

Package ‘cdmetapopR’

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Title Utility Functions for 'CDMetaPOP'

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

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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_cdmatrix	<i>Create cost distance matrix for CDMetaPOP simulation</i>
-----------------	---

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_cdmatrix(  
  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_cdmatrix(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_cdmatrix(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	<i>Function to facilitate the running of CDMetaPOP software from R</i>
------------------	--

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_cdmecipop(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	<i>Build PatchVars File from Template</i>
----------------	---

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	<i>Build PopVars File from Template</i>
--------------	---

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	<i>Build RunVars File from Template</i>
--------------	---

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	<i>Plot Pairwise FST Between Individual Groups</i>
------------------	--

Description

Calculates pairwise FST between groups, usually patches, from L#A# genotype columns in CD-MetaPOP 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 CD-MetaPOP 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 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	<i>Summarize CDMetaPOP Disease States</i>
-----------------	---

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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