Package ‘joinpointR’

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Type Package

Title Tidy Tools for Joinpoint Regression Models

Version 1.0.0

Description Provides tools to fit joinpoint regression models with a log-linear specification by levels of a categorical variable. The package acts as a wrapper around the 'segmented' package, facilitating model fitting, selection, and interpretation. It includes functions to estimate the Annual Percent Change (APC) and the Average Annual Percent Change (AAPC), along with their 95% confidence intervals, and to generate formatted summary tables and plots of results.

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Encoding UTF-8

Imports dplyr, purrr, tidyr, tibble, ggplot2, segmented, scales, flextable, rlang, stringr, stats, officer, forcats, cols4all

URL `https://github.com/datos-ine/joinpointR`

BugReports `https://github.com/datos-ine/joinpointR/issues`

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

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LazyData true

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Contents

`get_aapc` *Average Annual Percent Change (AAPC)*

Description

Estimates the Average Annual Percent Change (AAPC) and its corresponding 95% confidence interval for one or more regression models. Optionally, statistical significance can be displayed using significance stars instead of confidence intervals.

Usage

```
get_aapc(mods, digits = 1, show_ci = TRUE, dec = ".")
```

Arguments

`mods`	A joinpoint regression model, a list of joinpoint regression models returned by `model_jp()`, or linear regression models (`lm` objects).
`digits`	Integer. Number of decimal places used to display the results.
`show_ci`	Logical. If `TRUE`, displays the 95% confidence interval. If `FALSE`, displays significance stars.
`dec`	Character. Decimal separator to use (`"."` or `","`).

Value

A tibble with one row per model containing the estimated AAPC and either its 95% confidence interval or significance stars.

Author(s)

Tamara Ricardo

Examples

```
# Load example data
data(hiv_data)

# Fit joinpoint models
mods <- model_jp(
  data = hiv_data,
  value = "hiv_rate",
  time = "year",
  group = "region",
  k = 2,
  test = TRUE
)

# AAPC with 95% confidence intervals
get_aapc(mods, digits = 1, show_ci = TRUE, dec = ".")

# AAPC with significance stars
get_aapc(mods, show_ci = FALSE)

# AAPC for a single model
get_aapc(mods$Central)
```

`get_apc` *Annual Percent Change by Segment*

Description

Calculates the Annual Percent Change (APC) and corresponding 95% confidence intervals for each segment of one or more joinpoint regression models.

Usage

```
get_apc(mods, digits = 1, dec = ".")
```

Arguments

`mods`	A joinpoint regression model or a list of joinpoint regression models returned by `model_jp()`.
`digits`	Integer. Number of decimal places used to display the results.
`dec`	Character. Decimal separator to use (e.g. `"."` or `","`).

Value

A tibble with one row per segment and the variables `group`, `segment`, `apc`, `lower`, and `upper`, where `lower` and `upper` correspond to the limits of the 95\

Author(s)

Tamara Ricardo

Examples

```
# Load example data
data(hiv_data)

# Fit joinpoint models
mods <- model_jp(
  data = hiv_data,
  value = "hiv_rate",
  time = "year",
  group = "region",
  k = 2,
  test = TRUE
)

# APC and 95% confidence intervals for all models
get_apc(mods, digits = 1, dec = ".")

# APC and 95% confidence intervals for a single model
get_apc(mods$Central)
```

`gg_jpoint` *Plot Joinpoint Regression Models*

Description

Creates a ggplot showing observed values, fitted joinpoint regression lines, and optional joinpoints.

Usage

```
gg_jpoint(
  mods,
  obs = TRUE,
  psize = 2.5,
  ptr = 0.75,
  jp = TRUE,
  facets = c("wrap", "grid", "none"),
  ncol = 4,
  cb = TRUE,
 cbpal = c("viridis", "managua", "plasma", "roma", "vanimo", "algae", "arches2",
   "glasgow", "tokyo", "blue_fluoride")
)
```

Arguments

`mods`	A list of joinpoint regression models returned by `model_jp()`.
`obs`	Logical. If `TRUE`, observed data points are displayed.
`psize`	Numeric. Size of the observed data points.
`ptr`	Numeric. Transparency level of the observed data points (0-1).
`jp`	Logical. If `TRUE`, joinpoints are displayed as vertical dashed lines.
`facets`	Character. Determines the facet layout: `"none"` for a single panel, `"wrap"` for faceting by group, or `"grid"` for faceting by group and subgroup.
`ncol`	Numeric. Number of columns to display when `facets = "wrap"`.
`cb`	Logical. If `TRUE`, a colorblind-friendly palette is used.
`cbpal`	Character. Name of the colorblind-friendly palette to use. See Details.

Details

Available colorblind-friendly palettes from the `cols4all` package include:

Diverging palettes:

- `"managua"`
- `"plasma"`
- `"roma"`
- `"vanimo"`
- `"viridis"`

Sequential palettes:

- `"algae"`
- `"arches2"`
- `"blue_fluoride"`
- `"glasgow"`
- `"tokyo"`

Value

A `ggplot` object showing observed values, fitted joinpoint regression lines, and optional joinpoints.

Examples

```
# Load example data
data(hiv_data)

# Fit the joinpoint models
mods <- model_jp(
  data = hiv_data,
  value = hiv_rate,
  time = year,
```

```
    group = c("region", "sex"),
    k = 2,
    test = TRUE
  )

  # Plot results
  gg_jpoint(mods, obs = TRUE, jp = TRUE, facets = "wrap")

  # Facet by group and subgroup
  gg_jpoint(mods, obs = TRUE, jp = TRUE, facets = "grid")

  # Single panel without joinpoints
  gg_jpoint(mods, jp = FALSE, facets = "none")

  # Use a different colorblind-friendly palette
  gg_jpoint(
    mods,
    obs = TRUE,
    jp = TRUE,
    facets = "grid",
    cb = TRUE,
    cbpal = "managua"
  )

  # Use default ggplot2 palette (can be changed using `scale_color_`)
  gg_jpoint(
  mods,
  cb = FALSE
  )
```

`hiv_data` *Simulated HIV rates*

Description

Simulated annual HIV rates by region and sex from 2010 to 2025.

Usage

`hiv_data`

Format

A data frame with 160 rows and 4 variables:

year Calendar year.

region Geographic region.

sex Sex ("Male" or "Female").

hiv_rate Simulated HIV rate.

Source

Simulated data.

`jp_to_ft` *Summary Flextable for Joinpoint Regression Models*

Description

Creates a flextable object from the output of `summary_jp()`, displaying the number of joinpoints, time periods, Annual Percent Change (APC) with 95% confidence intervals, and Average Annual Percent Change (AAPC) with statistical significance.

Usage

```
jp_to_ft(tab, digits = 1, lan = c("en", "es"))
```

Arguments

`tab`	A tibble returned by `summary_jp()`.
`digits`	Integer. Number of decimal places used to display the results.
`lan`	Character. Output language: "en" (English) or "es" (Spanish).

Value

A `flextable` object containing summary statistics for the joinpoint regression models.

Author(s)

Tamara Ricardo

Examples

```
# Load example data
data(hiv_data)

# Fit the joinpoint models
mods <- model_jp(
  data = hiv_data,
  value = hiv_rate,
  time = year,
  group = c("region", "sex")
)

# Generate a flextable summary
tab <- summary_jp(mods, digits = 1)
jp_to_ft(tab)

# Change table language
jp_to_ft(tab, lan = "es")
```

`model_jp` *Joinpoint Regression Models by Groups*

Description

Fits segmented linear regression models by groups for age-standardized rates using joinpoint regression. Models can be fitted using either a stepwise selection procedure based on the Bayesian Information Criterion (BIC) or a fixed number of joinpoints. Internally, the function calls `segmented::selgmented()` or `segmented::segmented()` and applies a log transformation to the response variable.

Usage

```
model_jp(data, value, time, group, k = 2, step = TRUE, test = TRUE)
```

Arguments

`data`	A data frame containing age-standardized rates.
`value`	Response variable.
`time`	Time variable.
`group`	Names of one or more grouping variables.
`k`	Maximum number of joinpoints to estimate.
`step`	Logical. If `TRUE`, uses a stepwise procedure to select the number of joinpoints based on BIC. If `FALSE`, fits a model with a fixed number of joinpoints specified by `k`.
`test`	Logical. If `TRUE`, tests differences in slope t-values during the stepwise selection procedure. Only used when `step = TRUE`.

Details

The National Cancer Institute (NCI) recommends the following maximum number of joinpoints according to the length of the time series (Kim et al., 2000):

- 0–6 time points: 0 joinpoints.
- 7–11 time points: 1 joinpoint.
- 12–16 time points: 2 joinpoints.
- 17–21 time points: 3 joinpoints.
- 22–26 time points: 4 joinpoints.
- 27–31 time points: 5 joinpoints.
- 32–36 time points: 6 joinpoints.
- 37 or more time points: 7 joinpoints.

#' @references Kim HJ, Fay MP, Feuer EJ, Midthune DN (2000). "Permutation Tests for Joinpoint Regression with Applications to Cancer Rates." *Statistics in Medicine*, 19(3), 335–351. doi:10.1002/(sici)1097-0258(20000215)19:3<335::aid-sim336>3.0.co;2-z.

Value

A named list of joinpoint regression models by group.

Author(s)

Tamara Ricardo

Examples

```
# Load example data
data("hiv_data")

# Check group levels
levels(hiv_data$region)

# Fit models
mods <- model_jp(data = hiv_data, value = hiv_rate, time = year, group = c("region", "sex"),
 k = 2, step = TRUE, test = TRUE)

# Show the output of the first model by calling its index
mods[[1]]

# Same output will be obtained when calling model name
mods$Central
```

`summary_jp` *Summary Tables for Joinpoint Regression Models*

Description

Generates summary tables for one or more joinpoint regression models, including the number of joinpoints (JP), time periods, Annual Percent Change (APC) with 95% confidence intervals, and Average Annual Percent Change (AAPC) with statistical significance.

Usage

```
summary_jp(mods, digits = 1, dec = c(".", ","))
```

Arguments

`mods`	A list of models returned by `model_jp()`.
`digits`	Integer. Number of decimal places used to display the results.
`dec`	Character. Decimal separator to use (e.g. `"."` or `","`).

Value

A tibble with one row per segment containing the grouping variable(s), number of joinpoints (JP), time period(s), APC and its 95% confidence interval, and AAPC with significance stars.

Author(s)

Tamara Ricardo

Examples

```
# Load example data
data(hiv_data)

# Fit joinpoint models
mods <- model_jp(
  data = hiv_data,
  value = hiv_rate,
  time = year,
  group = "region"
)

# Summarize models
summary_jp(mods, digits = 1, dec = ".")
```

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