

# Package: ypr (via r-universe)

June 18, 2024

**Title** Yield Per Recruit

**Version** 0.6.0.9000

**Description** An implementation of equilibrium-based yield per recruit methods. Yield per recruit methods can be 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

**Suggests** covr, knitr, readr, rmarkdown, rstudioapi, scales, testthat (>= 3.0.0), tidy, usethis, withr

**VignetteBuilder** knitr

**ByteCompile** true

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-US

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Repository** <https://poissonconsulting.r-universe.dev>

**RemoteUrl** <https://github.com/poissonconsulting/ypr>

**RemoteRef** HEAD

**RemoteSha** 708f12e548716ff5cf4875af1b6d49980525a6fc

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`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_populations(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**

<code>x</code>	The object to coerce.
<code>...</code>	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	<i>Check Ecotypes</i>
----------------	-----------------------

---

**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_populations(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	<i>Quesnel Lake Bull Trout Population Parameters</i>
------------	--

---

**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	<i>Quesnel Lake Lake Trout Population Parameters</i>
------------	--

---

**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	<i>Age At Length</i>
-------------------	----------------------

---

**Description**

Age At Length

**Usage**

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

**Arguments**

population	An object of class <code>ypr_population()</code> .
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	<i>Exploitation Probability</i>
------------------	---------------------------------

---

### 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 recaptured 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	<i>Get Parameter Value</i>
-------------	----------------------------

---

**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	<i>Length At Age</i>
-------------------	----------------------

---

**Description**

Length At Age

**Usage**

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

**Arguments**

population	An object of class <code>ypr_population()</code> .
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	<i>Population(s) or Ecotype Names</i>
-----------	---------------------------------------

---

**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 **annual interval** 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 **annual interval** 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 <a href="#">ypr_population()</a> .
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	<i>Plot Population or Ecotypes Schedule Terms</i>
-------------------	---

---

**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 <code>ypr_population()</code> .
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 <code>ypr_population()</code> .
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	<i>Plot Yield by Capture</i>
----------------	------------------------------

---

**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.
L <sub>y</sub>	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	<i>Population Parameters</i>
----------------	------------------------------

---

### 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 <b>annual interval</b> natural mortality rate from age tR.
nL	The <b>annual interval</b> natural mortality rate from length Ln.
Ln	The length (or age if negative) at which the annual interval 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	<i>Populations</i>
-----------------	--------------------

---

**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 <code>ypr_population()</code> .
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**

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

**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  $R_{max} = 1$  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  $W_a$  (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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