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License GPL-2

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add_dens_polygon *Add a kernel density polygon*

Description

Add a kernel density polygon

Usage

```
add_dens_polygon(
  x,
  y,
  col,
  lwd = 1.7,
  alpha = c(0.25, 0.75),
  add_pts = FALSE,
  add_poly = TRUE
)
```

Arguments

x	x values
y	y values
col	Colour to add polygon with. Will be made into two levels of opacity.
lwd	lwd Line width
alpha	A numeric vector of length 2 that gives the confidence levels for the two kernel density polygons.
add_pts	Logical: should points be added?
add_poly	Add polygons?

annotate *Add annotations to panel*

Description

Add annotations to panel

Usage

```
annotate(label, xfrac = 0.008, yfrac = 0.18, pos = 4, cex = 0.9, ...)
```

Arguments

label	The text to add as a label
xfrac	Fraction over from the left
yfrac	Fraction down from the top
pos	Position of text to pass to text
cex	Character expansion value to pass to text
...	Anything else to pass to text

---

count_quasi_exts *Take meta_sim output objects and count quasi extinctions*

Description

Take meta_sim output objects and count quasi extinctions

Usage

```
count_quasi_exts(dat, quasi_thresh, ignore_pops_thresh = 5, duration = 1)
```

Arguments

dat	Input data. Should be a list of lists. The first level corresponds to the conservation plan and the second level corresponds to the replicate.
quasi_thresh	The quasi extinction threshold
ignore_pops_thresh	Threshold below which to ignore populations (e.g. if you started some populations with very low abundance and you don't want to count those populations.
duration	Number of years that the abundance must be below the quasi_thresh before being counted as quasi extinct.

Value

A list of matrices. The list elements correspond to the conservation plans. The columns of the matrix correspond to the subpopulations that were above the ignore_pops_thresh level. The rows of the matrix correspond to the replicates.

Examples

```
## Not run:
set.seed(1)
w_plans <- list()
w_plans[[1]] <- c(5, 1000, 5, 1000, 5, 5, 1000, 5, 1000, 5)
w_plans[[2]] <- c(5, 5, 5, 1000, 1000, 1000, 1000, 5, 5, 5)
w_plans[[3]] <- c(rep(1000, 4), rep(5, 6))
w_plans[[4]] <- rev(w_plans[[3]])
```

```
plans_name_sp <- c("Full range of responses", "Most stable only",
"Lower half", "Upper half")
 n_trials <- 50 # number of trials at each n conservation plan
 n_plans <- 4 # number of plans
 num_pops <- c(2, 4, 8, 16) # n pops to conserve
 w <- list()
 for(i in 1:n_plans) { # loop over number conserved
  w[[i]] <- list()
  for(j in 1:n_trials) { # loop over trials
    w[[i]][[j]] <- matrix(rep(625, 16), nrow = 1)
    w[[i]][[j]][-sample(1:16, num_pops[i])] <- 5
  }
 }
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)

x_arma_sp <- run_cons_plans(w, env_type = "arma", env_params = arma_env_params)
count_quasi_exts(x_arma_sp$plans_port, quasi_thresh = 200)

## End(Not run)
```

`create_asset_weights` *Create an asset weights matrix*

Description

Create an asset weight matrix to run through the Monte Carlo algorithm and test possible portfolios.

Usage

```
create_asset_weights(n_pop, n_sims, weight_lower_limit = 0.02)
```

Arguments

`n_pop`	The number of subpopulations.
`n_sims`	The number of simulations.
`weight_lower_limit`	The lowest fraction allowed for a subpopulation weight. For example, a value of 0.02 means a subpopulation will at least be assigned 2% of the total capacity

Value

A matrix. The columns represent subpopulations. The rows represent simulation repetitions.

Examples

```
create_asset_weights(n_pop = 5, n_sims = 10, weight_lower_limit = 0.001)
```

custom_bw *Custom bandwidth*

Description

Based on `bandwidth.nrd` from **MASS**. This version takes the absolute value of `var` to avoid errors.

Usage

```
custom_bw(x)
```

Arguments

`x`	A numeric vector

CVaR *Conditional Value at Risk*

Description

Get the conditional value at risk.

Usage

```
CVaR(x, probs = 0.05)
```

Arguments

`x`	A numeric vector
`probs`	The probability cutoff to pass to the CVaR function.

est_beta_params *Get beta parameters from mean and variance*

Description

Get beta parameters from mean and variance

Usage

```
est_beta_params(mu, var)
```

Arguments

`mu`	Mean
`var`	Variance

fastlm *Super fast linear regression*

Description

Super fast linear regression

Usage

```
fastlm(yr, Xr)
```

Arguments

yr	Vector of y values
Xr	Model matrix

fit_ricker *Fit Ricker linear regression*

Description

Fit a Ricker curve to spawner-recruit data and return the intercept (a) and slope (b). The model is fit via the **RcppArmadillo** package for speed..

Usage

```
fit_ricker(S, R)
```

Arguments

S	Spawners as a numeric vector.
R	Recruits or returns as a numeric vector.

Value

A named list with components a for the intercept and b for the slope.

Examples

```
S <- seq(100, 1000, length.out = 100)
v_t <- rnorm(100, 0, 0.1)
R <- mapply(ricker_v_t, spawners = S, v_t = v_t, a = 1.9, b = 900, d = 1)
plot(S, log(R/S))
fit_ricker(S, R)
```

`generate_env_ts` *Create an environmental time series.*

Description

Generate various types of environmental time series.

Usage

```
generate_env_ts(
  n_t,
  type = c("sine", "arma", "regime", "linear", "linear_arma", "constant"),
 sine_params = list(amplitude = 1, ang_frequency = 0.2, phase = 0, mean_value = 0, slope
    = 0, sigma_env = 0.02),
  arma_params = list(mean_value = 0, sigma_env = 0.5, ar = 0.4, ma = 0),
  regime_params = list(break_pts = c(25, 75), break_vals = c(-1, 0, 1)),
 linear_params = list(min_value = -1, max_value = 1, sigma_env = 0.1, start_t = 1),
 linear_arma_params = list(min_value = -1, max_value = 1, sigma_env = 0.1, start_t = 1,
    ar = 0.4, ma = 0),
  constant_params = list(value = 0)
)
```

Arguments

`n_t`	Length of time series.
`type`	Type of time series to produce.
`sine_params`	Parameters controlling sine wave time series.
`arma_params`	Parameters controlling ARMA time series.
`regime_params`	Parameters controlling regime-shift time series.
`linear_params`	Parameters controlling warming or cooling time series. Minimum environmental value, maximum environmental value, environmental standard deviation, and the year to start the linear trend (useful if you're going to throw out the early years as burn in).
`linear_arma_params`	A combination of `arma_params` and `linear_params`.
`constant_params`	Parameter controlling constant time series.

Examples

```
types <- c("sine", "arma", "regime", "linear", "linear_arma", "constant")
x <- list()
for(i in 1:6) x[[i]] <- generate_env_ts(n_t = 100, type = types[i])
op <- par(mfrow = c(5, 1), mar = c(3,3,1,0), cex = 0.7)
for(i in 1:6) plot(x[[i]], type = "o", main = types[i])
par(op)
```

generate_straying_matrix *Generate a matrix of straying proportions within a metapopulation*

Description

Generate a matrix of straying proportions within a metapopulation. Based on Eq. 2 in Cooper and Mangel (1999).

Usage

```
generate_straying_matrix(n_pop, stray_fraction, stray_decay_rate)
```

Arguments

n_pop	Number of subpopulations.
stray_fraction	Fraction of individuals that stray from a given subpopulation.
stray_decay_rate	Exponential rate that straying decays with distance between subpopulations.

References

Cooper, A.B. and Mangel, M. 1999. The dangers of ignoring metapopulation structure for the conservation of salmonids. Fish. Bull. 97(2): 213-226.

Examples

```
x <- generate_straying_matrix(10, 0.01, 0.3)
image(x, col = rev(heat.colors(12)))
```

get_conserv_plans_mv *Run simulation for conservation schemes*

Description

Run the metapopulation simulation for various conservation prioritization schemes.

Usage

```
get_conserv_plans_mv(
  weights,
  reps = 150,
  assess_freq = 5,
  burn = 1:30,
  risk_fn = var,
  ...
)
```

Arguments

weights	A matrix of habitat weights. Each row corresponds to another scenario. Each column is a different habitat location.
reps	Number of portfolios to simulate.
assess_freq	The frequency (in generations) of spawner-recruit re-assessment. Passed to meta_sim.
burn	Cycles to throw out as burn in.
risk_fn	Type of variance or risk metric. By default takes the variance. Instead you can supply any function that takes a numeric vector and returns some single numeric value. E.g. CVaR.
...	Other values to pass to meta_sim.

Value

Returns the portfolio mean and variance values and the simulation runs.

---

get_efficient_frontier

Get the efficient frontier from mean and variance values

Description

Get the efficient frontier from mean and variance values

Usage

```
get_efficient_frontier(m, v)
```

Arguments

m	A vector of mean values
v	A vector of variance values

get_port_vals *Get portfolio mean and variance values*

Description

Takes a list created by meta_sim and returns the mean and variance (or risk metric) values. This function is used by other internal functions, but can also be used as its own low-level function.

Usage

```
get_port_vals(x, risk_fn = var, burn = 1:30)
```

Arguments

x	A list object as returned from meta_sim
risk_fn	Type of variance or risk metric. By default takes the variance. Instead you can supply any function that takes a numeric vector and returns some single numeric value. E.g. CVaR.
burn	Number of years to throw out as burn in

Value

A data frame with columns for the mean (m) and variance (v).

See Also

plot_cons_plans

Examples

```
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)
base1 <- meta_sim(n_pop = 10, env_params = arma_env_params, env_type =
  "arma", assess_freq = 5)
get_port_vals(base1)
```

get_quantile_contour *Get quantile contour*

Description

Get quantile contour

Usage

```
get_quantile_contour(x, alpha = 0.8)
```

Arguments

x	Output from kde2d.
alpha	The quantile level.

---

gg_color_hue *ggplot2-like colour scale in HCL space*

Description

ggplot2-like colour scale in HCL space

Usage

```
gg_color_hue(n, hue_min = 10, hue_max = 280, l = 62, c = 100)
```

Arguments

n	Number of colours to return.
hue_min	Minimum hue value in the range [0,360]
hue_max	Maximum hue value in the range [0,360]
l	Luminance in the range [0,100]
c	Chroma of the colour.

Details

See the hcl function for details.

Value

A vector of colour values.

Examples

```
gg_color_hue(10)
```

`impl_error` *Add implementation error*

Description

Add implementation error with a beta distribution.

Usage

```
impl_error(mu, sigma_impl)
```

Arguments

`mu`	The mean
`sigma_impl`	Implementation error standard deviation

Value

A single numeric values representing a sample from a beta distribution with the specified mean and standard deviation.

References

Morgan, M. G. & Henrion, M. (1990). Uncertainty: A Guide to Dealing with Uncertainty in Quantitative Risk and Policy Analysis. Cambridge University Press.

Pestes, L. R., Peterman, R. M., Bradford, M. J., and Wood, C. C. (2008). Bayesian decision analysis for evaluating management options to promote recovery of a depleted salmon population. 22(2):351-361.

http://stats.stackexchange.com/questions/12232/calculating-the-parameters-of-a-beta-distribution-using-the-mean-and-variance

Examples

```
y <- sapply(1:200, function(x) impl_error(0.5, 0.2))
hist(y)

y <- sapply(1:200, function(x) impl_error(0.3, 0.1))
hist(y)
```

is_element *Check if x is an element of y.*

Description

Check if x is an element of y.

Usage

```
is_element(x, y)
```

Arguments

x	An integer to check
y	A vector to check if x is an element of y.

meta_sim *Run a single metapopulation simulation.*

Description

This is the master function for running **metafolio** simulations. It runs a single iteration of a simulation. The arguments can be manipulated with other functions in the package to use this function as part of a portfolio analysis.

Usage

```
meta_sim(
  n_t = 130,
  n_pop = 10,
  stray_decay_rate = 0.1,
  stray_fraction = 0.02,
  b = rep(1000, n_pop),
  spawners_0 = round(b),
  sigma_v = 0.7,
  v_rho = 0.4,
 a_width_param = c(seq(0.08, 0.04, length.out = n_pop/2), rev(seq(0.08, 0.04, length.out
    = n_pop/2))),
  optim_temp = seq(13, 19, length.out = n_pop),
  max_a = thermal_integration(n_pop),
  env_type = c("sine", "arma", "regime", "linear", "constant"),
 env_params = list(amplitude = 3.2, ang_frequency = 0.2, phase = runif(1, -pi, pi),
    mean_value = 15, slope = 0, sigma_env = 0.3),
  start_assessment = 20,
  a_lim = c(0.02, 4),
```

```
  b_lim = c(0.5, 1.5),
  silence_warnings = TRUE,
  sigma_impl = 0.1,
  assess_freq = 10,
  use_cache = FALSE,
  cache_env = FALSE,
  add_straying = TRUE,
  add_impl_error = TRUE,
  skip_saving_cache = FALSE,
  decrease_b = 0,
  debug = FALSE
)
```

Arguments

n_t	The number of years.
n_pop	Number of populations
stray_decay_rate	Rate that straying (exponentially) decays with distance.
stray_fraction	Fraction of fish that stray from natal streams.
b	Ricker density-dependent parameter. A vector with one numeric value per population.
spawners_0	A vector of spawner abundances at the start of the simulation. Length of the vector should equal the number of populations.
sigma_v	Stock-recruit residual standard deviation of the log-deviations.
v_rho	AR1 serial correlation of stock-recruit residuals.
a_width_param	Width of the thermal curves by population.
optim_temp	Optimal temperatures by population.
max_a	Maximum Ricker productivity parameters (a) by population. The value obtained at the optimum temperature. Note how the default argument uses the thermal_integration function.
env_type	The type of environmental time series to generate. One of "sine", "arma", "regime", "linear", or "constant". See generate_env_ts.
env_params	Parameters to pass on to generate_env_ts. You must provide the appropriate list given your chosen type of environmental signal.
start_assessment	Generation to start estimating the stock recruit relationship for escapement targets. The assessment is carried out using fit_ricker.
a_lim	A vector of length two giving the lower and upper limits for Ricker a values. If a value is estimated beyond these limits it will be set to the limit value.
b_lim	A vector of length two giving the lower and upper limits for the estimated Ricker b values *as fractions* of the previously assessed value. If a value is estimated beyond these limits it will be set to the limit value.

`silence_warnings`
: Should the warnings be skipped if the Ricker a or b values exceed their specified bounds? `meta_sim` will still print other warnings regardless of this argument value.

`sigma_impl`
: Implementation standard deviation for the implementation error beta distribution.

`assess_freq`
: How many generations before re-assessing Ricker a and b parameters.

`use_cache`
: Use the stochastically generated values (stock-recruit residuals and possibly environmental time series) from the previous run? See the Details section below.

`cache_env`
: Logical: Should the environmental time series be cached? If `use_cache = TRUE` then this will automatically happen. But, you could set `cache_env = TRUE` and `use_cache = FALSE` to only cache the environmental time series. See the Details section below.

`add_straying`
: Implement straying between populations?

`add_impl_error`
: Add implementation error? Implementation error is derived using `impl_error`.

`skip_saving_cache`
: Logical: if `TRUE` then no data will be cached for the next iteration. This will save time when running many simulations.

`decrease_b`
: A numeric value to decrease all streams by each generation. This is intended to be used to simulate habitat loss, for example though stream flow reduction with climate change.

`debug`
: Logical: if `TRUE` then `meta_sim` will print a number of debugging statements while it runs.

Details

To use either of the caching options, you must have run `meta_sim` at least once in the current session with both caching arguments set to `FALSE` to generate the cached values first. If you're running many iterations of `meta_sim` and you want to cache, then the first iteration should have both cache arguments set to `FALSE`, and subsequent runs can set one or both to `TRUE`. Internally, `meta_sim` caches by writing the appropriate data to an `.rda` file in a temporary directory.

Value

A list is returned that contains the following elements. All matrices that are returned (except the straying matrix) feature populations along the columns and generations/years along the rows.

`A` A matrix of abundances.

`F` A matrix of fishing mortality in numbers.

`E` A matrix of realized escapement.

`Eps` A matrix of (log) spawner-return residuals. These have been log-normal bias corrected so their expected value after exponentiation will be one.

`A_params` A matrix of actual Ricker a parameters.

`Strays_leaving` A matrix of strays leaving.

`Strays_joining` A matrix of strays joining.

`env_ts` A vector of the environmental time series.

`stray_mat` The straying matrix. These fractions are constant across generations/years. Rows and columns are populations.

`n_pop` The total possible populations as input in the simulation.

`n_t` The number of generations/years the simulation was run for.

`b` The original Ricker b values as specified.

`Est_a` A matrix of estimated Ricker a values.

`Est_b` A matrix of estimated Ricker b values.

Examples

```
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)
base1 <- meta_sim(n_pop = 10, env_params = arma_env_params,
  env_type = "arma", assess_freq = 5)

plot_sim_ts(base1, years_to_show = 70, burn = 30)
```

`metafolio` *metafolio: An R package to simulate metapopulations for portfolio optimization*

Description

The **metafolio** R package is a tool to simulate metapopulations and apply financial portfolio optimization concepts. The package was originally written for salmon simulations, so some of the language refers to salmon-specific terminology, but the package could be used and/or adopted for other taxonomic groups.

Details

The main simulation function is `meta_sim`. This function takes care of running an individual simulation iteration. The package also contains functions for exploring conservation scenarios with these simulations (see the "Assessing multiple conservation scenarios" section below), and find optimal conservation strategies (see the "Portfolio optimization section" below).

Running a simulation once

To run a single simulation iteration, see the function `meta_sim`. To plot the output from one of these simulations, see the function `plot_sim_ts`.

Assessing multiple conservation scenarios

You can use `run_cons_plans` to run `meta_sim` for multiple iterations and across multiple conservation strategies. These strategies could focus on the spatial distribution of conservation or on the number of populations conserved.

The function `plot_cons_plans` can plot the output from `run_cons_plans`.

Specifying environmental patterns

When you run `meta_sim` you can specify the environmental signal. One of the arguments is a list of options to pass to `generate_env_ts`, which controls the environmental pattern.

Diagnostic plots

metafolio contains some additional plotting functions to inspect the spawner-return relationships and the correlation between returns: `plot_rickers`, and `plot_correlation_between_returns`.

Portfolio optimization

metafolio also contains some experimental functions for finding optimal conservation strategies (an efficient frontier). This is analogous to financial portfolio where the goal is to find the investment weights that maximizes expected return for a level of expected risk, or vice-versa. Presently, these functions rely on Monte Carlo sampling, and so are rather slow.

For this purpose, the function `create_asset_weights` can generate a matrix of asset weights, which can then be passed to `monte_carlo_portfolios` to do the optimization itself. `plot_efficient_portfolios` can be used to plot the optimization output.

See the package vignette `vignette("metafolio")` for more extensive explanation of how to use **metafolio** along with some examples.

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- Michelle M. McClure [contributor]
- Nicholas K. Dulvy [contributor]
- Andrew B. Cooper [contributor]

See Also

Useful links:

- https://github.com/seananderson/metafolio
- Report bugs at https://github.com/seananderson/metafolio/issues

`metasim_base` *Base-level metapopulation simulation function*

Description

This is an Rcpp implementation of the main simulation. It is meant to be called by `meta_sim`.

Usage

```
metasim_base(
  n_pop,
  n_t,
  spawners_0,
  b,
  epsilon_mat,
  A_params,
  add_straying,
  stray_mat,
  assess_years,
  r_escp_goals,
  sigma_impl,
  add_impl_error,
  decrease_b,
  debug
)
```

Arguments

`n_pop`	Number of populations
`n_t`	The number of years.
`spawners_0`	A vector of spawner abundances at the start of the simulation. Length of the vector should equal the number of populations.
`b`	Ricker density-dependent parameter. A vector with one numeric value per population.
`epsilon_mat`	A matrix of recruitment deviations.
`A_params`	A matrix of Ricker a parameters
`add_straying`	Implement straying between populations?
`stray_mat`	A straying matrix.
`assess_years`	A vector of years to assess a and b in
`r_escp_goals`	A matrix of escapement goals.
`sigma_impl`	Implementation standard deviation for the implementation error beta distribution.
`add_impl_error`	Add implementation error? Implementation error is derived using `impl_error`.

decrease_b	A numeric value to decrease all streams by each generation. This is intended to be used to simulate habitat loss, for example though stream flow reduction with climate change.
debug	Boolean. Should some debuging messages be turned on?

`monte_carlo_portfolios` *Monte Carlo asset weights into portfolios*

Description

Monte Carlo the asset weights into portfolios and record the simulation output and portfolio metrics (mean and variance).

Usage

```
monte_carlo_portfolios(
  weights_matrix,
  n_sims = 500,
  mean_b = 1000,
  burn = 1:30,
  ...
)
```

Arguments

weights_matrix	A matrix of asset weights. The columns correspond to the different assets and the rows correspond to the simulation iterations.
n_sims	The number of simulations to run.
mean_b	The mean Ricker capacity value.
burn	The number of years to discard as burn in.
...	Anything else to pass to meta_sim.

Value

A list object with three elements: port_vals (a matrix with a column of mean rate of change and variance of rate of change), n_sims (the number of simulations ran), and sims_out (a list in which each element corresponds to the output from the run of meta_sim.

See Also

meta_sim, create_asset_weights

Examples

```
weights_matrix <- create_asset_weights(n_pop = 4, n_sims = 3,
  weight_lower_limit = 0.001)
mc_ports <- monte_carlo_portfolios(weights_matrix = weights_matrix,
  n_sims = 3, mean_b = 1000)
```

---

my.axis *Add a pretty axis*

Description

Add a pretty axis

Usage

```
my.axis(side, shade_years = NULL, ylab = "", yticks = NA)
```

Arguments

side	Number indicating the side to add an axis (as in the side number passed to axis).
shade_years	An optional numerical vector of length two giving the minimum and maximum years over which to add a light grey shading.
ylab	Y axis label
yticks	Logical: should y-axis ticks be added?

---

optim_thermal *Optimize to find optimal max productivity Ricker a*

Description

Optimize to find optimal max productivity Ricker a

Usage

```
optim_thermal(optim_temp, width_param, desired_area)
```

Arguments

optim_temp	The optimum temperature as a numeric value
width_param	The width parameter as a numeric value
desired_area	The desired area as a numeric value

plot_cons_plans *Plot conservation plans in mean-variance space*

Description

This makes a mean-variance plot of the portfolio output. It can take care of: plotting the individual portfolios, adding 2D kernel density polygons at two quantile levels, and adding an efficient frontier.

Usage

```
plot_cons_plans(
  plans_mv,
  plans_name,
  cols,
  xlim = NULL,
  ylim = NULL,
  add_pts = TRUE,
  add_all_efs = FALSE,
  x_axis = TRUE,
  y_axis = TRUE,
  add_legend = TRUE,
  legend_pos = "topright",
  w_show = "all",
  xlab = "Variance",
  ylab = "Mean",
  add_poly = TRUE,
  ...
)
```

Arguments

plans_mv	The plans_mv element of the output from run_cons_plans.
plans_name	A character vector of what to label each conservation plan.
cols	Colours for the conservation plan polygons.
xlim	X limits
ylim	Y limits
add_pts	Logical: add the points?
add_all_efs	Logical: add efficient frontiers?
x_axis	Logical: add x axis?
y_axis	Logical: add y axis?
add_legend	Logical: add y legend?
legend_pos	A character string to pass to legend denoting the position of the legend.
w_show	If "all" then all plans will be shown. If a numeric vector, then those plans will be shown. E.g. c(1, 3) will only show the first and third plans.

xlab	X axis label.
ylab	Y axis label.
add_poly	Add the kernal smoother quantile polygons?
...	Anything else to pass to plot.default.

Value

A plot. Also, the x and y limits are returned invisibly as a list. This makes it easy to make the first plot and then save those x and y limits to fix them in subsequent (multipanel) plots.

`plot_correlation_between_returns` *Plot correlation of returns (i.e. metapopulation abundance) across stocks.*

Description

Create a matrix plot showing the correlation between the log returns of each stock/asset.

Usage

```
plot_correlation_between_returns(
  x,
  burn = 1:30,
  pal = rev(gg_color_hue(x$n_pop)),
  xlab = "log of return abundance by population",
  ylab = "log of return abundance by population"
)
```

Arguments

x	A list output object from meta_sim.
burn	Number of years to discard at start as burn in.
pal	Colours to label each stock/asset.
xlab	X axis label
ylab	Y axis label

Value

A plot

Examples

```
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)
base1 <- meta_sim(n_pop = 10, env_params = arma_env_params, env_type =
  "arma", assess_freq = 5)
plot_correlation_between_returns(base1)
```

`plot_efficient_portfolios` *Basic plot of efficient portfolio and asset contributions*

Description

This function creates a mean-variance plot of the portfolios across possible asset weights, colour the efficient frontier, and show the contribution of the different stocks/assets. It also (invisibly) returns the values that make up the plot so you can create your own custom plots with the data. See the Returns section for more details.

Usage

```
plot_efficient_portfolios(
  port_vals,
  weights_matrix,
  pal,
  plot = TRUE,
  ylab_dots = "Mean of metapopulation growth rate",
  xlab_dots = "Variance of metapopulation growth rate",
  ylab_bars = "Percentage",
  xlab_bars = "Variance (multiplied by 1000)",
  port_cols = c("grey50", "red"),
  pch = 19,
  ...
)
```

Arguments

`port_vals`	A matrix of means and variances (down the two columns). This likely comes from the output of `monte_carlo_portfolios`.
`weights_matrix`	The same weight matrix that was passed to `monte_carlo_portfolios`.
`pal`	Colour palette for the stocks/assets in the barplot.
`plot`	Logical: should the plots be made?
`ylab_dots`	Y axis label for the mean-variance scatterplot.
`xlab_dots`	X axis label for the mean-variance scatterplot.
`ylab_bars`	Y axis label for the barplot.
`xlab_bars`	X axis label for the barplot.
`port_cols`	Colours for the dots. A vector of colours for the non-efficient and efficient portfolios.
`pch`	Dot type
`...`	Anything else to pass to both `plot.default` and `barplot`.

Value

A two panel plot and an (invisible) list of values calculated within the function. This list contains `pv` (mean, variance, and whether it was part of the efficient frontier); `ef_port_ids` (the portfolio IDs [run numbers] that are part of the efficient frontier; `min_var_port_id` (the portfolio ID for the minimum-variance portfolio); `ef_weights` (the weights of the portfolios on the efficient frontier).

Examples

```
## Not run:
weights_matrix <- create_asset_weights(n_pop = 6, n_sims = 3000,
weight_lower_limit = 0.001)
mc_ports <- monte_carlo_portfolios(weights_matrix = weights_matrix,
 n_sims = 3000, mean_b = 1000)

col_pal <- rev(gg_color_hue(6))
ef_dat <- plot_efficient_portfolios(port_vals = mc_ports$port_vals,
 pal = col_pal, weights_matrix = weights_matrix)
names(ef_dat)

## End(Not run)
```

---

plot_panel_lines *Standard matrix plot of values by stream for one panel:*

Description

Standard matrix plot of values by stream for one panel:

Usage

```
plot_panel_lines(dat, ymin = c("zero", "min"), ystretch = 1.1, ...)
```

Arguments

`dat`	The matrix of values to plot
`ymin`	Minimum y value for axis
`ystretch`	A fraction to multiply the max value of when setting the y axis limits. This is useful to make space for a panel label within the plot.
`...`	Anything else to pass to `matplot`.

plot_rickers *Plot sample Ricker curves for each stock*

Description

Make a plot of Ricker curves for each stock. Can be useful for visualizing how the simulation parameters are impacting the Ricker curves and how these vary with temperature across stocks. The colour of the lines corresponds to the relative thermal tolerance of that stock. The shaded region shows the range of spawners observed throughout the simulations.

Usage

```
plot_rickers(
  x,
  pal = rep("black", x$n_pop),
  n_samples = 40,
  add_y_axes_pops = c(1, 6),
  add_x_axes_pops = c(6:10),
  burn = 1:30,
  add_shading = TRUE,
  ...
)
```

Arguments

x	Output list from meta_sim.
pal	Colours for stocks.
n_samples	Number of sample lines to draw from the a parameters.
add_y_axes_pops	Panels to add y axes on.
add_x_axes_pops	Panels to add x axes on.
burn	Number of initial years to throw out as burn in.
add_shading	Logical: add the light grey shading for the range of observed spawner abundance?
...	Anything else to pass to plot.default.

Value

A plot

Examples

```
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)
base1 <- meta_sim(n_pop = 10, env_params = arma_env_params, env_type =
  "arma", assess_freq = 5)
plot_rickers(base1)
```

plot_sim_ts *Plot various time series from a simulation run*

Description

This function lets you quickly visualize the time series of output from a simulation run.

Usage

```
plot_sim_ts(
  x,
  pal = rev(gg_color_hue(x$n_pop)),
  years_to_show = 30,
  burn = 1:50,
  shade_years = NULL,
  adj = 0.02,
  add_units = FALSE,
  yticks = rep(list(NA), 10),
  oma = c(4, 4.5, 1, 1)
)
```

Arguments

x	A list output object from a simulation run of link{meta_sim}.
pal	A colour palette for the lines. One colour per line (each line is a population time series).
years_to_show	How many years to plot after the burn in period.
burn	The number of years to discard as burn in at the beginning of the time series.
shade_years	Shade some years? Give a vector. Shading will be applied from the minimum to maximum value. Can be used to show burn in period.
adj	adj parameter to pass to mtext for panel labels
add_units	Should the units be added to the y axis?
yticks	Position of ticks on the Y axis.
oma	oma vector to pass to par for outer margin space.

Value

A plot

Examples

```
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)
base1 <- meta_sim(n_pop = 10, env_params = arma_env_params, env_type =
  "arma", assess_freq = 5, decrease_b = 10)
plot_sim_ts(base1, years_to_show = 70, burn = 1:30)
```

plot_sp_A_ts *Plot sample time series from a portfolio simulation*

Description

Plot sample time series from a portfolio simulation

Usage

```
plot_sp_A_ts(
  X,
  ylim,
  x_axis = TRUE,
  y_axis = TRUE,
  rate = FALSE,
  lwd = 1.7,
  y_axis_ticks = NULL,
  start_new_plots = 1,
  labels = NULL,
  burn = 30,
  add_lm = FALSE,
  cols,
  ...
)
```

Arguments

X	Object to plot. Should be a list of outputs from meta_sim.
ylim	Y axis limits.
x_axis	Should an x axis be added?
y_axis	Should a y axis be added?
rate	If TRUE then the first difference (rate of change) will be plotted. If FALSE then the raw data will be plotted.
lwd	Line width of the lines.
y_axis_ticks	Location of the y-axis tick marks, if you want to specify them.
start_new_plots	On which elements of the list X should new panels be started? A numeric vector.
labels	Labels for the panels.
burn	Burn in period to discard.
add_lm	Add a regression trend line?
cols	Colours for the lines. A vector of character.
...	Anything else to pass to plot.default

Value

A plot, possibly with multiple panels.

Examples

```
w_plans <- list()
w_plans[[1]] <- c(5, 1000, 5, 1000, 5, 5, 1000, 5, 1000, 5)
w_plans[[2]] <- c(5, 5, 5, 1000, 1000, 1000, 1000, 5, 5, 5)
w_plans[[3]] <- c(rep(1000, 4), rep(5, 6))
w_plans[[4]] <- rev(w_plans[[3]])
w <- list()
for(i in 1:4) { # loop over plans
 w[[i]] <- list()
 for(j in 1:2) { # loop over trials
   w[[i]][[j]] <- matrix(w_plans[[i]], nrow = 1)
 }
}

cons_arma_ts <- list()
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)
for(i in 1:4) {
  use_cache <- ifelse(i == 1, FALSE, TRUE)
  cons_arma_ts[[i]] <- meta_sim(b = w[[i]][[1]], n_pop = 10, env_params =
    arma_env_params, env_type = "arma", assess_freq = 5,
    use_cache = use_cache)
}
cols <- RColorBrewer::brewer.pal(5, "Dark2")
par(mfrow = c(2, 1))
plot_sp_A_ts(cons_arma_ts, ylim = c(0000, 12400),
  start_new_plots = c(1, 3),
  labels = c("Balanced response diversity",
    "ignore", "Unbalanced response diversity", "ignore"), cols = cols)
```

`ricker` *A simple Ricker model*

Description

A simple Ricker model

Usage

```
ricker(spawners, a, b)
```

Arguments

`spawners`	Spawner abundance
`a`	Ricker productivity parameter. Recruits are e^a at the origin.
`b`	Ricker density dependent parameter.

Value

Returns the number of recruits.

Examples

```
S <- seq(100, 1000, length.out = 100)
R <- ricker(S, a = 1.9, b = 900)
plot(S, R)
```

`ricker_escapement` *Assign a salmon escapement target based on a Ricker curve*

Description

Sets escapement according to Hilborn and Walters (1992) p272, Table 7.2. Smsy = b(0.5 - 0.07*a).

Usage

```
ricker_escapement(a, b)
```

Arguments

a	Ricker productivity parameter.
b	Ricker density-dependent parameter.

References

Hilborn, R.W. and Walters, C. 1992. Quantitative fisheries stock assessment: Choice, dynamics, and uncertainty. Chapman and Hall, London.

Examples

```
ricker_escapement(1.1, 1000)
```

ricker_v_t *Ricker stock-recruit function with specified error*

Description

Ricker stock-recruit function with specified error

Usage

```
ricker_v_t(spawners, a, b, d, v_t)
```

Arguments

spawners	A single spawner abundance
a	Ricker productivity parameter. Recruits are e^a at the origin.
b	Ricker density dependent parameter.
d	Depensation parameter. A value of 1 means no depensation. Larger values indicate depensation.
v_t	A single residual on the curve. Will be exponentiated. Note that we are *not* bias correcting within this function (subtracting half the variance squared) and so the deviations will not be mean unbiased unless they were bias corrected previously.

Value

Returns a vector of recruits.

Examples

```
plot(1, 1, xlim = c(1, 100), ylim = c(0, 90), type = "n", xlab = "Spawners",
  ylab = "Returns")
for(i in 1:100) {
points(i, ricker_v_t(i, a = 1.1, b = 60, d = 1, v_t = rnorm(1, mean =
  -(0.1^2)/2, sd = 0.1)))
}
```

run_cons_plans *Run conservation plans and return the portfolio mean and variance values*

Description

This function takes a set of weights representing different conservation plans and gets the mean and variance in portfolio space. This function allows a maximally complicated set of weights to accommodate all possible scenarios. It can accommodate different spatial strategies of conservation, conserving different numbers of populations, and a lack of knowledge. You can do this by how you set your w weight object. See the example.

Usage

```
run_cons_plans(
  w,
  env_type,
  env_params,
  show_progress = TRUE,
  burn = 1:30,
  assess_freq = 5,
  risk_fn = var,
  ...
)
```

Arguments

w	A (nested) list of weights. The first list level contains the different plans. The next level contains repetitions for a given plan. E.g. cp[[2]][[1]] contains the first iteration of the second conservation plan. Each end element should be a matrix of weights with one row and the number of columns equal to the number of subpopulations.
env_type	The environmental type to pass to generate_env_ts
env_params	The environmental parameters to pass to generate_env_ts
show_progress	Logical: show an indication of progress?
burn	Cycles to throw out as burn in
assess_freq	How frequently (in years) to re-assess the Ricker a and b values.
risk_fn	A risk function to use. Can be any function that takes a numeric vector and returns a single value. Suggested values include var, or VaR, or CVaR. Defaults to variance.
...	Other values to pass to meta_sim

Value

A list with two high-level elements: the mean variance output (plans_mv) and the raw simulation output (plans_port). Within plans_mv, each element of the list contains a conservation plan. Each row of the data frames represents a trial run. Within plans_port, each first level of the list contains a weight element and each second level of the list contains a replicate.

Examples

```
## Not run:
set.seed(1)
w_plans <- list()
w_plans[[1]] <- c(5, 1000, 5, 1000, 5, 5, 1000, 5, 1000, 5)
w_plans[[2]] <- c(5, 5, 5, 1000, 1000, 1000, 1000, 5, 5, 5)
w_plans[[3]] <- c(rep(1000, 4), rep(5, 6))
w_plans[[4]] <- rev(w_plans[[3]])
plans_name_sp <- c("Full range of responses", "Most stable only",
"Lower half", "Upper half")
```

```
 n_trials <- 50 # number of trials at each n conservation plan
 n_plans <- 4 # number of plans
 num_pops <- c(2, 4, 8, 16) # n pops to conserve
 w <- list()
 for(i in 1:n_plans) { # loop over number conserved
  w[[i]] <- list()
  for(j in 1:n_trials) { # loop over trials
    w[[i]][[j]] <- matrix(rep(625, 16), nrow = 1)
    w[[i]][[j]][-sample(1:16, num_pops[i])] <- 5
  }
 }
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)

x_arma_sp <- run_cons_plans(w, env_type = "arma", env_params = arma_env_params)

plot_cons_plans(x_arma_sp$plans_mv, plans_name = plans_name_sp, cols =
  cols, add_all_efs = FALSE, xlim = c(0.02, 0.15), ylim = c(-0.017,
    0.017), add_legend = FALSE)

# In this version, the pops are wiped out; total abundance changes
n_trials <- 50 # number of trials at each n conservation plan
num_pops <- c(2, 4, 8, 16) # n pops to conserve
n_plans <- length(num_pops) # number of plans
w <- list()
for(i in 1:n_plans) { # loop over number conserved
 w[[i]] <- list()
 for(j in 1:n_trials) { # loop over trials
   w[[i]][[j]] <- matrix(rep(1000, 16), nrow = 1)
   w[[i]][[j]][-sample(1:16, num_pops[i])] <- 5
 }
}
plans_name_n <- paste(num_pops, "populations")
arma_env_params <- list(mean_value = 16, ar = 0.1, sigma_env = 2, ma = 0)

x_arma_n <- run_cons_plans(w, env_type = "arma", env_params =
  arma_env_params, max_a = thermal_integration(16))

plot_cons_plans(x_arma_n$plans_mv, plans_name = plans_name_n, cols =
  cols, add_all_efs = FALSE, xlim = c(0.02, 0.15), ylim = c(-0.017,
    0.017), add_legend = FALSE)

## End(Not run)
```

`thermal_area` *Return desired squared deviation between desired area and actual area under a curve*

Description

The function finds the lower and upper roots (where the thermal curve crosses 0) with the `uniroot` function and then integrates the area under the thermal curve with the `integrate` function. This is

useful as part of the optimization routine in optim_thermal.

Usage

```
thermal_area(
  max_a,
  desired_area,
  optim_temp,
  width_param,
  lower = -5,
  upper = 40
)
```

Arguments

max_a	Maximum Ricker a productivity value
desired_area	Desired area under the thermal curve
optim_temp	Optimal temperature
width_param	The width parameter as a numeric value
lower	Lower bound to pass to uniroot
upper	Upper bound to pass to uniroot

---

thermal_curve_a *Create thermal tolerance curves.*

Description

Creates a quadratic thermal tolerance curve of the form: width_param * (temp - optim_temp)^2 + max_a Negative values are *not* returned as 0 for speed of computation. You should check for this after.

Usage

```
thermal_curve_a(temp, optim_temp = 15, max_a = 1.4, width_param = 0.02)
```

Arguments

temp	The input temperature value.
optim_temp	The optimal temperature.
max_a	The maximum productivity parameter ‘a‘ from a Ricker model (or whatever the y-axis value is you want to return).
width_param	A parameter to control the width of the parabola. Smaller numbers make wider parabolas.

Value

A productivity parameter given the location on a thermal tolerance curve.

Examples

```
x <- seq(5, 30, length.out = 200)
plot(x, thermal_curve_a(x), ylab = "a", xlab = "Temperature", type
= "l")
```

`thermal_integration` *Integrate thermal tolerance curves to get maximum Ricker a values*

Description

Get maximum Ricker a values for a given number of populations. Useful for assembling multiple thermal tolerance curves in which each has the same total area under it.

Usage

```
thermal_integration(
  n_pop,
  width_params = c(seq(0.05, 0.02, length.out = n_pop/2), rev(seq(0.05, 0.02, length.out
    = n_pop/2))),
  optim_temps = seq(13, 19, length.out = n_pop),
  desired_area = 30
)
```

Arguments

`n_pop`	The number of populations.
`width_params`	Desired widths of the thermal tolerance curves.
`optim_temps`	Temperature value at which to reach the peak of each thermal tolerance curve.
`desired_area`	Desired area under each curve.

Value

A vector of Ricker a values

Examples

```
# Minimal example:
thermal_integration(16)

# Elaborate example:
optim_temps <- seq(13, 19, length.out = 10)
widths <- c(seq(0.05, 0.02, length.out = 5), rev(seq(0.05, 0.02,
      length.out = 5)))
```

```
heights <- c(seq(2.8, 2.2, length.out = 5), rev(seq(2.8, 2.2,
      length.out = 5)))
x <- seq(3, 29, length.out = 200)
plot(1, 1, xlim = c(4, 28), ylim = c(-0.01, 2.9), ylab = "Ricker
  productivity parameter (a)", xlab = "Environmental value", type =
  "n", yaxs = "i", las = 1)
for(i in 1:10) {
  a <- thermal_curve_a(x, optim_temp = optim_temps[i], max_a =
    heights[i], width_param = widths[i])
  lines(x, a, col = "grey40", lwd = 1.5)
}
```

VaR *Value at Risk*

Description

Get the value at risk.

Usage

```
VaR(x, probs = 0.05)
```

Arguments

x	A numeric vector
probs	The probability cutoff to pass to the value at risk.

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