Package: Rceattle (via r-universe)

June 10, 2026

Title Fits the Multispecies Assessment Model (CEATTLE) Using TMB

Version 4.5.0

Description Implements the CEATTLE model using Template Model Builder ('TMB'; Kristensen et al. 2015), which can be installed following <https://github.com/kaskr/adcomp/wiki/Download>. Structured similar to the original manuscript in terms of modularization. Separate functions estimate retrospective temperature- and size-specific predator rations, prey preference, and weight-at-age. These are then used as inputs to the CEATTLE model to evaluate how predation mortality, recruitment, and survival of three target species change under historical climate conditions and harvest rates.

URL https://grantdadams.github.io/Rceattle/, https://github.com/grantdadams/Rceattle

BugReports https://github.com/grantdadams/Rceattle/issues

License GPL (>= 2)

Encoding UTF-8

LazyData true

LazyDataCompression xz

Roxygen list(markdown = TRUE)

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Contents

`adjust_map_shared_params` *Helper to adjust map for shared catchability/selectivity indices*

Description

Enforces parameter sharing by mapping parameters for fleets with a common `Selectivity_index` or `Q_index` to the same value as the initial index.

Usage

```
adjust_map_shared_params(map_list, data_list)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.

Value

Updated `map_list`.

`as.data.frame.Rceattle`

Tidy long-format derived quantities from an Rceattle fit

Description

Returns the model's derived population quantities in long form so that custom plots and post-processing don't have to walk the deeply nested `quantities` list or inherit the dimnames decisions in `rename_output()`. Two shapes are flattened into one tidy frame: species-by-year quantities (e.g. `biomass`, `ssb`, `R`, `F_spp`) and species-by-sex-by-age-by-year quantities (e.g. `N_at_age`, `biomass_at_age`, `M_at_age`). For the species-level shapes, `sex` and `age` are returned as `NA`. Cells of the 4D arrays that are padded out to `max(nsex)` / `max(nages)` for species with fewer sexes or ages are dropped.

Usage

```
## S3 method for class 'Rceattle'
as.data.frame(
  x,
  row.names = NULL,
  optional = FALSE,
 which = c("biomass", "ssb", "R", "biomass_depletion", "ssb_depletion", "F_spp"),
  ci_level = 0.95,
  ...
)
```

Arguments

`x`	An object of class `"Rceattle"` returned by `fit_mod()`.
`row.names, optional`	Ignored; present for the `as.data.frame()` generic.
`which`	Character vector of quantity names to extract, or `"all"` for every quantity with a known shape. Defaults to a common population-level summary. See `names(Rceattle:::.RCEATTLE_QUA` for the full list.
`ci_level`	Confidence level for `lwr` and `upr`. Default `0.95`.
`...`	Currently unused.

Details

Standard errors (`se`) and confidence intervals (`lwr`, `upr`) are populated from the TMB `sdreport` for any quantity that was `ADREPORT`'d (currently `biomass`, `ssb`, `R`); other quantities and fits produced with `getsd` = `FALSE` get `NA` for `se` / `lwr` / `upr`. Set `ci_level` to widen or narrow the band.

Value

A `data.frame` with columns `year`, `species`, `sex`, `age`, `quantity`, `value`, `se`, `lwr`, `upr`. `species` is the character species name from `data_list$spnames`. Rows are sorted in the order `which` was given.

`Atka2022` *Data inputs for Atka mackerel CEATTLE model (2022)*

Description

A data list containing inputs for a single-species CEATTLE model fit to Aleutian Islands Atka mackerel data through 2022. See `BS2017SS` for format details.

Usage

```
Atka2022
```

Format

A list with the same structure as `BS2017SS`.

`BS2017MS` *Data inputs for multispecies CEATTLE of the Bering Sea from 1979 to 2017*

Description

A data list containing inputs for the three-species (walleye pollock, Pacific cod, arrowtooth flounder) multispecies CEATTLE model for the Eastern Bering Sea. See `BS2017SS` for format details.

Usage

```
BS2017MS
```

Format

A list with the same structure as `BS2017SS`.

`BS2017SS` *Data inputs for single species CEATTLE of the Bering Sea from 1979 to 2017*

Description

A dataset containing the inputs used for CEATTLE

Usage

`BS2017SS`

Format

Control

nspp Number of species included in CEATTLE

styr Start year of the hindcast

endyr End year of the hindcast

projyr End year of the forecast

nsex Number of sexes to model in the population (1 = combined/1sex, 2 = models both female/male)

spawn_month Spawning month of the population to adjust the numbers spawning

R_sexr Percent of recruitment that is female (ignored if nsex = 1)

nages Number of ages of each species included in the hindcast

minage Minimum age for each population (i.e.does recruitment correspond to age 0, 1, 2?)

nlengths Number of lengths of each species included in the hindcast

pop_wt_index Weight-at-age (weight) index to use for calculation of each species population derived quantities (SSB, Consumption/Ration, Suitability, etc)

ssb_wt_index Weight-at-age (weight) index to use for calculation of each species spawning biomass

pop_age_transition_index Age transition matrix (e.g. growth trajectory) index to use for derived quantities of the population to convert age to length (also used in length-based predation estimation)

sigma_rec_prior Standard deviation to use for recruitment

other_food Other food in the ecosystem for each species

estDynamics Estimate or fix numbers-at-age: 0 = estimate dynamics, 1 = use input numbers-at-age in NbyageFixed, 2 = multiply input numbers-at-age (NbyageFixed) by a single scaling coefficient, 3 = multiply input numbers-at-age (NbyageFixed) by age specific scaling coefficient.

est_M1 Estimate residual (multi-species mode) or total natural mortality (single-species mode). 0 = use fixed natural mortality from M1_base, 1 = estimate sex- and age-invariant M1, 2 = sex-specific (two-sex model), age-invariant M1, 3 = estimate sex- and age-specific M1.

fleet_control Survey and fishery data specifications

index_data Survey index in weight (kg) or numbers data

catch_data Total catch in weight (kg) or numbers data

comp_data Survey/fishery age or length composition data. Note if sex is 3, put female composition data then male composition data (similar to SS).

emp_sel Empirical/fixed selectivity for surveys and fisheries (leave empty if not used)

age_trans_matrix Age transition matrix (e.g. growth trajectory) used to convert age to length for length comp data. Can have multiple matrices for a species specified by Age_transition_index.

age_error Aging error matrices. Can have only one per species.

weight Weight-at-age (weight) to use for calculation of derived quantities (SSB, Consumption/Ration, Suitability, Total Catch, Survey Biomass, etc). Can have multiple weight-at-age data-sets for each species, but must be full for all years of the hindcast.

maturity Maturity-at-age for each species

sex_ratio Percent female at age for each species

M1_base Residual natural mortality for each species

aLW Parameters for weight-at-length power function for each species. . Used when estimating time-variant length-based gamma suitability (suitMode = 2) or time-variant length-based lognormal suitability (suitMode = 5)

Ceq Which bioenergetics equation to use for each species for ft to scale max consumtion: 1 = Exponential (Stewart et al 1983), 2 = Temperature-dependendence for warm-water species (Kitchell et al 1977; sensu Holsman et al 2015), 3 = temperature dependence for cool and cold-water species (Thornton and Lessem 1979)

Cindex Which environmental index in env_data to use to drive bioenergetics

Pvalue This scales the maximum consumption used for ration for each species; Pvalue is in Cmax*fT*Pvalue*ration_data

fday Number of foraging days per year for each species

CA Intercept of allometric mass function for calculating maximum consumption: CA * Weight ^ CB

CB Slope of allometric mass function for calculating maximum consumption: CA * Weight ^ CB

Qc Parameter for temperature scaling function of maximum consumption specified by Ceq

Tco Parameter for temperature scaling function of maximum consumption specified by Ceq

Tcm Parameter for temperature scaling function of maximum consumption specified by Ceq

Tcl Parameter for temperature scaling function of maximum consumption specified by Ceq

CK1 Parameter for temperature scaling function of maximum consumption specified by Ceq

CK4 Parameter for temperature scaling function of maximum consumption specified by Ceq

env_data Environmental indices such as bottom temperature data to incorporate into ration equation specificed by Ceq and Cindex. Also used to drive catchability if Catchability = 5. Will use the mean for missing years. Temperature should be in celcius.

ration_data Annual relative foraging rate by age or input consumption at age. Multiplied by pvalue and fday to scale maximum consumption to the number of days in a year that foraging occurs.

UobsAge Stomach proportion by numbers for each predator, prey, predator age, prey age combination. Can also be year specific by including the column, "Year"

UobsWtAge Stomach proportion by weight for each predator, prey, predator age, prey age combination. Can also be year specific by including the column, "Year"

fleet_control: controls for survey and fisheries data

Fleet_name Name of survey or fishery

Fleet_code Index of survey/fishery ACROSS species

Fleet_type 0 or 'Off' = Do not estimate; 1 = 'Fishery'; 2 = 'Survey'

Species Species number

Selectivity_index index to use if selectivities of different surveys are to be the same

Selectivity Selectivity to use for the species: 0 = "Fixed"; 1 = "Logistic"; 2 = "NonParametric" sensu Ianelli et al 2018; 3 = "DoubleLogistic"; 4 = "DescendingLogistic"; 5 = "Hake" non-parametric sensu Taylor et al; 6 = "2DAR1"; 7 = "3DAR1" sensu Cheng et al 2024; 8 = "DoubleNormal" (Gaussian ascending and descending limbs blended at a common peak — similar to SS3 pattern 24). Parameters: `sel_inf[1]` = peak bin/length; `sel_inf[2]` = logit(right_floor), right-tail floor analogous to SS3 P6/end_logit (logit=-10 → dome-shaped, logit=+10 → logistic ascending-only); `log_sel_slp[1]` = log(sigma_ascending); `log_sel_slp[2]` = log(sigma_descending). Supports the same time-varying modes as DoubleLogistic (IID, Block, RandomWalk).

Selectivity_dimension "Age" or "Length".

Nselages Number of ages to estimate non-parametric selectivity.

Time_varying_sel Whether a time-varying selectivity should be estimated for logistic, double logistic selectivity, or descending logistic. 0 = "Off", 1 = "IID" penalized deviates given sel_sd_prior or random effect, 2 = "AR1" (TODO), 3 = "Block" time blocks with no penalty, 4 = "RandomWalk" following Dorn, 5 = "RandomWalkAscending" on ascending portion of double logistic only.

Time_varying_sel_sd_prior The fixed or initial sd to use for time varying selectivity.

Bin_first_selected Age/length bin at which selectivity is non-zero

Acuumulation_age_lower Ages below this will be grouped to this age for composition data. For example, if set to 2, comp data for age 2 will include 1 and 2 year olds.

Acuumulation_age_upper Ages above this will be grouped to this age for composition data. For example, if set to 9 for a species with 10 ages, comp data for age 9 will include 9 and 10 year olds.

weight1_Numbers2 Is the observation in weight (kg) set as 1, if the observation is in numbers caught, set as 2

Weight_index Weight-at-age (weight) index to use for calculation of derived quantities

Age_transition_index Age transition matrix (e.g. growth trajectory) index to use for derived quantities to convert age to length

Q_index index to use if catchability coefficients are to be set the same

Catchability Estimate catchability? (0 or "Fixed" = fixed at prior; 1 or "Estimated" = Estimate single parameter; 2 or "Estimated-with-prior" = Estimate single parameter with prior; 3 or "Analytical" = Estimate analytical q from Ludwig and Walters 1994; - 4 = Estimate power equation; - 5 or "Environmental" = Linear equation log(q_y) = q_mu + beta * index_y; 6 or "AR1" = annual AR1 catchability deviates are fit to environmental index sensu Rogers et al 2025)

Q_prior Starting value or fixed value for catchability

Q_sd_prior Variance of q prior: dnorm (log_q, log_q_prior, q_sd_prior)

Time_varying_q Whether a time-varying q should be estimated. 0 = "Off", 1 = "IID" penalized deviate or random effect, 2 = "AR1" (TODO), 3 = "Block" time blocks with no penalty; 4 = "RandomWalk" random walk from mean following Dorn 2018 (dnorm(q_y - q_y-1, 0, sigma). If Catchability = 5 or 6, this determines the environmental index to be used in the equation log(q_y) = q_mu + beta * index_y

Time_varying_q_sd_prior The sd to use for the random walk of time varying q if set to 1

Estimate_survey_sd Estimate survey variance (0 = use CV from index_data, 1 = yes, 2 = analytically estimate following (Ludwig and Walters 1994)

Survey_sd_prior Starting value to be used if Estimate_sigma_index = 1

Estimate_catch_sd Estimate fishery variance (0 = use CV from index_data, 1 = yes, 2 = analytically estimate following (Ludwig and Walters 1994)

Catch_sd_prior Starting value to be used if Estimate_sigma_catch = 1

Comp_weights Composition weights to be used for multinomial likelihood. These are multiplied. After running model, these will update to McAllister & Ianelli 1997 weights using the harmonic mean.

Catch_units Units used for survey: 1 = kg; 2 = numbers

proj_F_prop The proportion of future fishing mortality assigned to this fleet

Sex sex codes: 0=combined; 1=use female only; 2=use male only; 3 = joint female and male

---

`build_bounds` *Build parameter bounds*

Description

Function to build parameter bounds based on Holsman et al 2015 and Kinzey and Punt 2010

Usage

```
build_bounds(param_list = NULL, data_list)
```

Arguments

`param_list`	Parameter list object built from `build_params`
`data_list`	a Rceattle data object

Value

List of upper and lower bounds

`build_growth` *Specify the growth model for Rceattle*

Description

Specify the growth model for Rceattle

Usage

```
build_growth(fun = "empirical", growth_age_L1 = NA, linkages = NULL)
```

Arguments

`fun`	Growth function. Either a string (GROWTH_FUNS: `"empirical"` (default), `"vonBertalanffy"`, `"Richards"`) or the equivalent integer code (`0`, `1`, `2`). The canonical string form is stored on the returned object.
`growth_age_L1`	Von Bertalanffy / Richards anchor age (the age at which mean length equals `L1`). Matches SS3's `Growth_Age_for_L1` control input. Scalar (recycled across species) or a length-nspp vector for per-species values. Default `NA` inherits `data_list$growth_age_L1` if supplied (e.g. from the SS3 converter), otherwise falls back to `max(0.5, minage[sp])` so `minage >= 1` models stay backwards-compatible and `minage = 0` models pick up an SS3-consistent half-year anchor.
`linkages`	Optional named list of `linkage_spec()` objects keyed by parameter name (must be one of GROWTH_LINKAGE_PARAMS). The mean-growth keys (`K`, `L1`, `Linf`, `m`) accept arbitrary one-sided formulas and produce year-varying offsets applied inside `growth.hpp`. The SD-endpoint keys (`sd_L1`, `sd_Linf`) only honor intercept-bearing formulas (typically ~ 1) – they thread `init`, bounds, and `priors` onto the underlying `growth_log_sd` parameter, giving the SDs the same prior/fix/initial-value contract as the mean parameters. Slope rows on SD specs raise a warning and have no effect; slope-only formulas (~ `0` + `temp`) error. Materialization into the global linkage table happens inside `fit_mod()` once `data_list$env_data` is in scope.

Value

A list of switches defining the growth model.

Examples

```
## Not run:
# Sex-specific von Bertalanffy with temperature on K, by species + sex
build_growth(
  fun = "vonBertalanffy",   # or fun = 1
  linkages = list(
    K = linkage_spec(
      formula = ~ temp,
      by      = ~ species + sex,
```

```
      priors  = list(temp = normal(0, 1))
    )
  )
)

## End(Not run)
```

`build_hcr` *Specify the harvest control rule (HCR) used for Rceattle*

Description

Defines the harvest control rule and associated reference points used in the Rceattle model.

Usage

```
build_hcr(
  HCR = 0,
  DynamicHCR = FALSE,
  Ftarget = 0.4,
  Flimit = 0.35,
  Ptarget = 0.4,
  Plimit = 0,
  Alpha = 0.05,
  Pstar = 0.45,
  Sigma = 0.5,
  Fmult = 1,
  HCRorder = 1
)
```

Arguments

`HCR`	Harvest control rule to use. Accepts an integer or equivalent string alias. Default = 0. See Details for the full list of available options.
`DynamicHCR`	TRUE/FALSE. Whether to use static or dynamic reference points (default = FALSE).
`Ftarget`	Target fishing mortality rate (yr^-1) (SPR or depletion based) or input F for projections. For example, if Ftarget is spr F40%, enter 0.40.
`Flimit`	Limit fishing mortality rate (yr^-1) (SPR or depletion based). For example, if Flimit is spr F35%, enter 0.35.
`Ptarget`	Target spawning-stock biomass as a percentage of static or dynamic spawning-stock-biomass at F = 0 (accounts for recruitment).
`Plimit`	Limit spawning-stock biomass as a percentage of static or dynamic spawning-stock-biomass at F = 0 (accounts for recruitment).
`Alpha`	Parameter used in NPFMC Tier 3 HCR.

`Pstar`	Quantile used for uncertainty buffer given `Flimit` and `Sigma`.
`Sigma`	Standard deviation used for normally distributed uncertainty buffer given `Flimit` and `Pstar`.
`Fmult`	Multiplier on the target F (default = 1). Used to scale the target fishing mortality following NEFSC convention.
`HCRorder`	For multi-species models, the order in which to project fishing (e.g., predators first, then prey).

Details

Harvest control rule formulations currently implemented in Rceattle:

`hcr = 0` or `"NoFishing"`: No catch. Estimate the hindcast.

`hcr = 1` or `"CMSY"`: CMSY. Maximize catch across all species simultaneously. CMSY can be constrained such that depletion does not fall below `Plimit`.

`hcr = 2` or `"ConstantF"`: Constant input F set at `Ftarget` for each species (vector or single F). SPR (single-species only) based Flimit is specified via `Flimit`.

`hcr = 3` or `"ConstantFSSB"`: F that achieves `Ftarget`% of SSB0 in the end of the projection.

`hcr = 4` or `"ConstantFSPR"`: Constant Fspr set at `Ftarget` for each species. Can be multiplied by `Fmult` following NEFSC.

`hcr = 5` or `"NPFMC"`: The North Pacific Fishery Management Council (NPFMC) Tier 3 spawner-per-recruit-based harvest control rule: Stock status: $SB > SBatFtarget$

$$Fofl = Flimit$$

$$Fuse = Ftarget$$

Stock status: $Alpha < SB/SBatFtarget \leq 1$

$$Fofl = Flimit * (SB/Ptarget - Alpha)/(1 - Alpha)$$

$$Fuse = Ftarget * (SB/Ptarget - Alpha)/(1 - Alpha)$$

Stock status: $SB/SBatFtarget \leq Alpha$ or $SB < Plimit * SB0$

$$Fofl = 0$$

$$Fuse = 0$$

`hcr = 6` or `"PFMC"`: An HCR based on the The Pacific Fishery Management Council (PFMC) category 1 40-10 annual catch limit (ABC) harvest control rule assuming Fofl is normally distributed with a standard deviation (sigma) = 0.5 and an uncertainty quantile buffer (P*) of 0.45 (PFMC 2020). The model uses Fspr if single-species or F that achieves X% of SSB0 for multi-species. Target biological reference points are calculated based on the normal cumulative distribution function (Phi(quantile,mean,standard deviation)), P*, and sigma as follows: Stock status: $SB > SB0 * Ptarget$

$$Fofl = Flimit$$

$$Fuse = Phi(Pstar, Flimit, Sigma)$$

Stock status: $SB0 * Plimit < SB \leq SB0 * Ptarget$

$$Fofl = Flimit$$

$$Fuse = Phi(Pstar, Flimit, Sigma) * \frac{SB0 * Ptarget * (SB - SB0 * Plimit)}{SB * SB0 * (Ptarget - Plimit)}$$

Stock status: $SB < SB0 * Plimit$

$$Fofl = 0$$

$$Fuse = 0$$

`hcr = 7` or `"SESSF"`: An HCR based on the The Southern and Eastern Scalefish and Shark Fishery (SESSF) spawner-per-recruit-based Tier 1 harvest control rule where F_Limit=F_(20%), B_Limit=SB_20, F_Target (AFMA 2017) calculated as follows: Stock status: $SB > SB0 * Ptarget$

$$Fofl = Flimit$$

$$Fuse = Ftarget$$

Stock status: $Ptarget > SB > SB0 * Plimit$

$$Fofl = Flimit * (SB/(SB0 * Ptarget) - 1)$$

$$Fuse = Ftarget * (SB/(SB0 * Ptarget) - 1)$$

Stock status: $SB < SB0 * Plimit$

$$Fofl = 0$$

$$Fuse = 0$$

NOTE: only HCRs 1, 2, 3, and 6 will work in multi-species mode.

Value

A `list` containing the harvest control rule and associated biological reference points.

`build_hcr_map` *Function to construct the TMB map argument for CEATTLE for projecting under alternative harvest control rules*

Description

Reads a data list and map to update the map argument based on the HCR specified in `build_hcr`

Usage

```
build_hcr_map(
  data_list,
  map,
  debug = FALSE,
  all_params_on = FALSE,
  HCRiter = 1
)
```

Arguments

`data_list`	an Rceattle data_list
`map`	a map object created from `build_map`.
`debug`	logical. If TRUE, turns off all parameters for debugging (default = FALSE).
`all_params_on`	logical. If TRUE, leaves all hindcast parameters turned on (default = FALSE).
`HCRiter`	for multi-species models, the order in which to project fishing (e.g. predators first, then prey)

Value

a list of map arguments for each parameter

`build_M1` *Define M1 specifications*

Description

Define M1 specifications

Usage

```
build_M1(
  M1_model = 0,
  M1_re = 0,
  updateM1 = FALSE,
  M1_use_prior = FALSE,
  M2_use_prior = FALSE,
  M_prior = 0.4,
  M_prior_sd = 0.35,
  M1_indices = NA,
  linkages = NULL
)
```

Arguments

`M1_model` Vector or scalar specifying the M1 structural fixed- effects model. Either an integer code or the equivalent string alias (both forms are accepted; the integer code is canonical):

- `0` / `"fixed"` – use the input `M1_base` (no estimation).
- `1` / `"sex_age_invariant"` – estimate one `M1_{spp}`.
- `2` / `"sex_specific"` – estimate `M1_{spp, sex}`.
- `3` / `"sex_age_specific"` – estimate `M1_{spp, sex, age}`.
- `4`, `5` – soft-deprecated env-driven codes; use the `linkages` argument instead. See `vignette("environmental-linkages-and-priors")`.

`M1_re`	Vector or scalar specifying the M1 random-effects model. Either an integer code or the equivalent string alias: `0` / `"none"`, `1` / `"iid_age"`, `2` / `"iid_year"`, `3` / `"iid_age_year"`, `4` / `"ar1_age"`, `5` / `"ar1_year"`, `6` / `"ar1_age_year"`.
`updateM1`	If using initial parameters, use M1 fixed effects from data (`M1_base`) instead. Default `FALSE`.
`M1_use_prior`	Vector or scalar; if `TRUE`, apply the lognormal `M_prior` / `M_prior_sd` to `M1` directly.
`M2_use_prior`	Vector or scalar; if `TRUE`, apply the lognormal prior to `M1` + `M2` in multi-species models.
`M_prior`	Mean (natural-scale) of the lognormal prior on M.
`M_prior_sd`	SD (log-scale) of the lognormal prior on M.
`M1_indices`	Soft-deprecated. Vector of column indices into `env_data` (excluding `Year`) for environmentally linked M1 when `M1_model %in% c(4, 5)`. Use the `linkages` argument instead; see `vignette("environmental-linkages-and-priors")`.
`linkages`	Optional named list of `linkage_spec()` objects keyed by M parameter name (currently the only valid key is `"M1"`). Each spec describes how `M1` depends on environmental covariates and on stratifying factors (species, sex, age). The offset enters additively (on the log scale) inside the `M1_at_age` compute. A row's `age_bin` == `NA` broadcasts the offset across ages; specific values pin it to that age slice.

Value

A list of switches for defining the M1 model.

Examples

```
## Not run:
# Sex/age-invariant M with a temperature linkage on M1
build_M1(
  M1_model = "sex_age_invariant",
  linkages = list(
    M1 = linkage_spec(
      formula = ~ temp,
      by      = ~ species,
      priors  = list(temp = normal(0, 0.5))
    )
  )
)

## End(Not run)
```

`build_map` *Main function to construct the TMB map argument for CEATTLE*

Description

Orchestrates the building of the TMB map object by calling specialized helper functions for each parameter block (Recruitment, M1, Predation, Selectivity, Catchability, etc.).

Usage

```
build_map(
  data_list,
  params,
  debug = FALSE,
  random_rec = FALSE,
  random_sel = FALSE
)
```

Arguments

`data_list`	an Rceattle data_list
`params`	A parameter list created from `build_params`.
`debug`	Logical. If TRUE, sets all map values to NA except the dummy parameter, running the model without parameter estimation.
`random_rec`	Logical. If TRUE, treats recruitment deviations as random effects, meaning the variance parameter (`R_log_sd`) is estimated.
`random_sel`	Logical. If TRUE, treats selectivity deviations as random effects, meaning the variance parameter (`sel_dev_log_sd`) is estimated.

Value

A list containing the factorized TMB map (`mapFactor`) and the original map matrix/array list (`mapList`).

`build_map_catchability` *Helper to set map for Catchability parameters*

Description

Maps survey catchability base parameters (`index_log_q`), time-varying deviations (`index_q_dev`), and environmental linkages (`index_q_beta`, `index_q_rho`).

Usage

```
build_map_catchability(map_list, data_list, nyrs_hind)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.
`nyrs_hind`	Number of historical years.

Value

Updated `map_list`.

`build_map_debug` *Helper to set map for debug mode*

Description

Sets all parameters in the map list to NA, except the `dummy` parameter, for use in debug or testing modes.

Usage

```
build_map_debug(map_list, debug)
```

Arguments

`map_list`	The current TMB map list.
`debug`	Logical. If TRUE, debug mode is activated.

Value

Updated `map_list`.

`build_map_f_and_data_weights` *Helper to set map for Fishing Mortality and Data Weights*

Description

Maps fishing mortality parameters (`log_F`) and related targets. Also maps data weighting parameters (`catch_log_sd`, `comp_weights`, `caal_weights`).

Usage

```
build_map_f_and_data_weights(map_list, data_list, nyrs_hind)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.
`nyrs_hind`	Number of historical years.

Value

Updated `map_list`.

`build_map_fixed_natage` *Helper to set map for Fixed N-at-Age models*

Description

Turns off (sets to NA) most population and fleet parameters for species where the dynamics are fixed (`estDynamics > 0`).

Usage

```
build_map_fixed_natage(map_list, data_list)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.

Value

Updated `map_list`.

`build_map_growth` *Helper to set map for growth parameters*

Description

Maps the fixed parameters (`log_growth_pars`) and the random effects parameters (`log_growth_par_devs`, `growth_dev_log_sd`, `growth_rho`) based on `growth_model` and `growth_re` settings.

Usage

```
build_map_growth(map_list, data_list, nyrs_hind)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.
`nyrs_hind`	Number of historical years.

Value

Updated `map_list`.

`build_map_m1` *Helper to set map for Natural Mortality (M1) parameters*

Description

Maps the fixed parameters (`log_M1`) and the random effects parameters (`log_M1_dev`, `M1_dev_log_sd`, `M1_rho`) based on `M1_model` and `M1_re` settings.

Usage

```
build_map_m1(map_list, data_list, nyrs_hind)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.
`nyrs_hind`	Number of historical years.

Value

Updated `map_list`.

`build_map_predation` *Helper to set map for Predation Mortality (M2) parameters*

Description

Maps predation suitability parameters (`log_gam_a`, `log_gam_b`, `log_phi`) and diet weight parameters based on `msmMode` and `suitMode`.

Usage

```
build_map_predation(map_list, data_list)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.

Value

Updated `map_list`.

`build_map_recruitment` *Helper to set map for Recruitment parameters*

Description

Maps the recruitment deviations (`rec_dev`, `init_dev`), stock-recruitment parameters (`rec_pars`) and Rec dev variances (`R_log_sd`)

see `build_srr()` for options,

Usage

```
build_map_recruitment(map_list, data_list, nyrs_hind, nyrs_proj, random_rec)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.
`nyrs_hind`	Number of historical years.
`nyrs_proj`	Total number of years (historical + projected).
`random_rec`	Logical indicating if recruitment deviations are random effects.

Value

Updated `map_list`.

`build_map_selectivity` *Helper to set map for Selectivity parameters*

Description

Maps base selectivity parameters (`log_sel_slp`, `sel_inf`, `sel_coff`) and time-varying deviations, based on `Selectivity` and `Time_varying_sel` settings in `fleet_control`.

`Selectivity` in `fleet_control` of the data determines shape of selectivity curve: `0` = "Fixed" empirical selectivity provided in `emp_sel` in the data `1` = "Logistic" `2` = "NonParametric" selecitivty sensu Ianelli et al 2018 `3` = "DoubleLogistic" `4` = "DescendingLogistic" `5` = "Hake" non-parametric selectivity sensu Taylor et al 2014 (Hake) `6` = "2DAR1" across age x year `7` = "3DAR1" across age x cohort x year (Cheng et al 2024) `8` = "DoubleNormal" Gaussian ascending/descending limbs blended at peak (analogous to SS3 pattern 24). Parameters: `sel_inf[1]` = peak; `sel_inf[2]` = logit(right_floor) (right-tail floor, SS3 P6/end_logit); `log_sel_slp[1]` = log(sigma_asc); `log_sel_slp[2]` = log(sigma_desc). right_floor→0: dome-shaped; right_floor→1: logistic ascending only.

`N_sel_bins` Number of age/length bins to estimate non-parametric selectivity when Selectivity = 2 or 5. Not used otherwise

`Time_varying_sel` determines if time-varying selectivity should be estimated for logistic, double logistic selectivity, descending logistic , non-parametric, or hake (`Selectivity` = `1, 2, 3, 4, or 5`). `0` = 'None' `1` = 'IID' penalized deviates given `sel_sd_prior` `3` = 'Block' time blocks with no penalty `4` = 'RandomWalk' random walk following Dorn `5` = 'RandomWalkAscending' random walk on ascending portion of double logistic only. `random_sel` in `fit_mod` treats random deviates and random walk parameters as random effects, estimating the variance.

Usage

```
build_map_selectivity(map_list, data_list, nyrs_hind, random_sel)
```

Arguments

`map_list`	The current TMB map list.
`data_list`	The data list containing model settings.
`nyrs_hind`	Number of historical years.
`random_sel`	Logical indicating if selectivity deviations are random effects.

Value

Updated `map_list`.

`build_params` *Build parameter list from cpp file*

Description

Function to read a TMB cpp file and construct parameter list object for Rceattle

Usage

```
build_params(data_list)
```

Arguments

`data_list`	an Rceattle data_list

Value

a list of map arguments for each parameter

`build_srr` *Specify the stock-recruit relationship (SRR) for Rceattle*

Description

Stock recruitment relationships currently implemented in Rceattle:

- `srr_fun` = `0` or `"mean"`: No stock recruit relationship. Recruitment is a function of R0 and annual deviates (i.e. steepness = 0.99).

$$R_y = exp(R0 + R_{dev,y})$$

- `srr_fun` = 2 or `"BevertonHolt"`: Beverton-holt stock-recruitment relationship

$$R_y = \frac{\alpha_{srr} * SB_{y-minage}}{1 + \beta_{srr} * SB_{y-minage}}$$

- `srr_fun` = 4 or `"Ricker"`: Ricker stock-recruitment relationship

$$R_y = \alpha_{srr} * SB_{y-minage} * exp(-\beta_{srr} * SB_{y-minage})$$

When `srr_pred_fun` > `0` and `srr_fun` = `0` recruitment in the hindcast is estimated as in `srr_fun` = `0`

$$R_y = exp(R0 + R_{dev,y})$$

, but an additional stock recruitment relationship defined by `srr_pred_fun` is estimated between `srr_hat_styr` and `srr_hat_endyr` and treated as an additional penalty. The stock recruitment relationship defined by `srr_pred_fun` is then used in the projection.

Usage

```
build_srr(
  srr_fun = 0,
  srr_pred_fun = srr_fun,
  proj_mean_rec = TRUE,
  srr_mse_switchyr = NULL,
  srr_hat_styr = NULL,
  srr_hat_endyr = NULL,
  srr_est_mode = 1,
  srr_prior = 4,
  srr_prior_sd = 1,
  srr_indices = NA,
  Bmsy_lim = NA,
  linkages = NULL
)
```

Arguments

`srr_fun`	Stock recruit function to be used for hindcast estimation of Rceattle (see @description below). Default = 0
`srr_pred_fun`	stock recruit function for projection, reference points, and penalties to be used for Rceattle (see below). When `srr_fun == 0`, it treats the stock-recruit curve as an additional penalty onto the annualy estimated recruitment from the hindcast (sensu AMAK and Jim Ianelli's pollock model). If `srr_fun > 0` then `srr_pred_fun = srr_fun` and no additional penalty is included.
`proj_mean_rec`	Project the model using: 0 = mean recruitment (average R of hindcast) or 1 = SRR(omega, srr_devs)
`srr_mse_switchyr`	is used for MSEs to deal with AMAK and Jim Ianelli's estimation where a stock recruit function is estimated as an additional penalty (srr_fun = 0 and srr_pred_fun > 0). It tells the model in what year to switch to the stock recruit function.
`srr_hat_styr`	Integer. The first year used for estimating the recruitment function as an additional penalty. It will add additional penalties sensu AMAK and Jim Ianelli's pollock model when `srr_pred_fun > 0` and `srr_fun = 0`, starting at `styr` + 1. Defaults to $styr + 1$ in $data_list$. Useful if environmental data used to condition stock-recruit relationships is not available until end-year, but projections are desired.
`srr_hat_endyr`	Integer. The last year used for estimating the recruitment function as an additional penalty. It will add an additional penalties sensu AMAK and Jim Ianelli's pollock model when `srr_pred_fun > 0` and `srr_fun = 0`. Recruitment Defaults to $endyr$ in $data_list$. Useful if environmental data used to condition stock-recruit relationships is not available for the full time-series, but projections are desired.
`srr_est_mode`	Switch to determine estimation mode. 0 = fix alpha to prior mean, 1 = freely estimate R0, alpha, and/or beta (default), 2 = use lognormally distributed prior

	for alpha (Ricker) or steepness (Beverton), 3 = use beta distributed prior for steepness (Beverton) given mean and sd.
`srr_prior`	mean for normally distributed prior for stock-recruit parameter
`srr_prior_sd`	Prior standard deviation for stock-recruit parameter
`srr_indices`	Soft-deprecated. Use the `linkages` argument instead. See `vignette("environmental-linkages-and-`
`Bmsy_lim`	Upper limit for Ricker based SSB-MSY (e.g 1/Beta). Will add a likelihood penalty if beta is estimated above this limit. Default `NA` is not used.
`linkages`	Optional named list of `linkage_spec()` objects keyed by recruitment parameter name (must be one of `"R0"`, `"alpha"`, `"beta"`). Each spec describes how that parameter depends on environmental covariates and on stratifying factors (species, sex). The offset enters additively (on the log scale) inside the recruitment compute. See `vignette("environmental-linkages-and-priors")` for details.

Value

A `list` containing the stock recruitment relationship settings

---

`check_mse` *Function to load .RDs files from MSE runs*

Description

Function to load .RDs files from MSE runs

Usage

```
check_mse(dir = NULL, file = NULL)
```

Arguments

`dir`	Directory used to save files from `run_mse`
`file`	file name used to save files from `run_mse`

Value

list of MSE simulations/run

`clean_data` *Function to clean data prior to Rceattle runs*

Description

Function to clean data prior to Rceattle runs

Usage

```
clean_data(data_list)
```

Arguments

`data_list`	Rceattle data list

`coef.Rceattle` *Extract estimated parameters from an Rceattle fit*

Description

Extract estimated parameters from an Rceattle fit

Usage

```
## S3 method for class 'Rceattle'
coef(object, ...)
```

Arguments

`object`	An object of class `"Rceattle"` returned by `fit_mod()`.
`...`	Currently unused.

Value

A named numeric vector of estimated fixed-effect parameters (the optimizer's `par`). Returns `NULL` if the model was not estimated.

`combine_data` *Combine data sets. Will use the env_data data set from data_set1 and diet data will have to be updated.*

Description

Combine data sets. Will use the env_data data set from data_set1 and diet data will have to be updated.

Usage

```
combine_data(data_list1 = NULL, data_list2 = NULL)
```

Arguments

`data_list1`	Rceattle data_list 1
`data_list2`	Rceattle data_list 2

`compare_sim` *Evaluate simulation performance*

Description

Function to evaluate the simulation performance with regard to bias using the median relative error (MRE) and precision using the coefficient of variation.

Usage

```
compare_sim(operating_mod, simulation_mods, object = "quantities")
```

Arguments

`operating_mod`	CEATTLE model object exported from `Rceattle` to be used as the operating model
`simulation_mods`	List of CEATTLE model objects exported from `Rceattle` fit to simulated data
`object`	character string specifying which part of the model to compare (default = "quantities")

Value

A data frame summarising simulation performance metrics

`convergence_diagnostics` *Convergence diagnostics for a fitted Rceattle model*

Description

Runs the post-fit convergence battery and returns a single structured object. Each check yields a record with a common schema (`id`, `tier`, `severity`, `message`, `data`); `severity` is one of `"OK"`, `"NOTE"`, `"WARN"`, `"FAIL"`. The object's `status` is the worst severity present.

Usage

```
convergence_diagnostics(object, ...)
```

Arguments

`object`	An object of class `"Rceattle"` returned by `fit_mod()`.
`...`	Currently unused.

Details

`fit_mod()` runs this automatically and attaches the result as `fit$convergence`; call `convergence_diagnostics()` directly to re-run it on any fit. Checks cover the optimizer gradient, Hessian positive-definiteness and conditioning, parameters on bounds, phasing, and parameter estimability.

Value

An object of class `"Rceattle_convergence"`: a list with `status` (overall worst severity) and `checks` (named list of records).

`EBS_ms_run` *Fitted multispecies CEATTLE model for the Eastern Bering Sea*

Description

A fitted `Rceattle` model object for the multispecies run of CEATTLE for the Eastern Bering Sea (walleye pollock, Pacific cod, arrowtooth flounder).

Usage

```
EBS_ms_run
```

Format

An object of class `Rceattle`.

`EBS_ss_M_run` *Fitted single-species CEATTLE model with estimated M for the Eastern Bering Sea*

Description

A fitted `Rceattle` model object for the single-species run of CEATTLE for the Eastern Bering Sea with natural mortality estimated.

Usage

```
EBS_ss_M_run
```

Format

An object of class `Rceattle`.

`EBS_ss_run` *Fitted single-species CEATTLE model for the Eastern Bering Sea*

Description

A fitted `Rceattle` model object for the single-species run of CEATTLE for the Eastern Bering Sea (walleye pollock, Pacific cod, arrowtooth flounder) without estimating natural mortality.

Usage

```
EBS_ss_run
```

Format

An object of class `Rceattle`.

`fit_control` *Bundle the optimizer / sdreport / phasing controls for* `fit_mod()`

Description

`fit_mod()` carries roughly a dozen optimizer- and reporting-related arguments (`bias.correct`, `getsd`, `loopnum`, `newtonsteps`, ...). That is a lot of surface area when the user mostly cares about "what model am I fitting" rather than "how is it being fit." `fit_control()` collects those knobs into a single object so calls to `fit_mod()` can stay focused on the model spec:

Usage

```
fit_control(
  bias.correct = FALSE,
  getsd = TRUE,
  getJointPrecision = TRUE,
  getReportCovariance = FALSE,
  use_gradient = TRUE,
  rel_tol = 1,
  loopnum = 5,
  newtonsteps = 0,
  phase = FALSE,
  TMBfilename = NULL,
  verbose = 1,
  nlminb_control = list(eval.max = 1e+09, iter.max = 1e+09, trace = 0)
)
```

Arguments

`bias.correct`	logical. If `TRUE`, applies bias correction via `TMB::sdreport()`. Default `FALSE`.
`getsd`	logical. If `TRUE`, run `TMB::sdreport()` after optimization. Default `TRUE`.
`getJointPrecision`	logical. Return the full Hessian of fixed and random effects. Default `TRUE` (matches `fit_mod()` default).
`getReportCovariance`	logical. Return the variance-covariance of `ADREPORT` variables. Default `FALSE`.
`use_gradient`	logical. Use the analytic gradient during phasing. Default `TRUE`.
`rel_tol`	Numeric tolerance used to flag discontinuous likelihood warnings (compares the TMB and `nlminb` objectives). Default `1`.
`loopnum`	Integer. Number of times to re-start optimization (`loopnum = 3` sometimes achieves a lower final gradient than `loopnum = 1`). Default `5`.
`newtonsteps`	Integer. Number of extra Newton steps to take after optimization (alternative to `loopnum`). Default `0`.

`phase`	`TRUE`/`FALSE` or a list. If `FALSE`, the model is not phased. If `TRUE`, default phasing is used. Can also accept a list of parameter object names with corresponding phase. Default `FALSE`.
`TMBfilename`	Optional character. Path (without `.cpp`) to an alternate TMB template for development. Default `NULL` (use the bundled `ceattle_v01_11`).
`verbose`	`0` = silent, `1` = print updates of model fit, `2` = print updates of model fit and TMB estimation progress. Default `1`.
`nlminb_control`	A list of control parameters passed to `stats::nlminb()`. See `?nlminb`. Default `list(eval.max = 1e9, iter.max = 1e9, trace = 0)`.

Details

```
fit <- fit_mod(
  data_list   = BS2017SS,
  msmMode     = 0,
  fit_control = fit_control(loopnum = 1, getsd = FALSE)
)
```

Pass the result via the `fit_control` argument to `fit_mod()`. When supplied, the values in the `fit_control` object override the corresponding individual arguments to `fit_mod()`. Individual arguments are kept for backward compatibility.

Value

A list of class `"Rceattle_fit_control"`.

Examples

```
# Quick-and-dirty fit: skip sdreport, single optimizer pass
ctl <- fit_control(getsd = FALSE, loopnum = 1)

# Production fit with bias correction and joint precision
ctl <- fit_control(bias.correct = TRUE, getJointPrecision = TRUE)
```

`fit_mod` *This function runs CEATTLE*

Description

This function estimates population parameters of CEATTLE using maximum likelihood in TMB.

Usage

```
fit_mod(
  data_list = NULL,
  inits = NULL,
  map = NULL,
  bounds = NULL,
```

```
  file = NULL,
  estimateMode = 0,
  projection_uncertainty = FALSE,
  random_rec = FALSE,
  random_q = FALSE,
  random_sel = FALSE,
  HCR = build_hcr(),
  niter = 3,
  recFun = build_srr(),
  M1Fun = build_M1(),
  growthFun = build_growth(),
  msmMode = 0,
  avgnMode = 0,
  initMode = "NonEquilibrium",
  suitMode = 0,
  suit_styr = NULL,
  suit_endyr = NULL,
  fit_control = NULL,
  ...
)
```

Arguments

`data_list`	A data list read in via `read_data` or built directly in R; see `vignette("data-without-excel", package = "Rceattle")`.
`inits`	(Optional) A named list of initial parameter values, as returned by `build_params` or extracted from a previous fit (`model$estimated_params`). If `NULL`, parameters are initialized from scratch via `build_params`.
`map`	(Optional) A map object from `build_map`.
`bounds`	(Optional) A bounds object from `build_bounds`.
`file`	(Optional) Filename where files will be saved. If NULL, no file is saved.
`estimateMode`	0 = Fit the hindcast model and projection with HCR specified via `HCR`. 1 = Fit the hindcast model only (no projection). 2 = Run the projection only with HCR specified via `HCR` given the initial parameters in `inits`. 3 = debug mode 1: runs the model through MakeADFun, but not nlminb, 4 = runs the model through MakeADFun and nlminb (will all parameters mapped out).
`projection_uncertainty`	logical. If TRUE, accounts for hindcast parameter uncertainty in projections when using an HCR. Default is FALSE for speed.
`random_rec`	logical. If TRUE, treats recruitment deviations as random effects using the laplace approximation.The default is FALSE.
`random_q`	logical. If TRUE, treats annual catchability deviations as random effects using the laplace approximation.The default is FALSE.
`random_sel`	logical. If TRUE, treats annual selectivity deviations as random effects using the laplace approximation.The default is FALSE.
`HCR`	HCR list object from `build_hcr`

`niter`	Number of iterations for multispecies model
`recFun`	The stock recruit-relationship parameterization from `build_srr`.
`M1Fun`	M1 parameterizations and priors. Use `build_M1`.
`growthFun`	The weight-at-age parameterization from `build_growth`.
`msmMode`	The predation mortality functions to used. Defaults to no predation mortality used.
`avgnMode`	The average abundance-at-age approximation to be used for predation mortality equations. 0 (default) is the $N/Z(1-exp(-Z))$, 1 is $Nexp(-Z/2)$, 2 is N.
`initMode`	how the population is initialized. 0 = initial age-structure estimated as free parameters; 1 = equilibrium age-structure estimated out from R0 + mortality (M1); 2 = non-equilibrium age-structure estimated out from R0, mortality (M1), and initial population deviates; 3 = non-equilibrium age-structure estimated out from initial fishing mortality (Finit), R0, mortality (M1), and initial population deviates; 4 = non-equilibrium age-structure version 2 where initial fishing mortality (Finit) scales R0.
`suitMode`	Switch for suitability derivation for each predator (single value or vector). 0 = empirical based on diet data (Holsman et al. 2015), 1 = length-based gamma suitability, 2 = weight-based gamma suitability, 3 = length-based lognormal suitability, 4 = weight-based lognormal suitability, 5 = length-based normal suitability, 6 = weight-based normal suitability.
`suit_styr`	Integer. The first year used to calculate mean suitability. Defaults to $styr$ in $data_list$. Used when diet data were sampled from a subset of years.
`suit_endyr`	Integer. The last year used to calculate mean suitability. Defaults to $endyr$ in $data_list$. Used when diet data were sampled from a subset of years.
`fit_control`	A list returned by `fit_control()` that bundles the optimizer / sdreport / phasing knobs (`phase`, `bias.correct`, `getsd`, `getJointPrecision`, `getReportCovariance`, `use_gradient`, `rel_tol`, `loopnum`, `newtonsteps`, `TMBfilename`, `verbose`, `nlminb_control`). Defaults to `fit_control()`. See `fit_control()` for the meaning and defaults of each field.
`...`	Deprecated optimizer / sdreport / phasing arguments (e.g. `phase`, `getsd`, `bias.correct`, `use_gradient`, `rel_tol`, `control`, `getJointPrecision`, `getReportCovariance`, `loopnum`, `newtonsteps`, `verbose`, `TMBfilename`). These are forwarded into `fit_control` with a deprecation warning; pass them via `fit_control()` instead.

Details

CEATTLE is an age-structured population dynamics model that can be fit with or without predation mortality. The default is to exclude predation mortality by setting `msmMode` to 0. Predation mortality can be included by setting `msmMode` with the following options:

- 0. Single species mode
- 1. Holsman et al. 2015 predation based on multi-species virtual population analysis (MSVPA) based predation formation.
- 2. MSVPA Holling Type III

Values 3 through 9 (Kinzey & Punt 2009 functional responses – Holling Type I/II/III, predator interference, predator preemption, Hassell-Varley, Ecosim) are blocked at runtime by `data_check()` because the implementations have not been validated against the current parameter set. See `src/TMB/predation.hpp`.

Value

A list of class "Rceattle" including:

- data_list: List of data inputs
- initial_params: List of starting parameters
- bounds: Parameter bounds used for estimation
- map: List of map used in TMB
- obj: TMB model object
- opt: Optimized model object from `nlminb`
- sdrep: Object of class `sdreport` exported by TMB including the standard errors of estimated parameters
- estimated_params: List of estimated parameters
- quantities: Derived quantities from CEATTLE
- run_time: Model run time

Examples

```
data(BS2017SS)
ss_run <- fit_mod(
  data_list    = BS2017SS,
  estimateMode = 0,
  msmMode      = 0,
  fit_control  = fit_control(phase = FALSE, verbose = 0)
)
```

`GeorgesBank3spp` *Data inputs for a three-species Georges Bank CEATTLE model*

Description

A data list containing inputs for a multispecies CEATTLE model fit to three groundfish species on Georges Bank. See `BS2017SS` for format details.

Usage

```
GeorgesBank3spp
```

Format

A list with the same structure as `BS2017SS`.

`get_growth_matrix_r` *Generate Length-at-Age Transition Matrix*

Description

This function calculates a probability transition matrix that defines the probability of a fish of a given age belonging to specific length bins. It supports Von Bertalanffy and Richards growth models and includes a Stock Synthesis (SS) style plus-group correction.

Usage

```
get_growth_matrix_r(
  fracyr,
  nsex_sp,
  nages_sp,
  nlengths_sp,
  nyrs,
  lengths_sp,
  minage_sp,
  maxage_sp,
  growth_params_sp,
  growth_log_sd_sp,
  growth_model_sp
)
```

Arguments

`fracyr`	Numeric. Fraction of the year (0 = Jan 1st).
`nsex_sp`	Integer. Number of sexes for the species.
`nages_sp`	Integer. Number of age classes.
`nlengths_sp`	Integer. Number of length bins.
`nyrs`	Integer. Number of years in the simulation.
`lengths_sp`	Vector. Boundaries of the length bins.
`minage_sp`	Numeric. The reference age (L1) for growth estimation.
`maxage_sp`	Numeric. The age at which growth enters the asymptotic phase.
`growth_params_sp`	Array. Dimensions (sex, yr, 4). Params: K, L1, Linf, Richards m.
`growth_log_sd_sp`	Array. Dimensions (sex, 2). Log-SD of length: 1st param is SD at minage, 2nd param is SD at maxage.
`growth_model_sp`	Integer. 1 = Von Bertalanffy, 2 = Richards.

Value

A 4D array of probabilities with dimensions (sex, age, length, year).

`get_weight_at_age_r` *Calculate Predicted Weight-at-Age*

Description

Converts a growth matrix (length-at-age probabilities) into mean weight-at-age using a length-weight relationship (W = a * L^b).

Usage

```
get_weight_at_age_r(
  nsex_sp,
  nages_sp,
  nlengths_sp,
  nyrs,
  lengths_sp,
  length_at_age,
  growth_matrix,
  lw_params
)
```

Arguments

`nsex_sp`	Integer. Number of sexes.
`nages_sp`	Integer. Number of age classes.
`nlengths_sp`	Integer. Number of length bins.
`nyrs`	Integer. Number of years.
`lengths_sp`	Vector. Boundaries of the length bins.
`length_at_age`	Array. Mean length at age from get_growth_matrix_r.
`growth_matrix`	Array. 4D array (sex, age, length, year) from get_growth_matrix_r.
`lw_params`	Array. Dimensions (sex, yr, 2). Params: 1st is alpha (a), 2nd is beta (b).

Details

The function calculates midpoints for length bins to avoid bias. For the first bin, it assumes the width is equal to the second bin's width. The final weight-at-age is the expected value across all length bins for that age.

Value

A 3D array of mean weights with dimensions (sex, age, year).

`GOA2018SS` *Data inputs for a single-species Gulf of Alaska CEATTLE model (2018)*

Description

A data list containing inputs for a single-species CEATTLE model fit to Gulf of Alaska groundfish data through 2018. See `BS2017SS` for format details.

Usage

```
GOA2018SS
```

Format

A list with the same structure as `BS2017SS`.

`GOAatf` *Data inputs for Gulf of Alaska arrowtooth flounder CEATTLE model*

Description

A data list containing inputs for a single-species CEATTLE model fit to Gulf of Alaska arrowtooth flounder data. See `BS2017SS` for format details.

Usage

```
GOAatf
```

Format

A list with the same structure as `BS2017SS`.

`GOAatf2023` *Data inputs for Gulf of Alaska arrowtooth flounder CEATTLE model (2023)*

Description

A data list containing inputs for a single-species CEATTLE model fit to Gulf of Alaska arrowtooth flounder data through 2023. See `BS2017SS` for format details.

Usage

```
GOAatf2023
```

Format

A list with the same structure as `BS2017SS`.

`GOAcod` *Data inputs for Gulf of Alaska Pacific cod CEATTLE model*

Description

A data list containing inputs for a single-species CEATTLE model fit to Gulf of Alaska Pacific cod data. See `BS2017SS` for format details.

Usage

```
GOAcod
```

Format

A list with the same structure as `BS2017SS`.

`GOApollock` *Data inputs for Gulf of Alaska walleye pollock CEATTLE model*

Description

A data list containing inputs for a single-species CEATTLE model fit to Gulf of Alaska walleye pollock data. See `BS2017SS` for format details.

Usage

```
GOApollock
```

Format

A list with the same structure as `BS2017SS`.

`GOAsafe2018` *Gulf of Alaska 2018 SAFE report reference values*

Description

A list containing biomass, spawning stock biomass, and recruitment reference values from the 2018 Gulf of Alaska Stock Assessment and Fishery Evaluation (SAFE) report.

Usage

```
GOAsafe2018
```

Format

A list with components:

biomass Total biomass time series

ssb Spawning stock biomass time series

recruitment Recruitment time series

`jitter` *Jitter analysis*

Description

Run's the Rceattle model at initial values that are +- N(0, sd) from the initial parameters.

Usage

```
jitter(
  Rceattle = NULL,
  njitter = 50,
  sd = 0.2,
  phase = FALSE,
  seed = 123,
  cores = NULL
)
```

Arguments

`Rceattle`	an Rceattle model fit using `fit_mod`
`njitter`	the number of jitters to run
`sd`	standard deviation for jitter (default = 0.2)
`phase`	as in `fit_mod` default = FALSE
`seed`	random number seed. Each jitter `i` uses `seed + i` so results are reproducible under both sequential and parallel execution.
`cores`	Number of cores to use for parallel jitters. Default `NULL` picks `parallel::detectCores() - 6`, capped at 2 when running under `R CMD check` (which sets `_R_CHECK_LIMIT_CORES_`). Set to 1 to force sequential execution.

Value

a list of Rceattle models

Examples

```
data(BS2017SS)
ss_run <- fit_mod(data_list = BS2017SS,
    inits = NULL, file = NULL,
    estimateMode = 0, random_rec = FALSE,
    msmMode = 0, avgnMode = 0,
    phase = FALSE, verbose = 0)
jitters <- jitter(ss_run, njitter = 10)
```

`linkage_spec` *Capture a linkage specification*

Description

Capture a linkage specification

Usage

```
linkage_spec(
  formula,
  param = NULL,
  data = NULL,
  by = ~species,
  species = NULL,
  sex = NULL,
  link = "log",
  init = NULL,
  bounds = NULL,
  priors = NULL,
  re_group = NA_character_,
  est_phase = 1L
)
```

Arguments

`formula`	one-sided R formula whose RHS describes the linear predictor for `param` (e.g. `~ 1`, `~ temp`, `~ temp + PDO`).
`param`	target parameter name on the natural scale (e.g. `"alpha"`, `"M1"`, `"K"`). May be `NULL` when the spec is built inside a `build_*()` call that infers the parameter name from the enclosing list key (see `build_growth()`).
`data`	(Optional) data frame for formula validation. Currently validation happens at materialization time inside `fit_mod()`.
`by`	one-sided formula naming stratifying factors that should each get their own coefficients. Allowed names are `species`, `sex`, and `age_bin`. The default `~species` produces one coefficient set per species (the typical multispecies assessment use case); pass `~species + sex` for per-(species, sex) coefficients, or `NULL` to share a single coefficient set across every species/sex.
`species`	optional integer vector of 1-based species ids that this spec applies to. `NULL` (default) means every species in `strata$species` at materialization time. Use this to give different species different formulas, e.g. by registering multiple specs against the same parameter – see `build_growth()` for the multi-spec syntax.
`sex`	optional vector of sex ids that this spec applies to. May be supplied as integers (`1L` = female, `2L` = male) or as character strings (`"Females"`/`"Males"`, case-insensitive; `"female"`, `"male"`, `"f"`, `"m"` are also accepted). `NULL` (default)

	means every sex in `strata$sex` at materialization time. Only meaningful when by includes `sex`; otherwise the filter is a no-op. Use this to register separate specs per sex (e.g. one prior on females, another on males) against the same parameter.
`link`	link function relating the linear predictor to the natural-scale target parameter. One of `"log"` (default) or `"identity"`. With `link = "log"`, `log(param) = X * beta` – slope contributions are multiplicative on the natural-scale parameter. With `link = "identity"`, `param = X * beta` – slope contributions are additive on the natural scale. All linkage targets currently expose log-scale TMB parameters, so `"log"` is the natural default; `"identity"` is reserved for future processes (e.g. logit for steepness).
`init`	optional named numeric vector of initial values keyed by the design-matrix column name (e.g. `c(`(Intercept)` = 4, temp = 0)`). Missing entries default to `0`.
`bounds`	optional named list of `c(lower, upper)` keyed the same way as `init`.
`priors`	optional named list whose entries are Rceattle_priors objects, keyed by design-matrix column name. Inside this argument the unprefixed shorthand `normal()`, `lognormal()`, `gamma()`, and `beta()` resolves to the corresponding `prior_*` constructors via a private data mask, so `priors = list(temp = normal(0, 1))` works without masking `base::gamma()` or `base::beta()` at the package level. Equivalent to `priors = list(temp = prior_normal(0, 1))`.
`re_group`	optional character: name of a random-effect grouping for these coefficients. `NA` (default) means fixed.
`est_phase`	optional integer estimation phase. Default `1L`.

Value

An `Rceattle_linkage_spec` object.

`load_mse` *Function to load .RDs files from MSE runs*

Description

Function to load .RDs files from MSE runs

Usage

```
load_mse(dir = NULL, file = NULL, exclude = NULL, include_em = TRUE)
```

Arguments

`dir`	Directory used to save files from `run_mse`
`file`	file name used to save files from `run_mse`
`exclude`	index of MSE simulations not to load
`include_em`	whether the EMs should be loaded or not (default = TRUE)

Value

list of MSE simulations/run

`logLik.Rceattle` *Log-likelihood of an Rceattle fit*

Description

Returns the joint negative-objective from `nlminb`, sign-flipped, as a `"logLik"` object. `df` is the number of estimated fixed-effect parameters. The `nobs` attribute is intentionally omitted: counting "observations" in a stock assessment likelihood (with composition cells, indices, catches, and priors) is not well-defined, so `stats::AIC()` works (uses `df`) while `stats::BIC()` does not.

Usage

```
## S3 method for class 'Rceattle'
logLik(object, ...)
```

Arguments

`object`	An object of class `"Rceattle"` returned by `fit_mod()`.
`...`	Currently unused.

Value

An object of class `"logLik"`, or `NULL` if the model was not estimated.

`model_average` *Model average of derived quantities*

Description

Model average of derived quantities

Usage

```
model_average(Rceattle, weights = NULL, uncertainty = FALSE, nboot = 10000)
```

Arguments

`Rceattle`	list of Rceattle model objects
`weights`	vector of weights to be used for weighting models
`uncertainty`	TRUE/FALSE Sample uncertainty across derived quantities using weighted bootstrap from the asymptotic distribution of MLEs
`nboot`	Number of bootstraps taken from asymptotic distribution of MLEs. Default = 10000

Value

an Rceattle object with derived quantities weighted by the specified weights. The length of the derived quantities spans the years which overlap across all models.

`mse_summary` *Management strategy evaluation performance metric summary*

Description

Management strategy evaluation performance metric summary

Usage

```
mse_summary(mse, om_only = FALSE)
```

Arguments

`mse`	MSE runs from `run_mse` or `load_mse`
`om_only`	only include performance metrics from OMs

Value

Alist of two data.frames with MSE summary statistics of performance metrics including: data.frame 1

1. Average annual catch across projection years and simulations per fleet and across fleets
2. Average interannual variation in catch (IAV) across projection years (n) per fleet and across fleets
3. % of years in which the fishery is closed across simulations (s)
4. Average relative mean squared error in estimate of spawning biomass in the terminal year across simulations
5. % of years in which the population is perceived as undergoing overfishing as determined from F_Limit across simulations via `build_hcr` in the EM
6. % of years in which the population is perceived to be overfished as determined from B_Limit across simulations via `build_hcr` in the EM
7. % of years in which the population is undergoing overfishing as determined from the “true” F_Limit across simulations via `build_hcr` in the OM
8. % of years in which the population is overfished as determined from the “true” B_Limit across simulations via `build_hcr` in the OM
9. Average ratio of spawning biomass over B_target in the terminal year across simulations in the OM 10-14. Terminal biomass, SSB, SSB depletion (relative to equilibrium), SSB depletion (relative to dynamic SB0)

`NorthernRockfish2022` *Data inputs for Northern Rockfish CEATTLE model (2022)*

Description

A data list containing inputs for a single-species CEATTLE model fit to Gulf of Alaska northern rockfish data through 2022. See `BS2017SS` for format details.

Usage

```
NorthernRockfish2022
```

Format

A list with the same structure as `BS2017SS`.

`plot.Rceattle` *Plot method for fitted Rceattle models*

Description

Thin S3 dispatcher around the package's existing `plot_*()` functions so that `plot(fit)` works the way users expect. Pick the panel with `what`; everything in `...` is forwarded to the underlying function.

Usage

```
## S3 method for class 'Rceattle'
plot(x, what = "biomass", ...)
```

Arguments

`x`	An object of class `"Rceattle"` returned by `fit_mod()`.
`what`	Character. One of `"biomass"` (default), `"ssb"`, `"recruitment"`, `"depletion"`, `"index"`, `"catch"`, `"selectivity"`, `"mortality"`, or `"data"`.
`...`	Passed to the underlying plotting function.

Value

Invisibly returns `NULL`. Called for the side effect of producing a plot.

`plot_b_eaten` *Plot biomass eaten*

Description

Function that plots the biomass consumed trends as estimated from Rceattle. Returns and saves a figure with the biomass eaten trajectory.

Usage

```
plot_b_eaten(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  width = 7,
  height = 6.5,
  minyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`spnames`	Species names for legend
`add_ci`	TRUE/FALSE, includes 95 percent confidence interval
`lwd`	Line width as specified by user
`save`	Save figure to file?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.

`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	first year to plot
`incl_proj`	TRUE/FALSE include projections years
`mod_cex`	Cex of text for model name legend
`alpha`	Shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?

`plot_b_eaten_prop` *Plot biomass consumed of each prey species by predator*

Description

Function that plots the biomass consumed trends as estimated from Rceattle. Returns and saves a figure with the biomass eaten trajectory.

Usage

```
plot_b_eaten_prop(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  spnames = NULL,
  species = NULL,
  lwd = 3,
  right_adj = 0,
  top_adj = 0.15,
  minyr = NULL,
  mohns = NULL,
  width = 7,
  height = 6.5,
  incl_proj = FALSE,
  incl_mean = FALSE,
  add_ci = FALSE,
  mod_cex = 1
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`spnames`	Species names for legend
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`lwd`	Line width as specified by user
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`top_adj`	Adjustment for top margin
`minyr`	first year to plot
`mohns`	data.frame of mohn's rows extracted from `retrospective`
`width`	Figure width in inches
`height`	Figure height in inches
`incl_proj`	TRUE/FALSE include projections years
`incl_mean`	TRUE/FALSE include horizontal long term mean
`add_ci`	TRUE/FALSE, includes 95 percent confidence interval
`mod_cex`	Cex of text for model name legend

`plot_biomass` *Plot biomass*

Description

Plots the mean minage+ biomass (million mt) and 95\

Usage

```
plot_biomass(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
```

```
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

Value

Returns and saves a figure with the biomass trajectory.

`plot_catch` *Landings fits*

Description

Plot of fitted landings data on natural-scale (r4ss-style)

Usage

```
plot_catch(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  right_adj = 0,
  top_adj = 1.2,
  incl_proj = FALSE,
  single.plots = FALSE,
  width = NULL,
  height = NULL,
  alpha = 0.4,
  lwd = 2,
  ymax = NULL,
  maxyr = NULL,
  mse = FALSE,
  error = TRUE,
  fleets = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Species names for legend
`right_adj`	How much right side of the x-axis for fitting the legend. As percentage.
`top_adj`	How much top side of the y-axis for fitting the legend. As percentage (default = 1.2).
`incl_proj`	TRUE/FALSE include projections years
`single.plots`	if TRUE plot invidual fits else make multiplot
`width`	plot width
`height`	plot hight

`alpha`	Transparency of lines for MSE plots
`lwd`	Line width
`ymax`	Fleet specific upper ylim
`maxyr`	Max year to plot
`mse`	Is if an MSE object from `load_mse` or `run_mse`. Will plot data from OMs.
`error`	Include observed data with error bars?
`fleets`	Which fishing fleets to include (defaults to all = NULL)

`plot_comp` *Plot time series of comp data*

Description

Function the plots the comp data as estimated from Rceattle

Usage

```
plot_comp(
  Rceattle,
  file = NULL,
  model_names = NULL,
  species = NULL,
  cex = 3,
  lwd = 3,
  right_adj = 0
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`species`	Species names for legend
`cex`	Line width as specified by user
`lwd`	Line width for observed data lines
`right_adj`	How many units of the x-axis to add to the right side of the figure for fitting the legend.

Value

Returns and saves a figure

`plot_data` *Timeline of data used in the model likelihoods*

Description

Plots a timeline of presence/absence (and optionally relative quantity) of the data sources contributing to an Rceattle model's likelihood, by year and fleet. Modelled after Stock Synthesis's `r4ss::SSplotData()`.

Usage

```
plot_data(
  Rceattle,
  file = NULL,
  subplots = 1:2,
  datatypes = "all",
  fleets = "all",
  species = "all",
  ghost = FALSE,
  fleetcol = "default",
  width = 7,
  height = 5,
  res = 200,
  ptsize = 10,
  margins = c(5.1, 2.1, 2.1, 10.1),
  cex = 2,
  lwd = 12,
  maxsize = 1,
  alphasize = 1,
  mainTitle = FALSE,
  cex.main = 1
)
```

Arguments

`Rceattle`	Either a single Rceattle model object exported from `Rceattle::fit_mod()`, or a raw `data_list` (e.g. one of the bundled datasets such as `BS2017MS`).
`file`	Path/prefix used to save the figure. If `NULL` (default) the plot is drawn to the active device only. When supplied, the figure is written to `paste0(file, "_data_plot.png")` (and `_data_plot2.png` for the bubble subplot).
`subplots`	Integer vector controlling which subplots are produced: • 1 — equal-size points showing presence/absence by year/fleet • 2 — points scaled to relative quantity / precision within each data type (catch tonnage, 1/SE for indices, sample size for comps)
`datatypes`	Either `"all"` or a subset of `c("catch", "index", "agecomp", "lencomp", "caal", "diet")`.

`fleets`	Either `"all"` or an integer vector of `Fleet_codes` to include. Diet "fleets" are encoded after the regular fleets (one per predator species).
`species`	Either `"all"` or an integer vector of species indices to include.
`ghost`	Logical. If `TRUE`, also include rows excluded from the likelihood (`Year < 0`). Defaults to `FALSE`.
`fleetcol`	Either `"default"` or a vector of colors (one per fleet shown after subsetting). Diet entries get an additional color appended.
`width`, `height`	Figure dimensions in inches.
`res`	Resolution (dpi) for the saved PNG.
`ptsize`	Pointsize passed to `png()`.
`margins`	`par("mar")` for the plot. Increase the right margin if long fleet names are clipped.
`cex`	Character expansion for points showing isolated years.
`lwd`	Line width for runs of consecutive years (subplot 1).
`maxsize`	Max bubble radius (in plot units) for subplot 2.
`alphasize`	Bubble fill transparency (0–1).
`mainTitle`	Logical; if `TRUE` add a default title.
`cex.main`	Title character expansion.

Details

Years with `Year > 0` contribute to the likelihood; rows with `Year < 0` (kept for fitting comparison only) are shown when `ghost = TRUE`. Diet data uses `Year == 0` for the fixed reference stomach composition; those entries are plotted at the model `endyr` and labelled per predator species.

Value

Invisibly, a list with `typetable` — the long data frame underlying the plot (year, fleet, data type, relative size).

`plot_depletion` *Plot biomass depletion*

Description

Plots the mean biomass depletion and 95\

Usage

```
plot_depletion(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot

`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

Value

Returns and saves a figure with the biomass depletion trajectory.

`plot_depletionSSB` *Plot SSB depletion*

Description

Plots the mean SSB depletion and 95\ Depletion reference lines for Ptarget and Plimit are drawn in blue and red respectively.

Usage

```
plot_depletionSSB(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
```

```
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

Value

Returns and saves a figure with the SSB depletion trajectory.

`plot_diet_comp` *Plot diet composition fits*

Description

If year == 0, diet data are averaged from suit_styr to suit_endyr If prey_age >= 0 diet data are diet proportion of prey-at-age in predator-at-age If prey_age < 0 diet data are diet proportion of prey-spp in predator-at-age (sum across prey ages) If prey_age < 0 and pred_age < 0, diet data are mean diet proportion of prey-spp in predator-spp (sum across prey ages and take mean across predator ages) If prey_age < 0 and pred_age < -500, diet data are weighted mean diet proportion of prey-spp in predator-spp (sum across prey ages and take weighted mean across predator ages)

Usage

```
plot_diet_comp(Rceattle, file = NULL, species = NULL)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`species`	Species names for legend

Value

Returns and saves a figure

`plot_exploitable_biomass` *Plot exploitable biomass*

Description

Plots the mean exploitable biomass (million mt) and 95\

Usage

```
plot_exploitable_biomass(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
```

```
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

Value

Returns and saves a figure with the exploitable biomass trajectory.

`plot_f` *plot F*

Description

Function that plots the F time series per species from Rceattle

Usage

```
plot_f(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  right_adj = 0,
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`spnames`	Species names for legend
`add_ci`	NOT WORKING If the confidence interval is to be added
`lwd`	Line width as specified by user

`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`width`	plot width
`height`	plot height
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`alpha`	shading for confidence intervals
`mod_avg`	is the list a model average? (DEPRECATED)
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?

Value

Returns and saves a figure with the population trajectory.

`plot_form` *Plot functional form*

Description

Function to plot the functional form estimated or specified by `Rceattle`

Usage

```
plot_form(params = NULL, pred = 1, pred_age = 1, prey = 1, msmMode = 3)
```

Arguments

`params`	Parameter list object from `build_params` or `Rceattle`
`pred`	Predator index
`pred_age`	Predator age
`prey`	Prey index
`msmMode`	Multispecies mode integer specifying functional form

`plot_index` *CPUE fits*

Description

Plot of fitted CPUE indices on natural-scale (r4ss-style)

Usage

```
plot_index(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  right_adj = 0,
  top_adj = 0.05,
  incl_proj = FALSE,
  single.plots = FALSE,
  width = NULL,
  height = NULL,
  error = TRUE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Species names for legend
`right_adj`	How much right side of the x-axis for fitting the legend. As percentage.
`top_adj`	How much top side of the y-axis for fitting the legend. As percentage.
`incl_proj`	TRUE/FALSE include projections years
`single.plots`	if TRUE plot invidual fits else make multiplot
`width`	plot width
`height`	plot hight
`error`	include observed data and error bars?

`plot_indexresidual` *CPUE residual*

Description

Plot of residuals CPUE indices on log-scale (r4ss-style)

Usage

```
plot_indexresidual(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  right_adj = 0,
  top_adj = 0.05,
  incl_proj = FALSE,
  single.plots = FALSE,
  width = NULL,
  height = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Species names for legend
`right_adj`	How much right side of the x-axis for fitting the legend. As percentage.
`top_adj`	How much top side of the y-axis for fitting the legend. As percentage.
`incl_proj`	TRUE/FALSE include projections years
`single.plots`	if TRUE plot invidual fits else make multiplot
`width`	plot width
`height`	plot hight

`plot_logindex` *log(CPUE) fits*

Description

Plot of fitted CPUE indices on log-scale (r4ss-style)

Usage

```
plot_logindex(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  right_adj = 0,
  top_adj = 0.05,
  incl_proj = FALSE,
  single.plots = FALSE,
  width = NULL,
  height = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Species names for legend
`right_adj`	How much right side of the x-axis for fitting the legend. As percentage.
`top_adj`	How much top side of the y-axis for fitting the legend. As percentage.
`incl_proj`	TRUE/FALSE include projections years
`single.plots`	if TRUE plot invidual fits else make multiplot
`width`	plot width
`height`	plot hight

`plot_m_at_age` *Plot natural mortality by age*

Description

Function that plots the natural mortality at age (M1 + M2) as estimated from Rceattle. Returns and saves a figure with the M-at-age trajectory.

Usage

```
plot_m_at_age(
  Rceattle,
  file = NULL,
  age = 1,
  model_names = NULL,
  line_col = NULL,
  spnames = NULL,
  species = NULL,
  lwd = 3,
  lty = 1,
  right_adj = 0,
  minyr = NULL,
  width = 7,
  height = 6.5,
  incl_proj = FALSE,
  incl_mean = FALSE,
  add_ci = FALSE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`age`	Age to plot M at age
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`spnames`	Species names for legend
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`lwd`	Line width as specified by user
`lty`	Line type
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`minyr`	first year to plot
`width`	Figure width in inches

`height`	Figure height in inches
`incl_proj`	TRUE/FALSE include projections years
`incl_mean`	TRUE/FALSE include time series mean as horizontal line
`add_ci`	TRUE/FALSE, includes 95 percent confidence interval

`plot_m2_at_age_prop` *Plot predation mortality by age and predator*

Description

Function that plots the predation mortality at age (M2) by predator as estimated from Rceattle. Returns and saves a figure with the M-at-age trajectory.

Usage

```
plot_m2_at_age_prop(
  Rceattle,
  file = NULL,
  age = 1,
  model_names = NULL,
  line_col = NULL,
  spnames = NULL,
  species = NULL,
  lwd = 3,
  right_adj = 0,
  top_adj = 0.15,
  minyr = NULL,
  width = 7,
  height = 6.5,
  incl_proj = FALSE,
  incl_mean = FALSE,
  add_ci = FALSE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`age`	Age to plot M at age
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`spnames`	Species names for legend
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`lwd`	Line width as specified by user

`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`top_adj`	Adjustment for top margin
`minyr`	first year to plot
`width`	Figure width in inches
`height`	Figure height in inches
`incl_proj`	TRUE/FALSE include projections years
`incl_mean`	TRUE/FALSE include time series mean as horizontal line
`add_ci`	TRUE/FALSE, includes 95 percent confidence interval

`plot_maturity` *Plot maturity*

Description

Function that plots the maturity of each species

Usage

```
plot_maturity(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  width = 4,
  height = 5.5,
  lwd = 3
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	Species names for legend
`width`	Figure width in inches
`height`	Figure height in inches
`lwd`	Line width as specified by user

`plot_mortality` *Plot M1 + M2*

Description

Function that plots the M1 and M2 as estimated from Rceattle

Usage

```
plot_mortality(
  Rceattle,
  file = NULL,
  incl_proj = FALSE,
  zlim = NULL,
  type = 0,
  width = 8,
  height = 5.5,
  title = NULL,
  log = FALSE,
  minyr = NULL,
  theta = 155,
  species = NULL,
  maxage = NULL,
  title_cex = 10,
  M2 = TRUE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`incl_proj`	Include the projection years (TRUE/FALSE)
`zlim`	zlim for M1 + M2 plots. Character - use max range across species in model. NULL - use species specific ranges. Vector of two.
`type`	0 = Tiles, 1 = contour, 2 = facet lines, 3 = persp
`width`	Plot width when saved "inches"
`height`	Plot height when saved "inches"
`title`	Additional title to add. Will also add species names if not NULL
`log`	TRUE/FALSE use log M1 + M2
`minyr`	First year to plot
`theta`	theta for persp plot
`species`	Species to plot. Plots all if null.
`maxage`	Plot up to this age. Plots all ages if NULL
`title_cex`	Font size for title
`M2`	TRUE/FALSE Use M2 only (True) or total M (False)

`plot_ration` *Plot ration*

Description

Function that plots the ration across ages (minage:nages) as estimated from Rceattle. Returns and saves a figure with the ration trajectory. Ration is multiplied by biomass-at-age/sex to get population level estimates

Usage

```
plot_ration(
  Rceattle,
  file = NULL,
  minage = 1,
  model_names = NULL,
  line_col = NULL,
  spnames = NULL,
  species = NULL,
  lwd = 3,
  lty = 1,
  right_adj = 0,
  minyr = NULL,
  width = 7,
  height = 6.5,
  incl_proj = FALSE,
  incl_mean = FALSE,
  add_ci = FALSE
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`minage`	minage to plot ration (i.e. age "minage"+)
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`spnames`	Species names for legend
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`lwd`	Line width as specified by user
`lty`	Line type
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`minyr`	first year to plot
`width`	Figure width in inches

`height`	Figure height in inches
`incl_proj`	TRUE/FALSE include projections years
`incl_mean`	TRUE/FALSE include time series mean as horizontal line
`add_ci`	TRUE/FALSE, includes 95 percent confidence interval

`plot_recruitment` *Plot recruitment*

Description

Plots the mean minage recruitment (millions) and 95\

Usage

```
plot_recruitment(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend

`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

Value

Returns and saves a figure with the recruitment trajectory.

`plot_selectivity` *Plot selectivity*

Description

Function that plots the fishery and survey selectivity as estimated from Rceattle

Usage

```
plot_selectivity(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  width = 7,
  height = 6.5,
  species = c("Walleye pollock", "Pacific cod", "Arrowtooth flounder"),
  lwd = 3
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`width`	Figure width in inches
`height`	Figure height in inches
`species`	Species names for legend
`lwd`	Line width as specified by user

`plot_selectivity_vs_maturity`

Plot fishery selectivity and maturity

Description

Function the plots the fishery selectivity and input maturity. Useful for debugging SPR based reference points.

Usage

```
plot_selectivity_vs_maturity(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  width = 7,
  height = 6.5,
  species = c("Walleye pollock", "Pacific cod", "Arrowtooth flounder"),
  lwd = 3
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`width`	Figure width in inches
`height`	Figure height in inches
`species`	Species names for legend
`lwd`	Line width as specified by user

`plot_ssb` *Plot spawning stock biomass (SSB)*

Description

Plots the mean SSB (million mt) and 95\

Usage

```
plot_ssb(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user

`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

Value

Returns and saves a figure with the SSB trajectory.

`plot_ssb_depletion` *Plot SSB depletion (deprecated name)*

Description

Deprecated alias for `plot_ssb_depletion`. Please use `plot_ssb_depletion()` instead.

Usage

```
plot_ssb_depletion(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  right_adj = 0,
  legend.pos = "topright",
  width = 7,
  height = 6.5,
```

```
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mod_avg = rep(FALSE, length(Rceattle)),
  mse = FALSE,
  OM = TRUE,
  reference = NULL
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mod_avg`	TRUE/FALSE
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model

`plot_stock_recruit` *Plot stock recruit function*

Description

Function the plots the stock recruit function as estimated from Rceattle

Usage

```
plot_stock_recruit(
  Rceattle,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  width = 7,
  height = 6.5,
  species = NULL,
  spnames = NULL,
  lwd = 3,
  lty = 1,
  incl_proj = FALSE,
  plot_env = FALSE,
  mod_cex = 1
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend
`line_col`	Colors of models to be used for line color
`width`	Figure width in inches
`height`	Figure height in inches
`species`	Which species to plot e.g. c(1,4). Default = NULL plots them all
`spnames`	Species names for legend
`lwd`	Line width as specified by user
`lty`	Line type
`incl_proj`	TRUE/FALSE, include projection years for environmental relationship
`plot_env`	TRUE/FALSE, plot environmental covariate relationship
`mod_cex`	Cex of text for model name legend

`plot_timeseries` *Plot time-series*

Description

Function that plots the time-series (SSB/B/R/Depletion) 95% CI trends as estimated from Rceattle

Usage

```
plot_timeseries(
  Rceattle,
  output = "biomass",
  ylab = NULL,
  file = NULL,
  model_names = NULL,
  line_col = NULL,
  species = NULL,
  spnames = NULL,
  add_ci = FALSE,
  lwd = 3,
  save = FALSE,
  legend.pos = "topright",
  right_adj = 0,
  width = 7,
  height = 6.5,
  minyr = NULL,
  maxyr = NULL,
  incl_proj = FALSE,
  mod_cex = 1,
  lty = rep(1, length(Rceattle)),
  alpha = 0.4,
  mse = FALSE,
  OM = TRUE,
  reference = NULL,
  mod_avg = rep(FALSE, length(Rceattle))
)
```

Arguments

`Rceattle`	Single or list of Rceattle model objects exported from `Rceattle`
`output`	derived quantity of interest: recruitment, biomass, ssb, depletion, or ssb_depletion. Uses same name as ".cpp" file.
`ylab`	Y-axis label
`file`	name of a file to identified the files exported by the function.
`model_names`	Names of models to be used in legend

`line_col`	Colors of models to be used for line color
`species`	What species to include 1:nspp
`spnames`	Species names for legend
`add_ci`	If the confidence interval is to be added
`lwd`	Line width as specified by user
`save`	Save derived quantity?
`legend.pos`	Position of the legend as used by `legend` (default = "topright").
`right_adj`	Multiplier for to add to the right side of the figure for fitting the legend.
`width`	Figure width in inches
`height`	Figure height in inches
`minyr`	First year to plot
`maxyr`	max year to plot
`incl_proj`	TRUE/FALSE, include projection years
`mod_cex`	Cex of text for model name legend
`lty`	line type
`alpha`	shading for confidence intervals
`mse`	Is an MSE object from `load_mse` or `run_mse`
`OM`	if mse == TRUE, use the OM (TRUE) or EM (FALSE) for plotting?
`reference`	Reference model
`mod_avg`	TRUE/FALSE

Value

Returns and saves a figure with the population trajectory.

`print.Rceattle` *Print method for fitted Rceattle models*

Description

Provides a compact summary so that auto-printing inside R Markdown / knitr / RStudio does not recurse into the (very deep) data and TMB objects stored on the fit. Only structural metadata, convergence status, headline derived quantities, and the package / TMB-DLL versions used to produce the fit are printed.

Usage

```
## S3 method for class 'Rceattle'
print(x, ...)
```

Arguments

`x`	An object of class `"Rceattle"` returned by `fit_mod()`.
`...`	Currently unused.

Details

For operational use, the package version line is meant to make it obvious which version of `Rceattle` produced an archived fit so that results can be reproduced even if `master` has moved on. Tag a release (`devtools::install_github("grantdadams/Rceattle@vX.Y.Z")`) and the same version string will reappear here on a fresh run.

Value

The input `x`, invisibly.

`prior_beta` *Beta prior on a linkage coefficient*

Description

Standard Beta(shape1, shape2) on (0, 1), matching `stats::dbeta()`. For priors on stock-recruit steepness on the standard (0.2, 1) interval, transform inside the model and use `prior_beta()` on the rescaled quantity.

Usage

```
prior_beta(shape1, shape2)
```

Arguments

`shape1, shape2`	positive shape parameters.

Value

An `Rceattle_prior` of family `"beta"`.

`prior_gamma` *Gamma prior on a linkage coefficient*

Description

Shape-rate parameterization, matching `stats::dgamma()`.

Usage

```
prior_gamma(shape, rate)
```

Arguments

`shape`	positive shape parameter.
`rate`	positive rate parameter.

Value

An `Rceattle_prior` of family `"gamma"`.

`prior_lognormal` *Lognormal prior on a linkage coefficient*

Description

Parameterized on the log scale (mean and sd of the log of the coefficient), matching `stats::dlnorm()`.

Usage

```
prior_lognormal(meanlog, sdlog)
```

Arguments

`meanlog`	prior mean of the log of the coefficient.
`sdlog`	prior standard deviation of the log (must be positive).

Value

An `Rceattle_prior` of family `"lognormal"`.

`prior_normal` *Normal prior on a linkage coefficient*

Description

Normal prior on a linkage coefficient

Usage

```
prior_normal(mean, sd)
```

Arguments

`mean`	prior mean.
`sd`	prior standard deviation (must be positive).

Value

An `Rceattle_prior` of family `"normal"`.

`profile.Rceattle` *Likelihood profile across one or more parameter cells*

Description

Re-fits an Rceattle model while holding selected cells of a parameter fixed at user-specified values. Supports profiling a single cell (e.g. `R_log_sd[species = 1]`) and arbitrary N-dimensional cross-profiles over multiple cells – e.g. `log_M1[1, 1, 1]` and `log_M1[1, 2, 1]` jointly, to profile residual M for males against females. For each grid point the targeted cells are fixed in the TMB map and the remaining parameters are re-estimated; the result is a grid of Rceattle models for downstream NLL surfaces.

Usage

```
## S3 method for class 'Rceattle'
profile(
  fitted = NULL,
  param = NULL,
  slots = NULL,
  values = NULL,
  transform = "log",
  cores = NULL,
  ...
)
```

Arguments

`fitted`	an Rceattle model fit using `fit_mod`
`param`	Name of the parameter to profile. Two ways to specify it: **Raw parameter slot** any name in `Rceattle$estimated_params`; tested for `"R_log_sd"`, `"rec_pars"`, and `"log_M1"`. `slots` must index into the full array and `transform` controls the scale. **Natural-scale alias** convenience shortcut for the three documented parameters. Aliases imply `transform = "log"` (values are taken in natural units and log'd before being substituted) and, for `rec_pars`, fill in the column from the alias name so `slots` only needs the species index: • `"sigmaR"`, `"R_sd"` -> `R_log_sd` • `"M1"` -> `log_M1` • `"R0"` -> `rec_pars[, 1]` • `"alpha"` -> `rec_pars[, 2]` • `"beta"` -> `rec_pars[, 3]` If `transform` is supplied with an alias it is ignored (with a warning).
`slots`	A list whose entries are integer index vectors, one entry per cell to fix. Each entry's length must equal the number of dimensions of the resolved parameter – 1 for vectors (`R_log_sd`), 2 for matrices (`rec_pars`), 3 for 3-D arrays (`log_M1`). When using the `"R0"`/`"alpha"`/`"beta"` aliases, supply only the species index (length 1); the column is filled in from the alias. E.g. `list(c(1, 2, 1))` fixes `log_M1[1, 2, 1]`; `list(c(1, 1, 1), c(1, 2, 1))` fixes both sex cells for a males-vs-females cross-profile of species 1; `list(1, 2)` with `param = "sigmaR"` cross-profiles species 1 and 2. If omitted, defaults to a single species-1 slot shaped to match the resolved parameter (e.g. `list(1)` for `R_log_sd`, `list(c(1, 1, 1))` for `log_M1`, `list(1)` for the `rec_pars` aliases) and emits a warning; pass `slots` explicitly to silence the warning. Defaulting requires `length(values) == 1L` (otherwise the user must explicitly say which cell each grid targets).
`values`	A list of numeric vectors, one per entry of `slots`. The full grid of fits is `expand.grid(values)`, so a single slot gives a 1-D profile and *k* slots give a *k*-D cross-profile.
`transform`	How to map user values onto the internal parameter scale before substituting them into `inits`. Either `"log"` (default), `"identity"`, or a unary function (e.g. `qlogis`). Applied element-wise to every grid value. Aliases override this with `"log"`.
`cores`	Number of cores to use for parallel fits. Default `NULL` picks `parallel::detectCores() - 6`, capped at 2 when running under `R CMD check` (which sets `_R_CHECK_LIMIT_CORES_`). Set to 1 to force sequential execution.
`...`	Unused; present for consistency with the `stats::profile` generic.

Value

A list with elements:

Rceattle_list list of fitted Rceattle models, one per grid row; entries for non-converged fits are `NULL` so positions stay aligned with `grid`.

grid data frame of grid values on the user scale (before `transform`); one column per profiled cell, named `slot_1`, `slot_2`, ...

nll numeric vector of joint negative log-likelihoods (`opt$objective`); `NA` where the fit did not converge.

param the profiled parameter name (echoed).

slots the slots list (echoed for downstream plotting).

Examples

```
data(BS2017SS)
ss_run <- fit_mod(data_list = BS2017SS,
    inits = NULL, file = NULL,
    estimateMode = 0, random_rec = FALSE,
    msmMode = 0, avgnMode = 0,
    phase = FALSE, verbose = 0)

# 1-D profile of sigmaR for species 1 (alias form -- natural scale)
p1 <- profile(ss_run,
    param  = "sigmaR",
    slots  = list(1),
    values = list(seq(0.1, 1.5, by = 0.1)))

# Equivalent raw form (log scale -- user does the transform)
p1_raw <- profile(ss_run,
    param     = "R_log_sd",
    slots     = list(1),
    values    = list(log(seq(0.1, 1.5, by = 0.1))),
    transform = "identity")

# 2-D cross-profile of M1 across species 1 and 2 (sex 1, age 1).
# BS2017SS is single-sex; with a multi-sex model the same form
# (e.g. c(1, 1, 1), c(1, 2, 1)) would cross-profile males vs females.
p2 <- profile(ss_run,
    param  = "M1",
    slots  = list(c(1, 1, 1), c(2, 1, 1)),
    values = list(seq(0.1, 0.4, length.out = 3),
                  seq(0.1, 0.4, length.out = 3)))

# 1-D profile of SRR alpha for species 1 (alias drops the rec_pars column)
p3 <- profile(ss_run,
    param  = "alpha",
    slots  = list(1),
    values = list(seq(2, 80, length.out = 20)))
```

`read_data` *Read a CEATTLE excel data file*

Description

Read a CEATTLE excel data file

Usage

```
read_data(file = "Rceattle_data.xlsx")
```

Arguments

`file`	Filname to be used. Must end with '.xlsx'

Examples

```
library(Rceattle)
data(BS2017SS)
out_file <- file.path(tempdir(), "BS2017SS.xlsx")
write_data(data_list = BS2017SS, file = out_file)
data_list <- read_data(file = out_file)
file.remove(out_file)
```

`rearrange_data` *Rearrange a data_list for TMB*

Description

Function to rearrange a `data_list` object to be read into TMB

`rearrange_dat()` is a deprecated alias for `rearrange_data()` kept for backwards compatibility; please use `rearrange_data()`.

Usage

```
rearrange_data(data_list)

rearrange_dat(data_list)
```

Arguments

`data_list`	an Rceattle data_list

`remove_F` *Rerun with F = 0.*

Description

Function to update hindcast and set F to 0. Useful for determining dynamic reference points for multi-species models under climate-change.

Usage

```
remove_F(Rceattle)
```

Arguments

`Rceattle`	A fitted Rceattle model object

`rename_output` *Function to rename derived quantities from Rceattle*

Description

Function to rename derived quantities from Rceattle

Usage

```
rename_output(data_list = NULL, quantities = NULL)
```

Arguments

`data_list`	an Rceattle data_list
`quantities`	list of "report" objects from Rceattle.

`residuals.Rceattle` *Observed-vs-fitted residuals from an Rceattle fit*

Description

Returns a long-format data frame of residuals across one or more of the four fitted data sources: `"index"` (survey indices), `"catch"` (fishery catches), `"comp"` (age- or length-composition proportions), and `"caal"` (conditional age-at-length proportions).

Usage

```
## S3 method for class 'Rceattle'
residuals(object, type = "index", scale = "log", ...)
```

Arguments

`object`	An object of class `"Rceattle"` returned by `fit_mod()`.
`type`	One or more of `"index"`, `"catch"`, `"comp"`, `"caal"`, or `"all"` (default `"index"`).
`scale`	`"log"` (default) or `"natural"`. Only affects `"index"` and `"catch"` residuals.
`...`	Currently unused.

Details

For `"index"` and `"catch"`, the `Residual` column is on the log scale by default (matching the lognormal observation likelihood) and can be switched to the natural scale via `scale = "natural"`. For `"comp"` and `"caal"`, residuals are Pearson residuals on the fitted proportions:

$$r = (p - \hat{p})/\sqrt{\hat{p}(1 - \hat{p})/N}$$

where N is the input sample size. Composition rows are returned in long form: one row per (observation, age/length bin).

Composition rows carry the `Age0_Length1` flag from `comp_data` (`0` for age comps, `1` for length comps) so age and length comps can be filtered apart. CAAL rows carry both the conditioning `Length` and the age `Bin`.

Value

A `data.frame` with columns `Source`, `Fleet_code`, `Fleet_name`, `Species`, `Sex`, `Year`, `Length`, `Bin`, `Age0_Length1`, `Sample_size`, `Observed`, `Fitted`, `Residual`. `Sex`, `Length`, `Bin`, `Age0_Length1`, and `Sample_size` are `NA` where they do not apply (e.g. for index/catch rows).

`retrospective` *Retrospective peels*

Description

Calculate Mohn's rho and run retrospective peels for an Rceattle model. The function also evaluates retrospective forecast skill. To evaluate both retrospective bias and forecast skill, the function uses the map functionality of TMB to peel the model:

1. Filters data, filters fixed inputs, and maps out time-varying parameters for the peeled years. All time-varying parameters for the peeled years are set to the terminal year of the model for that peel.
2. Fits the peeled model.
3. Turns off all hindcast parameters, turns on F for the peeled years, and fits to the peeled catch series to update the "forecast" dynamics given projection assumptions and observed catch from the peeled years.

Usage

```
retrospective(
  Rceattle = NULL,
  peels = 5,
  rescale = FALSE,
  nyrs_forecast = 3,
  cores = NULL
)
```

Arguments

`Rceattle`	an Rceattle model fit using `fit_mod`
`peels`	the number of retrospective peels to use in the calculation of rho and for model estimation
`rescale`	TRUE/FALSE whether to subset and rescale environmental predictors for the range of peel years.
`nyrs_forecast`	Number of forecast years to calculate Mohn's Rho in addition to terminal year
`cores`	Number of cores to use for parallel peels. Default `NULL` picks `parallel::detectCores() - 6`, capped at 2 when running under `R CMD check` (which sets `_R_CHECK_LIMIT_CORES_`). Set to 1 to force sequential execution.

Value

a list of 1. list of Rceattle models and 2. vector of Mohn's rho for each species

Examples

```
data(BS2017SS)
ss_run <- fit_mod(data_list = BS2017SS,
    inits = NULL, file = NULL,
    estimateMode = 0, random_rec = FALSE,
    msmMode = 0, avgnMode = 0,
    phase = FALSE, verbose = 0)
retro <- retrospective(ss_run, peels = 10)
```

`rich.colors.short` *Make a vector of colors.*

Description

A subset of rich.colors by Arni Magnusson from the gplots package, with the addition of alpha transparency (which is now available in the gplots version as well)

Usage

```
rich.colors.short(n, alpha = 1)
```

Arguments

`n`	Number of colors to generate.
`alpha`	Alpha transparency value for all colors in vector. Value is passed to rgb function.

Author(s)

Arni Magnusson, Ian Taylor

`run_mse` *Run a management strategy evaluation*

Description

Runs a forward projecting MSE. Main assumptions are the projected selectivity/catchability, foraging days, and weight-at-age are the same as the terminal year of the hindcast in the operating model. Assumes survey sd is same as average across historic time series, while comp data sample size is same as last year. No implementation error and no observation error for catch!

Usage

```
run_mse(
  om,
  em,
  nsim = 10,
  start_sim = 1,
  assessment_period = 1,
  sampling_period = 1,
  simulate_data = TRUE,
  regenerate_past = FALSE,
  sample_rec = TRUE,
  rec_trend = 0,
  fut_sample = 1,
  cap = NULL,
  catch_mult = NULL,
  seed = 666,
  regenerate_seed = seed,
  loopnum = 1,
  file = NULL,
  dir = NULL,
  timeout = 999,
  endyr = NA,
  cores = NULL
)
```

Arguments

`om`	CEATTLE model object exported from `Rceattle`
`em`	CEATTLE model object exported from `Rceattle`
`nsim`	Number of simulations to run (default 10)
`start_sim`	First simulation number to start at. Useful if the code stops at specific seed/sim (default = 1).
`assessment_period`	Period of years that each assessment is taken
`sampling_period`	Period of years data sampling is conducted. Single value or vector the same length as the number of fleets.
`simulate_data`	Include simulated random error proportional to that estimated/provided for the data from the OM.
`regenerate_past`	Refits the EM to historical/conditioning data prior to the MSE, where the data are generated from the OM with `simulate_data = TRUE` or without `simulate_data = FALSE` sampling error.
`sample_rec`	Include resampled recruitment deviates from the"hindcast" in the projection of the OM. Resampled deviates are used rather than sampling from N(0, sigmaR) because initial deviates bias R0 low. If false, uses mean of recruitment deviates.

`rec_trend`	Linear increase or decrease in mean recruitment from `endyr` to `projyr`. This is the terminal multiplier `mean rec * (1 + (rec_trend/projection years) * 1:projection years)`. Can be of length 1 or of length nspp. If length 1, all species get the same trend.
`fut_sample`	future sampling effort relative to last year. `Log_sd * 1 / fut_sample` for index and `Sample_size * fut_sample` for comps
`cap`	A cap on the catch in the projection. Can be a single number applied to all species (proportional to recommended catch) or vector of length `nspp` applied to each species. Default = NULL
`catch_mult`	A multiplier for the catch in the projection. Can be a single number or vector of length nspp. Default = NULL
`seed`	seed for the simulation
`regenerate_seed`	seed for regenerating data
`loopnum`	number of times to re-start optimization (where `loopnum=3` sometimes achieves a lower final gradient than `loopnum=1`)
`file`	(Optional) Filename where each OM simulation with EMs will be saved. If NULL, no files are saved.
`dir`	(Optional) Directory where each OM simulation is saved
`timeout`	length of time (minutes) estimation will run before stopping a sim (default 999 minutes)
`endyr`	Terminal year of the MSE projection. Default = NA uses `projyr` from the operating model.
`cores`	Number of cores to use for parallel simulations. Default `NULL` picks `parallel::detectCores() - 6`, capped at 2 when running under `R CMD check` (which sets `_R_CHECK_LIMIT_CORES_`). Set to 1 to force sequential execution.

Value

A list of operating models (differ by simulated recruitment determined by `nsim`) and estimation models fit to each operating model (differ by terminal year).

`sample_rec` *Sample historical recruitment deviates and place in the projection*

Description

Sample historical recruitment deviates and place in the projection

Usage

```
sample_rec(Rceattle, sample_rec = TRUE, update_model = TRUE, rec_trend = 0)
```

Arguments

`Rceattle`	CEATTLE model object exported from `Rceattle`
`sample_rec`	Include resampled recruitment deviates from the"hindcast" in the projection of the OM. Resampled deviates are used rather than sampling from N(0, sigmaR) because initial deviates bias R0 low. If false, uses mean of recruitment deviates.
`update_model`	Update model dynamics. Default = TRUE
`rec_trend`	Linear increase or decrease in mean recruitment from `endyr` to `projyr`. This is the terminal multiplier `mean rec * (1 + (rec_trend/projection years) * 1:projection years)`. Can be of length 1 or of length nspp. If length 1, all species get the same trend.

Value

Rceattle model

`self_test` *Self test simulation analysis analysis*

Description

Simulates data from an Rceattle model and refits the model to the simulated data. TODO add process variation (i.e. random devs) to simulation.

Usage

```
self_test(
  Rceattle = NULL,
  nsim = 50,
  simulate = TRUE,
  seed = 123,
  cores = NULL
)
```

Arguments

`Rceattle`	an Rceattle model fit using `fit_mod`
`nsim`	number of simulations
`simulate`	passed to `sim_mod`. If `TRUE` (default), data are simulated with observation error; if `FALSE`, expected values from the model are used.
`seed`	random number seed. Each simulation `i` uses `seed + i` so results are reproducible under both sequential and parallel execution.
`cores`	Number of cores to use for parallel simulations. Default `NULL` picks `parallel::detectCores() - 6`, capped at 2 when running under `R CMD check` (which sets `_R_CHECK_LIMIT_CORES_`). Set to 1 to force sequential execution.

Value

a list of Rceattle models

Examples

```
data(BS2017SS)
ss_run <- fit_mod(data_list = BS2017SS,
    inits = NULL, file = NULL,
    estimateMode = 0, random_rec = FALSE,
    msmMode = 0, avgnMode = 0,
    phase = FALSE, verbose = 0)
sims <- self_test(ss_run, nsim = 10)
```

`set_phases` *Function to set phasing order*

Description

Function to set phasing order

Usage

```
set_phases()
```

Value

list of parameter names with associated phase

`sim_mod` *Simulate Rceattle data*

Description

Simulates data used in Rceattle from the expected values estimated from an existing Rceattle model. The variances and uncertainty are consistent with those used in the operating model. The function simulates: survey biomass (log-normal), catch-at-age/length composition (multinomial or dirichlet-multinomial), conditional-age-at-length (CAAL; multinomial or dirichlet-multinomial), and total catch (log-normal).

Usage

```
sim_mod(Rceattle, simulate = FALSE)
```

Arguments

`Rceattle`	A CEATTLE model object exported from `Rceattle`.
`simulate`	Logical. If `TRUE`, simulates data from distributions. If `FALSE`, returns the expected values (hats).

Value

A `data_list` object containing the simulated or expected data values, formatted for use in `Rceattle`.

`summary.Rceattle` *Compact summary method for Rceattle fits*

Description

Compact summary method for Rceattle fits

Usage

```
## S3 method for class 'Rceattle'
summary(object, ...)
```

Arguments

`object`	An object of class `"Rceattle"` returned by `fit_mod()`.
`...`	Currently unused.

`switch_check` *Function to check for missing switches for map and parameter functions*

Description

Function to check for missing switches for map and parameter functions

Usage

```
switch_check(data_list)
```

Arguments

`data_list`	Rceattle data list

`t_col` *#https://www.dataanalytics.org.uk/make-transparent-colors-in-r/*

Description

#https://www.dataanalytics.org.uk/make-transparent-colors-in-r/

Usage

```
t_col(color, percent = 50, name = NULL)
```

Arguments

`color`	color name
`percent`	% transparency
`name`	an optional name for the color

`TMBAIC` *Calculate marginal AIC for a fitted model*

Description

`TMBAIC` calculates AIC for a given model fit

Usage

```
TMBAIC(opt, p = 2, n = Inf)
```

Arguments

`opt`	the output from `nlminb` or `optim`
`p`	the penalty on additional fixed effects (default=2, for AIC)
`n`	the sample size, for use in AICc calculation (default=Inf, for which AICc=AIC)

Value

AIC, where a parsimonious model has a AIC relative to other candidate models

---

`TMBphase` *Run TMB using phases*

Description

This function runs TMB with ADMB-like phasing of parameter estimation. Function with normal inputs, passed via "...", plus two additional arguments, "phase" Optimizer by default is nlminb phase is a tagged list where missing elements are populated with a vector of 1s, and non-missing elements are integers, and where the optimizer loops through values of phase while progressively changing map to turn on parameters

Usage

```
TMBphase(
  data,
  parameters,
  map,
  random,
  phases,
  model_name,
  silent,
  use_gradient = TRUE,
  control = list(eval.max = 1e+09, iter.max = 1e+09, trace = 0)
)
```

Arguments

`data`	A list to be passed to TMB
`parameters`	A list of parameters of the model
`map`	a list of map object from the model
`random`	A character vector of names of parameters that are random effects
`phases`	A list of the phases for the parameters of the model (same structure as your parameter list)
`model_name`	A string describing the model name. Must be the name of your .cpp file
`silent`	logical. If TRUE, suppresses output from TMB (default = TRUE).
`use_gradient`	logical. If TRUE, uses gradient in optimization (default = TRUE).
`control`	A list of control parameters. For details see `?nlminb`

Value

A list of parameter estimates and their standard errors

Author(s)

Gavin Fay https://github.com/kaskr/TMB_contrib_R/blob/master/TMBphase/R/TMBphase.R

`vcov.Rceattle` *Variance-covariance matrix for an Rceattle fit*

Description

Returns the fixed-effect covariance matrix produced by `TMB::sdreport()`. Random-effect covariance is not returned here — use `object$sdrep` for the full report.

Usage

```
## S3 method for class 'Rceattle'
vcov(object, ...)
```

Arguments

`object`	An object of class `"Rceattle"` returned by `fit_mod()`.
`...`	Currently unused.

Value

A numeric matrix, or `NULL` if `sdreport` was not run (i.e. the fit was produced with `getsd = FALSE`).

`whamGrowthData` *Data inputs for CEATTLE model with WHAM-estimated growth*

Description

A data list containing inputs for a CEATTLE model that uses growth estimated from the Woods Hole Assessment Model (WHAM). See `BS2017SS` for format details.

Usage

```
whamGrowthData
```

Format

A list with the same structure as `BS2017SS`.

`write_data` *Write data file*

Description

Write data file

Usage

```
write_data(data_list, file = "Rceattle_data.xlsx")
```

Arguments

`data_list`	Rceattle data_list object
`file`	Filname to be used. Must end with '.xlsx'

Examples

```
library(Rceattle)
data(BS2017SS)
out_file <- file.path(tempdir(), "BS2017SS.xlsx")
write_data(data_list = BS2017SS, file = out_file)
file.remove(out_file)
```

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