Package 'vital'

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Author Rob Hyndman [aut, cre, cph] (ORCID: <https://orcid.org/0000-0002-2140-5352>), Sixian Tang [aut] (ORCID: <https://orcid.org/0000-0002-7292-462X>), Miles McBain [ctb] (ORCID: <https://orcid.org/0000-0003-2865-2548>), Mitchell O'Hara-Wild [ctb] (ORCID: <https://orcid.org/0000-0001-6729-7695>)

Maintainer Rob Hyndman <Rob.Hyndman@monash.edu>

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age_components *Extract age components from a model*

Description

For a mable with a single model column, return the model components that are indexed by age.

Usage

```
age_components(object, ...)
```

Arguments

object	A vital mable object with a single model column.
...	Not currently used.

Value

vital object containing the age components from the model.

Examples

```
norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(lee_carter = LC(log(Mortality))) |>
  age_components()
```

as_vital *Coerce to a vital object*

Description

A vital object is a type of tsibble that contains vital statistics such as births, deaths, and population counts, and mortality and fertility rates. It is a tsibble with a special class that allows for special methods to be used. The object has an attribute that stores variables names needed for some functions, including age, sex, births, deaths and population.

Usage

```
as_vital(x, ...)

## S3 method for class 'demogdata'
as_vital(x, sex_groups = TRUE, ...)

## S3 method for class 'tbl_ts'
as_vital(
  x,
  .age = NULL,
  .sex = NULL,
  .deaths = NULL,
  .births = NULL,
  .population = NULL,
  reorder = FALSE,
  ...
)

## S3 method for class 'data.frame'
as_vital(
  x,
  key = NULL,
  index,
  .age = NULL,
  .sex = NULL,
  .deaths = NULL,
  .births = NULL,
  .population = NULL,
  reorder = TRUE,
  ...
)
```

Arguments

x	Object to be coerced to a vital format.
...	Other arguments passed to methods. For data frames, these are passed on to tsibble::as_tsibble().
sex_groups	Logical variable indicating if the groups denote sexes
.age	Character string with name of age variable
.sex	Character string with name of sex variable
.deaths	Character string with name of deaths variable
.births	Character string with name of births variable
.population	Character string with name of population variable
reorder	Logical indicating if the rows should be sorted by the index, the keys other than age, and then age. The default is TRUE for data frames and FALSE for tsibbles.

key	Variable(s) that uniquely determine time indices. NULL for empty key, and c() for multiple variables. It works with tidy selector (e.g. tidyselect::starts_with()).
index	A variable to specify the time index variable.

Value

A tsibble with class vital.

Author(s)

Rob J Hyndman

See Also

tsibble::tsibble()

Examples

```
# coerce demogdata object to vital
as_vital(demography::fr.mort)

# create a vital with only age as a key
data.frame(
  year = rep(2010:2015, 100),
  age = rep(0:99, each = 6),
  mx = runif(600, 0, 1)
) |>
  as_vital(
    index = year,
    key = age,
    .age = "age"
  )
```

---

autoplot.fbl_vtl_ts *Plot forecasts from a vital model*

Description

Produces a plot showing forecasts obtained from a model applied to a vital object.

Usage

```
## S3 method for class 'fbl_vtl_ts'
autoplot(object, ...)
```

Arguments

object	A fable object obtained from a vital model.
...	Further arguments ignored.

Value

A ggplot2 object.

Author(s)

Rob J Hyndman

Examples

```
library(ggplot2)
norway_mortality |>
  model(ave = FMEAN(Mortality)) |>
  forecast(h = 10) |>
  autoplot() + scale_y_log10()
```

`autoplot.mdl_vtl_df` *Plot output from a vital model*

Description

Produces a plot showing a model applied to a vital object. This can be applied to one type of model only. So use select() to choose the model column to plot. If there are multiple keys, separate models will be identified by colour.

Usage

```
## S3 method for class 'mdl_vtl_df'
autoplot(object, ...)
```

Arguments

`object`	A mable object obtained from a vital.
`...`	Further arguments ignored.

Value

A ggplot2 object.

Author(s)

Rob J Hyndman

Examples

```
library(ggplot2)
norway_mortality |>
  model(ave = FMEAN(Mortality)) |>
  autoplot() + scale_y_log10()
```

`autoplot.vital` *Rainbow plot of demographic data against age*

Description

Produce rainbow plot (coloured by time index) of demographic variable against age. If `object` has no age variable, the variable is plotted against time instead, with a line for each combination of keys.

Usage

```
## S3 method for class 'vital'
autoplot(object, .vars = NULL, age = NULL, ...)
```

Arguments

`object`	A vital including an age variable and the variable you wish to plot.
`.vars`	The name of the variable you wish to plot.
`age`	The name of the age variable. If not supplied, the function will attempt to find it.
`...`	Not used.

Value

A ggplot2 object.

Author(s)

Rob J Hyndman

References

Hyndman, Rob J & Shang, Han Lin (2010) Rainbow plots, bagplots, and boxplots for functional data. *Journal of Computational and Graphical Statistics*, 19(1), 29-45. https://robjhyndman.com/publications/rainbow-fda/

Examples

```
autoplot(norway_fertility, Fertility)
```

cohort_components *Extract cohort components from a model*

Description

For a mable with a single model column, return the model components that are indexed by birth year of the cohort.

Usage

```
cohort_components(object, ...)
```

Arguments

object	A vital mable object with a single model column.
...	Not currently used.

Value

tsibble object containing the cohort components from the model.

Examples

```
norway_mortality |>
  dplyr::filter(Sex == "Male", Age > 50, Year > 1960) |>
  model(apc = APC(Mortality)) |>
  cohort_components()
```

collapse_ages *Collapse upper ages into a single age group. Counts are summed while rates are recomputed where possible.*

Description

Collapse upper ages into a single age group. Counts are summed while rates are recomputed where possible.

Usage

```
collapse_ages(.data, max_age = 100)
```

Arguments

.data	A vital object including an age variable
max_age	Maximum age to include in the collapsed age group.

Details

If the object includes deaths, population and mortality rates, then deaths and population are summed and mortality rates are recomputed as deaths/population. But if the object contains mortality rates but not deaths and population, then the last rate remains unchanged (and a warning is generated).

Value

A vital object with the same variables as `.data`, but with the upper ages collapsed into a single age group.

Author(s)

Rob J Hyndman

Examples

```
norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  collapse_ages(max_age = 85)
```

FDM *Functional data model*

Description

Functional data model of mortality or fertility rates as a function of age. `FDM()` returns a functional data model applied to the formula's response variable as a function of age.

Usage

```
FDM(
  formula,
  order = 6,
  ts_model_fn = fable::ARIMA,
  coherent = FALSE,
  coherent_ts_model_fn = fable::ARFIMA,
  ...
)
```

Arguments

`formula`	Model specification.
`order`	Number of principal components to fit. Must be at least 1.
`ts_model_fn`	Univariate time series modelling function for the coefficients. Any model that works with the fable package is ok. Default is `fable::ARIMA()`.

coherent — If TRUE, fitted models are stationary, other than for the case of a key variable taking the value geometric_mean or mean. This is designed to work with vitals produced using make_pr() and make_sd. Default is FALSE.

coherent_ts_model_fn — Time series modelling function to be used for coherent fitting. ts_model_fn will be used for the geometric_mean or mean variables, with the other variables being modelled using coherent_ts_model_fn. Default is fable::ARFIMA().

... — Not used. An error is given if any arguments are supplied here, so that misspelled arguments are not silently ignored.

Value

A model specification.

Author(s)

Rob J Hyndman

References

Hyndman, R. J., and Ullah, S. (2007) Robust forecasting of mortality and fertility rates: a functional data approach. *Computational Statistics & Data Analysis*, 51, 4942-4956. https://robjhyndman.com/publications/funcfor/

Hyndman, R. J., Booth, H., & Yasmeen, F. (2013). Coherent mortality forecasting: the product-ratio method with functional time series models. *Demography*, 50(1), 261-283. https://robjhyndman.com/publications/coherentfdm/

Examples

```
hu <- norway_mortality |>
  dplyr::filter(Sex == "Female", Year > 2010) |>
  smooth_mortality(Mortality) |>
  model(hyndman_ullah = FDM(log(.smooth)))
report(hu)
autoplot(hu)
```

FMEAN *Functional mean model*

Description

FMEAN() returns an iid functional model applied to the formula's response variable as a function of age. Standard deviations that cannot be estimated, such as at ages with fewer than two finite residuals, are interpolated from neighbouring ages. Simulations from generate() with bootstrap = TRUE resample whole years of residuals, so they keep the correlation between ages. Otherwise, ages are simulated independently from normal distributions, which understates the uncertainty of quantities computed across ages, such as life expectancy.

Usage

```
FMEAN(formula, ...)
```

Arguments

formula	Model specification.
...	Not used. An error is given if any arguments are supplied here, so that misspelled arguments are not silently ignored.

Value

A model specification.

Author(s)

Rob J Hyndman

Examples

```
fmean <- norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(mean = FMEAN(Mortality))
report(fmean)
autoplot(fmean) + ggplot2::scale_y_log10()
```

FNAIVE *Functional naive model*

Description

FNAIVE() returns a random walk functional model applied to the formula's response variable as a function of age. Standard deviations that cannot be estimated, such as at ages with fewer than two finite residuals, are interpolated from neighbouring ages. Simulations from generate() with bootstrap = TRUE resample whole years of residuals, so they keep the correlation between ages. Otherwise, ages are simulated independently from normal distributions, which understates the uncertainty of quantities computed across ages, such as life expectancy.

Usage

```
FNAIVE(formula, ...)
```

Arguments

formula	Model specification.
...	Not used. An error is given if any arguments are supplied here, so that misspelled arguments are not silently ignored.

Value

A model specification.

Author(s)

Rob J Hyndman

Examples

```
fnaive <- norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(fit = FNAIVE(Mortality))
report(fnaive)
autoplot(fnaive) + ggplot2::scale_y_log10()
```

---

forecast.FDM *Produce forecasts from a vital model*

Description

The forecast function allows you to produce future predictions of a vital model, where the response is a function of age. The forecasts returned contain both point forecasts and their distribution.

Usage

```
## S3 method for class 'FDM'
forecast(
  object,
  new_data = NULL,
  h = NULL,
  point_forecast = list(.mean = mean),
  simulate = FALSE,
  bootstrap = FALSE,
  times = 5000,
  ...
)

## S3 method for class 'LC'
forecast(
  object,
  new_data = NULL,
  h = NULL,
  point_forecast = list(.mean = mean),
  simulate = FALSE,
  bootstrap = FALSE,
  times = 5000,
  ...
```

```
)

## S3 method for class 'GAPC'
forecast(
  object,
  new_data = NULL,
  h = NULL,
  point_forecast = list(.mean = mean),
  simulate = FALSE,
  bootstrap = FALSE,
  times = 5000,
  ...
)

## S3 method for class 'FMEAN'
forecast(
  object,
  new_data = NULL,
  h = NULL,
  point_forecast = list(.mean = mean),
  simulate = FALSE,
  bootstrap = FALSE,
  times = 5000,
  ...
)

## S3 method for class 'FNAIVE'
forecast(
  object,
  new_data = NULL,
  h = NULL,
  point_forecast = list(.mean = mean),
  simulate = FALSE,
  bootstrap = FALSE,
  times = 5000,
  ...
)

## S3 method for class 'mdl_vtl_df'
forecast(
  object,
  new_data = NULL,
  h = NULL,
  point_forecast = list(.mean = mean),
  simulate = FALSE,
  bootstrap = FALSE,
  times = 5000,
  ...
```

)

Arguments

object	A mable containing one or more models.
new_data	A tsibble containing future information used to forecast.
h	Number of time steps ahead to forecast. This can be used instead of new_data when there are no covariates in the model. It is ignored if new_data is provided.
point_forecast	A list of functions used to compute point forecasts from the forecast distribution.
simulate	If TRUE, then forecast distributions are computed using simulation from a parametric model.
bootstrap	If TRUE, then forecast distributions are computed using simulation with resampling.
times	The number of sample paths to use in estimating the forecast distribution when simulate = TRUE or bootstrap = TRUE.
...	Additional arguments passed to the specific model method.

Value

A fable containing the following columns:

- .model: The name of the model used to obtain the forecast. Taken from the column names of models in the provided mable.
- The forecast distribution. The name of this column will be the same as the dependent variable in the model(s). If multiple dependent variables exist, it will be named .distribution.
- Point forecasts computed from the distribution using the functions in the point_forecast argument.
- All columns in new_data, excluding those whose names conflict with the above.

Author(s)

Rob J Hyndman and Mitchell O'Hara-Wild

Examples

```
norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(naive = FNAIVE(Mortality)) |>
  forecast(h = 10)
```

GAPC *Generalized APC stochastic mortality model*

Description

A Generalized Age-Period-Cohort (GAPC) stochastic mortality model is defined in Villegas et al. (2018). The StMoMo package is used to fit the model. Separate functions are available to fit various special cases of the GAPC model.

Usage

```
GAPC(formula, use_weights = TRUE, clip = 0, zeroCohorts = NULL, ...)

LC2(
  formula,
  link = c("log", "logit"),
  const = c("sum", "last", "first"),
  use_weights = TRUE,
  clip = 0,
  zeroCohorts = NULL,
  ...
)

CBD(
  formula,
  link = c("log", "logit"),
  use_weights = TRUE,
  clip = 0,
  zeroCohorts = NULL,
  ...
)

RH(
  formula,
  link = c("log", "logit"),
  cohortAgeFun = c("1", "NP"),
  use_weights = TRUE,
  clip = 0,
  zeroCohorts = NULL,
  ...
)

APC(
  formula,
  link = c("log", "logit"),
  use_weights = TRUE,
  clip = 0,
```

```
  zeroCohorts = NULL,
  ...
)

M7(
  formula,
  link = c("log", "logit"),
  use_weights = TRUE,
  clip = 0,
  zeroCohorts = NULL,
  ...
)

PLAT(
  formula,
  link = c("log", "logit"),
  use_weights = TRUE,
  clip = 0,
  zeroCohorts = NULL,
  ...
)
```

Arguments

formula	Model specification
use_weights	If TRUE, will call genWeightMat with arguments clip and zeroCohorts.
clip	Passed to genWeightMat()
zeroCohorts	Passed to genWeightMat()
...	All other arguments passed to StMoMo()
link	The link function to use. Either "log" or "logit". When using logit, the mortality rates need to be between 0 and 1. If they are not, most likely you need to use initial rather than central population values when computing them.
const	defines the constraint to impose on the period index of the model ensure identifiability. The alternatives are "sum" (default), "last" and "first" which apply constraints $\sum_{t=1}^{T} \kappa_t = 0$, $\kappa_T = 0$ and $\kappa_1 = 0$ respectively.
cohortAgeFun	A function defining the cohort age modulating parameter $\beta_x^{(0)}$. It can take values: "NP" for a non-parametric age term or "1" for $\beta_x^{(0)} = 1$ (the default).

Details

LC2() provides an alternative implementation of the Lee-Carter model based on a GAPC specification. The advantage of this approach over LC() is that it allows for 0 rates in the mortality data. Note that it does not return identical results to LC() because the model formulation is different. For LC2(), do not take logs of the mortality rates because this is handled with the link function. For LC(), you need to take logs of the mortality rates when calling the function.

The Renshaw-Haberman (RH) model due to Renshaw and Haberman (2006) is another special case of a GAPC model, that can be considered an extension of a Lee-Carter model with an age-specific cohort effect.

The Age-Period-Cohort (APC) model is a special case of a GAPC model discussed by Renshaw and Haberman (2011).

The Cairns-Blake-Dowd (CBD) model due to Cairns et al (2006) can be considered another special case of a GAPC model that is primarily intended for forecasting mortality patterns in older populations.

Cairns et al (2009) extended the CBD model by adding a cohort effect and a quadratic age effect, giving the M7 model.

Plat (2009) combined the CBD model with some features of the Lee-Carter model to produce a model that is suitable for full age ranges and captures the cohort effect.

Each of these functions returns a GAPC model applied to the formula's response variable as a function of age. Use `autoplot()` on the fitted models to plot their age, period and cohort components. The model will optionally call `genWeightMat` with arguments `clip` and `zeroCohorts`. All other arguments are passed to `StMoMo`.

`forecast()` gives point forecasts only for these models. Use `forecast(..., simulate = TRUE)` to obtain forecast distributions and prediction intervals.

Value

A model specification.

Author(s)

Rob J Hyndman

References

Cairns, AJG, Blake, D, and Dowd, K (2006). A two-factor model for stochastic mortality with parameter uncertainty: Theory and calibration. *Journal of Risk and Insurance*, **73**(4), 687-718. doi:10.1111/j.1539-6975.2006.00195.x

Cairns AJG, Blake D, Dowd K, Coughlan GD, Epstein D, Ong A, Balevich I (2009). A quantitative comparison of stochastic mortality models using data from England and Wales and the United States. *North American Actuarial Journal*, **13**(1), 1–35. doi:10.1080/10920277.2009.10597538

Lee, RD, and Carter, LR (1992) Modeling and forecasting US mortality. *Journal of the American Statistical Association*, 87, 659-671. doi:10.1080/01621459.1992.10475265

Plat R (2009). On stochastic mortality modeling. *Insurance: Mathematics and Economics*, **45**(3), 393–404. doi:10.1016/j.insmatheco.2009.08.006

Renshaw, AE, and Haberman, S (2006). A cohort-based extension to the Lee-Carter model for mortality reduction factors. *Insurance: Mathematics and Economics*, **38**(3), 556-570. doi:10.1016/j.insmatheco.2005.12.001

Renshaw, AE, and Haberman, S (2011). A comparative study of parametric mortality projection models. *Insurance: Mathematics and Economics*, **48**(1), 35–55. doi:10.1016/j.insmatheco.2010.09.003

Villegas, AM, Millossovich, P, and Kaishev, VK (2018). StMoMo: An R package for stochastic mortality modelling. *Journal of Statistical Software*, **84**(3), 1-38. doi:10.18637/jss.v084.i03

See Also

LC()

Examples

```
# Fit the same CBD model using GAPC() and CBD()
gapc <- norway_mortality |>
  dplyr::filter(Sex == "Female", Age > 50, Year > 2000) |>
  model(
    cbd1 = GAPC(Mortality,
      link = "log",
      staticAgeFun = FALSE,
      periodAgeFun = c("1", function(x, ages) x - mean(ages))
    ),
    cbd2 = CBD(Mortality)
  )
glance(gapc)
gapc |>
  dplyr::select(cbd2) |>
  report()
gapc |>
  dplyr::select(cbd2) |>
  autoplot()
```

---

generate.mdl_vtl_df *Generate responses from a mable*

Description

Use a fitted model to simulate future data with similar behaviour to the response.

Usage

```
## S3 method for class 'mdl_vtl_df'
generate(x, new_data = NULL, h = NULL, bootstrap = FALSE, times = 1, ...)
```

Arguments

x	A mable.
new_data	Future data needed for generation (should include the time index and exogenous regressors)
h	The simulation horizon (can be used instead of new_data for regular time series with no exogenous regressors).

bootstrap	If TRUE, then forecast distributions are computed using simulation with resampled errors.
times	The number of replications.
...	Additional arguments

Details

Innovations are sampled by the model's assumed error distribution. If bootstrap is TRUE, innovations will be sampled from the model's residuals.

Value

A vital object with simulated values.

Author(s)

Rob J Hyndman and Mitchell O'Hara-Wild

Examples

```
norway_mortality |>
  model(lc = LC(log(Mortality))) |>
  generate(times = 3, bootstrap = TRUE)
```

---

generate_population *Future population simulation*

Description

Simulate future age-specific population given a starting population and models for fertility, mortality, and migration. If any model is NULL, it is assumed there are no future births, deaths or net migrants, respectively. This is an experimental function and has not been thoroughly tested. The simulation follows demography::pop.sim(), as described in Hyndman and Booth (2008).

Usage

```
generate_population(
  starting_population,
  mortality_model = NULL,
  fertility_model = NULL,
  migration_model = NULL,
  h = 10,
  n_reps = 1000,
  female = NULL
)
```

Arguments

starting_population	A vital object with the age-sex-specific starting population.
mortality_model	A mable object containing an age-sex-specific model for mortality rates, trained on data up to the year of the starting population. If NULL, there are zero future deaths.
fertility_model	A mable object containing an age-specific model for fertility rates, trained on data up to the year of the starting population. If NULL, there are zero future births.
migration_model	A mable object containing an age-sex-specific model for net migration numbers, trained on data up to the year of the starting population. Net migrants are indexed by age at the end of the year, as returned by net_migration(). If NULL, there are zero future net migrants.
h	The forecast horizon equal to the number of years to simulate into the future.
n_reps	The number of replicates to simulate.
female	A character string giving the name used for females in the sex variable of the starting_population. This is needed when computing births from the fertility rates. If missing, the function will try to identify the most likely value automatically.

Value

A vital object containing the simulated future population.

References

Hyndman and Booth (2008) Stochastic population forecasts using functional data models for mortality, fertility and migration. *International Journal of Forecasting*, 24(3), 323-342.

Examples

```
# Norwegian data, with ages above 100 combined
nor <- norway_mortality |>
  dplyr::filter(Sex != "Total") |>
  collapse_ages(max_age = 100)
# Models trained on data up to the year of the starting population
mortality <- nor |>
  dplyr::filter(Year > 2010) |>
  model(fmean = FMEAN(log(Mortality)))
fertility <- norway_fertility |>
  dplyr::filter(Year > 2010) |>
  model(fmean = FMEAN(Fertility))
migration <- net_migration(nor, norway_births) |>
  dplyr::filter(Year > 2010) |>
  model(fmean = FMEAN(NetMigration))
# Simulate 5 future populations for 3 years, starting from the final year of data
```

```
generate_population(
  starting_population = nor |> dplyr::filter(Year == max(Year)),
  mortality_model = mortality,
  fertility_model = fertility,
  migration_model = migration,
  h = 3,
  n_reps = 5
)
```

`interpolate.mdl_vtl_df` *Interpolate missing values using a vital model*

Description

Uses a fitted vital model to interpolate missing values from a dataset.

Usage

```
## S3 method for class 'mdl_vtl_df'
interpolate(object, new_data, ...)
```

Arguments

`object`	A mable containing a single model column.
`new_data`	A dataset with the same structure as the data used to fit the model.
`...`	Other arguments passed to interpolate methods.

Value

A vital object with missing values interpolated.

Author(s)

Rob J Hyndman

Examples

```
nor_female <- norway_mortality |>
  dplyr::filter(Sex == "Female")
nor_female |>
  model(mean = FMEAN(Mortality)) |>
  interpolate(nor_female)
```

LC *Lee-Carter model*

Description

Lee-Carter model of mortality or fertility rates. `LC()` returns a Lee-Carter model applied to the formula's response variable as a function of age. This produces a standard Lee-Carter model by default, although many other options are available. Missing rates are set to the geometric mean rate for the relevant age.

Usage

```
LC(
  formula,
  adjust = c("dt", "dxt", "e0", "none"),
  jump_choice = c("fit", "actual"),
  scale = FALSE,
  ...
)
```

Arguments

`formula`	Model specification. It should include the log of the variable to be modelled. See the examples.
`adjust`	method to use for adjustment of coefficients k_t. Possibilities are `"dt"` (Lee-Carter method), `"dxt"` (BMS method), `"e0"` (Lee-Miller method based on life expectancy) and `"none"`. If omitted, `"dt"` is used when the data contain deaths and population (see `vital_vars()`), and `"none"` otherwise, or when the data contain product-ratios from `make_pr()`. The `"dt"` and `"dxt"` methods require deaths and population.
`jump_choice`	Method used for computation of jump-off point for forecasts. Possibilities: `"actual"` (use actual rates from final year) and `"fit"` (use fitted rates). The original Lee-Carter method used `"fit"` (the default), but Lee and Miller (2001) and most other authors prefer `"actual"`. With `"actual"`, fitted rates are used (with a warning) for ages whose rate is zero or missing in the final year.
`scale`	If TRUE, `bx` and `kt` are rescaled so that `kt` has drift parameter = -1 (i.e., `kt` decreases by 1 per year on average).
`...`	Not used. An error is given if any arguments are supplied here, so that misspelled arguments are not silently ignored.

Value

A model specification.

Author(s)

Rob J Hyndman

References

Basellini, U, Camarda, C G, and Booth, H (2022) Thirty years on: A review of the Lee-Carter method for forecasting mortality. *International Journal of Forecasting*, 39(3), 1033-1049.

Booth, H., Maindonald, J., and Smith, L. (2002) Applying Lee-Carter under conditions of variable mortality decline. *Population Studies*, **56**, 325-336.

Lee, R D, and Carter, L R (1992) Modeling and forecasting US mortality. *Journal of the American Statistical Association*, 87, 659-671.

Lee R D, and Miller T (2001). Evaluating the performance of the Lee-Carter method for forecasting mortality. *Demography*, 38(4), 537–549.

See Also

`LC2()`, `FDM()`

Examples

```
lc <- norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(lee_carter = LC(log(Mortality)))
report(lc)
autoplot(lc)
```

`life_expectancy` *Compute life expectancy from age-specific mortality rates*

Description

Returns remaining life expectancy at a given age (0 by default).

Usage

```
life_expectancy(.data, from_age = 0, mortality)
```

Arguments

`.data`	A vital object including an age variable and a variable containing mortality rates.
`from_age`	Age at which life expectancy to be calculated. Either a scalar or a vector of ages.
`mortality`	Variable in `.data` containing Mortality rates (mx). If omitted, the variable with name `mx`, `Mortality` or `Rate` will be used (not case sensitive).

Value

A `vital` object with life expectancy in column `ex`.

Author(s)

Rob J Hyndman

References

Chiang CL. (1984) *The life table and its applications*. Robert E Krieger Publishing Company: Malabar.

Keyfitz, N, and Caswell, H. (2005) *Applied Mathematical Demography*, Springer-Verlag: New York.

Preston, S.H., Heuveline, P., and Guillot, M. (2001) *Demography: measuring and modeling population processes*. Blackwell

See Also

`life_table()`

Examples

```
# Compute Norwegian life expectancy for females over time
norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  life_expectancy()
```

---

life_table *Compute period life tables from age-specific mortality rates*

Description

All available years and ages are included in the tables. $qx = mx/(1 + ((1-ax) * mx))$ as per Chiang (1984). Ages can be single years, abridged (0, 1, 5, 10, ...), or 5-year groups starting at age 5 or above. Missing mortality rates are interpolated (on the log scale) from neighbouring ages, with a warning.

Usage

```
life_table(.data, mortality)
```

Arguments

`.data`	A `vital` including an age variable and a variable containing mortality rates.
`mortality`	Variable in `.data` containing Mortality rates (mx). If omitted, the variable with name `mx`, `Mortality` or `Rate` will be used (not case sensitive).

Value

A vital object containing the index, keys, and the new life table variables `mx`, `qx`, `lx`, `dx`, `Lx`, `Tx`, `ex`, `rx` (survivorship ratios), `nx` (widths of the age groups) and `ax` (average years lived in each age group by those dying in it).

Author(s)

Rob J Hyndman

References

Chiang CL. (1984) *The life table and its applications*. Robert E Krieger Publishing Company: Malabar.

Keyfitz, N, and Caswell, H. (2005) *Applied mathematical demography*, Springer-Verlag: New York.

Preston, S.H., Heuveline, P., and Guillot, M. (2001) *Demography: measuring and modeling population processes*. Blackwell

Examples

```
# Compute Norwegian life table for females in 2003
norway_mortality |>
  dplyr::filter(Sex == "Female", Year == 2003) |>
  life_table()
```

---

make_pr *Do a product/ratio transformation*

Description

Make a new vital containing products and ratios of a measured variable by a key variable. The most common use case of this function is for mortality rates by sex. That is, we want to compute the geometric mean of age-specific mortality rates, along with the ratio of mortality to the geometric mean for each sex. The latter are equal to the male/female and female/male ratios of mortality rates.

Usage

```
make_pr(.data, .var, key = Sex)
```

Arguments

.data	A vital object
.var	A bare variable name of the measured variable to use.
key	A bare variable name specifying the key variable to use.

Details

When a measured variable takes value 0, it is set to 10^-5 to avoid infinite values in the ratio.

Value

A vital object

References

Hyndman, R.J., Booth, H., & Yasmeen, F. (2013). Coherent mortality forecasting: the product-ratio method with functional time series models. *Demography*, 50(1), 261-283.

Examples

```
pr <- norway_mortality |>
  dplyr::filter(Year > 2015, Sex != "Total") |>
  make_pr(Mortality)
pr |>
  dplyr::filter(Sex == "geometric_mean") |>
  autoplot(Mortality) +
  ggplot2::scale_y_log10()
```

---

make_sd *Do a sum/difference transformation*

Description

Make a new vital containing means and differences of a measured variable by a key variable. The most common use case of this function is for migration numbers by sex. That is, we want to compute the age-specific mean migration, along with the difference of migration to the mean for each sex. The latter are equal to half the male/female and female/male differences of migration numbers.

Usage

```
make_sd(.data, .var, key = Sex)
```

Arguments

.data	A vital object
.var	A bare variable name of the measured variable to use.
key	A bare variable name specifying the key variable to use.

Value

A vital object

References

Hyndman, R.J., Booth, H., & Yasmeen, F. (2013). Coherent mortality forecasting: the product-ratio method with functional time series models. *Demography*, 50(1), 261-283.

Examples

```
mig <- net_migration(norway_mortality, norway_births) |>
  dplyr::filter(Sex != "Total")
sd <- mig |>
  make_sd(NetMigration)
sd |>
  autoplot(NetMigration)
```

`model.vital` *Estimate models for vital data*

Description

Trains specified model definition(s) on a dataset. This function will estimate the a set of model definitions (passed via `...`) to each series within `.data` (as identified by the key structure). The result will be a mable (a model table), which neatly stores the estimated models in a tabular structure. Rows of the data identify different series within the data, and each model column contains all models from that model definition. Each cell in the mable identifies a single model.

Usage

```
## S3 method for class 'vital'
model(.data, ..., .safely = TRUE)
```

Arguments

`.data`	A vital object including an age variable.
`...`	Definitions for the models to be used. All models must share the same response variable.
`.safely`	If a model encounters an error, rather than aborting the process a NULL model will be returned instead. This allows for an error to occur when computing many models, without losing the results of the successful models.

Value

A mable containing the fitted models.

Parallel

It is possible to estimate models in parallel using the future package. By specifying a `future::plan()` before estimating the models, they will be computed according to that plan.

Progress

Progress on model estimation can be obtained by wrapping the code with `progressr::with_progress()`. Further customisation on how progress is reported can be controlled using the `progressr` package.

Author(s)

Rob J Hyndman and Mitchell O'Hara-Wild

Examples

```
norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(
    naive = FNAIVE(Mortality),
    mean = FMEAN(Mortality)
  )
```

`net_migration` *Calculate net migration from a vital object*

Description

Calculate net migration from a vital object

Usage

```
net_migration(deaths, births)
```

Arguments

`deaths`	A vital object containing at least a time index, age, population at 1 January, and death rates.
`births`	A vital object containing at least a time index and number of births per time period. It is assumed that the population variable is the same as in the deaths object, and that the same keys other than age are present in both objects.

Value

A vital object containing population, estimated deaths (not actual deaths) and net migration. Net migration at age x in year t is for the cohort aged x at the end of year t (on 1 January of year t+1), so it equals the population aged x on 1 January of year t+1, minus the cohort's population on 1 January of year t (births during year t for age 0, and the two oldest ages combined for the open age group), plus the cohort's deaths during year t. Deaths are estimated from the survivorship ratios of the life table, as in `demography::netmigration()`.

References

Hyndman and Booth (2008) Stochastic population forecasts using functional data models for mortality, fertility and migration. *International Journal of Forecasting*, 24(3), 323-342.

Examples

```
net_migration(norway_mortality, norway_births)
## Not run:
# Files downloaded from the [Human Mortality Database](https://mortality.org)
deaths <- read_hmd_files(c("Population.txt", "Mx_1x1.txt"))
births <- read_hmd_files("Births.txt")
mig <- net_migration(deaths, births)

## End(Not run)
```

`norway_births` *Norwegian mortality and births data*

Description

`norway_births` is an annual `vital` object covering the years 1900-2023, as provided by the Human Mortality Database on 19 August 2025.

`norway_fertility` is an annual `vital` covering the years 1967-2022, as provided by the Human Fertility Database on 19 August 2025.

`norway_mortality` is an annual `vital` covering the years 1900-2023, as provided by the Human Mortality Database on 19 August 2025.

Format

Time series of class `vital`

Source

Human Mortality Database https://mortality.org

Human Fertility Database https://www.humanfertility.org

Examples

```
library(ggplot2)
# Births
norway_births
norway_births |>
  autoplot(Births)
# Deaths
norway_mortality
norway_mortality |>
  dplyr::filter(Age < 85, Year < 1950, Sex != "Total") |>
  autoplot(Mortality) +
  scale_y_log10()
# Fertility
norway_fertility
norway_fertility |>
  autoplot(Fertility)
```

read_hfd *Read data directly from HFD and construct a* vital *object for use in other functions*

Description

read_hfd reads single-year and single-age data from the Human Fertility Database (HFD https://www.humanfertility.org) and constructs a vital object suitable for use in other functions. This function uses HMDHFDplus::readHFDweb() to download the required data. It is designed to handle age-specific fertility rates. It may be extended to handle other types of data in the future.

Usage

```
read_hfd(country, username, password, variables = "asfrRR")
```

Arguments

country	Country code as used by the HFD. For instance, Norway = "NOR".
username	HFD username (case-sensitive)
password	HFD password (case-sensitive)
variables	List of variables to download from the HFD. By default, the age-specific fertility rate (asfrRR) is downloaded.

Details

In order to read the data, users are required to create an account with the HFD website (https://www.humanfertility.org), and obtain a valid username and password.

Value

read_hfd returns a vital object combining the downloaded data.

Author(s)

Rob J Hyndman

Examples

```
## Not run:
norway <- read_hfd(
  country = "NOR",
  username = "Nora.Weigh@mymail.com",
  password = "FF!5xeEFa6"
)

## End(Not run)
```

`read_hfd_files` *Read data from files downloaded from HFD and construct a* `vital` *object for use in other functions*

Description

`read_hfd_files` reads single-year and single-age data from files downloaded from the Human Fertility Database (HFD https://www.humanfertility.org) and constructs a `vital` object suitable for use in other functions. This function uses `HMDHFDplus::readHFD()` to parse the files.

Usage

```
read_hfd_files(files)
```

Arguments

`files`	Vector of file names containing data downloaded from the HFD. The file names are used to determine what they contain. If the file names are as per the HFD, then the function will automatically determine the contents. If it is unclear what a file contains, the columns will be named according to the filename. If the data contains a mixture of age-specific and non-age-specific variables, then the non-age-specific data will be repeated for each age. If you have HFD files for many countries, all with the same names, then you should put them in separate folders to avoid confusion, and to save changing all the filenames.

Value

`read_hfd_files` returns a `vital` object combining the downloaded data.

Author(s)

Rob J Hyndman

Examples

```
## Not run:
# File downloaded from the [Human Fertility Database](https://www.humanfertility.org)
fertility <- read_hfd_files("NORasfrRR.txt")

## End(Not run)
```

read_hmd *Read data directly from HMD and construct a* vital *object for use in other functions*

Description

read_hmd reads single-year and single-age data from the Human Mortality Database (HMD https://www.mortality.org) and constructs a vital object suitable for use in other functions. This function uses HMDHFDplus::readHMDweb() to download the required data. It is designed to handle Deaths, Population, Exposure, Death Rates and Births. By default, Deaths, Population, Exposure and Death Rates are downloaded. It is better to handle Births separately as they are not age-specific.

Usage

```
read_hmd(
  country,
  username,
  password,
  variables = c("Deaths", "Exposures", "Population", "Mx")
)
```

Arguments

country	Country name or country code as specified by the HMD. For instance, Australian data can be obtained using country = "Australia" or country = "AUS".
username	HMD username (case-sensitive)
password	HMD password (case-sensitive)
variables	List of variables to download from the HMD. If the data contains a mixture of age-specific and non-age-specific variables, then the non-age-specific data will be repeated for each age.

Details

In order to read the data, users are required to create an account with the HMD website (https://www.mortality.org), and obtain a valid username and password.

Value

read_hmd returns a vital object combining the downloaded data.

Author(s)

Rob J Hyndman

Examples

```
## Not run:
norway <- read_hmd(
  country = "Norway",
  username = "Nora.Weigh@mymail.com",
  password = "FF!5xeEFa6"
)
norway_births <- read_hmd(
  country = "Norway",
  username = "Nora.Weigh@mymail.com",
  password = "FF!5xeEFa6",
  variables = "Births"
)

## End(Not run)
```

---

read_hmd_files *Read data from files downloaded from HMD and construct a* `vital` *object for use in other functions*

Description

`read_hmd_files` reads single-year and single-age data from files downloaded from the Human Mortality Database (HMD https://www.mortality.org) and constructs a `vital` object suitable for use in other functions. This function uses `HMDHFDplus::readHMD()` to parse the files.

Usage

```
read_hmd_files(files)
```

Arguments

`files`	Vector of file names containing data downloaded from the HMD. The file names are used to determine what they contain. If the file names are as per the HMD, then the function will automatically determine the contents. If it is unclear what a file contains, the columns will be named according to the filename. If the data contains a mixture of age-specific and non-age-specific variables, then the non-age-specific data will be repeated for each age. If you have HMD files for many countries, all with the same names, then you should put them in separate folders to avoid confusion, and to save changing all the filenames.

Value

`read_hmd_files` returns a `vital` object combining the downloaded data.

Author(s)

Rob J Hyndman

Examples

```
## Not run:
# Files downloaded from the [Human Mortality Database](https://mortality.org)
mortality <- read_hmd_files(
  c("Deaths_1x1.txt", "Exposures_1x1.txt", "Population.txt", "Mx_1x1.txt")
)
births <- read_hmd_files("Births.txt")

## End(Not run)
```

`read_ktdb` *Read old-age mortality from Kannisto-Thatcher (K-T) database and construct a* `vital` *object for use in other functions*

Description

`read_ktdb` reads old-age mortality data classified by sex, age, year of birth, and calendar year for more than 30 countries. The series is available in Kannisto-Thatcher (K-T) database (https://www.demogr.mpg.de/cgi-bin/databases/ktdb/datamap.plx) and constructs a `vital` object suitable for use in other functions.

Usage

```
read_ktdb(country, triangle = 1)
```

Arguments

`country`	Country name or country code as specified by the KT database. For instance, Australian data can be obtained using `country = "Australia"` or `country = 1`.
`triangle`	Lexis triangle number, 1 (default) is lower triangle, 2 is upper triangle.

Value

`read_ktdb` returns a `vital` object combining the downloaded data.

Author(s)

Sixian Tang

Examples

```
australia <- read_ktdb(country = "Australia")
```

read_ktdb_files *Read old-age mortality data from files downloaded from K-T database*

Description

read_ktdb_files reads old-age mortality data from files downloaded from K-T database (https://www.demogr.mpg.de/cgi-bin/databases/ktdb/datamap.plx) and constructs a vital object suitable for use in other functions. If two files are provided, the function will treat them as data for each gender, returning a combined dataset. If only one file is provided, the function will assume that it represents data for a single gender.

Usage

```
read_ktdb_files(male = NULL, female = NULL, triangle = 1)
```

Arguments

male	File containing male mortality downloaded from the K-T database.
female	File containing female mortality downloaded from the K-T database.
triangle	Lexis triangle number, 1 (default) is lower triangle, 2 is upper triangle.

Value

read_ktdb_files returns a vital object combining the downloaded data.

Author(s)

Sixian Tang

Examples

```
## Not run:
# File downloaded from the K-T database
australia_male <- read_ktdb_files("maustl.txt")

## End(Not run)
```

`read_stmf` *Read Short-Term Mortality Fluctuations data from the Human Mortality Database*

Description

`read_stmf` reads weekly mortality data from the Short-term Mortality Fluctuations (STMF) series available in the Human Mortality Database (HMD) https://www.mortality.org/Data/STMF, and constructs a `vital` object suitable for use in other functions. The HMD requires a login to download STMF data.

Usage

```
read_stmf(country, username, password)
```

Arguments

`country`	Country name or country code as specified by the HMD. For instance, Australian data can be obtained using `country = "Australia"` or `country = "AUS"`.
`username`	HMD username (case-sensitive)
`password`	HMD password (case-sensitive)

Value

A `vital` object combining the downloaded data.

Author(s)

Sixian Tang

See Also

`read_stmf_files()` for reading STMF files that have already been downloaded.

Examples

```
## Not run:
norway <- read_stmf(
  country = "NOR",
  username = "Nora.Weigh@mymail.com",
  password = "FF!5xeEFa6"
)

## End(Not run)
```

read_stmf_files *Read STMF data from files downloaded from HMD*

Description

read_stmf_files reads weekly mortality data from a file downloaded from the Short-term Mortality Fluctuations (STMF) series available in the Human Mortality Database (HMD) https://www.mortality.org/Data/STMF, and constructs a vital object suitable for use in other functions.

Usage

```
read_stmf_files(file)
```

Arguments

file	Name of a file containing data downloaded from the HMD.

Value

read_stmf_files returns a vital object combining the downloaded data.

Author(s)

Rob J Hyndman

See Also

read_stmf() for downloading and reading STMF data directly from the HMD.

Examples

```
## Not run:
# File downloaded from the Human Mortality Database STMF series
# (https://www.mortality.org/Data/STMF)
mortality <- read_stmf_files("AUSstmfout.csv")

## End(Not run)
```

`smooth_mortality_law` *Function to smooth mortality rates using MortalityLaw package*

Description

This smoothing function allows smoothing of a variable in a vital object using the MortalityLaw package. The vital object is returned along with some additional columns containing information about the smoothed variable: `.smooth` containing the smoothed values, and `.smooth_se` containing the corresponding standard errors. If `.data` has deaths and population variables (see `vital_vars()`), the law is fitted to these; otherwise it is fitted to `.var`. The standard errors are approximate: they are the smoothed values multiplied by the residual standard deviation of the log rates and by $\sqrt{p/n}$, where p is the number of parameters of the law and n is the number of ages with positive rates.

Usage

```
smooth_mortality_law(.data, .var, law = "gompertz", ...)
```

Arguments

`.data`	A vital object
`.var`	name of variable to smooth. This should contain mortality rates.
`law`	name of mortality law. See `availableLaws` for the available options. Argument ignored if a custom law supplied.
`...`	Additional arguments are passed to `MortalityLaw`.

Value

vital with added columns containing smoothed values and their standard errors

Author(s)

Sixian Tang and Rob J Hyndman

Examples

```
norway_mortality |> smooth_mortality_law(Mortality)
```

smooth_spline *Functions to smooth demographic data*

Description

These smoothing functions allow smoothing of a variable in a vital object. The vital object is returned along with some additional columns containing information about the smoothed variable: usually `.smooth` containing the smoothed values, and `.smooth_se` containing the corresponding standard errors.

Usage

```
smooth_spline(.data, .var, age_spacing = 1, k = -1)

smooth_mortality(.data, .var, age_spacing = 1, b = 65, power = 0.4, k = 30)

smooth_fertility(.data, .var, age_spacing = 1, lambda = 1e-10)

smooth_loess(.data, .var, age_spacing = 1, span = 0.2)
```

Arguments

`.data`	A vital object
`.var`	name of variable to smooth
`age_spacing`	Spacing between ages for smoothed vital. Default is 1.
`k`	Number of knots to use for penalized regression spline estimate.
`b`	Lower age for monotonicity. Above this, the smooth curve is assumed to be monotonically increasing.
`power`	Power transformation for age variable before smoothing. Default is 0.4 (for mortality data).
`lambda`	Penalty for constrained regression spline.
`span`	Span for loess smooth.

Details

`smooth_mortality()` use penalized regression splines applied to log mortality with a monotonicity constraint above age `b`. The methodology is based on Wood (1994). `smooth_fertility()` uses weighted regression B-splines with a concavity constraint, based on He and Ng (1999). The function `smooth_loess()` uses locally quadratic regression, while `smooth_spline()` uses penalized regression splines.

Value

vital with added columns containing smoothed values and their standard errors

Author(s)

Rob J Hyndman

References

Hyndman, R.J., and Ullah, S. (2007) Robust forecasting of mortality and fertility rates: a functional data approach. *Computational Statistics & Data Analysis*, 51, 4942-4956. https://robjhyndman.com/publications/funcfor/

Examples

```
library(dplyr)
norway_mortality |>
  filter(Sex == "Female", Year > 2000) |>
  smooth_mortality(Mortality)
norway_fertility |>
  filter(Year > 2000) |>
  smooth_fertility(Fertility)
```

---

time_components *Extract time components from a model*

Description

For a mable with a single model column, return the model components that are indexed by time.

Usage

```
time_components(object, ...)
```

Arguments

object	A vital mable object with a single model column.
...	Not currently used.

Value

tsibble object containing the time components from the model.

Examples

```
norway_mortality |>
  dplyr::filter(Sex == "Female") |>
  model(lee_carter = LC(log(Mortality))) |>
  time_components()
```

total_fertility_rate *Compute total fertility rate from age-specific fertility rates*

Description

Total fertility rate is the expected number of babies per woman in a life-time given the fertility rate at each age of a woman's life. Rates for age groups wider than one year (e.g., 5-year age groups) are multiplied by the width of each group, with the oldest group assumed to be as wide as the one before it.

Usage

```
total_fertility_rate(.data, fertility)
```

Arguments

`.data`	A vital object including an age variable and a variable containing fertility rates.
`fertility`	Variable in `.data` containing fertility rates. If omitted, the variable with name `fx`, `Fertility` or `Rate` will be used (not case sensitive).

Value

A vital object with total fertility in column `tfr`.

Author(s)

Rob J Hyndman

Examples

```
# Compute Norwegian total fertility rates over time
norway_fertility |>
  total_fertility_rate()
```

undo_pr *Undo a product/ratio transformation*

Description

Make a new vital from products and ratios of a measured variable by a key variable. The most common use case of this function is for computing mortality rates by sex, from the sex ratios and geometric mean of the rates.

Usage

```
undo_pr(.data, .var, key = Sex, times = 2000)
```

Arguments

.data	A vital object
.var	A bare variable name of the measured variable to use.
key	A bare variable name specifying the key variable to use. This key variable must include the value geometric_mean.
times	When the variable is a distribution, the product must be computed by simulation. This argument specifies the number of simulations to use.

Details

Note that when a measured variable takes value 0, make_pr() sets it to 10^-5 to avoid infinite values in the ratio. Therefore, when the transformation is undone, the results will not be identical to the original in the case that the original data was 0.

Value

A vital object

References

Hyndman, R.J., Booth, H., & Yasmeen, F. (2013). Coherent mortality forecasting: the product-ratio method with functional time series models. *Demography*, 50(1), 261-283.

Examples

```
# Make products and ratios
orig_data <- norway_mortality |>
  dplyr::filter(Year > 2015, Sex != "Total")
pr <- orig_data |>
  make_pr(Mortality)
# Compare original data with product/ratio version
orig_data
pr
# Undo products and ratios
pr |> undo_pr(Mortality)
```

---

undo_sd *Undo a mean/difference transformation*

Description

Make a new vital from means and differences of a measured variable by a key variable. The most common use case of this function is for computing migration numbers by sex, from the sex differences and mean of the numbers.

Usage

```
undo_sd(.data, .var, key = Sex, times = 2000)
```

Arguments

.data	A vital object
.var	A bare variable name of the measured variable to use.
key	A bare variable name specifying the key variable to use. This key variable must include the value mean.
times	When the variable is a distribution, the sum must be computed by simulation. This argument specifies the number of simulations to use.

Value

A vital object

References

Hyndman, R.J., Booth, H., & Yasmeen, F. (2013). Coherent mortality forecasting: the product-ratio method with functional time series models. *Demography*, 50(1), 261-283.

Examples

```
# Make sums and differences
mig <- net_migration(norway_mortality, norway_births) |>
  dplyr::filter(Sex != "Total")
sd <- mig |>
  make_sd(NetMigration)
# Undo means and differences
sd |> undo_sd(NetMigration)
```

---

vital *Create a vital object*

Description

A vital object is a type of tsibble that contains vital statistics such as births, deaths, and population counts, and mortality and fertility rates. It is a tsibble with a special class that allows for special methods to be used. The object has an attribute that stores variables names needed for some functions, including age, sex, births, deaths and population.

Usage

```
vital(
  ...,
  key = NULL,
  index,
  .age = NULL,
  .sex = NULL,
  .deaths = NULL,
  .births = NULL,
```

```
  .population = NULL,
  regular = TRUE,
  .drop = TRUE
)
```

Arguments

...	A set of name-value pairs
key	Variable(s) that uniquely determine time indices. NULL for empty key, and c() for multiple variables. It works with tidy selector (e.g. tidyselect::starts_with())
index	A variable to specify the time index variable.
.age	Character string with name of age variable
.sex	Character string with name of sex variable
.deaths	Character string with name of deaths variable
.births	Character string with name of births variable
.population	Character string with name of population variable
regular	Regular time interval (TRUE) or irregular (FALSE). The interval is determined by the greatest common divisor of index column, if TRUE.
.drop	If TRUE, empty key groups are dropped.

Value

A tsibble with class vital.

Author(s)

Rob J Hyndman

See Also

tsibble::tsibble()

Examples

```
# create a vital with only age as a key
vital(
  year = rep(2010:2015, 100),
  age = rep(0:99, each = 6),
  mx = runif(600, 0, 1),
  index = year,
  key = age,
  .age = "age"
)
```

vital_vars *Return vital variables*

Description

A vital object is a special case of a tsibble object with additional attributes identifying the age, sex, deaths, births and population variables. `vital_vars()` returns a character vector of the names of the vital variables.

Usage

```
vital_vars(x)
```

Arguments

x	A tsibble object.

Value

A character vector of the names of the vital variables.

Examples

```
vital_vars(norway_mortality)
```

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