Package: cdmetapopR (via r-universe)

July 10, 2026

Title Utility Functions for 'CDMetaPOP'

Version 1.0.0

Description Provides a set of helper functions to launch, analyze, and visualize the output files of 'CDMetaPOP' <`https://computationalecologylab.github.io/cdmetapop_web/`>.

Imports ggplot2, tidyr, tidyselect, dplyr, adegenet, gdistance, graph4lg, poppr, shiny, shinyBS, terra

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Encoding UTF-8

RoxygenNote 7.3.3

Suggests knitr, pkgload, rmarkdown, tidyverse, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

Language en-US

NeedsCompilation no

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Config/pak/sysreqs libabsl-dev cmake libgdal-dev gdal-bin libgeos-dev libglpk-dev make libicu-dev libuv1-dev libxml2-dev libssl-dev libproj-dev libsqlite3-dev libudunits2-dev zlib1g-dev

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

Date/Publication 2026-07-09 09:10:14 UTC

RemoteUrl https://github.com/cran/cdmetapopR

RemoteRef HEAD

RemoteSha f8488854a0bbf42c419c35ad934fcf7cac006097

Contents

`age_structure_proportions` *Determine the proportions of the age structure of the population*

Description

This function summarizes the proportions of the age structure in the simulated population. It is calculated counting the values in the column 'age' of the chosen 'ind' generation.

Usage

```
age_structure_proportions(
  path = system.file("extdata", "Example_dat", package = "cdmetapopR"),
  runs = 1,
  gen = 49,
  species = 0
)
```

Arguments

`path`	path to the simulation folder
`runs`	integer referring to the number of montecarlo simulations output files to examine. It refers to the mcruns option in the RunVars CDMetaPOP input file. Right now it defaults to 1, which would be only one montecarlo run.
`gen`	Simulation run time (generation or year). Refers to runtime in the RunVars of CDMetaPOP input file. Currently defaults to 49.
`species`	If the simulation includes more species... The code for this needs to be adjusted

Value

a dataframe with a column for each montecarlo run (MC) with the proportion of the population for each given age (in rows) and the last column with the average value across all montecarlo runs at any given age.

Examples

```
mypath <- system.file("extdata", "Example_dat", package = "cdmetapopR")
age_structure_proportions(path = paste0(mypath, "/"), runs = 1, gen = 9)
```

`allele_frequencies_ind` *Plot Individual-Level Allele Frequencies*

Description

Calculates allele frequencies from `L#A#` genotype columns in CDMetaPOP `ind##.csv` or `ind##_Sample.csv` files.

Usage

```
allele_frequencies_ind(
  path,
  year = 0,
  run = 0,
  batch = 0,
  mc = 0,
  species = 0,
  file_type = "ind",
  patches = "all",
  loci = NULL,
  group_col = "PatchID",
  jitter = TRUE
)
```

Arguments

`path`	A dataframe, file path, vector of file paths, run directory, or top-level output directory containing individual files.
`year`	Integer. Year/generation to plot for one-year plots. Defaults to `0`.
`run`	Integer. Run index used when `path` is a directory. Defaults to `0`.
`batch`	Integer. Batch index used when `path` is a directory. Defaults to `0`.
`mc`	Integer. Monte Carlo index used when `path` is a directory. Defaults to `0`.
`species`	Integer. Species index used when `path` is a directory. Defaults to `0`.

`file_type`	Character. Which individual file type to read. Use `"ind"` for `ind##.csv` files or `"ind_Sample"` for `ind##_Sample.csv` files. Defaults to `"ind"`.
`patches`	Patch IDs to include. Use `"all"` to include all patches, a single patch ID such as `5`, or a vector/range such as `c(1, 3, 8)` or `1:20`. Defaults to `"all"`.
`loci`	Optional vector of loci to include, such as `c("L0", "L1")` or `c(0, 1)`. Defaults to all detected loci.
`group_col`	Column used for grouping frequencies. Defaults to `"PatchID"`.
`jitter`	Logical. If `TRUE`, overlay jittered group-level points on the boxplots. Defaults to `TRUE`.

Value

A ggplot object with frequency data in `plot$data`.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")
allele_frequencies_ind(ex_dir, year = 9)
allele_frequencies_ind(ex_dir, year = 9, jitter = FALSE)
```

`cdmetapop_to_gene` *Convert CDMetaPOP data to GENEPOP or GENALEX format*

Description

This function reads a `CDMetaPOP` CSV file, processes the genetic loci, and converts the data into `GENEPOP` or `GENALEX` formats.

Usage

```
cdmetapop_to_gene(path, format = "genepop", output_dir = tempdir())
```

Arguments

`path`	Character string; the file path to the `CDMetaPOP` CSV file.
`format`	A character string indicating the desired output format: "genepop" or "genalex". Genepop is default.
`output_dir`	Character string; the directory where output files will be written. Defaults to tempdir().

Value

The function writes the GENEPOP or GENALEX formatted data to the specified output directory.

Examples

```
path <- system.file("extdata", "Example_dat",
  "run0batch0mc0species0", "ind9.csv",
  package = "cdmetapopR")
cdmetapop_to_gene(path = path, format = "genepop")
cdmetapop_to_gene(path = path, format = "genalex")
```

`create_cdmat` *Create cost distance matrix for CDMetaPOP simulation*

Description

Takes input coordinates and produces a symmetrical cost distance matrix with options for Euclidean distance, equal distance, or least cost paths based on a provided resistance surface

Usage

```
create_cdmat(
  coords,
  method = c("euclidean", "equal", "lcp"),
  resistance = NULL
)
```

Arguments

`coords`	A set of spatial coordinates in the form of a 2-column data frame or matrix
`method`	Method for creating the cost distance matrix, must be "euclidean", "equal", or "lcp"
`resistance`	Raster object representing resistance surface for generating cost distance matrix

Details

Hello

Value

An NxN matrix of cost distances among patch locations

Examples

```
x <- c(1,2,3,4,5,6)
y <- c(1,2,3,4,5,6)
test <- data.frame(x=x, y=y)
create_cdmat(coords=test)

x <- runif(6, min=0, max=10)
y <- runif(6, min=0, max=10)
coords <- data.frame(x=x, y=y)
```

```
r <- terra::rast(nrows=10, ncols=10, xmin = 0, xmax = 10, ymin = 0, ymax = 10)
terra::values(r) <- 1
create_cdmat(coords=coords, method="lcp", resistance=r)
```

`heterozygosity_ind` *Plot Individual-Level Heterozygosity*

Description

Calculates observed and expected heterozygosity from `L#A#` genotype columns in CDMetaPOP `ind##.csv` files.

Usage

```
heterozygosity_ind(
  path,
  year = 0,
  run = 0,
  batch = 0,
  mc = 0,
  species = 0,
  file_type = "ind",
  patches = "all",
  loci = NULL,
  group_col = "PatchID",
  jitter = TRUE
)
```

Arguments

`path`	A dataframe, file path, vector of file paths, run directory, or top-level output directory containing individual files.
`year`	Integer. Year/generation to plot for one-year plots. Defaults to `0`.
`run`	Integer. Run index used when `path` is a directory. Defaults to `0`.
`batch`	Integer. Batch index used when `path` is a directory. Defaults to `0`.
`mc`	Integer. Monte Carlo index used when `path` is a directory. Defaults to `0`.
`species`	Integer. Species index used when `path` is a directory. Defaults to `0`.
`file_type`	Character. Which individual file type to read. Use `"ind"` for `ind##.csv` files or `"ind_Sample"` for `ind##_Sample.csv` files. Defaults to `"ind"`.
`patches`	Patch IDs to include. Use `"all"` to include all patches, a single patch ID such as 5, or a vector/range such as `c(1, 3, 8)` or `1:20`. Defaults to `"all"`.
`loci`	Optional vector of loci to include, such as `c("L0", "L1")` or `c(0, 1)`. Defaults to all detected loci.
`group_col`	Column used for grouping frequencies. Defaults to `"PatchID"`.
`jitter`	Logical. If `TRUE`, overlay jittered group-level points on the boxplots. Defaults to `TRUE`.

Value

A ggplot object with heterozygosity data in `plot$data`.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")
heterozygosity_ind(ex_dir, year = 9)
heterozygosity_ind(ex_dir, year = 9, jitter = FALSE)
```

`launch_cdmetapop` *Function to facilitate the running of CDMetaPOP software from R*

Description

Function to run CDMetaPOP from R

Usage

```
launch_cdmetapop(
  pythonFilepath = "python",
  CDMetaPOPFilepath = "CDMetaPOP.py",
  runvarsDirectory = NULL,
  runvarsFilename = "RunVars.csv",
  outputDirectory = "test_"
)
```

Arguments

`pythonFilepath`	Location of Python executable, or just 'python' if the environment is already established
`CDMetaPOPFilepath`	Location of the CDMetaPOP.py file, if already in the working directory then this can just be 'CDMetaPOP.py'
`runvarsDirectory`	Location of the directory where the RunVars.csv file is stored for the run
`runvarsFilename`	Name of the RunVars file to run
`outputDirectory`	Name of output directory to be stored in the same location as runvarsDirectory

Details

This function will launch a command prompt (Windows) or terminal (Linux/Mac) that will call Python and supply the 5 arguments needed to launch CDMetaPOP simulations

Value

No return value. This function is called for its side effect of launching a CDMetaPOP simulation in a terminal window.

Examples

```
# Example: This function launches a system command to initiate CDMetaPOP.
pythonFilepath="C:/Users/User1/anaconda3/python.exe"
CDMetaPOPFilepath="C:/Users/User1/CDMetaPOP_v3.03/src/CDMetaPOP.py"
runvarsDirectory = "C:/Users/User1/CDMetaPOP_v3.03/example_files/"
runvarsFilename = "RunVars.csv"
outputDirectory = "test_"

mymodel <- launch_cdmetapop(pythonFilepath,
                            CDMetaPOPFilepath,
                            runvarsDirectory,
                            runvarsFilename,
                            outputDirectory = "test_")
```

`make_classvars` *Build ClassVars File from Template*

Description

This function loads a provided ClassVars template, allows the user to edit selected areas, and saves the modified version as a new file.

Usage

```
make_classvars(output_file = "my_new_classvars.csv")
```

Arguments

`output_file`	The name of the output file. Defaults to 'my_new_classvars.csv'.

Value

A Shiny app instance.

`make_patchvars` *Build PatchVars File from Template*

Description

This function loads a provided PatchVars template, allows the user to edit selected areas, and saves the modified version as a new file.

Usage

```
make_patchvars(output_file = "my_new_patchvars.csv")
```

Arguments

`output_file`	The name of the output file. Defaults to 'my_new_patchvars.csv'.

Value

A Shiny app instance.

`make_popvars` *Build PopVars File from Template*

Description

This function loads a provided PopVars template, allows the user to edit selected areas, and saves the modified version as a new file.

Usage

```
make_popvars(output_file = "my_new_popvars.csv")
```

Arguments

`output_file`	The name of the output file. Defaults to 'my_new_popvars.csv'.

Value

A Shiny app instance.

`make_runvars` *Build RunVars File from Template*

Description

This function loads a provided runVars template, allows the user to edit selected areas, and saves the modified version as a new file.

Usage

```
make_runvars(output_file = "my_new_runvars.csv")
```

Arguments

`output_file`	The name of the output file. Defaults to 'my_new_runvars.csv'.

Value

A Shiny app instance.

`pairwise_fst_ind` *Plot Pairwise FST Between Individual Groups*

Description

Calculates pairwise FST between groups, usually patches, from `L#A#` genotype columns in CDMetaPOP `ind##.csv` files. FST is calculated per locus and then averaged across loci for each pair.

Usage

```
pairwise_fst_ind(
  path,
  year = 0,
  run = 0,
  batch = 0,
  mc = 0,
  species = 0,
  file_type = "ind",
  patches = "all",
  loci = NULL,
  group_col = "PatchID"
)
```

Arguments

`path`	A dataframe, file path, vector of file paths, run directory, or top-level output directory containing individual files.
`year`	Integer. Year/generation to plot for one-year plots. Defaults to `0`.
`run`	Integer. Run index used when `path` is a directory. Defaults to `0`.
`batch`	Integer. Batch index used when `path` is a directory. Defaults to `0`.
`mc`	Integer. Monte Carlo index used when `path` is a directory. Defaults to `0`.
`species`	Integer. Species index used when `path` is a directory. Defaults to `0`.
`file_type`	Character. Which individual file type to read. Use `"ind"` for `ind##.csv` files or `"ind_Sample"` for `ind##_Sample.csv` files. Defaults to `"ind"`.
`patches`	Patch IDs to include. Use `"all"` to include all patches, a single patch ID such as `5`, or a vector/range such as `c(1, 3, 8)` or `1:20`. Defaults to `"all"`.
`loci`	Optional vector of loci to include, such as `c("L0", "L1")` or `c(0, 1)`. Defaults to all detected loci.
`group_col`	Column used for grouping frequencies. Defaults to `"PatchID"`.

Value

A ggplot heatmap with pairwise FST data in `plot$data`.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")
pairwise_fst_ind(ex_dir, year = 9)
```

`summary_class` *Plot CDMetaPOP Class Summary Dynamics*

Description

Summarizes and plots data from `summary_classAllTime.csv` files. Inputs can be a data frame, one file path, multiple file paths, or a CDMetaPOP output directory containing `summary_classAllTime.csv` files.

Usage

```
summary_class(
  data,
  type = "age_class",
  batch_labels = NULL,
  show_mc = TRUE,
  show_ci = TRUE,
  run = 0,
  batch = 0,
```

```
  mc = 0,
  species = 0,
  ...
)
```

Arguments

`data`	A dataframe, file path (`.csv`, `.rds`, `.RData`), vector of file paths, or a directory containing `summary_classAllTime.csv` files.
`type`	String specifying the plot type: `"age_class"` or `"age_plus_one"`.
`batch_labels`	Optional named character vector used to relabel faceted source groups. Names should match folder names such as `N.out1776184541` and values should be the labels displayed in the facet strips.
`show_mc`	Logical. If `TRUE`, plot individual Monte Carlo trajectories when multiple source files are supplied for line-based plots. Defaults to `TRUE`.
`show_ci`	Logical. If `TRUE`, plot the mean and a 95% confidence band across Monte Carlo replicates when multiple source files are supplied for line-based plots. Defaults to `TRUE`.
`run`	Integer run index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all runs.
`batch`	Integer batch index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all batches.
`mc`	Integer Monte Carlo index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all Monte Carlo replicates.
`species`	Integer species index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all species.
`...`	Additional arguments passed to specific plot types. Use `n` to choose the year interval for `"age_class"` plots.

Value

A ggplot object.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")

summary_class(ex_dir, type = "age_class", n = 10)
summary_class(ex_dir, type = "age_plus_one")
```

`summary_dataframe` *Return CDMetaPOP Output Data as Data Frames*

Description

Reads CDMetaPOP population, class, disease-state, or individual output files and returns data frames for custom plotting or downstream summaries.

Usage

```
summary_dataframe(
  data,
  type = c("pop", "class", "disease", "ind"),
  run = 0,
  batch = 0,
  mc = 0,
  species = 0,
  years = NULL,
  file_type = "ind",
  patches = "all",
  state_names = NULL,
  cumulative_states = NULL,
  state_column = "States_SecondUpdate",
  disease_format = c("long", "wide"),
  summary_format = c("long", "wide")
)
```

Arguments

`data`	A data frame, file path, vector of file paths, run directory, or top-level CDMetaPOP output directory.
`type`	Character. Which file type to read: `"pop"` for `summary_popAllTime.csv`, `"class"` for `summary_classAllTime.csv`, `"disease"` for `summary_popAllTime_DiseaseStates.csv`, or `"ind"` for `ind##.csv` / `ind##_Sample.csv` files.
`run`	Integer run index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all runs.
`batch`	Integer batch index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all batches.
`mc`	Integer Monte Carlo index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all Monte Carlo replicates.
`species`	Integer species index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all species.
`years`	Optional integer vector of years/generations to include for `type = "ind"`.
`file_type`	Character. Which individual file type to read for `type = "ind"`. Use `"ind"` for `ind##.csv` files or `"ind_Sample"` for `ind##_Sample.csv` files. Defaults to `"ind"`.

`patches`	Patch IDs to include for `type = "ind"`. Use `"all"` to include all patches, a single patch ID, or a vector/range of patch IDs. Defaults to `"all"`.
`state_names`	Character vector used to name disease states for `type = "disease"`. If `NULL`, states are named numerically.
`cumulative_states`	Character vector of disease state names to calculate as running totals for `type = "disease"`.
`state_column`	Character. Disease-state column to parse for `type = "disease"`. Defaults to `"States_SecondUpdate"`.
`disease_format`	Character. Use `"long"` to return one row per year/source/state, or `"wide"` to return one column per state. Defaults to `"long"`.
`summary_format`	Character. Use `"long"` to split pipe-delimited `summary_popAllTime.csv` and `summary_classAllTime.csv` columns into one row per patch or class while keeping metrics in separate columns. Use `"wide"` to return the raw summary columns with metadata. Defaults to `"long"`.

Value

A data frame with source metadata columns. For `type = "pop"` and `type = "class"`, the default long format includes `PatchID` or `ClassID` indexing values split from pipe-delimited metric columns. For `type = "disease"`, the default long format includes `State` and `Count` columns.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")

pop_df <- summary_dataframe(ex_dir, type = "pop")
class_df <- summary_dataframe(ex_dir, type = "class")
disease_df <- summary_dataframe(ex_dir, type = "disease")
ind_df <- summary_dataframe(ex_dir, type = "ind", years = 9)

all_mc_pop_df <- summary_dataframe(ex_dir, type = "pop", mc = "all")
```

`summary_disease` *Summarize CDMetaPOP Disease States*

Description

Scans CDMetaPOP output directories, pulls state totals from `summary_popAllTime_DiseaseStates.csv` files, and returns a faceted ggplot comparing disease states across batches.

Usage

```
summary_disease(
  base_path,
  state_names = NULL,
  scenario_names = NULL,
```

```
  cumulative_states = NULL,
  state_column = "States_SecondUpdate"
)
```

Arguments

`base_path`	Character. Path to a CDMetaPOP output directory containing `run#batch#mc#species#` folders, or a parent directory containing those folders.
`state_names`	Character vector. Optional labels for disease states. If `NULL`, states are named numerically (`"1"`, `"2"`, `"3"`, ...).
`scenario_names`	Character vector. Optional labels for batches. The first value labels batch 0, the second labels batch 1, and so on.
`cumulative_states`	Character vector. Names of states to calculate as running totals within each Monte Carlo replicate.
`state_column`	Character. Disease-state column to summarize. Defaults to `"States_SecondUpdate"`.

Value

A ggplot object.

Examples

```
ex_dir <- system.file(
  "extdata",
  "Example_dat",
  package = "cdmetapopR"
)

summary_disease(ex_dir)

summary_disease(
  ex_dir,
  state_names = c("Susceptible", "Infected", "Recovered"),
  scenario_names = c("Batch 0", "Batch 1"),
  cumulative_states = "Recovered"
)
```

`summary_ind` *Plot CDMetaPOP Individual File Summaries*

Description

Plots simple summaries from CDMetaPOP `ind##.csv` or `ind##_Sample.csv` files. Inputs can be a data frame, one individual file, multiple individual files, a single run folder, or a top-level CDMetaPOP output directory containing run folders.

Usage

```
summary_ind(
  path,
  type = "age",
  year = 0,
  years = NULL,
  run = 0,
  batch = 0,
  mc = 0,
  species = 0,
  file_type = "ind",
  patches = "all",
  bins = 30
)
```

Arguments

`path`	A dataframe, file path, vector of file paths, run directory, or top-level output directory containing individual files.
`type`	String specifying the plot type: `"cdist"`, `"hindex"`, `"age"`, `"size"`, `"age_size"`, or `"movement"`.
`year`	Integer. Year/generation to plot for one-year plots. Defaults to `0`.
`years`	Integer vector. Years/generations to include for movement plots. If `NULL`, all discovered years are used for `"movement"`.
`run`	Integer. Run index used when `path` is a directory. Defaults to `0`.
`batch`	Integer. Batch index used when `path` is a directory. Defaults to `0`.
`mc`	Integer. Monte Carlo index used when `path` is a directory. Defaults to `0`.
`species`	Integer. Species index used when `path` is a directory. Defaults to `0`.
`file_type`	Character. Which individual file type to read. Use `"ind"` for `ind##.csv` files or `"ind_Sample"` for `ind##_Sample.csv` files. Defaults to `"ind"`.
`patches`	Patch IDs to include. Use `"all"` to include all patches, a single patch ID such as `5`, or a vector/range such as `c(1, 3, 8)` or `1:20`. Defaults to `"all"`.
`bins`	Integer. Number of bins for continuous histograms. Defaults to `30`.

Value

A ggplot object.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")

summary_ind(ex_dir, type = "age", year = 9)
summary_ind(ex_dir, type = "age_size", year = 9)
summary_ind(ex_dir, type = "movement", years = 0:9, batch = 1, mc = 1)
```

`summary_patch_map` *Map CDMetaPOP Patch Abundance*

Description

Creates a faceted patch map from CDMetaPOP `ind##.csv` or `ind##_Sample.csv` files. Points are drawn at patch coordinates and scaled by the number of individuals in each patch.

Usage

```
summary_patch_map(
  path,
  type = "abundance",
  years = 0,
  run = 0,
  batch = 0,
  mc = 0,
  species = 0,
  file_type = "ind",
  patches = "all",
  states = NULL,
  facet_by_state = FALSE,
  locus = NULL,
  allele = NULL,
  metric = "Ho",
  labels = FALSE,
  log_scale = FALSE,
  crs = NULL
)
```

Arguments

`path`	A dataframe, file path, vector of file paths, run directory, or top-level output directory containing individual files.
`type`	Character. What to map: `"abundance"`, `"allele_frequency"`, or `"heterozygosity"`. Defaults to `"abundance"`.
`years`	Integer vector. Years/generations to map. Defaults to `0`.
`run`	Integer. Run index used when `path` is a directory. Defaults to `0`.
`batch`	Integer. Batch index used when `path` is a directory. Defaults to `0`.
`mc`	Integer. Monte Carlo index used when `path` is a directory. Defaults to `0`.
`species`	Integer. Species index used when `path` is a directory. Defaults to `0`.
`file_type`	Character. Which individual file type to read. Use `"ind"` for `ind##.csv` files or `"ind_Sample"` for `ind##_Sample.csv` files. Defaults to `"ind"`.
`patches`	Patch IDs to include. Use `"all"` to include all patches, a single patch ID such as `5`, or a vector/range such as `c(1, 3, 8)` or `1:20`. Defaults to `"all"`.

`states`	Optional vector of disease states to include. If `NULL`, all individuals are used.
`facet_by_state`	Logical. If `TRUE`, facet by disease state as well as year. Defaults to `FALSE`.
`locus`	Locus to map for genetic summaries, such as `"L0"` or `0`. Required when `type` is `"allele_frequency"` or `"heterozygosity"`.
`allele`	Allele to map for `type = "allele_frequency"`, such as `"A1"` or `1`.
`metric`	Heterozygosity metric to map for `type = "heterozygosity"`. Use `"Ho"` or `"He"`. Defaults to `"Ho"`.
`labels`	Logical. If `TRUE`, add patch ID labels to the map. Defaults to `FALSE`.
`log_scale`	Logical. If `TRUE`, use log1p-transformed abundance for point sizes when `type = "abundance"`. Defaults to `FALSE`.
`crs`	Optional coordinate reference system label. For example, use `5070` or `"EPSG:5070"` for NAD83 / Conus Albers. Coordinates are not transformed; this is used for labeling and stored as plot data metadata.

Value

A ggplot object with patch-level summary data in `plot$data`.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")

summary_patch_map(ex_dir, years = c(0, 5, 9), crs = 5070)
summary_patch_map(ex_dir, years = c(0, 5, 9), states = 1, crs = 5070)
summary_patch_map(ex_dir, years = c(0, 9), states = c(0, 1), facet_by_state = TRUE, crs = 5070)
summary_patch_map(ex_dir, type = "allele_frequency", years = 9, locus = "L0", allele = "A1")
summary_patch_map(ex_dir, type = "heterozygosity", years = 9, locus = "L0", metric = "Ho")
```

`summary_pop` *Plot CDMetaPOP Population Summary Dynamics*

Description

Summarizes and plots data from `summary_popAllTime.csv` files. Inputs can be a data frame, one file path, multiple file paths, or a CDMetaPOP output directory containing `summary_popAllTime.csv` files.

Usage

```
summary_pop(
  data,
  type = "N_initial",
  batch_labels = NULL,
  show_mc = TRUE,
  show_ci = TRUE,
  run = 0,
```

```
  batch = 0,
  mc = 0,
  species = 0,
  ...
)
```

Arguments

`data`	A dataframe, file path (`.csv`, `.rds`, `.RData`), vector of file paths, or a directory containing `summary_popAllTime.csv` files.
`type`	String specifying the plot type: `"N_initial"`, `"sex"`, `"mature"`, `"births"`, `"myy_ratio"`, `"patch"`, `"allelic_richness"`, or `"het"`.
`batch_labels`	Optional named character vector used to relabel faceted source groups. Names should match folder names such as `N.out1776184541` and values should be the labels displayed in the facet strips.
`show_mc`	Logical. If `TRUE`, plot individual Monte Carlo trajectories when multiple source files are supplied. Defaults to `TRUE`.
`show_ci`	Logical. If `TRUE`, plot the mean and a 95% confidence band across Monte Carlo replicates when multiple source files are supplied. Defaults to `TRUE`.
`run`	Integer run index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all runs.
`batch`	Integer batch index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all batches.
`mc`	Integer Monte Carlo index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all Monte Carlo replicates.
`species`	Integer species index used when `data` is a directory. Defaults to `0`. Use `"all"` to include all species.
`...`	Additional arguments passed to specific plot types. Use `include_yys = TRUE` for `"sex"` or `"mature"` plots, or `years` for `"patch"` plots.

Value

A ggplot object.

Examples

```
ex_dir <- system.file("extdata", "Example_dat", package = "cdmetapopR")

summary_pop(ex_dir, type = "N_initial")
summary_pop(ex_dir, type = "sex")
summary_pop(ex_dir, type = "mature", include_yys = TRUE)
summary_pop(ex_dir, type = "allelic_richness")
summary_pop(ex_dir, type = "het")
```

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