifTool with CSV output enabled and numeric values returned where applicable. When parse_hs = TRUE, the HierarchicalSubject field is split into structured columns.

Value

A tibble where each row represents one image file and each column represents a metadata field.

See Also

- ct_get_hs() to retrieve hierarchical subjects
- ct_create_hs() to add hierarchical subjects
- ct_remove_hs() to remove hierarchical subjects

Examples

```
## Not run:
# Example image path
image_path <- file.path(system.file("img", package = "ct"), "large.jpeg")

# Extract all metadata
ct_read_metadata(path = image_path)

# Extract a predefined standard set of metadata
ct_read_metadata(path = image_path, tags = "standard")

# Extract custom tags
ct_read_metadata(path = image_path,
                 tags = c("DateTimeOriginal", "GPSLatitude", "GPSLongitude"))

# Parse hierarchical subject fields into columns
```

```
ct_read_metadata(path = image_path,
                 tags = "standard",
                 parse_hs = TRUE)

## End(Not run)
```

`ct_remove_hs` *Remove hierarchical subject (hs) values from image metadata*

Description

Removes specific hierarchical subjects or clears the entire HierarchicalSubject field from image metadata using ExifTool. Can remove one or multiple specific parent|child hierarchies, or clear all hierarchical subjects at once.

This function supports processing individual files or entire directories (with optional recursion), applying the removal to all supported image files found.

Usage

```
ct_remove_hs(
  path,
  hierarchy = NULL,
  recursive = FALSE,
  intern = TRUE,
  quiet = TRUE,
  ...
)
```

Arguments

`path`	A character string specifying the full path to an image file or directory. If a directory is provided, hierarchical subjects will be removed from all supported image files in that directory.
`hierarchy`	A named character vector specifying hierarchies to remove. Names represent parent categories, values represent child categories. Example: `c("Species" = "Vulture")` removes "Species|Vulture". If `NULL` (default), removes all hierarchical subjects from the image(s).
`recursive`	Logical. If `TRUE` and `path` is a directory, searches for images recursively in subdirectories. Default: `FALSE`.
`intern`	Logical. If `TRUE`, returns output as a character vector. Default: `TRUE`.
`quiet`	Logical. If `TRUE`, suppresses command output. Default: `TRUE`.
`...`	Additional arguments passed to `system2()`.

Details

When removing specific hierarchies from a single file, the function validates that they exist before attempting removal. If the last hierarchy is removed, the entire HierarchicalSubject field is cleared from the metadata. The function handles multiple hierarchies in a single call.

When processing directories, the function applies the removal to all supported image files found. Use `recursive = TRUE` to include subdirectories. Note that validation of existing hierarchies is only performed for single files.

Value

Invisibly returns `TRUE` on success, `FALSE` if specified hierarchy doesn't exist. Displays informative messages about the operation. Called primarily for side effects (modifying image metadata).

See Also

- `ct_get_hs()` to retrieve hierarchical subjects
- `ct_create_hs()` to add hierarchical subjects
- `ct_read_metadata()` to read image metadata

Examples

```
## Not run:
# Path to example image
image_path <- file.path(system.file("img", package = "ct"), "large.jpeg")

# Add some hierarchical subjects
ct_create_hs(image_path, c("Species" = "Vulture", "Location" = "Africa"))
ct_get_hs(image_path)

# Remove a specific hierarchy
ct_remove_hs(image_path, hierarchy = c("Species" = "Vulture"))
ct_get_hs(image_path) # Only "Location|Africa" remains

# Remove multiple hierarchies at once
ct_create_hs(image_path, c("Species" = "Eagle", "Status" = "Endangered"))
ct_remove_hs(
  image_path,
  hierarchy = c("Species" = "Eagle", "Status" = "Endangered")
)

# Remove all hierarchical subjects
ct_remove_hs(image_path, hierarchy = NULL)
ct_get_hs(image_path) # Returns NULL

# Attempting to remove non-existent hierarchy
ct_remove_hs(image_path, hierarchy = c("Species" = "NonExistent"))

# Remove all hierarchical subjects from all images in a directory
image_dir <- system.file("img", package = "ct")
ct_remove_hs(path = image_dir, recursive = FALSE)
```

```
# Remove recursively from directory and subdirectories
ct_remove_hs(path = image_dir, recursive = TRUE)

# Remove specific hierarchy from all images in a directory
ct_remove_hs(
  path = image_dir,
  hierarchy = c("Species" = "Vulture"),
  recursive = TRUE
)

## End(Not run)
```

`ct_rest_activity` *Prepare activity (time-of-day) data for REST*

Description

Keeps independent detections of each species and converts their time of day to radians for circular activity modelling.

Usage

```
ct_rest_activity(
  detection_data,
  station_column = "Station",
  species_column = "Species",
  datetime_column = "DateTime",
  independence_minutes = 30
)
```

Arguments

`detection_data`	A data frame with one row per detection.
`station_column, datetime_column`	Columns for the station ID and datetime in `detection_data`.
`species_column`	Column for species in `detection_data`.
`independence_minutes`	Minimum gap (minutes) between successive detections at a station for them to count as independent.

Value

A tibble with columns `Species`, `Station`, `time` (radians).

Examples

```
data(rest_detection)

activity <- ct_rest_activity(rest_detection, independence_minutes = 30)
head(activity)
```

`ct_rest_effort` *Add camera-trapping effort (days) to formatted station data*

Description

Effort is approximated as the span between the first and last detection. When `term_col` is given, effort is computed per survey term and summed per station so inactive gaps between terms are not counted.

Usage

```
ct_rest_effort(
  detection_data,
  station_data,
  station_column = "Station",
  datetime_column = "DateTime",
  term_column = NULL,
  plot = FALSE
)
```

Arguments

`detection_data`	A data frame with one row per detection.
`station_data`	A data frame from `ct_rest_passes()` (must have a `Station` column).
`station_column, datetime_column`	Columns for the station ID and datetime in `detection_data`.
`term_column`	Optional column identifying survey terms; `NULL` to ignore.
`plot`	If `TRUE`, draw a Gantt-style plot of operation periods.

Value

`station_data` with an added `Effort` column (days). Stations with no or zero effort are dropped with a warning.

Examples

```
data(rest_detection)
data(rest_station)

stations <- ct_rest_passes(rest_detection, rest_station, model = "REST")
ct_rest_effort(rest_detection, stations)
```

`ct_rest_passes` *Aggregate the number of animal passes per station for REST / RAD-REST*

Description

Aggregate the number of animal passes per station for REST / RAD-REST

Usage

```
ct_rest_passes(
  detection_data,
  station_data,
  station_column = "Station",
  species_column = "Species",
  passes_column = "y",
  model = c("REST", "RAD-REST")
)
```

Arguments

`detection_data`	A data frame with one row per video / detection.
`station_data`	A data frame with one row per camera station.
`station_column, species_column`	Columns giving the station ID and species in `detection_data`.
`passes_column`	Column holding the number of passes per video.
`model`	Either `"REST"` (totals as `Y`) or `"RAD-REST"` (per-video pass counts spread into `y_0`, `y_1`, ... plus the video total `N`).

Value

A tibble with one row per station x species, ready for `ct_rest_effort()`.

Examples

```
data(rest_detection)
data(rest_station)

# Original REST: total passes (Y) per station
ct_rest_passes(rest_detection, rest_station, model = "REST")

# RAD-REST: videos split by number of passes (y_0, y_1, ...)
ct_rest_passes(rest_detection, rest_station, model = "RAD-REST")
```

`ct_rest_select_stay` *Choose a staying-time distribution for REST by WAIC*

Description

Fits the REST staying-time survival sub-model under one or more candidate distributions (and, optionally, covariate combinations) and ranks them by WAIC, with a Bayesian p-value as a goodness-of-fit check. Use the winning `stay_distribution` in `ct_fit_rest()`.

Usage

```
ct_rest_select_stay(
  stay_data,
  species,
  stay_formula = Stay ~ 1,
  stay_distribution = c("lognormal", "gamma", "weibull", "exponential"),
  stay_random_effect = NULL,
  compare_models = FALSE,
  iterations = 5000,
  burnin = 1000,
  thin = 4,
  chains = 3,
  cores = 3,
  quiet = FALSE
)
```

Arguments

`stay_data`	Staying-time data from `ct_rest_stay()`.
`species`	Single species name to analyse.
`stay_formula`	Staying-time formula, e.g. `Stay ~ 1` or `Stay ~ 1 + habitat`.
`stay_distribution`	One or more of `"lognormal"`, `"gamma"`, `"weibull"`, `"exponential"` to compare.

stay_random_effect
: Optional column in stay_data for a random effect on staying time. Tidy-selected (string, bare name, or position).

compare_models
: If TRUE, also compare every covariate combination of stay_formula.

iterations, burnin, thin, chains, cores
: MCMC settings.

quiet
: If TRUE, suppress progress messages.

Value

An object of class ct_rest_stay with a waic ranking tibble, a summary of the mean staying time for the best model, and its samples.

See Also

ct_fit_rest()

Examples

```
data(rest_detection)
data(rest_station)

stay <- ct_rest_stay(rest_detection, rest_station)

## Not run:
# Compare candidate staying-time distributions by WAIC (requires 'nimble')
ct_rest_select_stay(
  stay, species = "Red duiker",
  stay_distribution = c("lognormal", "gamma", "weibull"),
  iterations = 3000, burnin = 1000, chains = 2, cores = 2
)

## End(Not run)
```

---

ct_rest_stay *Prepare staying-time data for REST*

Description

Selects and standardises the staying-time and censoring columns from a detection table and attaches per-station covariates.

Usage

```
ct_rest_stay(
  detection_data,
  station_data,
  station_column = "Station",
```

```
  species_column = "Species",
  stay_column = "Stay",
  censor_column = "Cens"
)
```

Arguments

`detection_data`	A data frame with one row per video / detection.
`station_data`	A data frame with one row per camera station.
`station_column, species_column`	Columns giving the station ID and species in `detection_data`.
`stay_column`	Column holding the staying time in seconds.
`censor_column`	Column holding the censoring flag (1 = censored, 0 = fully observed).

Value

A tibble with columns `Station`, `Species`, `Stay`, `Cens` plus any station covariates, ready for `ct_fit_rest()`.

Examples

```
data(rest_detection)
data(rest_station)

# Column names can be strings, bare names, or positions:
stay <- ct_rest_stay(rest_detection, rest_station, stay_column = Stay)
head(stay)
```

`ct_select_model` *Model selection for Distance Sampling detection functions*

Description

Implements a two-step model selection procedure for distance sampling detection functions following the approach of Howe et al (2019).

Usage

```
ct_select_model(models, chat = NULL, k = 2)
```

Arguments

`models`	A list of fitted detection function models (objects returned by `Distance::ds()` or `ct_fit_ds()`).
`chat`	Optional numeric value of overdispersion ($\hat{c}$). If not provided, it is estimated from the most parameterised model in each key function set.
`k`	Numeric. The penalty term used in QAIC (default is 2).

Details

Step 1: Within each key function family (e.g., half-normal, hazard-rate), models are compared using the quasi-Akaike Information Criterion (QAIC). Overdispersion ($\hat{c}$) is estimated if not provided. The best model per key function family is identified as the one with the lowest QAIC.

Step 2: The best models from each key function family are compared using overall goodness-of-fit statistics based on chi-squared divided by degrees of freedom (χ^2/df). The model with the lowest χ^2/df is selected as the final detection function model.

Value

A named list with the following elements:

- `QAIC`: A tibble summarizing QAIC results for each model within key function families.
- `Best QAIC models`: A subset of models, one per key function, that minimize QAIC.
- `Chiq2`: A tibble comparing the best models by chi-squared goodness-of-fit criteria.
- `Final model`: The selected detection function model with the lowest chi-squared/df.

References

Howe, E. J., Buckland, S. T., Després-Einspenner, M., & Kühl, H. S. (2019). Model selection with overdispersed distance sampling data. **Methods in Ecology and Evolution**, 10(1), 38-47. doi:10.1111/2041210X.13082

See Also

`ct_QAIC()`, `ct_chi2_select()`

Examples

```
library(Distance)
library(dplyr)

data("duiker")
duiker_data <- duikers$DaytimeDistances %>%
  dplyr::slice_sample(prop = .3) # sample 30% of rows
truncation <- list(left = 2, right = 15) # Keep only distance between 2-15 m

# fit hazard-rate key models
w3_hr0 <- ds(duiker_data, transect = "point", key = "hr", adjustment = NULL,
             truncation = truncation)
w3_hr1 <- ds(duiker_data, transect = "point", key = "hr", adjustment = "cos",
             order = 2, truncation = truncation)
w3_hr2 <- ds(duiker_data, transect = "point", key = "hr", adjustment = "cos",
             order = c(2, 4), truncation = truncation)
# fit half-normal key models
w3_hn0 <- ds(duiker_data, transect = "point", key = "hn", adjustment = NULL,
             truncation = truncation)
w3_hn1 <- ds(duiker_data, transect = "point", key = "hn", adjustment = "cos",
             order = 2, truncation = truncation)
w3_hn2 <- ds(duiker_data, transect = "point", key = "hn", adjustment = "cos",
```

```
             order = c(2, 4), truncation = truncation)
# fit uniform key models
w3_u0 <- ds(duiker_data, transect = "point", key = "unif", adjustment = NULL,
            truncation = truncation)
w3_u1 <- ds(duiker_data, transect = "point", key = "unif", adjustment = "cos",
            order = 2, truncation = truncation)
w3_u2 <- ds(duiker_data, transect = "point", key = "unif", adjustment = "cos",
            order = c(2, 4), truncation = truncation)

# Create model list
model_list <- list(w3_hn0, w3_hn1, w3_hn2,
                   w3_hr0, w3_hr1, w3_hr2,
                   w3_u0, w3_u1, w3_u2)

# Compute model QAICs
ct_QAIC(list(w3_hr0, w3_hr1, w3_hr2)) # All key functions must be the same
ct_QAIC(list(w3_hn0, w3_hn1, w3_hn2)) # All key functions must be the same

# Compute Chi-squared Goodness-of-fit
ct_chi2_select(list(w3_hn0, w3_hr0, w3_u0)) # All key functions must be different
ct_chi2_select(list(w3_hn2, w3_hr1, w3_u0)) # All key functions must be different

# Two-step model selection
ct_select_model(model_list)
```

`ct_solartime` *Transform time to solar time anchored to sunrise and sunset*

Description

This function converts local time to solar time based on the sunrise and sunset times for a given location. Solar time is a timekeeping system where the day is defined by the position of the sun in the sky, with sunrise marking the start of the day and sunset marking the end.

Usage

```
ct_solartime(
  data = NULL,
  date,
  longitude,
  latitude,
  crs = NULL,
  format,
  time_zone,
  ...
)
```

Arguments

data	A data frame containing the date, longitude, and latitude columns. If NULL, the function will use the date, longitude, and latitude parameters directly. Default is NULL.
date	A vector of date-time values or a column name in data representing the date-time values to be converted to solar time. This can be a character vector or a POSIXlt object.
longitude	A numeric vector or a column name in data representing the longitude of the location(s). Longitude should be in decimal degrees.
latitude	A numeric vector or a column name in data representing the latitude of the location(s). Latitude should be in decimal degrees.
crs	A coordinate reference system (CRS) string or object specifying the current CRS of the input coordinates. If provided, the function will transform the coordinates to longitude and latitude (WGS84). This is useful when the input coordinates are in a projected system (e.g., UTM). Default is NULL.
format	character string giving a date-time format as used by strptime().
time_zone	A numeric vector representing the time zone offset(s) from UTC (in hours). If data is provided, this should match the number of unique locations in the data.
...	Additional arguments passed to as.POSIXlt for date parsing.

Details

The function calculates solar time by first determining the sunrise and sunset times for the given location(s) and date(s). It then uses these times to anchor the solar time calculation. The solar time is computed by transforming the local clock time based on the position of the sun in the sky.

If data is provided, the function will process each unique location in the data and return a tibble with the solar time for each date-time value. If data is NULL, the function will process the date, longitude, and latitude parameters directly.

Value

A tibble with the following columns:

- input: The original date-time values.
- clock: The local clock time.
- solar: The calculated solar time.

If data is provided, the tibble will also include the longitude and latitude columns.

References

Rowcliffe, M. (2023). activity: Animal Activity Statistics. R package version 1.3.4. https://CRAN.R-project.org/package=activity

Examples

```
library(dplyr)
data(penessoulou)

cam_data <- penessoulou %>%
  dplyr::filter(project == "Last") %>%
 dplyr::filter(species == "Erythrocebus patas") %>%
 # Select independent events based on a given threshold
 ct::ct_independence(species_column = species,
                          datetime = datetimes, threshold = 60*5, # 5 minutes
                          format = "%Y-%m-%d %H:%M:%S"
                          ) %>%
 # Transform Time to Solar Time
 ct_solartime(data = ., date = datetime, longitude = longitude, latitude = latitude,
              crs = "EPSG:32631", time_zone = 1)
```

`ct_spatial_coverage` *Estimate species spatial coverage from camera trap detections*

Description

Estimates spatial coverage a species from camera-trap detection data using a kernel density approach. The kernel bandwidth $\hat{\sigma}$ is estimated from the spatial spread of detection sites via **Silverman's reference bandwidth rule** (Silverman 1986).

Usage

```
ct_spatial_coverage(
  data,
  site_column,
  longitude,
  latitude,
  crs = c(4326, NULL),
  study_area = NULL,
  mask = NULL,
  resolution,
  isopleth = 0.95,
  n_boot = 200
)
```

Arguments

`data`	A data frame of species detection records.
`site_column`	Column name of the camera-trap site identifier.
`longitude`	Column name of site longitude (or UTM easting).
`latitude`	Column name of site latitude (or UTM northing).

crs	A vector of length two specifying the coordinate reference systems: c(crs_in, crs_out). • crs_in represents the current CRS of the data (e.g., 4326 for latitude/longitude). • crs_out represents the CRS to transform into (e.g., "EPSG:32631", a UTM EPSG code) for accurate distance calculations. If crs_out is NULL, no transformation is applied. Defaults to c(4326, NULL)
study_area	Optional sf polygon defining the full study extent. If provided, the raster grid is extended to cover the polygon.
mask	Optional sf polygon (or multipolygon) of areas to **exclude** from the coverage estimate (e.g. water bodies, settlements, cliffs). Raster cells inside the mask are set to NA in the output. Note that Euclidean distances are used throughout; the mask filters the final surface but does not reroute distance calculations around barriers.
resolution	Numeric. Side length of one grid cell in the units of the active CRS (metres if projected).
isopleth	Numeric in (0, 1]. Isopleth level for home-range delineation. 0.95 (default) returns the smallest area containing 95 % of the total kernel density - the standard 95 % kernel home range.
n_boot	Integer. Bootstrap resamples for the standard error of $\hat{\sigma}$. Set to 0 to skip (default 200).

Details

The term home range is typically associated with dynamic movement data, such as those recorded by radio-tracking or GPS devices, which provide continuous or near-continuous tracking of an individual animal's movements. Since camera traps are static and only capture presence/absence or activity within their specific locations, the concept of home range might not fully apply.

Method:

Each camera station where the species was detected contributes equally (binary detection). A Gaussian kernel is centred at each detection site and the average surface is computed:

$$\hat{f}(\mathbf{x}) = \frac{1}{n} \sum_{i=1}^{n} \exp\left(-\frac{\|\mathbf{x} - \mathbf{x}_i\|^2}{2\,\hat{\sigma}^2} \right)$$

Bandwidth estimation:

The bandwidth $\hat{\sigma}$ is the **reference bandwidth** (Silverman 1986, eq. 4.14, extended to 2-D):

$$\hat{\sigma} = \sqrt{\hat{\sigma}_x\,\hat{\sigma}_y}\; n^{-1/6}$$

where $\hat{\sigma}_x$ and $\hat{\sigma}_y$ are the standard deviations of the detection-site coordinates and n is the number of detection sites. This is the asymptotically MISE-optimal bandwidth under a bivariate normal reference distribution. It shrinks with more sites and widens when detections are spatially dispersed.

The standard error of $\hat{\sigma}$ is obtained by **nonparametric bootstrap**: sites are resampled with replacement n_boot times and $\hat{\sigma}$ recomputed each time; the SE is the standard deviation of those bootstrap estimates, and the 95 % CI is their 2.5th - 97.5th percentiles.

Home-range isopleth:

Cells are ranked by kernel density (descending). The `isopleth` isopleth retains the smallest set of cells whose cumulative density equals `isopleth` of the total - the standard minimum-volume contour estimator (Worton 1989).

Value

A named list with three elements:

`Coverage raster` A `SpatRaster` (`terra`) containing the kernel density surface, clipped to the `isopleth` isopleth, with masked and out-of-isopleth cells set to `NA`.

`Bandwidth` A named numeric vector: `sigma` (estimated bandwidth in CRS units), `SE` (bootstrap SE; `NA` if `n_boot = 0`), `CI_low` and `CI_high` (95 % bootstrap CI), `n_sites`, and `isopleth`.

`Coverage stats` A one-row tibble: coverage area in km^2, $\hat{\sigma}$ +/- SE, detection-site count, and isopleth level.

References

Silverman, B. W. (1986). *Density Estimation for Statistics and Data Analysis*. Chapman and Hall, London.

Worton, B. J. (1989). Kernel methods for estimating the utilization distribution in home-range studies. *Ecology*, **70**(1), 164-168. doi:10.2307/1938423

Examples

```
library(dplyr)
data(penessoulou)
cam_data <- penessoulou %>%
  dplyr::filter(project == "First") %>%
  dplyr::filter(species == "Erythrocebus patas", number > 0)


spc <- ct_spatial_coverage(
  data = cam_data,
  site_column = camera,
  longitude = longitude,
  latitude = latitude,
  crs = "EPSG:32631",
  resolution = 30 # meter
)

# Plot coverage raster
library(terra)
terra::plot(spc$`Coverage raster`)

## Bandwidth estimate with uncertainty
spc$Bandwidth

## Coverage area summary
spc$`Coverage stats`
```

ct_stack_df *Stack a list of data frame*

Description

The function takes a list of data frames and stacks them into a single data frame. It ensures that all columns from the input data frames in the list are included in the output, filling in missing columns with NA values where necessary.

Usage

```
ct_stack_df(df_list)
```

Arguments

df_list	list of data frame to be stacked

Value

data frame

Examples

```
x <- data.frame(age = 15, fruit = "Apple", weight = 12)
y <- data.frame(age = 51, fruit = "Tomato")
z <- data.frame(age = 26, fruit = "Lemo", weight = 12, height = 45)
alldf <- list(x,y,z)
ct_stack_df(alldf)
```

ct_standardize *Standardize community data matrix*

Description

This function standardizes a given data matrix using different methods such as total sum scaling, max normalization, frequency scaling, standardization, presence-absence transformation, chi-square transformation, Hellinger transformation, log transformation, and others.

Usage

```
ct_standardize(
  data,
  method,
  margin,
  range_global,
  logbase = 2,
  na.rm = FALSE,
  ...
)
```

Arguments

data	A numeric matrix or data frame to be standardized.
method	A character string specifying the standardization method (see details). Available methods are: • "total": Divides each entry by the total sum in the given margin. • "max": Divides each entry by the maximum value in the given margin. • "frequency": Frequency transformation. • "normalize": Normalization by Euclidean norm. • "range": Standardizes by range (min-max scaling). • "rank": Converts values to ranks. • "rrank": Relative rank transformation. • "standardize": Standardization (z-score normalization). • "pa": Presence-absence transformation (binary). • "chi.square": Chi-square standardization. • "hellinger": Hellinger transformation. • "log": Log transformation. • "clr": Centered log-ratio transformation. • "rclr": Robust centered log-ratio transformation. • "alr": Additive log-ratio transformation.
margin	An integer specifying the margin for standardization: • 1: Rows • 2: Columns
range_global	A matrix specifying the range for standardization (optional, used with "range" method).
logbase	The base for logarithmic transformation (default is 2).
na.rm	Logical. If TRUE, missing values (NA) are removed before calculations.
...	Additional arguments passed to transformation functions.

Details

The function provides the following standardization methods for community data:

- `"total"`: Divides by margin total (default `margin = 1`).
- `"max"`: Divides by margin maximum (default `margin = 2`).
- `"frequency"`: Divides by margin total and multiplies by the number of non-zero items, ensuring the average of non-zero entries is one (Oksanen 1983; default `margin = 2`).
- `"normalize"`: Scales data so that the sum of squares along the specified margin equals one (default `margin = 1`).
- `"range"`: Standardizes values into the range `[0,1]` (default `margin = 2`). If all values are constant, they will be transformed to 0.
- `"rank"`, `"rrank"`:
  - `"rank"` replaces abundance values by their increasing ranks, leaving zeros unchanged.
  - `"rrank"` is similar but uses relative ranks with a maximum of 1 (default `margin = 1`).
- `"standardize"`: Scales `x` to zero mean and unit variance (default `margin = 2`).
- `"pa"`: Converts `x` to presence/absence scale (0/1).
- `"chi.square"`: Divides by row sums and the square root of column sums, then adjusts for the square root of the matrix total (Legendre & Gallagher 2001). When used with Euclidean distance, the distances should be similar to Chi-square distances in correspondence analysis (default `margin = 1`).
- `"hellinger"`: Computes the square root of `method = "total"` (Legendre & Gallagher 2001).
- `"log"`: Logarithmic transformation suggested by Anderson et al. (2006):

  $$\log_b(x) + 1$$

  for $x > 0$, where b is the base of the logarithm. Zeros remain unchanged. Higher bases give less weight to quantities and more to presences.
- `"alr"`: Additive log ratio (ALR) transformation (Aitchison 1986). Reduces skewness and compositional bias. Requires positive values; pseudocounts can be added. The transformation is defined as:

  $$alr = [\log(x_1/x_D), ..., \log(x_{D-1}/x_D)]$$

  where the denominator sample x_D can be chosen arbitrarily.
- `"clr"`: Centered log ratio (CLR) transformation (Aitchison 1986). Common in microbial ecology (Gloor et al. 2017). Only supports positive data; pseudocounts can be used to handle zeros. The transformation is defined as:

  $$clr = \log(x/g(x)) = \log x - \log g(x)$$

  where x is a single value, and $g(x)$ is the geometric mean of x.
- `"rclr"`: Robust CLR transformation. Unlike CLR, this method allows zeros without requiring pseudocounts. It divides values by the geometric mean of observed (non-zero) features, preserving zeros (Martino et al. 2019). The transformation is defined as:

  $$rclr = \log(x/g(x > 0))$$

  where x is a single value, and $g(x > 0)$ is the geometric mean of sample-wide values x that are positive ($x > 0$).

Standardization, as contrasted to transformation, means that the entries are transformed relative to other entries.

All methods have a default margin. `margin=1` means rows (sites in a normal data set) and `margin=2` means columns (species in a normal data set).

Command `wisconsin` is a shortcut to common Wisconsin double standardization where species (`margin=2`) are first standardized by maxima (`max`) and then sites (`margin=1`) by site totals (`tot`).

Most standardization methods will give nonsense results with negative data entries that normally should not occur in the community data. If there are empty sites or species (or constant with `method = "range"`), many standardization will change these into `NaN`.

Function `decobackstand` can be used to transform standardized data back to original. This is not possible for all standardization and may not be implemented to all cases where it would be possible. There are round-off errors and back-transformation is not exact, and it is wise not to overwrite the original data. With `zap=TRUE` original zeros should be exact.

Value

A standardized matrix or tibble with attributes specifying the transformation applied.

Note

This function is adapted from the `decostand` function in the `vegan` R package, with modifications to improved handling.

References

Aitchison, J. The Statistical Analysis of Compositional Data (1986). London, UK: Chapman & Hall.

Anderson, M.J., Ellingsen, K.E. & McArdle, B.H. (2006) Multivariate dispersion as a measure of beta diversity. *Ecology Letters* **9**, 683–693.

Egozcue, J.J., Pawlowsky-Glahn, V., Mateu-Figueras, G., Barcel'o-Vidal, C. (2003) Isometric logratio transformations for compositional data analysis. *Mathematical Geology* **35**, 279–300.

Gloor, G.B., Macklaim, J.M., Pawlowsky-Glahn, V. & Egozcue, J.J. (2017) Microbiome Datasets Are Compositional: And This Is Not Optional. *Frontiers in Microbiology* **8**, 2224.

Legendre, P. & Gallagher, E.D. (2001) Ecologically meaningful transformations for ordination of species data. *Oecologia* **129**, 271–280.

Martino, C., Morton, J.T., Marotz, C.A., Thompson, L.R., Tripathi, A., Knight, R. & Zengler, K. (2019) A novel sparse compositional technique reveals microbial perturbations. *mSystems* **4**, 1.

Oksanen, J. (1983) Ordination of boreal heath-like vegetation with principal component analysis, correspondence analysis and multidimensional scaling. *Vegetatio* **52**, 181–189.

Examples

```
# Example usage with sample data
library(dplyr)
data(penessoulou)

cam_data <- penessoulou %>%
```

```
  dplyr::filter(project == "Last")
cam_data <- cam_data %>%
  ct_to_community(site_column = camera, species_column = species,
                  size_column = number, values_fill = 0)

standardized_data <- ct_standardize(data = cam_data[, 2:11], method = "total")
standardized_data
```

`ct_summarise_camtrap_activity` *Create activity summary statistics*

Description

Calculates summary statistics for camera trap activity periods.

Usage

```
ct_summarise_camtrap_activity(
  data,
  deployment_column,
  datetime_column,
  threshold = 5,
  time_unit = "days",
  format = NULL
)
```

Arguments

`data`	A data frame containing the datetime column.
`deployment_column`	Character. Column name for deployment identifiers.
`datetime_column`	The datetime column.
`threshold`	A numeric value indicating the minimum gap to be considered a break (default is 10).
`time_unit`	The unit for the threshold. Supported values include "secs", "mins", "hours", "days", and "weeks".
`format`	Optional. A character string specifying the datetime format, passed to `as.POSIXlt`.

Value

A tibble with activity summary statistics for each deployment.

Examples

```
# Get activity summary
library(dplyr)
data(penessoulou)
camtrap_data <- penessoulou %>%
  filter(project == "Last")

ct_summarise_camtrap_activity(data = camtrap_data,
                              deployment_column = "camera",
                              datetime_column = datetimes,
                              threshold = 15,
                              time_unit = "days")
```

---

ct_survey_design *Create a survey design for camera trap deployment*

Description

This function designs a survey for deploying camera traps within a specified study area. It supports various sampling methods, including random, regular, and clustered sampling, with options for minimum distance constraints and padding around the study area.

Usage

```
ct_survey_design(
  study_area,
  method = "random",
  total_site,
  total_cluster,
  type_in = "random",
  min_distance = NULL,
  distance = NULL,
  padding = 10,
  nest_padding = 0,
  set_seed = NULL,
  verbose = TRUE
)
```

Arguments

study_area	An sf polygon representing the area where the survey will be conducted.
method	A character string specifying the sampling method. Options include: • "random": Randomly distributes camera trap sites within the study area. • "regular": Creates a regularly spaced grid of sites. • "regular_cluster": Generates regularly spaced clusters within which sites are sampled..

- "random_cluster": Creates randomly clusters within which sites are sampled.
- "mask": Uses existing features in the `study_area` object to define sampling areas, with user-defined site allocation.

`total_site` An integer specifying the number of sites to be sampled per cluster (for "regular_cluster" and "random_cluster") or the total number of sites (for "random" and "regular" methods). For the "mask" method, this can be a single value (applied to all features) or a vector specifying the number of sites per feature in `study_area`.

`total_cluster` An integer defining the number of clusters (required for "random_cluster").

`type_in` A character string indicating the within-cluster sampling type. Options:

- "regular": Places sites in a structured grid within each cluster or feature (for "mask" method).
- "random": Distributes sites randomly within each cluster or feature (for "mask" method).

`min_distance` A numeric value specifying the minimum allowed distance (in meter) between sampled sites (applied only for the random methods).

`distance` A numeric vector specifying the distance (x and y spacing in meter) between grid cells for regular sampling methods. If a single value is provided, it is used for both dimensions.

`padding` A numeric value defining the buffer distance to exclude areas near the edge of the study area.

`nest_padding` A numeric value defining an additional buffer applied within each cluster or mask feature to avoid placing sites near the edges of those units.

`set_seed` An optional integer for setting the random seed to ensure reproducibility.

`verbose` A logical indicating whether to display warnings and messages (default: `TRUE`).

Value

An `sf` object containing the sampled points within the study area.

Note

The function ensures that the study area has a projected coordinate reference system (CRS) before proceeding. If a geographic CRS is detected, an error is raised.

Examples

```
library(ggplot2)
# Load example dataset
data("pendjari")

# Transform study area to a projected coordinate system
pendjari_trans <- pendjari %>%
  sf::st_transform(crs = "EPSG:32631")
```

```
# Random sampling method with 15 sites, ensuring a minimum distance of 5000 meters between sites
random_sdes <- ct_survey_design(study_area = pendjari_trans, method = "random", verbose = TRUE,
                                total_site = 15, min_distance = 5000, padding = 2000,
                                set_seed = 123)

# Regular sampling method using a grid with cell sizes of 4000m x 6000m
regular_sdes <- ct_survey_design(study_area = pendjari_trans, method = "regular", verbose = TRUE,
                               distance = c(4000, 6000), padding = 2500, set_seed = 123)

# Random-cluster sampling: 8 clusters, each containing 5 sites, ensuring a
# minimum site distance of 2000 meters
rand_c_sdes <- ct_survey_design(study_area = pendjari_trans,
                                method = "random_cluster", verbose = TRUE,
                                total_cluster = 8, total_site = 5,
                                distance = c(7000, 3000), min_distance = 2000,
                                padding = 2000, nest_padding = 500, set_seed = 123)

# Random-cluster sampling with regularly distributed sites: 22 clusters, each
# with 8 regularly spaced sites
rand_c_reg_sdes <- ct_survey_design(study_area = pendjari_trans,
                                    method = "random_cluster", verbose = TRUE,
                                total_cluster = 22, total_site = 8, type_in = "regular",
                                    distance = c(6000, 3000),
                                    padding = 1000, nest_padding = 0, set_seed = 123)

# Regular-cluster sampling: Grid with 3 sites per cluster, ensuring a minimum
# distance of 2000 meters between sites
reg_c_sdes <- ct_survey_design(study_area = pendjari_trans,
                               method = "regular_cluster", verbose = TRUE,
                               total_site = 3, distance = c(7000, 6000),
                               min_distance = 2000, padding = 2000, set_seed = 123)

# Regular-cluster sampling with regularly distributed sites within clusters
reg_c_reg_sdes <- ct_survey_design(study_area = pendjari_trans,
                                   method = "regular_cluster", verbose = TRUE,
                             total_site = 3, distance = c(7000, 6000), type_in = "regular",
                                   padding = 1000, set_seed = 123)
# A plot with
ggplot()+
  geom_sf(data = pendjari_trans)+
  geom_sf(data = reg_c_reg_sdes)

# Mask-based sampling: Sites are sampled within existing features of the study area
mask_sdes <- ct_survey_design(study_area = pendjari_trans,
                              method = "mask", verbose = TRUE,
                              total_site = 13, distance = c(7000, 6000),
                              min_distance = 2000, nest_padding = 2000, set_seed = 123)

# Mask-based sampling with regularly spaced sites per feature
mask_regular_sdes <- ct_survey_design(study_area = pendjari_trans,
                                    method = "mask", verbose = TRUE, type_in = "regular",
                                      total_site = c(8, 2, 13), distance = c(7000, 6000),
                                  min_distance = 2000, nest_padding = 1000, set_seed = 123)
```

`ct_temporal_shift` *Calculate the temporal shift of one species' activity over two periods*

Description

Estimates and analyzes the temporal shift in the activity of a species between two time periods using kernel density estimation. The activity distributions are compared and the magnitude, direction, and (optionally) a bootstrap confidence interval for the shift size are returned.

Usage

```
ct_temporal_shift(
  first_period,
  second_period,
  convert_time = FALSE,
  xscale = 24,
  xcenter = c("noon", "midnight"),
  n_grid = 128,
  kmax = 3,
  adjust = 1,
  width_at = 1/2,
  format = "%H:%M:%S",
  time_zone,
  n_boot = 999,
  boot_ci = 0.95,
  plot = TRUE,
  linestyle_1 = list(),
  linestyle_2 = list(),
  posestyle_1 = list(),
  posestyle_2 = list(),
  period_names = c("First period", "Second period"),
  legend_title = "Period",
  ...
)
```

Arguments

`first_period`	A numeric vector of activity times in radians for the first period.
`second_period`	A numeric vector of activity times in radians for the second period.
`convert_time`	Logical. If `TRUE`, converts times to radians before analysis.
`xscale`	A numeric value to scale the x-axis. Default is 24 for representing time in hours.

xcenter	A string indicating the center of the x-axis. Options are "noon" (default) or "midnight".
n_grid	An integer specifying the number of grid points for density estimation. Default is 128.
kmax	An integer indicating the maximum number of modes allowed in the activity pattern. Default is 3.
adjust	A numeric value to adjust the bandwidth of the kernel density estimation. Default is 1.
width_at	Numeric. Fraction of peak density at which the activity window width is measured (default 0.5, i.e. half-maximum).
format	Character. Input time format (default "%H:%M:%S"). Only used when convert_time = TRUE.
time_zone	Character. Time zone for conversion. Required when convert_time = TRUE.
n_boot	Integer. Number of bootstrap resamples used to compute a confidence interval for the shift size. Set to 0 to skip bootstrapping (default 999).
boot_ci	Numeric. Confidence level for the bootstrap CI, strictly between 0 and 1 (default 0.95).
plot	Logical. If TRUE, prints and returns a ggplot comparing the activity distributions of the two periods.
linestyle_1	List. Line style for the first period's density curve. Accepts: linetype, linewidth, color.
linestyle_2	List. Line style for the second period's density curve. Accepts: linetype, linewidth, color.
posestyle_1	List. Marker style for the first period's activity-range indicator. Accepts: shape, size, color, alpha.
posestyle_2	List. Marker style for the second period's activity-range indicator. Accepts: shape, size, color, alpha.
period_names	Character vector of length 2 giving the legend labels for the first and second periods (default c("First period", "Second period")). For example, c("Dry", "Rainy").
legend_title	Character. Title shown above the period legend (default "Period").
...	Additional arguments (currently unused).

Value

When plot = FALSE: a tibble. When plot = TRUE: a list whose first element is the tibble and whose $plot element is a ggplot2 object. The tibble contains:

`First period range` Start and end of the active window for the first period.

`Second period range` Start and end of the active window for the second period.

`Shift size (in hour)` Absolute difference in activity-window duration between periods.

`Displacement (in hour)` Signed shift of the activity window along the day, measured at its midpoint: positive means the second period is active later, negative earlier. Unlike `Shift size` (a duration change), this captures a pure time shift, so a window that slides without changing length has `Shift size` near 0 but a non-zero `Displacement`.

`Shift CI lower (XX%)`/`Shift CI upper (XX%)` Bootstrap CI bounds (only when `n_boot > 0`).

`Move` Direction/type of shift: `"Forward"`, `"Backward"`, `"Enlarged"`, `"Contracted"`, `"Constant"`, `"Forward Edge"`, `"Backward Edge"`, `"Contracted Edge (Max)"`, `"Contracted Edge (Min)"`, or `"Undefined"`.

Examples

```
library(ggplot2)

# Using radians as input
first_period  <- c(1.3, 2.3, 2.5, 5.2, 6.1, 2.3)
second_period <- c(1.8, 2.2, 2.5)
result <- ct_temporal_shift(
  first_period, second_period, plot = TRUE, xcenter = "noon", n_boot = 100,
  linestyle_1 = list(color = "gray10", linetype = 1, linewidth = 1),
  posestyle_1 = list(color = "gray10"),

  linestyle_2 = list(color = "#b70000", linetype = 5, linewidth = 0.5),
  posestyle_2 = list(color = "#b70000")
)

result

# Customize the returned plot
result$plot + theme(legend.position = "top")

# Using time strings as input
first_period  <- c("12:03:05", "13:10:09", "14:08:10", "14:18:30", "18:22:11")
second_period <- c("13:00:20", "14:20:10", "15:55:20", "16:03:01", "16:47:00")
result <- ct_temporal_shift(
  first_period, second_period,
  convert_time = TRUE, format = "%H:%M:%S", time_zone = "UTC"
)
```

---

ct_to_community *Convert data to a community matrix*

Description

The function transforms input data into a community matrix where rows represent sites, columns represent species, and values indicate the count or abundance of each species at each site.

Usage

```
ct_to_community(
  data,
  site_column,
  species_column,
```

```
  size_column,
  values_fill = NULL
)
```

Arguments

data	A data frame containing the input data.
site_column	The column in the data frame representing site identifiers. Can be specified as a string or unquoted column name.
species_column	The column in the data frame representing species identifiers. Can be specified as a string or unquoted column name.
size_column	(Optional) The column representing the size or abundance of the species at each site. If not provided, counts of species occurrences are calculated.
values_fill	(Optional) A value to fill missing cells in the resulting community matrix. Defaults to NULL.

Details

The function creates a site-by-species matrix suitable for ecological analysis. If size_column is not provided, the function counts occurrences of each species per site. If size_column is provided, its values are used as the measure for species abundance.

Value

A tibble where rows represent sites, columns represent species, and values represent the count or abundance of each species.

Examples

```
# Example data
df <- dplyr::tibble(
  site = c("A", "A", "B", "B", "C"),
  species = c("sp1", "sp2", "sp1", "sp3", "sp2"),
  abundance = c(5, 2, 3, 1, 4)
)

# Convert to community matrix with counts
ct_to_community(df, site_column = site, species_column = species)

# Convert to community matrix with abundance
ct_to_community(df, site_column = site, species_column = species, size_column = abundance)

# Fill missing cells with 0
ct_to_community(df, site_column = site, species_column = species, values_fill = 0)
```

`ct_to_occupancy` *Convert camera trap data to occupancy format*

Description

This function transforms camera trap detection data into an occupancy format suitable for analysis. It aggregates detections into user-defined time windows and optionally converts counts into presence-absence (0/1) data.

Usage

```
ct_to_occupancy(
  data,
  date_column,
  format = "%Y-%m-%d",
  site_column,
  species_column,
  size_column,
  by_day = 7,
  presence_absence = TRUE
)
```

Arguments

`data`	A data frame containing camera trap detection records.
`date_column`	The name of the column containing detection dates.
`format`	a character string. If not specified when converting from a character representation, it will try c("%Y-%m-%d", "%Y/%m/%d") one by one, and give an error if none works. Otherwise, the processing is via `strptime()` whose help page describes available conversion specifications.
`site_column`	The name of the column identifying sampling sites.
`species_column`	The name of the column containing species names. Can be NULL if species information is not needed.
`size_column`	The name of the column representing detection counts.
`by_day`	An integer specifying the number of days per time window (default: 7).
`presence_absence`	Logical. If `TRUE`, converts counts to presence-absence data (1 = detected, 0 = not detected). Default is `TRUE`.

Value

A wide-format data frame where rows represent sites (and optionally species), and columns represent detection windows. Values indicate either detection counts or presence-absence (0/1).

See Also

ct_to_community()

Examples

```
data <- data.frame(
  date = c("01-01-2023", "03-01-2023", "10-01-2023", "15-01-2023"),
  site = c("A", "A", "B", "B"),
  species = c("Tiger", "Tiger", "Deer", "Deer"),
  count = c(1, 2, 3, 1)
)

occupancy_data <- ct_to_occupancy(
  data,
  date_column = date,
  site_column = site,
  species_column = species,
  size_column = count,
  by_day = 7,
  presence_absence = TRUE
)

occupancy_data
```

---

ct_to_radian *Convert time to radians*

Description

This function converts time values into radians, which is often used in circular statistics and time-of-day analyses.

Usage

```
ct_to_radian(data, times, format = "%H:%M:%S", time_zone = "UTC")
```

Arguments

data	A data frame containing a column with time values. Optional. If NULL, the times parameter is treated as a standalone vector.
times	A column name in the data or a vector of time values to be converted. Time values should be in a format recognized by as.POSIXct().
format	A string specifying the format of the time values, using the standard POSIX formatting syntax. Default is "%H:%M:%S".
time_zone	A string specifying the time zone for interpreting the time values. Default is "UTC".

Details

This function converts time values into radians based on a 24-hour clock:

- A full day (24 hours) corresponds to 2π radians.
- The fractional time of the day is calculated as:

$$\text{Fraction of the day} = \frac{\text{hours}}{24} + \frac{\text{minutes}}{1440} + \frac{\text{seconds}}{86400}$$

For example, for a time of 23 hours, 6 minutes, and 12 seconds:

$$\text{Fraction of the day} = \frac{23}{24} + \frac{6}{1440} + \frac{12}{86400}$$

To convert this fraction into radians:

$$\text{Radians} = \text{Fraction of the day} \times 2\pi$$

Value

If `data` is provided, the function returns the input data frame with an additional column named `time_radian`. If `data` is not provided, the function returns a numeric vector of time values converted to radians.

Examples

```
# Convert a standalone vector of time values
times <- c("00:00:00", "06:00:00", "12:00:00", "18:00:00")
ct_to_radian(times = times, format = "%H:%M:%S")

# Convert a column of time values in a data frame
data <- data.frame(times = c("00:00:00", "06:00:00", "12:00:00", "18:00:00"))
ct_to_radian(data = data, times = times, format = "%H:%M:%S")
```

---

ct_to_time *Convert radian to time*

Description

This function converts an angle in radians (representing a fraction of a full circle) into a time in the format '%H:%M:%S'. The conversion assumes that the radian value represents a fraction of a 24-hour day (i.e., 0 radians is midnight and 2π radians is the next midnight).

Usage

```
ct_to_time(radian)
```

Arguments

radian	A numeric value or vector representing an angle in radians. The value must lie within the range $[0, 2\pi]$, where 0 corresponds to midnight (00:00:00) and 2π corresponds to the next midnight (24:00:00).

Value

A character string representing the time in the format '%H:%M:%S'.

See Also

ct_to_radian()

Examples

```
# Convert 1.6 radians to time
ct_to_time(1.6)
# Output: "06:06:42"
```

---

ct_traprate_data *Prepare data for trap rate estimation*

Description

Calculates observation counts and associated monitoring effort per deployment to support trap rate estimation.

Usage

```
ct_traprate_data(
  observation_data,
  use_deployment = TRUE,
  deployment_data = NULL,
  deployment_column,
  start_column = NULL,
  end_column = NULL,
  datetime_column = NULL,
  format = NULL,
  time_zone = "",
  time_unit = "days"
)
```

Arguments

observation_data	A data frame of detection records (e.g., camera trap images or events).
use_deployment	Logical. If TRUE (default), effort is derived from deployment data. If FALSE, effort is estimated from observation timestamps.
deployment_data	Optional. A data frame of deployment metadata; required if use_deployment = TRUE.
deployment_column	The column name (unquoted or as a string) that uniquely identifies the deployment (e.g., camera ID).
start_column	Optional. Start datetime column in the deployment data. Required if use_deployment = TRUE.
end_column	Optional. End datetime column in the deployment data. Required if use_deployment = TRUE.
datetime_column	Optional. The datetime column in observation_data; used if use_deployment = FALSE.
format	A character string specifying the format of the datetime columns. If NULL, defaults to ISO 8601 format.
time_zone	The time zone used to parse datetime values. Default is "" (i.e., system time zone).
time_unit	Unit of time to compute effort and trap rate. One of "secs", "mins", "hours", "days", or "weeks". Default is "days".

Value

A data frame with columns:

- deployment_column: Deployment identifier
- n: Number of observations per deployment
- effort: Monitoring duration
- effort_unit: Time unit used for effort

See Also

ct_get_effort()

Examples

```
data("ctdp")
deployments <- ctdp$data$deployments
observations <- ctdp$data$observations %>%
                 dplyr::filter(scientificName == "Vulpes vulpes")

ct_traprate_data(observation_data = observations,
                 deployment_data = deployments,
```

```
use_deployment = TRUE,
deployment_column = deploymentID,
datetime_column = timestamp,
start = start, end = 'end'
)
```

`ct_traprate_estimate` *Estimate trap rate*

Description

Computes the estimated trap rate and uncertainty using bootstrapping, with optional support for stratified estimation based on area-weighted averaging.

Usage

```
ct_traprate_estimate(data, strata = NULL, n_bootstrap = 1000)
```

Arguments

`data`	A data frame as returned by `ct_traprate_data()` with columns `n` and `effort`.
`strata`	Optional. A data frame defining strata, with columns `stratumID` and `area`.
`n_bootstrap`	Number of bootstrap replicates to estimate uncertainty. Default is 1000.

Value

A data frame with the following columns:

- `estimate`: Trap rate estimate (e.g., detections per day)
- `se`: Standard error of the estimate
- `cv`: Coefficient of variation
- `lower_ci`: Lower bound of the 95\
- `upper_ci`: Upper bound of the 95\
- `n`: Number of deployments or observation used
- `unit`: Effort unit

See Also

`ct_get_effort()`, `ct_traprate_data()`

Examples

```
data("ctdp")
deployments <- ctdp$data$deployments
observations <- ctdp$data$observations %>%
                  dplyr::filter(scientificName == "Vulpes vulpes")

trap_rate <- ct_traprate_data(observation_data = observations,
                              deployment_data = deployments,
                              use_deployment = FALSE,
                              deployment_column = deploymentID,
                              datetime_column = timestamp,
                              start = start, end = 'end'
)

ct_traprate_estimate(data = trap_rate, n_bootstrap = 1000)
```

---

ctdp *Camera trap data package example*

Description

Data and metadata from an example study exported from the Agouti camera trap data management platform in camtrap-DP format. Metadata includes study name, authors, location and other details. Data is held in element data, itself a list holding dataframes deployments, media and observations. See https://tdwg.github.io/camtrap-dp for details.

Usage

```
ctdp
```

Format

A list holding study data and metadata.

Author(s)

Marcus Rowcliffe

`duikers` *Maxwell's duiker camera-trap distance & video-start data*

Description

The `duikers` dataset is a **named list** of three tibbles derived from Maxwell's duiker (*Philantomba maxwellii*) camera trap and distance sampling data collected in Taï National Park, Côte d'Ivoire (2014), and archived as the Dryad dataset *Distance sampling with camera traps* (Howe et al., 2018)

Usage

```
duikers
```

Format

A named list with these tibbles:

DaytimeDistances: A tibble of all Maxwell's duiker distance observations (including non peak periods) recorded at camera stations during daytime deployments. It has the following columns:

- `distance`: the midpoint (m) of the assigned distance interval between animal and camera.
- `Sample.Label`: camera station identifier.
- `Effort`: number of active 2 second time steps the camera operated (i.e. temporal effort).
- `Region.Label`: stratum name (only a single stratum in this dataset).
- `Area`: study area size (km^2; in this dataset, 40.4).
- `multiplier`: spatial effort: fraction of a full circle covered, based on the camera's 42 deg field of view (42/360).
- `utm.e`: UTM easting (metres) of the camera station.
- `utm.n`: UTM northing (metres) of the camera station.
- `object`: a unique identifier for each observation

PeakDistances: A tibble with the **same column structure** as **DaytimeDistances**, but includes **only** observations during the species' peak activity periods (no dawn or late day records).

VideoStartTimesFullDays: A tibble of camera-trigger times for duiker videos that were recorded on **full day deployments** (i.e. days without researcher visits). Columns include:

- `order`: sequential order of video events at each station/day.
- `folder`: local folder (e.g. `"A1"`) for grouping videos by station or session.
- `vid.no`: unique video identifier number.
- `ek.no`: event key number (original trigger event id).
- `easting`: UTM easting (metres) for the video event.
- `northing`: UTM northing (metres) for the video event.
- `month`: calendar month (1-12) of the video event.
- `day`: day of the month (1-31).

- `hour`: hour (24h clock) when the video started.
- `minute`: minute of that hour when the video started.
- `date`: Date of the record
- `time`: Time of the record
- `datetime`: date pasted with time

References

Howe, E. J., Buckland, S. T., Després-Einspenner, M. L., Kühl, H. S., & Buckland, S. T. (2018). Data from: Distance sampling with camera traps. doi:10.5061/dryad.b4c70

`lama` *Camera trap survey of the Lama Classified Forest*

Description

Detection-level camera-trap records and camera deployment intervals from a multispecies survey of terrestrial mammals in the Lama Classified Forest, a semi-deciduous forest remnant in the Dahomey Gap, southern Benin. Twenty-three camera traps operated from June to December 2024 (about 4,256 trap-days), recording 18 mammal taxa. The survey was designed for camera-trap distance sampling, so each detection carries a radial `distance` and detection `angle` alongside station coordinates and anthropogenic-gradient covariates.

Usage

```
lama
```

Format

A list with two tibbles that share the `camera` column:

`observation` One row per recorded image (7,963 rows, 11 columns): `camera` (station identifier), `species` (scientific name), `datetime` (detection date-time, UTC), `distance` (radial distance to the animal, m), `angle` (detection angle, degrees), `size` (group size), `x`/`y` (station coordinates, UTM zone 31N, EPSG:32631), `region` (survey stratum), `d_villages` and `d_track` (distance to the nearest village and track, m).

`deployment` One row per camera (23 rows, 11 columns): `camera`, `start` and `end` (install and pull-out date-times, UTC), `x`/`y`, `fov` (field of view, degrees), `radius` (maximum detection distance, m), `height` (camera height, m), `region`, `d_villages`, `d_track`.

Source

Adounké, G.R.M., Lecompte, E., Gandaho, S.M., Toyi, M.S., Azihou, A.F., Hugueny, B., Sinsin, B.A., Gaubert, P., & Djagoun, C.A.M.S. (submitted). Camera-trap distance sampling reveals density patterns and anthropogenic drivers of terrestrial mammals in a remnant forest refuge in West Africa. *Ecology and Evolution*.

Examples

```
data(lama)
str(lama, max.level = 2)
sort(table(lama$observation$species), decreasing = TRUE)
```

---

pendjari *Pendjari national park and surrounding areas*

Description

A dataset containing spatial boundaries of Pendjari National Park and its surrounding hunting zones in Benin.

Usage

```
pendjari
```

Format

A tibble with 3 rows and 2 columns:

- `NOM`: The name of the protected area or hunting zone.
- `geometry`: The spatial geometry of the area, stored in decimal degrees (EPSG:4326).

Examples

```
# Load the dataset
data("pendjari")

# Plot the data
library(sf)
plot(pendjari, main = "Pendjari National Park and Surrounding Areas")
legend("topright", legend = pendjari$NAME, fill = c("gray10", "gray50", "gray90"))
```

---

penessoulou *Camera-trap detections from the Penessoulou Classified Forest*

Description

Camera-trap image records in the Penessoulou Classified Forest, Benin. One row per recorded image in 2024.

Usage

```
penessoulou
```

Format

A tibble with 4724 rows and 12 columns, including:

`project` Survey/project name.

`image_name` Source image file name.

`camera` Camera station identifier.

`make`, `model` Camera mak and mode

`species` Recorded species name.

`number` Number of individuals in the record.

`dates`, `times` Date and time parts of the record.

`datetimes` Record date-time as a `"YYYY-MM-DD HH:MM:SS"` string.

`longitude`, `latitude` Station coordinates in decimal degrees.

Source

Ayegnon, D.T.D., Nobimè, G., Azihou, F., Houinato, M., & Djagoun, C.A.M.S. (2026). Seasonal variation in the diversity, abundance, and spatial distribution of terrestrial mammals in the Pénéssoulou Classified Forest. *Wild*, 3(1), 2. doi:10.3390/wild3010002

Examples

```
head(penessoulou)
```

`rest_detection` *Simulated camera-trap detections for the REST / RAD-REST workflow*

Description

A small simulated dataset illustrating the inputs needed by `ct_fit_rest()` and the `ct_rest_*` preparation helpers. It contains detections of a focal species (`"Red duiker"`) recorded at 8 stations over roughly one month, together with two background species.

Usage

```
rest_detection
```

Format

A tibble with one row per video (detection) and columns:

- `Station`: Camera station ID.
- `Species`: Detected species name.
- `DateTime`: Capture time as a `"YYYY-MM-DD HH:MM:SS"` string.
- `y`: Number of passes through the focal area in that video (`NA` for background species).
- `Stay`: Staying time within the focal area in seconds (`NA` when the animal did not enter).
- `Cens`: Right-censoring flag for `Stay` (1 = censored, 0 = observed).

See Also

rest_station, ct_fit_rest()

Examples

```
data(rest_detection)
head(rest_detection)
```

---

rest_station *Camera-station table for the REST / RAD-REST example*

Description

Per-station information to accompany rest_detection, with one row per station and a habitat covariate that can be used in density_formula or stay_formula.

Usage

```
rest_station
```

Format

A tibble with one row per station and columns:

- Station: Camera station ID.
- Habitat: Habitat type at the station ("forest" or "savanna").

See Also

rest_detection, ct_fit_rest()

Examples

```
data(rest_station)
rest_station
```

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