Package ‘ypr’

May 8, 2026

Title Yield Per Recruit

Version 0.6.0

Description An implementation of equilibrium-based yield per recruit methods. Yield per recruit methods can used to estimate the optimal yield for a fish population as described by Walters and Martell (2004) <isbn:0-691-11544-3>. The yield can be based on the number of fish caught (or harvested) or biomass caught for all fish or just large (trophy) individuals.

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URL `https://github.com/poissonconsulting/ypr`

BugReports `https://github.com/poissonconsulting/ypr/issues`

Depends R (>= 3.6)

Imports chk, ggplot2, graphics, lifecycle, purrr, stats, tibble, tidyplus, tools, yesno

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Contents

`adams_bt_03` *Adams Lake Bull Trout Population Parameters (2003)*

Description

The population parameters for Bull Trout in Adams Lake from Bison et al (2003)

Usage

```
adams_bt_03
```

Format

An object of class `ypr_population()`.

References

Bison, R., O'Brien, D., and Martell, S.J.D. 2003. An Analysis of Sustainable Fishing Options for Adams Lake Bull Trout Using Life History and Telemetry Data. BC Ministry of Water Land and Air Protection, Kamloops, B.C.

See Also

Other data: `chilliwack_bt_05`, `kootenay_bt_13`, `kootenay_rb_13`, `kootenay_rb`, `quesnel_bt`, `quesnel_lt`, `quesnel_rb`

Examples

```
adams_bt_03
ypr_plot_yield(adams_bt_03)
```

`as_ypr_ecotypes` *Coerce to an Ecotypes Object*

Description

Coerce to an Ecotypes Object

Usage

```
as_ypr_ecotypes(x, ...)

## S3 method for class 'data.frame'
as_ypr_ecotypes(x, ...)

## S3 method for class 'ypr_population'
as_ypr_ecotypes(x, ...)

## S3 method for class 'ypr_populations'
as_ypr_ecotypes(x, ...)

## S3 method for class 'ypr_ecotypes'
as_ypr_ecotypes(x, ...)
```

Arguments

`x`	The object to coerce.
`...`	Additional arguments.

Value

An object of class ypr_ecotypes.

Methods (by class)

- `as_ypr_ecotypes(data.frame)`: Coerce a data.frame to an Ecotypes Object
- `as_ypr_ecotypes(ypr_population)`: Coerce a Population Object to an Ecotypes Object
- `as_ypr_ecotypes(ypr_populations)`: Coerce a Populations Object to an Ecotypes Object
- `as_ypr_ecotypes(ypr_ecotypes)`: Coerce an Ecotypes Object to an Ecotypes Object

See Also

Other ecotypes: `ypr_ecotypes()`

Examples

```
as_ypr_ecotypes(as.data.frame(ypr_ecotypes(Ls = c(10, 15, 20))))
as_ypr_ecotypes(ypr_population())
as_ypr_ecotypes(ypr_populations(Ls = c(10, 15, 20)))
as_ypr_ecotypes(ypr_ecotypes(Ls = c(10, 15, 20)))
```

`as_ypr_population` *Coerce to a Population Object*

Description

Coerce to a Population Object

Usage

```
as_ypr_population(x, ...)

## S3 method for class 'data.frame'
as_ypr_population(x, ...)

## S3 method for class 'ypr_population'
as_ypr_population(x, ...)

## S3 method for class 'ypr_populations'
as_ypr_population(x, ...)

## S3 method for class 'ypr_ecotypes'
as_ypr_population(x, ...)

## S3 method for class 'data.frame'
as_ypr_populations(x, ...)
```

Arguments

`x`	The object to coerce.
`...`	Unused.

Value

An object of class ypr_population.

Methods (by class)

- `as_ypr_population(data.frame)`: Coerce a data.frame to an Population Object
- `as_ypr_population(ypr_population)`: Coerce a Population Object to an Population Object
- `as_ypr_population(ypr_populations)`: Coerce a Populations Object of length 1 to a Population Object
- `as_ypr_population(ypr_ecotypes)`: Coerce a Ecotypes Object of length 1 to a Population Object

Functions

- `as_ypr_populations(data.frame)`: Coerce a data.frame to a Populations Object

Examples

```
as_ypr_population(as.data.frame(ypr_population()))
as_ypr_population(ypr_populations())
as_ypr_population(ypr_populations())
as_ypr_population(ypr_ecotypes())
as_ypr_populations(as.data.frame(ypr_populations(Rk = c(3, 4))))
```

`as_ypr_populations` *Coerce to a Populations Object*

Description

Coerce to a Populations Object

Usage

```
as_ypr_populations(x, ...)

## S3 method for class 'ypr_population'
as_ypr_populations(x, ...)

## S3 method for class 'ypr_populations'
as_ypr_populations(x, ...)

## S3 method for class 'ypr_ecotypes'
as_ypr_populations(x, ...)
```

Arguments

`x`	The object to coerce.
`...`	Unused.

Value

An object of class ypr_ecotypes.

Methods (by class)

- `as_ypr_populations(ypr_population)`: Coerce a Population Object to an Population Object
- `as_ypr_populations(ypr_populations)`: Coerce a Populations Object of length 1 to a Population Object
- `as_ypr_populations(ypr_ecotypes)`: Coerce a Ecotypes Object of length 1 to a Population Object

See Also

Other populations: `chilliwack_bt_05`, `ypr_plot_yield()`, `ypr_populations_expand()`, `ypr_populations()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Examples

```
as_ypr_populations(ypr_population())
as_ypr_populations(ypr_populations())
as_ypr_populations(ypr_ecotypes())
```

`check_ecotypes` *Check Ecotypes*

Description

Checks if an ypr_ecotypes object with valid parameter values.

Usage

```
check_ecotypes(x, x_name = NULL)
```

Arguments

`x`	The object to check.
`x_name`	A string of the name of object x or NULL.

Value

An informative error if the test fails or an invisible copy of x.

See Also

Other check: `check_populations()`, `check_population()`

Examples

```
check_ecotypes(ypr_ecotypes())
```

`check_population` *Check Population*

Description

Checks if an ypr_population object with valid parameter values.

Usage

```
check_population(x, x_name = NULL)
```

Arguments

`x`	The object to check.
`x_name`	A string of the name of object x or NULL.

Value

An informative error if the test fails or an invisible copy of x.

See Also

Other check: `check_ecotypes()`, `check_populations()`

Examples

```
check_population(ypr_population())
```

`check_populations` *Check Populations*

Description

Checks if an ypr_populations object with valid parameter values.

Usage

```
check_populations(x, x_name = NULL)
```

Arguments

`x`	The object to check.
`x_name`	A string of the name of object x or NULL.

Value

An informative error if the test fails or an invisible copy of x.

See Also

Other check: `check_ecotypes()`, `check_population()`

Examples

```
check_populations(ypr_populations())
```

`chilliwack_bt_05` *Chilliwack Lake Bull Trout Populations Parameters (2005)*

Description

The populations parameters for Bull Trout in Chilliwack Lake from Taylor (2005)

Usage

```
chilliwack_bt_05
```

Format

An object of class `ypr_populations()`.

References

Taylor, J.L. 2005. Sustainability of the Chilliwack Lake Char Fishery. Ministry of Water, Land and Air Protection, Surrey, B.C.

See Also

Other populations: `as_ypr_populations()`, `ypr_plot_yield()`, `ypr_populations_expand()`, `ypr_populations()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other data: `adams_bt_03`, `kootenay_bt_13`, `kootenay_rb_13`, `kootenay_rb`, `quesnel_bt`, `quesnel_lt`, `quesnel_rb`

Examples

```
chilliwack_bt_05
yield <- ypr_tabulate_yield(chilliwack_bt_05, type = "optimal")
yield$pi <- round(yield$pi, 2)
yield <- yield[c("Llo", "Hm", "Rk", "pi")]
yield <- tidyr::spread(yield, Rk, pi)
yield <- yield[order(-yield$Hm), ]
yield
## Not run:
```

```
ypr_plot_yield(chilliwack_bt_05, plot_values = FALSE) +
  ggplot2::facet_grid(Rk ~ Hm) +
  ggplot2::aes(group = Llo, linetype = Llo)

## End(Not run)
```

`is.ypr_population` *Tests if is a Population, Populations or Ecotypes*

Description

Tests if is a Population, Populations or Ecotypes

Usage

```
is.ypr_population(x)

is_ypr_population(x)

is.ypr_populations(x)

is_ypr_populations(x)

is.ypr_ecotypes(x)

is_ypr_ecotypes(x)
```

Arguments

`x`	The object to test.

Functions

- `is_ypr_population()`: Test if is a Population
- `is.ypr_populations()`: Test if is a Populations
- `is_ypr_populations()`: Test if is a Populations
- `is.ypr_ecotypes()`: Test if is an Ecotypes
- `is_ypr_ecotypes()`: Test if is an Ecotypes

Examples

```
is.ypr_population(ypr_population())
is_ypr_population(ypr_population())
is.ypr_populations(ypr_populations())
is_ypr_population(ypr_populations())
is.ypr_ecotypes(ypr_ecotypes())
is_ypr_ecotypes(ypr_ecotypes())
```

`kootenay_bt_13` *Kootenay Lake Bull Trout Population Parameters (2013)*

Description

The population parameters for Bull Trout in Kootenay Lake from Andrusak and Thorley (2013)

Usage

```
kootenay_bt_13
```

Format

An object of class `ypr_population()`.

Details

The estimates should not be used for management.

References

Andrusak, G.F., and Thorley, J.L. 2013. Kootenay Lake Exploitation Study: Fishing and Natural Mortality of Large Rainbow Trout and Bull Trout: 2013 Annual Report. A Poisson Consulting Ltd. and Redfish Consulting Ltd. Report, Habitat Conservation Trust Foundation, Victoria, BC.

See Also

Other data: `adams_bt_03`, `chilliwack_bt_05`, `kootenay_rb_13`, `kootenay_rb`, `quesnel_bt`, `quesnel_lt`, `quesnel_rb`

Examples

```
kootenay_bt_13
ypr_plot_yield(kootenay_bt_13)
```

`kootenay_rb` *Kootenay Lake Rainbow Trout Population Parameters*

Description

The population parameters for Rainbow Trout in Kootenay Lake.

Usage

```
kootenay_rb
```

Format

An object of class `ypr_population()`.

Details

The estimates are liable to change and should not be used for management.

References

Thorley, J.L., and Andrusak, G.F. 2017. The fishing and natural mortality of large, piscivorous Bull Trout and Rainbow Trout in Kootenay Lake, British Columbia (2008–2013). PeerJ 5: e2874. doi:10.7717/peerj.2874.

See Also

Other data: `adams_bt_03`, `chilliwack_bt_05`, `kootenay_bt_13`, `kootenay_rb_13`, `quesnel_bt`, `quesnel_lt`, `quesnel_rb`

Examples

```
kootenay_rb
ypr_plot_yield(kootenay_rb)
```

`kootenay_rb_13` *Kootenay Lake Rainbow Trout Population Parameters (2013)*

Description

The population parameters for Rainbow Trout in Kootenay Lake from Andrusak and Thorley (2013)

Usage

```
kootenay_rb_13
```

Format

An object of class `ypr_population()`.

Details

The estimates should not be used for management.

References

Andrusak, G.F., and Thorley, J.L. 2013. Kootenay Lake Exploitation Study: Fishing and Natural Mortality of Large Rainbow Trout and Bull Trout: 2013 Annual Report. A Poisson Consulting Ltd. and Redfish Consulting Ltd. Report, Habitat Conservation Trust Foundation, Victoria, BC.

See Also

Other data: `adams_bt_03`, `chilliwack_bt_05`, `kootenay_bt_13`, `kootenay_rb`, `quesnel_bt`, `quesnel_lt`, `quesnel_rb`

Examples

```
kootenay_rb_13
ypr_plot_yield(kootenay_rb_13)
```

`plot.ypr_population` *Plot Population Schedule*

Description

Plot Population Schedule

Usage

```
## S3 method for class 'ypr_population'
plot(x, type = "b", ...)
```

Arguments

`x`	The population to plot.
`type`	A string specifying the plot type. Possible values include 'b', 'p' and 'l'.
`...`	Additional arguments passed to graphics::plot function.

Value

An invisible copy of the original object.

See Also

graphics::plot

Examples

```
## Not run:
plot(ypr_population())

## End(Not run)
```

`quesnel_bt` *Quesnel Lake Bull Trout Population Parameters*

Description

The population parameters for Bull Trout in Quesnel Lake, BC.

Usage

```
quesnel_bt
```

Format

An object of class `ypr_population()`.

Details

The estimates are liable to change and should not be used for management.

See Also

Other data: `adams_bt_03`, `chilliwack_bt_05`, `kootenay_bt_13`, `kootenay_rb_13`, `kootenay_rb`, `quesnel_lt`, `quesnel_rb`

Examples

```
quesnel_bt
ypr_plot_yield(quesnel_bt)
```

`quesnel_lt` *Quesnel Lake Lake Trout Population Parameters*

Description

The population parameters for Lake Trout in Quesnel Lake, BC.

Usage

```
quesnel_lt
```

Format

An object of class `ypr_population()`.

Details

The estimates are liable to change and should not be used for management.

See Also

Other data: `adams_bt_03`, `chilliwack_bt_05`, `kootenay_bt_13`, `kootenay_rb_13`, `kootenay_rb`, `quesnel_bt`, `quesnel_rb`

Examples

```
quesnel_lt
ypr_plot_yield(quesnel_lt)
```

`quesnel_rb` *Quesnel Lake Rainbow Trout Population Parameters*

Description

The population parameters for Rainbow Trout in Quesnel Lake, BC.

Usage

```
quesnel_rb
```

Format

An object of class `ypr_population()`.

Details

The estimates are liable to change and should not be used for management.

See Also

Other data: `adams_bt_03`, `chilliwack_bt_05`, `kootenay_bt_13`, `kootenay_rb_13`, `kootenay_rb`, `quesnel_bt`, `quesnel_lt`

Examples

```
quesnel_rb
ypr_plot_yield(quesnel_rb)
```

`ypr_age_at_length` *Age At Length*

Description

Age At Length

Usage

```
ypr_age_at_length(population, length)
```

Arguments

`population`	An object of class `ypr_population()`.
`length`	A numeric vector of the length (cm).

Value

A double vector of the lengths.

See Also

Other calculate: `ypr_exploitation()`, `ypr_length_at_age()`, `ypr_optimize()`, `ypr_yields()`, `ypr_yield()`

Examples

```
ypr_age_at_length(ypr_population(), seq(0, 100, by = 10))
```

`ypr_detabulate_parameters` *Detabulate Population Parameters*

Description

Detabulate Population Parameters

Usage

```
ypr_detabulate_parameters(x)
```

Arguments

`x`	A data frame with columns Parameter and Value specifying one or more parameters and their values.

Value

An object of class `ypr_population()`

See Also

Other tabulate: `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other parameters: `ypr_tabulate_parameters()`

Examples

```
ypr_detabulate_parameters(ypr_tabulate_parameters(ypr_population()))
```

`ypr_ecotypes` *Create Ecotypes Object*

Description

Creates an ypr_ecotypes object.

Usage

```
ypr_ecotypes(..., names = NULL)
```

Arguments

`...`	Unused parameters.
`names`	A character vector of unique ecotype names.

Value

An `ypr_ecotypes()` objects

See Also

Other ecotypes: `as_ypr_ecotypes()`

Examples

```
ypr_ecotypes(Linf = c(1, 2))
ypr_ecotypes(Linf = c(1, 2), t0 = c(0, 0.5))
```

`ypr_exploitation` *Exploitation Probability*

Description

Converts capture probabilities into exploitation probabilities based on the release and handling mortality probabilities where the probability of exploitation includes handling mortalities. The calculation assumes that a released fish cannot be recaught in the same year.

Usage

```
ypr_exploitation(object, pi = ypr_get_par(object))
```

Arguments

`object`	The population or populations.
`pi`	A vector of capture probabilities to calculate the exploitation probabilities for.

Details

In the case of no release (or 100% handling mortalities) the exploitation probability is identical to the capture probability. Otherwise it is less.

Value

A vector of exploitation probabilities.

See Also

Other calculate: `ypr_age_at_length()`, `ypr_length_at_age()`, `ypr_optimize()`, `ypr_yields()`, `ypr_yield()`

Examples

```
ypr_exploitation(ypr_population(pi = 0.4))
ypr_exploitation(ypr_population(pi = 0.4, rho = 0.6, Hm = 0.2))
```

`ypr_get_par` *Get Parameter Value*

Description

Get Parameter Value

Usage

```
ypr_get_par(object, par = "pi")
```

Arguments

`object`	A ypr object.
`par`	A string of the parameter.

Value

A numeric or integer scalar or vector of the parameter value.

Examples

```
ypr_get_par(ypr_population())
```

`ypr_length_at_age` *Length At Age*

Description

Length At Age

Usage

```
ypr_length_at_age(population, age)
```

Arguments

`population`	An object of class `ypr_population()`.
`age`	A numeric vector of the age (yr).

Value

A double vector of the lengths.

See Also

Other calculate: `ypr_age_at_length()`, `ypr_exploitation()`, `ypr_optimize()`, `ypr_yields()`, `ypr_yield()`

Examples

```
ypr_length_at_age(ypr_population(), seq(0, 5, by = 0.5))
```

`ypr_names` *Population(s) or Ecotype Names*

Description

Generates set of unique names based on differences in parameter values.

Usage

```
ypr_names(x, ...)

## S3 method for class 'ypr_population'
ypr_names(x, ...)

## S3 method for class 'ypr_populations'
ypr_names(x, ...)

## S3 method for class 'ypr_ecotypes'
ypr_names(x, ...)
```

Arguments

`x`	An object of class ypr_population, ypr_populations or ypr_ecotypes.
`...`	Unused.

Details

Parameter RPR is ignored because it is irrelevant to population(s) and does not distinguish between ecotypes.

Value

A character vector of the unique parameter based names.

Methods (by class)

- `ypr_names(ypr_population)`: Population Names
- `ypr_names(ypr_populations)`: Populations Names
- `ypr_names(ypr_ecotypes)`: Ecotypes Names

Examples

```
ypr_names(ypr_population())
ypr_names(ypr_populations())
ypr_names(ypr_populations())
```

`ypr_optimize` *Optimize Capture*

Description

Finds the interval annual capture probability (pi) that maximises the yield for a given population.

Usage

```
ypr_optimize(object, Ly = 0, harvest = TRUE, biomass = FALSE)
```

Arguments

`object`	The population or populations.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.

Value

The interval annual capture probability (pi) that maximises the yield.

See Also

Other calculate: `ypr_age_at_length()`, `ypr_exploitation()`, `ypr_length_at_age()`, `ypr_yields()`, `ypr_yield()`

Examples

```
ypr_optimize(ypr_population())
```

`ypr_plot_biomass` *Plot Biomass*

Description

Produces a frequency histogram of the total fish 'Biomass' or 'Eggs' deposition by 'Age' class.

Usage

```
ypr_plot_biomass(population, y = "Biomass", color = NULL)
```

Arguments

`population`	An object of class `ypr_population()`.
`y`	A string of the term on the y-axis.
`color`	A string of the color around each bar (or NULL).

Value

A ggplot2 object.

See Also

`ggplot2::geom_histogram()`

Other biomass: `ypr_tabulate_biomass()`

Other plot: `ypr_plot_fish()`, `ypr_plot_schedule()`, `ypr_plot_sr()`, `ypr_plot_yield()`

Examples

```
ypr_plot_biomass(ypr_population(), color = "white")
```

`ypr_plot_fish` *Plot Fish*

Description

Produces a frequency histogram of the number of fish in the 'Survivors', 'Spawners', 'Caught', 'Harvested' or 'Released' categories by 'Length', 'Age' or 'Weight' class.

Usage

```
ypr_plot_fish(
  population,
  x = "Age",
  y = "Survivors",
  percent = FALSE,
  binwidth = 1L,
  color = NULL
)
```

Arguments

`population`	An object of class `ypr_population()`.
`x`	The object to coerce.
`y`	A string of the term on the y-axis.
`percent`	A flag specifying whether to plot the number of fish as a percent or frequency (the default).
`binwidth`	A positive integer of the width of the bins for grouping.
`color`	A string of the color around each bar (or NULL).

Value

A ggplot2 object.

See Also

`ggplot2::geom_histogram()`

Other fish: `ypr_tabulate_fish()`

Other plot: `ypr_plot_biomass()`, `ypr_plot_schedule()`, `ypr_plot_sr()`, `ypr_plot_yield()`

Examples

```
ypr_plot_fish(ypr_population(), color = "white")
```

`ypr_plot_schedule` *Plot Population or Ecotypes Schedule Terms*

Description

Produces a bivariate line plot of two schedule terms.

Usage

```
ypr_plot_schedule(population, x = "Age", y = "Length")
```

Arguments

`population`	An object of class `ypr_population()`.
`x`	A string of the term on the x-axis.
`y`	A string of the term on the y-axis.

Value

A ggplot2 object.

See Also

Other schedule: `ypr_tabulate_schedule()`

Other plot: `ypr_plot_biomass()`, `ypr_plot_fish()`, `ypr_plot_sr()`, `ypr_plot_yield()`

Examples

```
ypr_plot_schedule(ypr_population())
```

`ypr_plot_sr` *Plot Stock-Recruitment Curve*

Description

Plot Stock-Recruitment Curve

Usage

```
ypr_plot_sr(
  population,
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  plot_values = TRUE
)
```

Arguments

`population`	An object of class `ypr_population()`.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`plot_values`	A flag specifying whether to plot the actual and optimal values.

Value

A ggplot2 object.

See Also

Other sr: `ypr_sr()`, `ypr_tabulate_sr()`

Other plot: `ypr_plot_biomass()`, `ypr_plot_fish()`, `ypr_plot_schedule()`, `ypr_plot_yield()`

Examples

```
ypr_plot_sr(ypr_population(Rk = 10))
ypr_plot_sr(ypr_population(Rk = 10, BH = 0L))
```

`ypr_plot_yield` *Plot Yield by Capture*

Description

Plots the 'Yield', 'Age', 'Length', 'Weight', 'Effort', or 'YPUE' by the annual interval capture/exploitation probability.

Usage

```
ypr_plot_yield(object, ...)

## Default S3 method:
ypr_plot_yield(
  object,
  y = "Yield",
  pi = seq(0, 1, length.out = 100),
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  u = harvest,
  plot_values = TRUE,
  ...
)

## S3 method for class 'ypr_populations'
ypr_plot_yield(
  object,
  y = "Yield",
  pi = seq(0, 1, length.out = 100),
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  u = harvest,
```

```
  plot_values = TRUE,
  ...
)
```

Arguments

`object`	The population or populations.
`...`	Unused parameters.
`y`	A string of the term on the y-axis.
`pi`	A vector of probabilities of capture to calculate the yield for.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`u`	A flag specifying whether to plot the exploitation rate as opposed to the capture rate.
`plot_values`	A flag specifying whether to plot the actual and optimal values.

Value

A ggplot2 object.

Methods (by class)

- `ypr_plot_yield(default)`: Plot Yield by Capture
- `ypr_plot_yield(ypr_populations)`: Plot Yield by Capture

See Also

Other populations: `as_ypr_populations()`, `chilliwack_bt_05`, `ypr_populations_expand()`, `ypr_populations()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other yield: `ypr_tabulate_yield()`, `ypr_yields()`, `ypr_yield()`

Other plot: `ypr_plot_biomass()`, `ypr_plot_fish()`, `ypr_plot_schedule()`, `ypr_plot_sr()`

Examples

```
## Not run:
ypr_plot_yield(ypr_populations(
  Rk = c(2.5, 4.6),
  Llo = c(0, 60)
),
plot_values = FALSE
) +
  ggplot2::facet_wrap(~Llo) +
  ggplot2::aes_string(group = "Rk", color = "Rk") +
  ggplot2::scale_color_manual(values = c("black", "blue"))
```

```
ypr_plot_yield(ypr_populations(Rk = c(2.5, 4.6), Llo = c(0, 60))) +
  ggplot2::facet_grid(Rk ~ Llo)

## End(Not run)

ypr_plot_yield(ypr_population())
```

`ypr_population` *Population Parameters*

Description

Generates an object of class `ypr_population`.

Usage

```
ypr_population(
  tmax = 20L,
  k = 0.15,
  Linf = 100,
  t0 = 0,
  k2 = 0.15,
  Linf2 = 100,
  L2 = 1000,
  Wb = 3,
  Ls = 50,
  Sp = 100,
  es = 1,
  Sm = 0,
  fb = 1,
  tR = 1L,
  BH = 1L,
  Rk = 3,
  n = 0.2,
  nL = 0.2,
  Ln = 1000,
  Lv = 50,
  Vp = 100,
  Llo = 0,
  Lup = 1000,
  Nc = 0,
  pi = 0.2,
  rho = 0,
  Hm = 0,
  Rmax = 1,
  Wa = 0.01,
  fa = 1,
```

```
  q = 0.1,
  RPR = 1
)
```

Arguments

`tmax`	The maximum age (yr).
`k`	The VB growth coefficient (yr-1).
`Linf`	The VB mean maximum length (cm).
`t0`	The (theoretical) age at zero length (yr).
`k2`	The VB growth coefficient after length L2 (yr-1).
`Linf2`	The VB mean maximum length after length L2 (cm).
`L2`	The length (or age if negative) at which growth switches from the first to second phase (cm or yr).
`Wb`	The weight (as a function of length) scaling exponent.
`Ls`	The length (or age if negative) at which 50 % mature (cm or yr).
`Sp`	The maturity (as a function of length) power.
`es`	The annual probability of a mature fish spawning.
`Sm`	The spawning mortality probability.
`fb`	The fecundity (as a function of weight) scaling exponent.
`tR`	The age from which survival is density-independent (yr).
`BH`	Recruitment follows a Beverton-Holt (1) or Ricker (0) relationship.
`Rk`	The lifetime spawners per spawner at low density (or the egg to tR survival if between 0 and 1).
`n`	The annual interval natural mortality rate from age tR.
`nL`	The annual interval natural mortality rate from length Ln.
`Ln`	The length (or age if negative) at which the natural mortality rate switches from n to nL (cm or yr).
`Lv`	The length (or age if negative) at which 50 % vulnerable to harvest (cm or yr).
`Vp`	The vulnerability to harvest (as a function of length) power.
`Llo`	The lower harvest slot length (cm).
`Lup`	The upper harvest slot length (cm).
`Nc`	The slot limits non-compliance probability.
`pi`	The annual capture probability.
`rho`	The release probability.
`Hm`	The hooking mortality probability.
`Rmax`	The number of recruits at the carrying capacity (ind).
`Wa`	The (extrapolated) weight of a 1 cm individual (g).
`fa`	The (theoretical) fecundity of a 1 g female (eggs).
`q`	The catchability (annual probability of capture) for a unit of effort.
`RPR`	The relative proportion of recruits that are of the ecotype.

Value

An object of class `ypr_population`.

Examples

```
ypr_population(k = 0.1, Linf = 90)
```

`ypr_populations` *Populations*

Description

Populations

Usage

```
ypr_populations(..., expand = TRUE, names = NULL)
```

Arguments

`...`	Unused parameters.
`expand`	A flag specifying whether to expand parameter combinations.
`names`	A character vector of unique ecotype names.

Value

A list of `ypr_population()` objects

See Also

Other populations: `as_ypr_populations()`, `chilliwack_bt_05`, `ypr_plot_yield()`, `ypr_populations_expand()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Examples

```
ypr_populations(Rk = c(2.5, 4.6), Hm = c(0.2, 0.05))
```

`ypr_populations_expand` *Expand Populations*

Description

An object of class `ypr_population()` of all unique combinations of parameter values.

Usage

```
ypr_populations_expand(populations)
```

Arguments

`populations`	An object of class `ypr_populations()`.

Value

An object of class `ypr_population`.

See Also

Other populations: `as_ypr_populations()`, `chilliwack_bt_05`, `ypr_plot_yield()`, `ypr_populations()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Examples

```
ypr_populations_expand(
  ypr_populations(
    Rk = c(2.5, 4, 2.5),
    Hm = c(0.1, 0.2, 0.1)
  )
)
```

`ypr_population_names` *Population Names*

Description

Generates set of unique names based on differences in parameter values. **[Deprecated]**

Usage

```
ypr_population_names(population)
```

Arguments

`population`	An object of class ypr_population, ypr_populations or ypr_ecotypes.

Value

A character vector of the unique parameter based names.

See Also

`ypr_names()`

`ypr_population_update` *Update a Population Object*

Description

[Deprecated] for `ypr_update()`.

Usage

```
ypr_population_update(population, ...)
```

Arguments

`population`	A ypr_population object.
`...`	One or more parameter values from `ypr_population()`.

`ypr_report` *Report*

Description

Creates an Rmd file that can be used to generate a report.

Usage

```
ypr_report(
  population,
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  title = "Population Report",
  description = "",
  date = Sys.Date(),
  file = "report",
  view = FALSE,
  ask = TRUE
)
```

Arguments

`population`	An object of class `ypr_population()`.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`title`	A string of the report title.
`description`	A string describing the population.
`date`	A date of the report date.
`file`	A string of the path to the file (without the extension).
`view`	A flag specifying whether to view the report (after rendering it to html).
`ask`	A flag specifying whether to ask before overwriting or creating a file.

Value

An invisible character vector of the contents of the file.

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Examples

```
## Not run:
ypr_report(ypr_population(), file = tempfile(), ask = FALSE)

## End(Not run)
```

`ypr_sr` *Stock-Recruitment Parameters*

Description

Returns a single rowed data frame of the SR parameters:

alpha	Survival from egg to age tR at low density
beta	Density-dependence
Rk	Lifetime spawners per spawner at low density
phi	Lifetime eggs deposited per recruit at unfished equilibrium
phiF	Lifetime eggs deposited per recruit at the fished equilibrium
R0	Age tR recruits at the unfished equilibrium
R0F	Age tR recruits at the fished equilibrium
S0	Spawners at the unfished equilibrium
S0F	Spawners at the fished equilibrium

Usage

```
ypr_sr(object)
```

Arguments

`object`	The population or populations.

Value

A data frame of the SR parameters.

See Also

Other sr: `ypr_plot_sr()`, `ypr_tabulate_sr()`

Examples

```
ypr_sr(ypr_population()) # Beverton-Holt
ypr_sr(ypr_population(BH = 0L)) # Ricker
```

`ypr_tabulate_biomass` *Tabulate Biomass (and Eggs)*

Description

Produces a data frame of the ’Weight’ and ’Fecundity’ and the number of ’Survivors’ and ’Spawners’ and the total ’Biomass’ and ’Eggs’ by ’Age’ class.

Usage

```
ypr_tabulate_biomass(population)
```

Arguments

`population`	An object of class `ypr_population()`.

Value

A data frame

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other biomass: `ypr_plot_biomass()`

Examples

```
ypr_tabulate_biomass(ypr_population())
```

`ypr_tabulate_fish` *Tabulate Fish Numbers*

Description

Produces a data frame of the number of fish in the 'Survivors', 'Spawners', 'Caught', 'Harvested', 'Released' and 'HandlingMortalities' categories by 'Length', 'Age' or 'Weight' class and 'Ecotype' (NA if not applicable)

Usage

```
ypr_tabulate_fish(population, x = "Age", binwidth = 1L)
```

Arguments

`population`	An object of class `ypr_population()`.
`x`	The object to coerce.
`binwidth`	A positive integer of the width of the bins for grouping.

Value

A data frame

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_parameters`
`ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other fish: `ypr_plot_fish()`

Examples

```
ypr_tabulate_fish(ypr_population())
```

`ypr_tabulate_parameters` *Tabulate Population Parameters*

Description

Tabulate Population Parameters

Usage

```
ypr_tabulate_parameters(population)
```

Arguments

`population`	An object of class `ypr_population()`.

Value

A table of population parameters

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other parameters: `ypr_detabulate_parameters()`

Examples

```
ypr_tabulate_parameters(ypr_population())
```

`ypr_tabulate_schedule` *Life-History Schedule*

Description

Generates the life-history schedule by age for a population.

Usage

```
ypr_tabulate_schedule(object, ...)

## S3 method for class 'ypr_population'
ypr_tabulate_schedule(object, ...)

## S3 method for class 'ypr_ecotypes'
ypr_tabulate_schedule(object, ...)
```

Arguments

`object`	The population or populations.
`...`	Unused parameters.

Value

A tibble of the life-history schedule by age.

Methods (by class)

- `ypr_tabulate_schedule(ypr_population)`: Tabulate Schedule
- `ypr_tabulate_schedule(ypr_ecotypes)`: Tabulate Schedule

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other schedule: `ypr_plot_schedule()`

Examples

```
ypr_tabulate_schedule(ypr_population())
ypr_tabulate_schedule(ypr_ecotypes(Linf = c(10, 20)))
```

`ypr_tabulate_sr` *Tabulate Stock-Recruitment Parameters*

Description

Tabulate Stock-Recruitment Parameters

Usage

```
ypr_tabulate_sr(object, ...)

## Default S3 method:
ypr_tabulate_sr(
  object,
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  all = FALSE,
  ...
)

## S3 method for class 'ypr_populations'
ypr_tabulate_sr(
  object,
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  all = FALSE,
  ...
)
```

Arguments

`object`	The population or populations.
`...`	Unused parameters.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).

`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`all`	A flag specifying whether to include all parameter values.

Value

A data.frame of stock-recruitment parameters.

Methods (by class)

- `ypr_tabulate_sr(default)`: Tabulate Stock-Recruitment Parameters
- `ypr_tabulate_sr(ypr_populations)`: Tabulate Stock-Recruitment Parameters

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_schedule()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other populations: `as_ypr_populations()`, `chilliwack_bt_05`, `ypr_plot_yield()`, `ypr_populations_expand()`, `ypr_populations()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

Other sr: `ypr_plot_sr()`, `ypr_sr()`

Examples

```
ypr_tabulate_sr(ypr_population()) # Beverton-Holt
ypr_tabulate_sr(ypr_population(BH = 0L)) # Ricker
ypr_tabulate_sr(ypr_populations(Rk = c(2.5, 4.6)))
```

`ypr_tabulate_yield` *Tabulate Yield*

Description

Tabulate Yield

Usage

```
ypr_tabulate_yield(object, ...)

## Default S3 method:
ypr_tabulate_yield(
  object,
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  type = "both",
```

```
  all = FALSE,
  ...
)

## S3 method for class 'ypr_populations'
ypr_tabulate_yield(
  object,
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  type = "both",
  all = FALSE,
  ...
)
```

Arguments

`object`	The population or populations.
`...`	Unused parameters.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`type`	A string indicating whether to include 'both' or just the 'actual' or 'optimal' yield.
`all`	A flag specifying whether to include all parameter values.

Value

A data frame.

Methods (by class)

- `ypr_tabulate_yield(default)`: Tabulate Yield
- `ypr_tabulate_yield(ypr_populations)`: Tabulate Yield

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`

Other populations: `as_ypr_populations()`, `chilliwack_bt_05`, `ypr_plot_yield()`, `ypr_populations_expand()`, `ypr_populations()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`

Other yield: `ypr_plot_yield()`, `ypr_yields()`, `ypr_yield()`

Examples

```
ypr_tabulate_yield(ypr_population())
ypr_tabulate_yield(ypr_populations(Rk = c(3, 5)))
```

`ypr_tabulate_yields` *Tabulate Yields*

Description

Tabulate Yields

Usage

```
ypr_tabulate_yields(object, ...)

## Default S3 method:
ypr_tabulate_yields(
  object,
  pi = seq(0, 1, length.out = 100),
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  all = FALSE,
  ...
)

## S3 method for class 'ypr_populations'
ypr_tabulate_yields(
  object,
  pi = seq(0, 1, length.out = 100),
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE,
  all = FALSE,
  ...
)
```

Arguments

`object`	The population or populations.
`...`	Unused parameters.
`pi`	A vector of probabilities of capture to calculate the yield for.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`all`	A flag specifying whether to include all parameter values.

Value

A data frame.

Methods (by class)

- `ypr_tabulate_yields(default)`: Tabulate Yields
- `ypr_tabulate_yields(ypr_populations)`: Tabulate Yields

See Also

Other tabulate: `ypr_detabulate_parameters()`, `ypr_report()`, `ypr_tabulate_biomass()`, `ypr_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_schedule()`, `ypr_tabulate_sr()`, `ypr_tabulate_yield()`

Other populations: `as_ypr_populations()`, `chilliwack_bt_05`, `ypr_plot_yield()`, `ypr_populations_expand()`, `ypr_populations()`, `ypr_tabulate_sr()`, `ypr_tabulate_yield()`

Examples

```
ypr_tabulate_yields(ypr_population())
ypr_tabulate_yields(
  ypr_populations(
    Rk = c(3, 5)
  ),
  pi = seq(0, 1, length.out = 10)
)
ypr_tabulate_yields(ypr_ecotypes(Linf = c(10, 20)))
```

`ypr_update` *Update a YPR Object Currently just works with scalar parameters for populations and ecotypes.*

Description

Update a YPR Object Currently just works with scalar parameters for populations and ecotypes.

Usage

```
ypr_update(x, ...)

## S3 method for class 'ypr_population'
ypr_update(x, ...)

## S3 method for class 'ypr_populations'
ypr_update(x, ...)

## S3 method for class 'ypr_ecotypes'
ypr_update(x, ...)
```

Arguments

`x`	A population, populations or ecotypes object to update.
`...`	One or more parameter values from `ypr_population()`.

Methods (by class)

- `ypr_update(ypr_population)`: Update Population Parameters
- `ypr_update(ypr_populations)`: Update Populations Parameters
- `ypr_update(ypr_ecotypes)`: Update Populations Parameters

Examples

```
ypr_update(ypr_population(), Rk = 2.5)
ypr_update(ypr_populations(Rk = c(2.5, 4)), Rk = 2.5)
ypr_update(ypr_ecotypes(Linf = c(2.5, 4)), k = 1.5)
```

`ypr_yield` *Yield*

Description

Calculates the yield for a population.

Usage

```
ypr_yield(object, Ly = 0, harvest = TRUE, biomass = FALSE, ...)
```

Arguments

`object`	The population or populations.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.
`...`	Unused parameters.

Details

By default, with `Rmax = 1` the number of individuals is the proportion of the recruits at the carrying capacity. If the yield is given in terms of the biomass (kg) then the scaling also depends on the value of `Wa` (g).

Value

The yield as number of fish or biomass.

See Also

Other yield: `ypr_plot_yield()`, `ypr_tabulate_yield()`, `ypr_yields()`

Other calculate: `ypr_age_at_length()`, `ypr_exploitation()`, `ypr_length_at_age()`, `ypr_optimize()`, `ypr_yields()`

Examples

```
ypr_yield(ypr_population())
ypr_yield(ypr_ecotypes(Linf = c(100, 200)))
```

`ypr_yields` *Yields*

Description

Calculates the yield(s) for a population based on one or more capture rates.

Usage

```
ypr_yields(
  object,
  pi = seq(0, 1, length.out = 100),
  Ly = 0,
  harvest = TRUE,
  biomass = FALSE
)
```

Arguments

`object`	The population or populations.
`pi`	A vector of probabilities of capture to calculate the yield for.
`Ly`	The minimum length (trophy) fish to consider when calculating the yield (cm).
`harvest`	A flag specifying whether to calculate the yield for harvested fish or captures.
`biomass`	A flag specifying whether to calculate the yield in terms of the biomass versus number of individuals.

Value

A numeric vector of the yields.

See Also

Other yield: `ypr_plot_yield()`, `ypr_tabulate_yield()`, `ypr_yield()`

Other calculate: `ypr_age_at_length()`, `ypr_exploitation()`, `ypr_length_at_age()`, `ypr_optimize()`, `ypr_yield()`

Examples

```
pi <- seq(0, 1, length.out = 30)
plot(pi, ypr_yields(ypr_population(), pi), type = "l")
```

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