

# Package ‘ypr’

July 10, 2020

**Version** 0.5.1

**Title** Yield Per Recruit

**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.

**License** MIT + file LICENSE

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

**BugReports** <https://github.com/poissonconsulting/ypr/issues>

**Depends** R (>= 3.4)

**Imports** chk, yesno, ggplot2, graphics, scales, stats, tools, purrr,  
lifecycle

**Suggests** covr, testthat, knitr, rmarkdown, rstudioapi, tidyr

**Encoding** UTF-8

**LazyData** true

**ByteCompile** true

**RoxygenNote** 7.1.1.9000

**VignetteBuilder** knitr

**Language** en-US

**NeedsCompilation** no

**Author** Joe Thorley [aut, cre] (<<https://orcid.org/0000-0002-7683-4592>>),  
Poisson Consulting [cph, fnd]

**Maintainer** Joe Thorley <joe@poissonconsulting.ca>

**Repository** CRAN

**Date/Publication** 2020-07-10 17:10:02 UTC

**R topics documented:**

adams_bt_03 . . . . .	3
as_ypr_population . . . . .	3
as_ypr_populations . . . . .	4
chilliwack_bt_05 . . . . .	5
kootenay_bt_13 . . . . .	5
kootenay_rb . . . . .	6
kootenay_rb_13 . . . . .	7
plot.ypr_population . . . . .	7
quesnel_bt . . . . .	8
quesnel_lt . . . . .	9
quesnel_rb . . . . .	9
update.ypr_population . . . . .	10
update.ypr_populations . . . . .	11
ypr_age_at_length . . . . .	12
ypr_detabulate_parameters . . . . .	12
ypr_exploitation . . . . .	13
ypr_length_at_age . . . . .	14
ypr_optimize . . . . .	14
ypr_plot_biomass . . . . .	15
ypr_plot_fish . . . . .	16
ypr_plot_schedule . . . . .	17
ypr_plot_sr . . . . .	17
ypr_plot_yield . . . . .	18
ypr_plot_yield.ypr_population . . . . .	19
ypr_plot_yield.ypr_populations . . . . .	20
ypr_population . . . . .	21
ypr_populations . . . . .	23
ypr_populations_expand . . . . .	24
ypr_population_names . . . . .	24
ypr_report . . . . .	25
ypr_schedule . . . . .	26
ypr_sr . . . . .	26
ypr_tabulate_biomass . . . . .	27
ypr_tabulate_fish . . . . .	28
ypr_tabulate_parameters . . . . .	28
ypr_tabulate_sr . . . . .	29
ypr_tabulate_yield . . . . .	30
ypr_tabulate_yields . . . . .	32
ypr_yield . . . . .	33
ypr_yields . . . . .	34

---

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.

**Examples**

```
adams_bt_03
ypr_plot_yield(adams_bt_03)
```

---

as\_ypr\_population

*Coerce to a Population Parameter Object*


---

**Description**

Coerce to a Population Parameter Object

**Usage**

```
as_ypr_population(x, ...)

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

**Arguments**

x                    The object to coerce.  
...                    Unused.

**Methods (by class)**

- `data.frame`: Coerce data frame to `ypr_population`

**Examples**

```
as_ypr_population(as.data.frame(ypr_population()))
```

---

`as_ypr_populations`      *Coerce to a Populations Parameter Object*

---

**Description**

Coerce to a Populations Parameter Object

**Usage**

```
as_ypr_populations(x, ...)
```

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

**Arguments**

<code>x</code>	The object to coerce.
<code>...</code>	Unused.

**Methods (by class)**

- `data.frame`: Coerce data frame to `ypr_populations`

**Examples**

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

---

`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.

**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)
```

---

`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.

**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.

**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**

`kootenay_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 <a href="#">graphics::plot</a> function.

**Value**

An invisible copy of the original object.

**See Also**

[graphics::plot](#), [ypr\\_population\(\)](#) and [ypr\\_tabulate\\_schedule\(\)](#)

**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.

**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.

**Examples**

```
quesnel_lt  
ypr_plot_yield(quesnel_lt)
```

---

quesnel_rb	<i>Quesnel Lake Rainbow Trout Population Parameters</i>
------------	---

---

**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.

**Examples**

```
quesnel_rb  
ypr_plot_yield(quesnel_rb)
```

---

update.ypr\_population *Update Population Parameters*

---

### Description

Updates an object of class `ypr_population()`.

### Usage

```
## S3 method for class 'ypr_population'  
update(object, ...)  
  
ypr_population_update(population, ...)
```

### Arguments

<code>object</code>	The populations or populations.
<code>...</code>	One or more of the arguments from <code>ypr_population()</code> .
<code>population</code>	An object of class <code>ypr_population()</code> .

### Value

An object of class `ypr_population`.

### Methods (by generic)

- `update`: Update Population Parameters

### See Also

`ypr_population()`

### Examples

```
ypr_population_update(ypr_population(), Rk = 2.5)
```

---

`update.ypr_populations`*Update Population Parameters*

---

**Description**

Updates an object of class `ypr_population()`.

**Usage**

```
## S3 method for class 'ypr_populations'  
update(object, ...)
```

```
ypr_populations_update(populations, ...)
```

**Arguments**

<code>object</code>	The populations or populations.
<code>...</code>	One or more of the arguments from <code>ypr_population()</code> .
<code>populations</code>	An object of class <code>ypr_populations()</code> .

**Value**

An object of class `ypr_population`.

**Methods (by generic)**

- `update`: Update Populations Parameters

**See Also**

`ypr_population()`

**Examples**

```
ypr_populations_update(ypr_populations(Rk = c(2.5, 4)), Rk = 2.5)
```

---

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.

**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**

[ypr\\_tabulate\\_parameters\(\)](#)

**Examples**

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

---

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(population, pi = population$pi)
```

**Arguments**

population	An object of class <a href="#">ypr_population()</a> .
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**

[ypr\\_population\(\)](#)

**Examples**

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

---

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.

### Examples

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

---

ypr\_optimize            *Optimize Capture*

---

### Description

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

### Usage

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

### 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.

### Value

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

**See Also**

[ypr\\_population\(\)](#) and [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 <a href="#">ypr_population()</a> .
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**

[ypr\\_population\(\)](#) and [ggplot2::geom\\_histogram\(\)](#)

**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**

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

**Value**

A `ggplot2` object.

**See Also**

`ypr_population()` and `ggplot2::geom_histogram()`

**Examples**

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



---

ypr\_plot\_schedule      *Plot Population 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 <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**

[ypr\\_population\(\)](#) and [ypr\\_tabulate\\_schedule\(\)](#)

**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**

`ypr_population()` and `ypr_sr()`

**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 probability.

**Usage**

```
ypr_plot_yield(object, ...)
```

**Arguments**

object	The populations or populations.
...	Unused parameters.

**Value**

A ggplot2 object.

**See Also**

`ypr_population()` and `ypr_yields()`

**Examples**

```
ypr_plot_yield(ypr_population())
```

---

ypr\_plot\_yield.ypr\_population

*Plot Yield by Exploitation/Capture Probability*


---

### Description

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

### Usage

```
## S3 method for class 'ypr_population'
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 populations or populations.
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.
...	Unused parameters.

### Value

A ggplot2 object.

### See Also

[ypr\\_population\(\)](#) and [ypr\\_yields\(\)](#)

**Examples**

```
ypr_plot_yield(ypr_population())
```

---

```
ypr_plot_yield.ypr_populations
```

*Plot Yield by Exploitation/Capture Probability*

---

**Description**

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

**Usage**

```
## 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 populations or populations.
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.
...	Unused parameters.

**Value**

A ggplot2 object.

**See Also**

[ypr\\_populations\(\)](#) and [ypr\\_yields\(\)](#)

**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\_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
)

```

### Arguments

tmax	The maximum age (yr).
k	The VB growth coefficient (yr <sup>-1</sup> ).
Linf	The VB mean maximum length (cm).
t0	The (theoretical) age at zero length (yr).
k2	The VB growth coefficient after length L2 (yr <sup>-1</sup> ).
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.
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.

**Value**

An object of class `ypr_population`.

**See Also**

[ypr\\_population\\_update\(\)](#), [ypr\\_tabulate\\_schedule\(\)](#), [ypr\\_yield\(\)](#) and [ypr\\_optimize\(\)](#).

**Examples**

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

---

ypr_populations	<i>Populations</i>
-----------------	--------------------

---

**Description**

Populations

**Usage**

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

**Arguments**

...	Unused parameters.
expand	A flag specifying whether to expand parameter combinations.

**Value**

A list of [ypr\\_population\(\)](#) objects

**See Also**

[ypr\\_population\(\)](#)

**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**

[ypr\\_population\(\)](#)

**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**

Population Names

**Usage**

```
ypr_population_names(populations)
```

**Arguments**

populations     An object of class `ypr_populations()`.

**Value**

A character vector of the unique population names.



**Examples**

```
ypr_population_names(ypr_populations(Rk = c(2.5, 3, 2.5), expand = FALSE))
```

---

ypr_report	<i>Report</i>
------------	---------------

---

**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.

**Examples**

```
ypr_report(ypr_population(), file = tempfile(), ask = FALSE)
```

---

ypr\_schedule                      *Life-History Schedule*

---

### Description

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

### Usage

```
ypr_schedule(population)
```

```
ypr_tabulate_schedule(population)
```

### Arguments

population            An object of class `ypr_population()`.

### Value

A tibble of the life-history schedule by age.

### Functions

- `ypr_schedule`: Tabulate Schedule (Deprecated)

### See Also

`ypr_population()`

### Examples

```
ypr_tabulate_schedule(ypr_population())
```

---

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(population)
```

**Arguments**

population      An object of class `ypr_population()`.

**Value**

A data frame of the SR parameters.

**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_tabulate_fish()`, `ypr_tabulate_parameters()`, `ypr_tabulate_sr()`, `ypr_tabulate_yields()`, `ypr_tabulate_yield()`

**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.

**Usage**

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

**Arguments**

population      An object of class [ypr\\_population\(\)](#).  
 x                A string of the term on the x-axis.  
 binwidth        A positive integer of the width of the bins for grouping.

**Value**

A data frame

**See Also**

Other tabulate: [ypr\\_tabulate\\_biomass\(\)](#), [ypr\\_tabulate\\_parameters\(\)](#), [ypr\\_tabulate\\_sr\(\)](#), [ypr\\_tabulate\\_yields\(\)](#), [ypr\\_tabulate\\_yield\(\)](#)

**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**

[ypr\\_detabulate\\_parameters\(\)](#)

Other tabulate: [ypr\\_tabulate\\_biomass\(\)](#), [ypr\\_tabulate\\_fish\(\)](#), [ypr\\_tabulate\\_sr\(\)](#), [ypr\\_tabulate\\_yields\(\)](#), [ypr\\_tabulate\\_yield\(\)](#)

**Examples**

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

---

ypr_tabulate_sr	<i>Tabulate Stock-Recruitment Parameters</i>
-----------------	--

---

**Description**

Tabulate Stock-Recruitment Parameters

**Usage**

```
ypr_tabulate_sr(object, ...)
```

```
## S3 method for class 'ypr_population'
```

```
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 populations 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\_population: Tabulate Stock-Recruitment Parameters
- ypr\_populations: Tabulate Stock-Recruitment Parameters

**See Also**

Other tabulate: [ypr\\_tabulate\\_biomass\(\)](#), [ypr\\_tabulate\\_fish\(\)](#), [ypr\\_tabulate\\_parameters\(\)](#), [ypr\\_tabulate\\_yields\(\)](#), [ypr\\_tabulate\\_yield\(\)](#)

**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, ...)

## S3 method for class 'ypr_population'
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 populations 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\_population: Tabulate Yield
- ypr\_populations: Tabulate Yield

### See Also

Other tabulate: [ypr\\_tabulate\\_biomass\(\)](#), [ypr\\_tabulate\\_fish\(\)](#), [ypr\\_tabulate\\_parameters\(\)](#), [ypr\\_tabulate\\_sr\(\)](#), [ypr\\_tabulate\\_yields\(\)](#)

### 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, ...)

## S3 method for class 'ypr_population'
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 populations 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\_population: Tabulate Yields
- ypr\_populations: Tabulate Yields

**See Also**

Other tabulate: [ypr\\_tabulate\\_biomass\(\)](#), [ypr\\_tabulate\\_fish\(\)](#), [ypr\\_tabulate\\_parameters\(\)](#), [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\_yield

*Yield*

---

**Description**

Calculates the yield for a population.

**Usage**

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

**Arguments**

population	An object of class <a href="#">ypr_population()</a> .
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.

**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**

[ypr\\_population\(\)](#) and [ypr\\_optimize\(\)](#)

**Examples**

```
ypr_yield(ypr_population())
```

---

ypr\_yields

*Yields*

---

**Description**

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

**Usage**

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

**Arguments**

population	An object of class <a href="#">ypr_population()</a> .
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**

[ypr\\_yield\(\)](#)

**Examples**

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

# Index

- \* **datasets**
  - adams\_bt\_03, 3
  - chilliwack\_bt\_05, 5
  - kootenay\_bt\_13, 5
  - kootenay\_rb, 6
  - kootenay\_rb\_13, 7
  - quesnel\_bt, 8
  - quesnel\_lt, 9
  - quesnel\_rb, 9
- \* **tabulate**
  - ypr\_tabulate\_biomass, 27
  - ypr\_tabulate\_fish, 28
  - ypr\_tabulate\_parameters, 28
  - ypr\_tabulate\_sr, 29
  - ypr\_tabulate\_yield, 30
  - ypr\_tabulate\_yields, 32
- adams\_bt\_03, 3
- as\_ypr\_population, 3
- as\_ypr\_populations, 4
- chilliwack\_bt\_05, 5
- ggplot2::geom\_histogram(), 15, 16
- graphics::plot, 8
- kootenay\_bt\_13, 5
- kootenay\_rb, 6
- kootenay\_rb(), 7
- kootenay\_rb\_13, 7
- plot.ypr\_population, 7
- quesnel\_bt, 8
- quesnel\_lt, 9
- quesnel\_rb, 9
- update.ypr\_population, 10
- update.ypr\_populations, 11
- ypr\_age\_at\_length, 12
- ypr\_detabulate\_parameters, 12
- ypr\_detabulate\_parameters(), 29
- ypr\_exploitation, 13
- ypr\_length\_at\_age, 14
- ypr\_optimise (ypr\_optimize), 14
- ypr\_optimize, 14
- ypr\_optimize(), 23, 34
- ypr\_plot\_biomass, 15
- ypr\_plot\_fish, 16
- ypr\_plot\_schedule, 17
- ypr\_plot\_sr, 17
- ypr\_plot\_yield, 18
- ypr\_plot\_yield.ypr\_population, 19
- ypr\_plot\_yield.ypr\_populations, 20
- ypr\_population, 21
- ypr\_population(), 3, 6–19, 23–28, 33, 34
- ypr\_population\_names, 24
- ypr\_population\_update
  - (update.ypr\_population), 10
- ypr\_population\_update(), 23
- ypr\_populations, 23
- ypr\_populations(), 5, 11, 21, 24
- ypr\_populations\_expand, 24
- ypr\_populations\_update
  - (update.ypr\_populations), 11
- ypr\_report, 25
- ypr\_schedule, 26
- ypr\_sr, 26
- ypr\_sr(), 18
- ypr\_tabulate\_biomass, 27, 28–31, 33
- ypr\_tabulate\_fish, 27, 28, 29–31, 33
- ypr\_tabulate\_parameters, 27, 28, 28, 30, 31, 33
- ypr\_tabulate\_parameters(), 13
- ypr\_tabulate\_schedule (ypr\_schedule), 26
- ypr\_tabulate\_schedule(), 8, 17, 23
- ypr\_tabulate\_sr, 27–29, 29, 31, 33
- ypr\_tabulate\_yield, 27–30, 30, 33
- ypr\_tabulate\_yields, 27–31, 32

ypr\_yield, [33](#)  
ypr\_yield(), [15](#), [23](#), [34](#)  
ypr\_yields, [34](#)  
ypr\_yields(), [18](#), [19](#), [21](#)