

# Package: growthPheno (via r-universe)

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**Title** Functional Analysis of Phenotypic Growth Data to Smooth and Extract Traits

**Depends** R (>= 3.5.0)

**Imports** dae, GGally, ggplot2, grDevices, Hmisc, JOPS, methods, RColorBrewer, readxl, reshape, stats, stringi, utils

**Suggests** testthat, nlme, R.rsp, scales

**VignetteBuilder** R.rsp

**Description** Assists in the plotting and functional smoothing of traits measured over time and the extraction of features from these traits, implementing the SET (Smoothing and Extraction of Traits) method described in Brien et al. (2020) Plant Methods, 16. Smoothing of growth trends for individual plants using natural cubic smoothing splines or P-splines is available for removing transient effects and segmented smoothing is available to deal with discontinuities in growth trends. There are graphical tools for assessing the adequacy of trait smoothing, both when using this and other packages, such as those that fit nonlinear growth models. A range of per-unit (plant, pot, plot) growth traits or features can be extracted from the data, including single time points, interval growth rates and other growth statistics, such as maximum growth or days to maximum growth. The package also has tools adapted to inputting data from high-throughput phenotyping facilities, such from a Lemna-Tec Scanalyzer 3D (see [https://www.youtube.com/watch?v=MRAF\\_mAEa7E/](https://www.youtube.com/watch?v=MRAF_mAEa7E/) for more information). The package 'growthPheno' can also be installed from <http://chris.brien.name/rpackages/>.

**License** GPL (>= 2)

**URL** <http://chris.brien.name/>

**BugReports** <https://github.com/briencj/growthPheno/issues>

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growthPheno-package	<i>Functional Analysis of Phenotypic Growth Data to Smooth and Extract Traits</i>
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## Description

Assists in the plotting and functional smoothing of traits measured over time and the extraction of features from these traits, implementing the SET (Smoothing and Extraction of Traits) method described in Brien et al. (2020) Plant Methods, 16. Smoothing of growth trends for individual plants using natural cubic smoothing splines or P-splines is available for removing transient effects and segmented smoothing is available to deal with discontinuities in growth trends. There are graphical tools for assessing the adequacy of trait smoothing, both when using this and other packages, such as those that fit nonlinear growth models. A range of per-unit (plant, pot, plot) growth traits or features can be extracted from the data, including single time points, interval growth rates and other growth statistics, such as maximum growth or days to maximum growth. The package also has tools adapted to inputting data from high-throughput phenotyping facilities, such from a Lemna-Tec

Scanalyzer 3D (see [https://www.youtube.com/watch?v=MRAF\\_mAEa7E/](https://www.youtube.com/watch?v=MRAF_mAEa7E/) for more information). The package 'growthPheno' can also be installed from <http://chris.brien.name/rpackages/>.

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## Index

The following list of functions does not include those that are soft-deprecated, i.e. those that have been available in previous versions of growthPheno but will be removed in future versions. For a description of the use of the listed functions and vignettes that are available, see the Overview section below.

### (i) Wrapper functions

<code>traitSmooth</code>	Obtain smooths for a trait by fitting spline functions and, having compared several smooths, allows one of them to be chosen and returned in a <code>data.frame</code> .
<code>traitExtractFeatures</code>	Extract features, that are single-valued for each individual, from smoothed traits over time.

### (ii) Helper functions

<code>args4chosen_plot</code>	Creates a list of the values for the options of profile plots for the chosen smooth.
<code>args4chosen_smooth</code>	Creates a list of the values for the smoothing parameters for which a smooth is to be extracted.
<code>args4meddevn_plot</code>	Creates a list of the values for the options of median deviations plots for smooths.
<code>args4profile_plot</code>	Creates a list of the values for the options of profile plots for comparing smooths.
<code>args4smoothing</code>	Creates a list of the values for the smoothing parameters to be passed to a smoothing function.

### (iii) Data

<code>exampleData</code>	A small data set to use in function examples.
<code>RicePrepped.dat</code>	Prepped data from an experiment to investigate a rice germplasm panel.
<code>RiceRaw.dat</code>	Data for an experiment to investigate a rice germplasm panel.
<code>tomato.dat</code>	Longitudinal data for an experiment to investigate tomato response to mycorrhizal fungi and zinc.

### (iv) Plots

<code>plotAnom</code>	Identifies anomalous individuals and produces profile plots without them and with just them.
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<code>plotCorrmatrix</code>	Calculates and plots correlation matrices for a set of responses.
<code>plotDeviationsBoxes</code>	Produces boxplots of the deviations of the observed values from the smoothed values over values of x.
<code>plotImagetimes</code>	Plots the time within an interval versus the interval. For example, the hour of the day carts are imaged against the days after planting (or some other number of days after an event).
<code>plotMedianDeviations</code>	Calculates and plots the medians of the deviations of the smoothed values from the observed values.
<code>plotProfiles</code>	Produces profile plots of longitudinal data for a set of individuals.
<code>plotSmoothsComparison</code>	Plots several sets of smoothed values for a response, possibly along with growth rates and optionally including the unsmoothed values, as well as deviations boxplots.
<code>plotSmoothsMedianDevns</code>	Calculates and plots the medians of the deviations from the observed values of several sets for smoothed values stored in a <code>data.frame</code> in long format.
<code>probeSmooths</code>	Computes and compares, for a set of smoothing parameters, a response and the smooths of it, possibly along with growth rates calculated from the smooths.
(v) Smoothing and calculation of growth rates and water use traits for each individual (Indv)	
<code>byIndv4Intvl_GRsAvg</code>	Calculates the growth rates for a specified time interval for individuals in a <code>data.frame</code> in long format by taking weighted averages of growth rates for times within the interval.
<code>byIndv4Intvl_GRsDiff</code>	Calculates the growth rates for a specified time interval for individuals in a <code>data.frame</code> in long format by differencing the values for a response within the interval.
<code>byIndv4Intvl_ValueCalc</code>	Calculates a single value that is a function of the values of an individual for a response in a <code>data.frame</code> in long format over a specified time interval.
<code>byIndv4Intvl_WaterUse</code>	Calculates, water use traits (WU, WUR, WUI) over a specified time interval for each individual in a <code>data.frame</code> in long format.
<code>byIndv4Times_GRsDiff</code>	Adds, to a 'data.frame', the growth rates calculated for consecutive times for individuals in a <code>data.frame</code> in long format by differencing response values.
<code>byIndv4Times_SplinesGRs</code>	For a response in a <code>data.frame</code> in long format, computes, for a single set of smoothing parameters, smooths of the response, possibly along with

<code>byIndv_ValueCalc</code>	growth rates calculated from the smooths. Applies a function to calculate a single value from an individual's values for a response in a <code>data.frame</code> in long format.
<code>smoothSpline</code>	Fit a spline to smooth the relationship between a response and an <code>x</code> in a <code>data.frame</code> , optionally computing growth rates using derivatives.
<code>probeSmooths</code>	For a response in a <code>data.frame</code> in long format, computes and compares, for sets of smoothing parameters, smooths of the response, possibly along with growth rates calculated from the smooths.

## (vi) Data frame manipulation

<code>as.smooths.frame</code>	Forms a <code>smooths.frame</code> from a <code>data.frame</code> , ensuring that the correct columns are present.
<code>designFactors</code>	Adds the factors and covariates for a blocked, split-unit design.
<code>getTimesSubset</code>	Forms a subset of 'responses' in 'data' that contains their values for the nominated times.
<code>importExcel</code>	Imports an Excel imaging file and allows some renaming of variables.
<code>is.smooths.frame</code>	Tests whether an object is of class <code>smooths.frame</code> .
<code>prepImageData</code>	Selects a set variables to be retained in a data frame of longitudinal data.
<code>smooths.frame</code>	Description of a <code>smooths.frame</code> object,
<code>twoLevelOpcreate</code>	Creates a <code>data.frame</code> formed by applying, for each response, a binary operation to the values of two different treatments.
<code>validSmoothsFrame</code>	Checks that an object is a valid <code>smooths.frame</code> .

## (vii) General calculations

<code>anom</code>	Tests if any values in a vector are anomalous in being outside specified limits.
<code>calcLagged</code>	Replaces the values in a vector with the result of applying an operation to it and a lagged value.
<code>calcTimes</code>	Calculates for a set of times, the time intervals after an origin time and the position of each within a time interval
<code>cumulate</code>	Calculates the cumulative sum, ignoring the first element if <code>exclude.1st</code> is <code>TRUE</code> .
<code>GrowthRates</code>	Calculates growth rates (AGR, PGR, RGRdiff) between a pair of values in a vector.
<code>WUI</code>	Calculates the Water Use Index (WUI) for a value of the response and of the water use.

## (viii) Principal variates analysis (PVA)

<code>intervalPVA.data.frame</code>	Selects a subset of variables using PVA, based on the observed values within a specified time interval
<code>PVA.data.frame</code>	Selects a subset of variables stored in a <code>data.frame</code> using PVA.
<code>PVA.matrix</code>	Selects a subset of variables using PVA based on a correlation matrix.
<code>rcontrib.data.frame</code>	Computes a measure of how correlated each variable in a set is with the other variable, conditional on a nominated subset of them.
<code>rcontrib.matrix</code>	Computes a measure of how correlated each variable in a set is with the other variable, conditional on a nominated subset of them.

## Overview

This package can be used to perform a functional analysis of growth data using splines to smooth the trend of individual plant traces over time and then to extract features or tertiary traits for further analysis. This process is called smoothing and extraction of traits (SET) by Brien et al. (2020), who detail the use of growthPheno for carrying out the method. However, growthPheno now has the two wrapper, or primary, functions `traitSmooth` and `traitExtractFeatures` that implement the SET approach. These may be the only functions that are used in that the complete SET process can be carried out using only them. The Tomato vignette illustrates their use for the example presented in Brien et al. (2020).

The function `traitSmooth` utilizes the secondary functions `probeSmooths`, `plotSmoothsComparison` and `plotSmoothsMedianDevns` and accepts the arguments of the secondary functions. The function `probeSmooths` utilizes the tertiary functions `byIndv4Times_SplinesGRs` and `byIndv4Times_GRsDiff`, which in turn call the function `smoothSpline`. The function `plotSmoothsComparison` calls `plotDeviationsBoxes`. All of these functions play a role in choosing the smoothing method and parameters for a data set.

The primary function `traitExtractFeatures` uses the secondary functions `getTimesSubset` and the set of `byIndv4Intvl_` functions. These functions are concerned with the extraction of traits that yield a single value for each individual in the data.

Recourse to the secondary and tertiary functions may be necessary for special cases. Their use is illustrated in the Rice vignette.

Use `vignette("Tomato", package = "growthPheno")` or `vignette("Rice", package = "growthPheno")` to access either of the vignettes.

In addition to functions that implement SET approach, growthPheno also has functions for importing and organizing the data that are generally applicable, although they do have defaults that make them particularly adapted to data from a high-throughput phenotyping facility based on a Lemna-Tec Scanalyzer 3D system.

Data suitable for use with this package consists of columns of data obtained from a set of individuals (e.g. plants, pots, carts, plots or units) over time. There should be a unique identifier for each individual and a time variable, such as Days after Planting (DAP), that contain no repeats for an individual. The combination of the identifier and a time for an individual should be unique to that individual. For imaging data, the individuals may be arranged in a grid of Lanes  $\times$  Positions. That is, the minimum set of columns is an individuals, a times and one or more primary trait columns.

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**References**

Brien, C., Jewell, N., Garnett, T., Watts-Williams, S. J., & Berger, B. (2020). Smoothing and extraction of traits in the growth analysis of noninvasive phenotypic data. *Plant Methods*, **16**, 36. [doi:10.1186/s13007020005776](https://doi.org/10.1186/s13007020005776).

**See Also**

[dae](#)

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anom	<i>Tests if any values in a vector are anomalous in being outside specified limits</i>
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**Description**

Test whether any values in x are less than the value of lower, if it is not NULL, or are greater than the value of upper, if it is not NULL, or both.

**Usage**

```
anom(x, lower=NULL, upper=NULL, na.rm = TRUE)
```

**Arguments**

x	A <a href="#">vector</a> containing the values to be tested.
lower	A <a href="#">numeric</a> such that values in x below it are considered to be anomalous.
upper	A <a href="#">numeric</a> such that values in x above it are considered to be anomalous.
na.rm	A <a href="#">logical</a> indicating whether NA values should be stripped before the testing proceeds.

**Value**

A [logical](#) indicating whether any values have been found to be outside the limits specified by lower or upper or both.

**Author(s)**

Chris Brien

**Examples**

```
data(exampleData)
anom.val <- anom(longi.dat$sPSA.AGR, lower=2.5)
```



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args4chosen_plot	<i>Creates a list of the values for the options of profile plots for the chosen smooth</i>
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## Description

Creates a list of the values for the options of profile plots (and boxplots facets) for comparing smooths. Note that `plots.by`, `facet.x`, `facet.y` and `include.raw` jointly define the organization of the plots. The default settings are optimized for `traitSmooth`.

## Usage

```
args4chosen_plot(plots.by = NULL,
                  facet.x = ".", facet.y = ".",
                  include.raw = "no",
                  collapse.facets.x = FALSE, collapse.facets.y = FALSE,
                  facet.labeller = NULL, facet.scales = "fixed",
                  breaks.spacing.x = -2, angle.x = 0,
                  colour = "black", colour.column = NULL,
                  colour.values = NULL, alpha = 0.3,
                  addMediansWhiskers = TRUE,
                  ggplotFuns = NULL,
                  ...)
```

## Arguments

<code>plots.by</code>	A <a href="#">character</a> that gives the names of the set of <a href="#">factors</a> by which the data is to be grouped and a separate plot produced for each group. If <code>NULL</code> , no groups are formed. If a set of <a href="#">factors</a> , such as <code>Type</code> , <code>Tuning</code> and <code>Method</code> , that uniquely index the combinations of the smoothing-parameter values is specified, then groups are formed for each combination of the levels of the these <a href="#">factors</a> , and a separate plot is produced for each combination.
<code>facet.x</code>	A <a href="#">character</a> giving the names of the <a href="#">factors</a> to be used to form subsets to be plotted in separate columns of the profiles plots. The default of <code>"."</code> results in no split into columns.
<code>facet.y</code>	A <a href="#">character</a> giving the <a href="#">factors</a> to be used to form subsets to be plotted in separate rows of the profiles plots. The default of <code>"."</code> results in no split into rows.
<code>include.raw</code>	A <a href="#">character</a> indicating whether plots of the raw (unsmoothed) trait, corresponding to the plots of the smoothed traits, are to be included in profile plots. The options are <code>no</code> , <code>alone</code> , <code>facet.x</code> , or <code>facet.y</code> . That is, the plots of the raw traits are plotted separately or as part of either <code>facet.x</code> or <code>facet.y</code> .
<code>collapse.facets.x</code>	A <a href="#">logical</a> to indicate whether all variables specified by <code>facets.x</code> are to be collapsed to a single variable. Note that the smoothing-parameters factors, if present, are always collapsed.

<code>collapse.facets.y</code>	A <b>logical</b> to indicate whether all variables specified by <code>facets.y</code> are to be collapsed to a single variable. Note that the smoothing-parameters factors, if present, are always collapsed.
<code>facet.labeller</code>	A <code>ggplot</code> function for labelling the facets of a plot produced using the <code>ggplot</code> function. For more information see <code>ggplot</code> .
<code>facet.scales</code>	A <b>character</b> specifying whether the scales are shared across all facets of a plot ("fixed"), or do they vary across rows (the default, "free_x"), columns ("free_y"), or both rows and columns ("free")?
<code>breaks.spacing.x</code>	A <b>numeric</b> whose absolute values specifies the distance between major breaks for the x-axis in a sequence beginning with the minimum x value and continuing up to the maximum x value. If it is negative, the breaks that do not have x values in data will be omitted. Minor breaks will be at half major break value or, if these do not correspond to x-values in data when <code>breaks.spacing.x</code> is negative, have a spacing of one. Thus, when <code>breaks.spacing.x</code> is negative, grid lines will only be included for x-values that occur in data. These settings can be overwritten by supplying, in <code>ggplotFuncs</code> , a <code>scale_x_continuous</code> function from <code>ggplot2</code> .
<code>angle.x</code>	A <b>numeric</b> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in <code>ggplotFuncs</code> , a theme function from <code>ggplot2</code> .
<code>colour</code>	A <b>character</b> specifying a single colour to use in drawing the lines for the profiles. If colouring according to the values of a variable is required then use <code>colour.column</code> .
<code>colour.column</code>	A <b>character</b> giving the name of a column in data over whose values the colours of the lines are to be varied. The colours can be specified using <code>colour.values</code> .
<code>colour.values</code>	A <b>character</b> vector specifying the values of the colours to use in drawing the lines for the profiles. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) within the limits of the scale.
<code>alpha</code>	A <b>numeric</b> specifying the degrees of transparency to be used in plotting the responses. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
<code>addMediansWhiskers</code>	A <b>logical</b> indicating whether plots over time of the medians and outer whiskers are to be added to the plot. The outer whiskers are related to the whiskers on a box-and-whisker and are defined as the median plus (and minus) 1.5 times the interquartile range (IQR). Points lying outside the whiskers are considered to be potential outliers.
<code>ggplotFuncs</code>	A <b>list</b> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied in creating the <code>ggplot</code> object for a profiles plot.
<code>...</code>	allows arguments to be passed to other functions; not used at present.

**Value**

A named [list](#).

**Author(s)**

Chris Brien

**See Also**

[traitSmooth](#), [probeSmooths](#), [plotSmoothsComparison](#) and [args4profile\\_plot](#).

**Examples**

```
args4chosen_plot(plots.by = "Type",
                 facet.x = "Tuning", facet.y = c("Smarthouse", "Treatment.1"),
                 include.raw = "facet.x",
                 alpha = 0.4,
                 colour.column = "Method",
                 colour.values = c("orange", "olivedrab"))
```

---

args4chosen_smooth	<i>Creates a list of the values for the smoothing parameters for which a smooth is to be extracted</i>
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---

**Description**

Creates a [list](#) of the values for the smoothing parameters for which a smooth is to be extracted. The default settings for these are optimized for [traitSmooth](#).

**Usage**

```
args4chosen_smooth(smoothing.methods = "logarithmic",
                   spline.types = "PS",
                   df = NULL,
                   lambdas = NULL,
                   combinations = "single")
```

**Arguments**

smoothing.methods	A <a href="#">character</a> giving the smoothing method for the chosen smooth. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response.
spline.types	A <a href="#">character</a> giving the type of spline for the chosen smooth. Currently, the possibilities are (i) "NCSS", for natural cubic smoothing splines, and (ii) "PS", for P-splines.

df	A <a href="#">numeric</a> with single value that specifies, for natural cubic smoothing splines (NCSS), the desired equivalent numbers of degrees of freedom of the chosen smooth (trace of the smoother matrix). Lower values result in more smoothing.
lambdas	A named <a href="#">list</a> or a <a href="#">numeric</a> specifying the positive penalties for which the chosen smooth is required.
combinations	Generally, this argument should be set to <code>single</code> so that only one value should be supplied to the functions arguments. Also, only one of <code>df</code> or <code>lambdas</code> should be set.

**Value**

A named [list](#).

**Author(s)**

Chris Brien

**See Also**

[traitSmooth](#) and [probeSmooths](#).

**Examples**

```
args4chosen_smooth(smoothing.methods = "direct",
                   spline.types = "NCSS", df = 4)
args4chosen_smooth(smoothing.methods = "log",
                   spline.types = "PS", lambdas = 0.36)
```

---

args4devnboxes_plot	<i>Creates a list of the values for the options of profile plots for comparing smooths</i>
---------------------	--

---

**Description**

Creates a list of the values for the options of deviations boxplots for comparing smooths. Note that `plots.by`, `facet.x` and `facet.y` jointly define the organization of the plots. The default settings are optimized for [traitSmooth](#) so that, if you want to change any of these from their default settings when using `args4devnboxes_plot` with a function other than [traitSmooth](#), then it is recommended that you specify all of them to ensure that the complete set has been correctly specified. Otherwise, the default settings will be those shown here and these may be different to the default settings shown for the function with which you are using `args4devnboxes_plot`.

**Usage**

```
args4devnboxes_plot(plots.by = "Type",
                    facet.x = c("Method", "Tuning"), facet.y = ".",
                    collapse.facets.x = TRUE, collapse.facets.y = FALSE,
                    facet.labeller = NULL, facet.scales = "fixed",
                    angle.x = 0,
                    which.plots = "none",
                    ggplotFuncs = NULL,
                    ...)
```

**Arguments**

- |                   |  |
|-------------------|--|
| plots.by          | A <a href="#">character</a> that gives the names of the set of <a href="#">factors</a> by which the data is to be grouped and a separate plot produced for each group. If NULL, no groups are formed. If a set of <a href="#">factors</a> , such as Type, Tuning and Method, that uniquely index the combinations of the smoothing-parameter values is specified, then groups are formed for each combination of the levels of these <a href="#">factors</a> , and a separate plot is produced for each combination. |
| facet.x           | A <a href="#">character</a> giving the names of the <a href="#">factors</a> to be used to form subsets to be plotted in separate columns of the profiles plots and deviations boxplots. The default of "." results in no split into columns.   |
| facet.y           | A <a href="#">character</a> giving the <a href="#">factors</a> to be used to form subsets to be plotted in separate rows of the profiles plots and deviations boxplots. The default of "." results in no split into rows.  |
| collapse.facets.x | A <a href="#">logical</a> to indicate whether all variables specified by facets.x are to be collapsed to a single variable. Note that the smoothing-parameters factors, if present, are always collapsed.  |
| collapse.facets.y | A <a href="#">logical</a> to indicate whether all variables specified by facets.y are to be collapsed to a single variable. Note that the smoothing-parameters factors, if present, are always collapsed.  |
| facet.labeller    | A ggplot function for labelling the facets of a plot produced using the ggplot function. For more information see ggplot.  |
| facet.scales      | A <a href="#">character</a> specifying whether the scales are shared across all facets of a plot ("fixed"), or do they vary across rows (the default, "free_x"), columns ("free_y"), or both rows and columns ("free")?  |
| angle.x           | A <a href="#">numeric</a> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in ggplotFuncs, a theme function from ggplot2.   |
| which.plots       | A <a href="#">logical</a> indicating which plots are to be produced. The options are either none or absolute.deviations and/or relative.deviations. Boxplots of the absolute deviations are specified by absolute.boxplots, the absolute deviations being the values of a trait minus their smoothed values (observed - smoothed). Boxplots of the relative deviations are specified by relative.boxplots, the relative deviations being the absolute deviations divided by the smoothed values of the trait.        |

`ggplotFuncs` A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the `list` function with a ggplot function call for each element. These functions are applied in creating the ggplot object for a boxplot.

`...` allows arguments to be passed to other functions; not used at present.

**Value**

A named [list](#).

**Author(s)**

Chris Brien

**See Also**

[traitSmooth](#), [probeSmooths](#), [plotSmoothsComparison](#) and [args4chosen\\_plot](#).

**Examples**

```
args4devnboxes_plot(plots.by = "Type",
                    facet.x = "Tuning",
                    facet.y = c("Smarthouse", "Treatment.1"),
                    which.plots = "absolute")
```

---

args4meddevn_plot	<i>Creates a list of the values for the options of median deviations plots for smooths</i>
-------------------	--

---

**Description**

Creates a list of the values for the options of median deviations plots for smooths. Note that the arguments `plots.by`, `plots.group`, `facet.x` and `facet.y` jointly define the organization of the plots. The default settings are optimized for [traitSmooth](#) so that, if you want to change any of these from their default settings when using `args4meddevn_plot` with a function other than [traitSmooth](#), then it is recommended that you specify all of them to ensure that the complete set has been correctly specified. Otherwise, the default settings will be those shown here and these may be different to the default settings shown for the function with which you are using `args4meddevn_plot`.

**Usage**

```
args4meddevn_plot(plots.by = NULL, plots.group = "Tuning",
                  facet.x = c("Method", "Type"), facet.y = ".",
                  facet.labeller = NULL, facet.scales = "free_x",
                  breaks.spacing.x = -4, angle.x = 0,
                  colour.values = NULL, shape.values = NULL,
                  alpha = 0.5,
```

```
propn.note = TRUE, propn.types = NULL,
ggplotFuncs = NULL,
...)
```

## Arguments

plots.by	A <b>character</b> that give the names of the set of <b>factors</b> by which medians deviations data is to be grouped and a separate plot produced for each group. If NULL, no groups are formed. If a set of <b>factors</b> , such as Type, Tuning and Method, that uniquely index the combinations of the smoothing-parameter values is specified, then groups are formed for each combination of the levels of these <b>factors</b> , and a separate plot is produced for each combination.
plots.group	A <b>character</b> that gives the names of the set of <b>factors</b> by which the subset of medians deviations data within a single facet in a single plot is to be grouped for plotting as separate lines.
facet.x	A <b>character</b> giving the <b>factors</b> to be used to form subsets to be plotted in separate columns of the medians deviations plots. The default of "." results in no split into columns.
facet.y	A <b>character</b> giving the <b>factors</b> to be used to form subsets to be plotted in separate rows of the medians deviations plots. The default of "." results in no split into rows.
facet.labeller	A ggplot function for labelling the facets of a plot produced using the ggplot function. For more information see ggplot.
facet.scales	A <b>character</b> specifying whether the scales are shared across all facets of a plot ("fixed"), or do they vary across rows (the default, "free_x"), columns ("free_y"), or both rows and columns ("free")?
breaks.spacing.x	A <b>numeric</b> whose absolute values specifies the distance between breaks for the x-axis in a sequence beginning with the minimum x value and continuing up to the maximum x value. If it is negative, the breaks that do not have x values in data will be omitted. Minor breaks will be at half this value or, if these do not correspond to x-values in data when breaks.spacing.x is negative, have a spacing of one. Thus, when breaks.spacing.x is negative, grid lines will only be included for x-values that occur in data. These settings can be overwritten by supplying, in ggplotFuncs, a scale_x_continuous function from ggplot2.
angle.x	A <b>numeric</b> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in ggplotFuncs, a theme function from ggplot2.
colour.values	A <b>character</b> vector specifying the values of the colours to use in drawing the lines for the medians deviations within a facet. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) within the limits of the scale.
shape.values	A <b>numeric</b> vector specifying the values of the shapes to use in drawing the points for the medians deviations within a facet. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order.

alpha	A <b>numeric</b> specifying the degrees of transparency to be used in plotting a median deviations plot. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
propn.note	A <b>logical</b> indicating whether a note giving the proportion of the median value of the response for each time is to be included in the medians.deviations plots.
propn.types	A <b>numeric</b> giving, for each of the <code>trait.types</code> , the proportion of the median value of the response for each time to be used to plot envelopes in the median deviations plots. If set to <code>NULL</code> , the plots of the proportion envelopes are omitted.
ggplotFuncs	A <b>list</b> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied in creating the <code>ggplot</code> object for a median-deviations plot.
...	allows arguments to be passed to other functions; not used at present.

**Value**

A named **list**.

**Author(s)**

Chris Brien

**See Also**

[traitSmooth](#), [probeSmooths](#) and [plotSmoothsMedianDevns](#).

**Examples**

```
args4meddevn_plot(plots.by = "Type", plots.group = "Tuning",
  facet.x = "Method", facet.y = ".",
  propn.types = c(0.02, 0.1, 0.2))
```

---

args4profile_plot	<i>Creates a list of the values for the options of profile plots for comparing smooths</i>
-------------------	--

---

**Description**

Creates a list of the values for the options of profile plots for comparing smooths. Note that `plots.by`, `facet.x`, `facet.y` and `include.raw` jointly define the organization of the plots. The default settings are optimized for [traitSmooth](#) so that, if you want to change any of these from their default settings when using `args4profile_plot` with a function other than [traitSmooth](#), then it is recommended that you specify all of them to ensure that the complete set has been correctly specified. Otherwise, the default settings will be those shown here and these may be different to the default settings shown for the function with which you are using `args4profile_plot`.



**Usage**

```
args4profile_plot(plots.by = "Type",
                  facet.x = c("Method", "Tuning"), facet.y = ".",
                  include.raw = "facet.x",
                  collapse.facets.x = TRUE, collapse.facets.y = FALSE,
                  facet.labeller = NULL, facet.scales = "fixed",
                  breaks.spacing.x = -4, angle.x = 0,
                  colour = "black", colour.column = NULL,
                  colour.values = NULL, alpha = 0.3,
                  addMediansWhiskers = TRUE,
                  ggplotFuncs = NULL,
                  ...)
```

**Arguments**

- |                   |  |
|-------------------|--|
| plots.by          | A <a href="#">character</a> that gives the names of the set of <a href="#">factors</a> by which the data is to be grouped and a separate plot produced for each group. If NULL, no groups are formed. If a set of <a href="#">factors</a> , such as Type, Tuning and Method, that uniquely index the combinations of the smoothing-parameter values is specified, then groups are formed for each combination of the levels of the these <a href="#">factors</a> , and a separate plot is produced for each combination. |
| facet.x           | A <a href="#">character</a> giving the names of the <a href="#">factors</a> to be used to form subsets to be plotted in separate columns of the profiles plots and deviations boxplots. The default of "." results in no split into columns.   |
| facet.y           | A <a href="#">character</a> giving the <a href="#">factors</a> to be used to form subsets to be plotted in separate rows of the profiles plots and deviations boxplots. The default of "." results in no split into rows.  |
| include.raw       | A <a href="#">character</a> indicating whether plots of the raw (unsmoothed) trait, corresponding to the plots of the smoothed traits, are to be included in profile plots. The options are no, alone, facet.x, or facet.y. That is, the plots of the raw traits are plotted separately or as part of either facet.x or facet.y.   |
| collapse.facets.x | A <a href="#">logical</a> to indicate whether all variables specified by facets.x are to be collapsed to a single variable. Note that the smoothing-parameters factors, if present, are always collapsed.  |
| collapse.facets.y | A <a href="#">logical</a> to indicate whether all variables specified by facets.y are to be collapsed to a single variable. Note that the smoothing-parameters factors, if present, are always collapsed.  |
| facet.labeller    | A ggplot function for labelling the facets of a plot produced using the ggplot function. For more information see ggplot.  |
| facet.scales      | A <a href="#">character</a> specifying whether the scales are shared across all facets of a plot ("fixed"), or do they vary across rows (the default, "free_x"), columns ("free_y"), or both rows and columns ("free")?  |
| breaks.spacing.x  | A <a href="#">numeric</a> whose absolute values specifies the distance between breaks for the x-axis in a sequence beginning with the minimum x value and continuing up  |

	to the maximum x value. If it is negative, the breaks that do not have x values in data will be omitted. Minor breaks will be at half this value or, if these do not correspond to x-values in data when <code>breaks.spacing.x</code> is negative, have a spacing of one. Thus, when <code>breaks.spacing.x</code> is negative, grid lines will only be included for x-values that occur in data. These settings can be overwritten by supplying, in <code>ggplotFuncs</code> , a <code>scale_x_continuous</code> function from <code>ggplot2</code> .
<code>angle.x</code>	A <a href="#">numeric</a> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in <code>ggplotFuncs</code> , a theme function from <code>ggplot2</code> .
<code>colour</code>	A <a href="#">character</a> specifying a single colour to use in drawing the lines for the profiles. If colouring according to the values of a variable is required then use <code>colour.column</code> .
<code>colour.column</code>	A <a href="#">character</a> giving the name of a column in data over whose values the colours of the lines are to be varied. The colours can be specified using <code>colour.values</code> .
<code>colour.values</code>	A <a href="#">character</a> vector specifying the values of the colours to use in drawing the lines for the profiles. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) within the limits of the scale.
<code>alpha</code>	A <a href="#">numeric</a> specifying the degrees of transparency to be used in plotting the responses. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
<code>addMediansWhiskers</code>	A <a href="#">logical</a> indicating whether plots over time of the medians and outer whiskers are to be added to the plot. The outer whiskers are related to the whiskers on a box-and-whisker and are defined as the median plus (and minus) 1.5 times the interquartile range (IQR). Points lying outside the whiskers are considered to be potential outliers.
<code>ggplotFuncs</code>	A list, each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied in creating the <code>ggplot</code> object for a profile plot.
<code>...</code>	allows arguments to be passed to other functions; not used at present.

**Value**

A named [list](#).

**Author(s)**

Chris Brien

**See Also**

[traitSmooth](#), [probeSmooths](#), [plotSmoothsComparison](#) and [args4chosen\\_plot](#).

## Examples

```
args4profile_plot(plots.by = "Type",
                  facet.x = "Tuning", facet.y = c("Smarthouse", "Treatment.1"),
                  include.raw = "facet.x",
                  alpha = 0.4,
                  colour.column = "Method",
                  colour.values = c("orange", "olivedrab"))
```

---

args4smoothing	<i>Creates a list of the values for the smoothing parameters to be passed to a smoothing function</i>
----------------	---

---

## Description

Creates a [list](#) of the values for the smoothing parameters to be passed to a smoothing function. Note that `smoothing.methods`, `spline.types`, `df` and `lambdas` are combined to define the set of smooths. The default settings are optimized for [traitSmooth](#) so that, if you want to change any of these from their default settings when using `args4smoothing` with a function other than [traitSmooth](#), then it is recommended that you specify all of them to ensure that the complete set has been correctly specified. Otherwise, the default settings will be those shown here and these may be different to the default settings shown for the function with which you are using `args4smoothing`.

## Usage

```
args4smoothing(smoothing.methods = "logarithmic",
               spline.types = c("NCSS", "PS"),
               df = 5:7,
               lambdas = list(PS = round(10^c(-0.5, 0, 0.5, 1),
                                           digits = 3)),
               smoothing.segments = NULL,
               npspline.segments = NULL,
               na.x.action="exclude", na.y.action = "trimx",
               external.smooths = NULL,
               correctBoundaries = FALSE,
               combinations = "allvalid",
               ...)
```

## Arguments

<code>smoothing.methods</code>	A <a href="#">character</a> giving the smoothing method to use. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response and then back-transforming by taking the exponential of the fitted values.
<code>spline.types</code>	A <a href="#">character</a> giving the type of spline to use. Currently, the possibilities are (i) "NCSS", for natural cubic smoothing splines, and (ii) "PS", for P-splines.

df	A <b>numeric</b> with at least one value that specifies, for natural cubic smoothing splines (NCSS), the desired equivalent numbers of degrees of freedom of the smooths (trace of the smoother matrix). Lower values result in more smoothing. If df = NULL, the amount of smoothing can be controlled by including a component named NCSS in the <b>list</b> for <b>lambdas</b> . If df is NULL and <b>lambda</b> does not include a component named NCSS, then an error is issued.
<b>lambdas</b>	A named <b>list</b> or a <b>numeric</b> specifying the positive penalties to apply in order to control the amount of smoothing. The amount of smoothing decreases as <b>lamda</b> decreases. If <b>lambdas</b> is a <b>list</b> , then include a components with <b>lambdas</b> values and named for each of the specified values of <b>spline.types</b> for which <b>lambdas</b> are to be used. If <b>spline.types</b> includes PS, then a component named PS with at least one numeric value must be present. If a <b>numeric</b> , then it will be converted to a <b>list</b> with the single component named PS.
<b>smoothing.segments</b>	A named <b>list</b> , each of whose components is a numeric pair specifying the first and last values of an times-interval whose data is to be subjected as an entity to smoothing using splines. The separate smooths will be combined to form a whole smooth for each individual. If <b>get.rates</b> includes smoothed or is TRUE, <b>rates.method</b> is differences and <b>ntimes2span</b> is 2, the smoothed growth rates will be computed over the set of segments; otherwise, they will be computed within segments. If <b>smoothing.segments</b> is NULL, the data is not segmented for smoothing.
<b>npspline.segments</b>	A <b>numeric</b> specifying, for P-splines (PS), the number of equally spaced segments between min(x) and max(x), excluding missing values, to use in constructing the B-spline basis for the spline fitting. If <b>npspline.segments</b> is NULL, <b>npspline.segments</b> is set to the maximum of 10 and $\text{ceiling}((\text{nrow}(\text{data})-1)/2)$ i.e. there will be at least 10 segments and, for more than 22 times values, there will be half as many segments as there are times values. The amount of smoothing decreases as <b>npspline.segments</b> increases. When the data has been segmented for smoothing ( <b>smoothing.segments</b> is not NULL), an <b>npspline.segments</b> value can be supplied for each segment.
<b>na.x.action</b>	A character string that specifies the action to be taken when values of x are NA. The possible values are fail, exclude or omit. For exclude and omit, predictions and derivatives will only be obtained for nonmissing values of x. The difference between these two codes is that for exclude the returned <b>data.frame</b> will have as many rows as data, the missing values have been incorporated.
<b>na.y.action</b>	A character string that specifies the action to be taken when values of y, or the response, are NA. The possible values are fail, exclude, omit, allx, trimx, ltrimx or rtrimx. For all options, except fail, missing values in y will be removed before smoothing. For exclude and omit, predictions and derivatives will be obtained only for nonmissing values of x that do not have missing y values. Again, the difference between these two is that, only for exclude will the missing values be incorporated into the returned <b>data.frame</b> . For allx, predictions and derivatives will be obtained for all nonmissing x. For trimx, they will be obtained for all nonmissing x between the first and last nonmissing y values that have been ordered for x; for ltrimx and utrimx either the lower or upper missing y values, respectively, are trimmed.

`external.smooths`

A [data.frame](#) containing the one or more smooths of a response in the column specified by `smoothed.response`. Multiple smooths should be supplied in `long.format` with the same columns as the `smooths.frame` data, except for the smoothing-parameter columns `Type`, `TunePar`, `TuneVal`, `Tuning` and `Method`. Only those smoothing-parameter columns that are to be used in any of `plots.by`, `plots.group`, `facet.x` and `facet.y` should be included with labels appropriate to the `external.smooths`. Those smoothing-parameter columns not included in `external.smooths` will have columns of "Other" added to `external.smooths`. The growth rates will be computed by differencing according to the settings of `get.rates` and `trait.types` in the function that calls `args4smoothing`.

`correctBoundaries`

A [logical](#) indicating whether the fitted spline values are to have the method of Huang (2001) applied to them to correct for estimation bias at the end-points. Note that `spline.type` must be `NCSS` and `lambda` and `deriv` must be `NULL` for `correctBoundaries` to be set to `TRUE`.

`combinations`

A [character](#) specifying how the values of the different smoothing parameters are to be combined to specify the smooths that are to be obtained. The option `allvalid` results in a smooth for each of the combinations of the values of `smoothing.methods`, `spline.types`, `df` and `lambdas` that are valid; the other `smoothing.args` will be the same for all smooths.

The option `parallel` specifies that, if set, each of four smoothing parameters, `smoothing.methods`, `spline.types`, `df` and `lambdas`, must have the same number of values and that this number is the number of different smooths to be produced. The values of the parameters in the same position within each parameter collectively specify a single smooth. Because the value of only one of `df` and `lambdas` must be specified for a smooth, one of these must be set to `NA` and the other to the desired value for each smooth. If all values for one of them is `NA`, then the argument may be omitted or set to `NULL`.

The option `single` is for the specification of a single smooth. This will mean that only one of `df` or `lambdas` should be set.

...

allows arguments to be passed to other functions; not used at present.

## Value

A named [list](#).

## Author(s)

Chris Brien

## See Also

[traitSmooth](#) and [probeSmooths](#).

## Examples

```
args4smoothing(smoothing.methods = "direct",
```

```

      spline.types = "NCSS", df = NULL, lambdas = NULL,
      smoothing.segments = NULL, npspline.segments = NULL,
      combinations = "allvalid")
args4smoothing(smoothing.methods = c("log", "dir", "log"),
      spline.types = c("NCSS", "NCSS", "PS"),
      df = c(4, 5, NA), lambdas = c(NA, NA, 0.36),
      combinations = "parallel")
args4smoothing(smoothing.methods = "log",
      spline.types = "PS", df = NULL,
      lambdas = 0.36, combinations = "single")

```

---

as.smooths.frame	<i>Forms a <a href="#">smooths.frame</a> from a <a href="#">data.frame</a>, ensuring that the correct columns are present.</i>
------------------	--

---

## Description

Creates a [smooths.frame](#) from a [data.frame](#) by adding the class [smooths.frame](#) and a set of [attributes](#) to it.

## Usage

```
as.smooths.frame(data, individuals = NULL, times = NULL)
```

## Arguments

data	A <a href="#">data.frame</a> containing the results of smoothing the data on a set of individuals over time, the data being arranged in long format both with respect to the times and the smoothing-parameter values. It must contain the columns Type, TunePar, TuneVal, Tuning and Method that give the smoothing-parameter values that were used to produce each smooth of the data, as well as the columns identifying the individuals, the observation times of the responses and the unsmoothed and smoothed responses. Each response occupies a single column.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the <a href="#">numeric</a> , or <a href="#">factor</a> with numeric levels, that contains the values of the predictor variable to be supplied to <a href="#">smooth.spline</a> and to be plotted on the x-axis.

## Value

A [smooths.frame](#)

## Author(s)

Chris Brien

**See Also**

[validSmoothsFrame](#), [as.smooths.frame](#)

**Examples**

```
dat <- read.table(header = TRUE, text = "
Type TunePar TuneVal Tuning Method ID DAP PSA sPSA
NCSS df 4 df-4 direct 045451-C 28 57.446 51.18456
NCSS df 4 df-4 direct 045451-C 30 89.306 87.67343
NCSS df 7 df-7 direct 045451-C 28 57.446 57.01589
NCSS df 7 df-7 direct 045451-C 30 89.306 87.01316
")
dat[1:7] <- lapply(dat[1:6], factor)
dat <- as.smooths.frame(dat, individuals = "ID", times = "DAP")
is.smooths.frame(dat)
validSmoothsFrame(dat)
```

---

byIndv4Intvl_GRsAvg	<i>Calculates the growth rates for a specified time interval for individuals in a data.frame in long format by taking weighted averages of growth rates for times within the interval.</i>
---------------------	--

---

**Description**

Using previously calculated growth rates over time, calculates the Absolute Growth Rates for a specified interval using the weighted averages of AGRs for each time point in the interval (AGR) and the Relative Growth Rates for a specified interval using the weighted geometric means of RGRs for each time point in the interval (RGR).

**Usage**

```
byIndv4Intvl_GRsAvg(data, responses,
                     individuals = "Snapshot.ID.Tag", times = "DAP",
                     which.rates = c("AGR", "RGR"),
                     suffices.rates=c("AGR", "RGR"), sep.rates = ".",
                     start.time, end.time,
                     suffix.interval, sep.suffix.interval = ".",
                     sep.levels=".", na.rm=FALSE)
```

**Arguments**

data	A <a href="#">data.frame</a> containing the columns from which the growth rates are to be calculated.
responses	A <a href="#">character</a> giving the names of the responses for which there are columns in data that contain the growth rates that are to be averaged. The names of the growth rates should have either AGR or RGR appended to the responses names.

individuals	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <b>character</b> giving the name of the column in data containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used in calculating growth rates and, if a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
which.rates	A <b>character</b> giving the growth rates that are to be averaged to obtain growth rates for an interval. It should be a combination of one or more of "AGR" and "RGR".
suffices.rates	A <b>character</b> giving the suffices to be appended to response to form the names of the columns containing the calculated the growth rates and in which growth rates are to be stored. Their elements will be matched with those of which.rates.
sep.rates	A <b>character</b> giving the character(s) to be used to separate the suffices.rates value from a response value in constructing the name for a new rate. For no separator, set to "".
start.time	A <b>numeric</b> giving the times, in terms of values in times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the start of the interval for which the growth rate is to be calculated.
end.time	A <b>numeric</b> giving the times, in terms of values times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the end of the interval for which the growth rate is to be calculated.
suffix.interval	A <b>character</b> giving the suffix to be appended to response.suffices.rates to form the names of the columns containing the calculated the growth rates.
sep.suffix.interval	A <b>character</b> giving the separator to use in appending suffix.interval to a growth rate. For no separator, set to "".
sep.levels	A <b>character</b> giving the separator to use when the levels of individuals are combined. This is needed to avoid using a <b>character</b> that occurs in a <b>factor</b> to delimit levels when the levels of individuals are combined to identify subsets.
na.rm	A <b>logical</b> indicating whether NA values should be stripped before the calculation of weighted means proceeds.

## Details

The AGR for an interval is calculated as the weighted mean of the AGRs for times within the interval. The RGR is calculated as the weighted geometric mean of the RGRs for times within the interval; in fact the exponential is taken of the weighted means of the logs of the RGRs. The weights are obtained from the times. They are taken as the sum of half the time subintervals before and after each time, except for the end points; the end points are taken to be the subintervals at the start and end of the interval.

## Value

A **data.frame** with the growth rates. The name of each column is the concatenation of (i) one of responses, (ii) one of AGR, PGR or RGR, or the appropriate element of suffices.rates, and (iii)



suffix.interval, the three components being separated by full stops.

### Author(s)

Chris Brien

### See Also

[byIndv4Intvl\\_GRsDiff](#), [byIndv4Intvl\\_WaterUse](#), [splitValueCalculate](#), [getTimesSubset](#), [GrowthRates](#), [byIndv4Times\\_SplinesGRs](#), [splitContGRdiff](#)

### Examples

```
data(exampleData)
longi.dat <- byIndv4Times_SplinesGRs(data = longi.dat,
                                     response="PSA", response.smoothed = "sPSA",
                                     individuals = "Snapshot.ID.Tag",
                                     times = "DAP",
                                     df = 4,
                                     rates.method = "deriv",
                                     which.rates = c("AGR", "RGR"),
                                     suffices.rates = c("AGRdv", "RGRdv"))
sPSA.GR <- byIndv4Intvl_GRsAvg(data = longi.dat,
                               response="sPSA", times = "DAP",
                               which.rates = c("AGR", "RGR"),
                               suffices.rates = c("AGRdv", "RGRdv"),
                               start.time = 31, end.time = 35,
                               suffix.interval = "31to35")
```

---

byIndv4Intvl_GRsDiff	<i>Calculates the growth rates for a specified time interval for individuals in a data.frame in long format by differencing the values for a response within the interval.</i>
----------------------	--

---

### Description

Using the values of the responses, calculates the specified combination of the Absolute Growth Rates using differences (AGR), the Proportionate Growth Rates (PGR) and Relative Growth Rates using log differences (RGR) between two nominated time points.

### Usage

```
byIndv4Intvl_GRsDiff(data, responses,
                     individuals = "Snapshot.ID.Tag", times = "DAP",
                     which.rates = c("AGR", "PGR", "RGR"),
                     suffices.rates=NULL, sep.rates = ".",
                     start.time, end.time,
                     suffix.interval, sep.suffix.interval = ".")
```

## Arguments

data	A <code>data.frame</code> containing the column from which the growth rates are to be calculated.
responses	A <code>character</code> giving the names of the columns in data from which the growth rates are to be calculated.
individuals	A <code>character</code> giving the name of the <code>factor</code> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <code>character</code> giving the name of the column in data containing the times at which the data was collected, either as a <code>numeric</code> , <code>factor</code> , or <code>character</code> . It will be used in calculating growth rates and, if a <code>factor</code> or <code>character</code> , the values should be numerics stored as characters.
which.rates	A <code>character</code> giving the growth rates that are to be calculated. It should be a combination of one or more of "AGR", "PGR" and "RGR".
suffices.rates	A <code>character</code> giving the characters to be appended to the names of the responses in constructing the names of the columns containing the calculated growth rates. The order of the suffices in <code>suffices.rates</code> should correspond to the order of the elements of <code>which.rates</code> .
sep.rates	A <code>character</code> giving the character(s) to be used to separate the <code>suffices.rates</code> value from a response value in constructing the name for a new rate. For no separator, set to "".
start.time	A <code>numeric</code> giving the times, in terms of values in <code>times</code> , that will give a single value for each <code>Snapshot.ID.Tag</code> and that will be taken as the observation at the start of the interval for which the growth rate is to be calculated.
end.time	A <code>numeric</code> giving the times, in terms of values <code>times</code> , that will give a single value for each <code>Snapshot.ID.Tag</code> and that will be taken as the observation at the end of the interval for which the growth rate is to be calculated.
suffix.interval	A <code>character</code> giving the suffix to be appended to response to form the names of the columns containing the calculated the growth rates.
sep.suffix.interval	A <code>character</code> giving the separator to use in appending <code>suffix.interval</code> to a growth rate. For no separator, set to "".

## Details

The AGR is calculated as the difference between the values of response at the `end.time` and `start.time` divided by the difference between `end.time` and `start.time`. The PGR is calculated as the ratio of response at the `end.time` to that at `start.time` and the ratio raised to the power of the reciprocal of the difference between `end.time` and `start.time`. The RGR is calculated as the log of the PGR and so is equal to the difference between the logarithms of response at the `end.time` and `start.time` divided by the difference between `end.time` and `start.time`.

**Value**

A `data.frame` with the growth rates. The name of each column is the concatenation of (i) one of responses, (ii) one of AGR, PGR or RGR, or the appropriate element of `suffices.rates`, and (iii) `suffix.interval`, the three components being separated by full stops.

**Author(s)**

Chris Brien

**See Also**

`byIndv4Intvl_GRsAvg`, `byIndv4Intvl_WaterUse`, `getTimesSubset`, `GrowthRates`,  
`byIndv4Times_SplinesGRs`, `splitContGRdiff`

**Examples**

```
data(exampleData)
sPSA.GR <- byIndv4Intvl_GRsDiff(data = longi.dat,
                                responses = "sPSA", times = "DAP",
                                which.rates = c("AGR", "RGR"),
                                start.time = 31, end.time = 35,
                                suffix.interval = "31to35")
```

---

`byIndv4Intvl_ValueCalc`

*Calculates a single value that is a function of the values of an individual for a response in a data.frame in long format over a specified time interval.*

---

**Description**

Splits the values of a response into subsets corresponding individuals and applies a function that calculates a single value from each individual's observations during a specified time interval. It includes the ability to calculate the observation number that is closest to the calculated value of the function and the associated values of a `factor` or `numeric`.

**Usage**

```
byIndv4Intvl_ValueCalc(data, response,
                        individuals = "Snapshot.ID.Tag", times = "DAP",
                        FUN = "max", which.obs = FALSE, which.values = NULL,
                        addFUN2name = TRUE, sep.FUNname = ".",
                        start.time=NULL, end.time=NULL,
                        suffix.interval=NULL, sep.suffix.interval = ".",
                        sep.levels=".", weights=NULL, na.rm=TRUE, ...)
```

**Arguments**

data	A <code>data.frame</code> containing the column from which the function is to be calculated.
response	A <code>character</code> giving the name of the column in data from which the values of FUN are to be calculated.
individuals	A <code>character</code> giving the name of the <code>factor</code> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <code>character</code> giving the name of the column in data containing the times at which the data was collected, either as a <code>numeric</code> , <code>factor</code> , or <code>character</code> . It will be used in calculating growth rates and, if a <code>factor</code> or <code>character</code> , the values should be numerics stored as characters.
FUN	A <code>character</code> giving the name of the function that calculates the value for each subset.
which.obs	A <code>logical</code> indicating whether or not to determine the observation number corresponding to the observed value that is closest to the value of the function, in addition to the value of the function itself. That is, FUN need not return an observed value of the response, e.g. quantile.
which.values	A <code>character</code> giving the name of the <code>factor</code> or <code>numeric</code> whose values are associated with the response values and whose value is to be returned for the observation number whose response value corresponds to the observed value closest to the value of the function. That is, FUN need not return an observed value of the response, e.g. quantile. In the case of multiple observed response values satisfying this condition, the value of the <code>which.values</code> vector for the first of these is returned.
addFUN2name	A <code>logical</code> that, if TRUE, indicates that the FUN name is to be added to the names of the columns in the <code>data.frame</code> returned by <code>byIndv4Intvl_ValueCalc</code> .
sep.FUNname	A <code>character</code> giving the character(s) to be used to separate the name of FUN from the response value in constructing the name for a new response. For no separator, set to "".
start.time	A <code>numeric</code> giving the times, in terms of levels of <code>times.factor</code> , that will give a single value for each <code>Snapshot.ID.Tag</code> and that will be taken as the observation at the start of the interval for which a value is to be calculated. If <code>start.time</code> is NULL, the interval will start with the first observation. In the case of multiple observed response values satisfying this condition, the first is returned.
end.time	A <code>numeric</code> giving the times, in terms of levels of <code>times.factor</code> , that will give a single value for each <code>Snapshot.ID.Tag</code> and that will be taken as the observation at the end of the interval for which a value is to be calculated. If <code>end.time</code> is NULL, the interval will end with the last observation.
suffix.interval	A <code>character</code> giving the suffix to be appended to response to form the name of the column containing the calculated values. If it is NULL then nothing will be appended.
sep.suffix.interval	A <code>character</code> giving the separator to use in appending <code>suffix.interval</code> to a growth rate. For no separator, set to "".



---

byIndv4Intvl\_WaterUse *Calculates, water use traits (WU, WUR, WUI) over a specified time interval for each individual in a data.frame in long format.*

---

### Description

Calculates one or more of water use (WU), water use rate (WUR), and, for a set of responses, water use indices (WUI)s over a specified time interval for each individual in a data.frame in long format.

### Usage

```
byIndv4Intvl_WaterUse(data, water.use = "Water.Use", responses = NULL,
  individuals = "Snapshot.ID.Tag", times = "DAP",
  trait.types = c("WU", "WUR", "WUI"),
  suffix.rate = "R", suffix.index = "I",
  sep.water.traits = "", sep.responses = ".",
  start.time, end.time,
  suffix.interval = NULL, sep.suffix.interval = ".",
  na.rm = FALSE)
```

### Arguments

data	A <a href="#">data.frame</a> containing the column from which the water use traits are to be calculated.
water.use	A <a href="#">character</a> giving the names of the column in data that contains the water use values.
responses	A <a href="#">character</a> giving the names of the columns in data for which WUIs are to be calculated.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used identifying the intervals and, if a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
trait.types	A <a href="#">character</a> listing the trait types to compute and return. It should be some combination of WU, WUR and WUI, or be all. See Details for how each is calculated.
suffix.rate	A <a href="#">character</a> giving the label to be appended to the value of water.use to form the name of the WUR.
suffix.index	A <a href="#">character</a> giving the label to be appended to the value of water.use to form the name of the WUI.

sep.water.traits	A <a href="#">character</a> giving the character(s) to be used to separate the suffix.rate and suffix.index values from the responses values in constructing the name for a new rate/index. The default of "" results in no separator.
sep.responses	A <a href="#">character</a> giving the character(s) to be used to separate the suffix.rate value from aresponses value in constructing the name for a new index. For no separator, set to "".
start.time	A <a href="#">numeric</a> giving the times, in terms of values in times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the start of the interval for which the WUI is to be calculated.
end.time	A <a href="#">numeric</a> giving the times, in terms of values times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the end of the interval for which the WUI is to be calculated.
suffix.interval	A <a href="#">character</a> giving the suffix to be appended to the names of the columns for the water use traits to indicate the interval for which the traits have been calculated.
sep.suffix.interval	A <a href="#">character</a> giving the separator to use in appending suffix.inteval to a growth rate. For no separator, set to "".
na.rm	A <a href="#">logical</a> indicating whether NA values should be stripped before the calculation proceeds.

## Details

WU is the water use and is the sum of the water use after start.time until end.time. Thus, the water use up to start.time is not included.

WUR is the Water Use Rate and is WU divided by the difference between end.time and start.time.

WUI is the Water Use Index and is calculated as a response difference between the start.time and the end.time, which s then divided by the WU.

## Value

A [data.frame](#) containing the individuals column, WU and/or WUR and, if requested, a WUI for each element of responses. The names of WU and WUR will have suffix.interval appended, if it is not NULL, separated by a full stop ('.'). The name of each WUI will be the concatenation of an element of responses with WUI and, if not NULL, suffix.interval, the three components being separated by a full stop ('.').

## Author(s)

Chris Brien

## See Also

[byIndv4Intvl\\_GRsAvg](#), [byIndv4Intvl\\_GRsDiff](#), [splitValueCalculate](#), [getTimesSubset](#), [GrowthRates](#)

## Examples

```
data(exampleData)
WU.WUI_31_35 <- byIndv4Intvl_WaterUse(data = longi.dat,
                                     water.use = "WU", responses = "PSA",
                                     times = "DAP",
                                     trait.types = c("WUR", "WUI"),
                                     suffix.rate = ".Rate",
                                     suffix.index = ".Index",
                                     start.time = 31, end.time = 35,
                                     suffix.interval = "31to35")
```

---

`byIndv4Times_GRsDiff` *Adds, to a data.frame, the growth rates calculated for consecutive times for individuals in a data.frame in long format by differencing response values.*

---

## Description

Uses [AGRdiff](#), [PGR](#) and [RGRdiff](#) to calculate growth rates continuously over time for the response by differencing pairs of pairs of response values and stores the results in data. The subsets are those values with the same levels combinations of the [factors](#) listed in individuals.

If `avail.time.diffs` is FALSE, the differences between consecutive time values are calculated. For this, it is assumed that the same first times value is present in data for all individuals.

## Usage

```
byIndv4Times_GRsDiff(data, responses,
                     individuals = "Snapshot.ID.Tag", times = "DAP",
                     which.rates = c("AGR", "PGR", "RGR"),
                     suffices.rates=NULL, sep.rates = ".",
                     avail.times.diffs = FALSE, ntimes2span = 2)
```

## Arguments

<code>data</code>	A <a href="#">data.frame</a> containing the columns for which growth rates are to be calculated.
<code>responses</code>	A <a href="#">character</a> giving the names of the columns in data for which growth rates are to be calculated.
<code>individuals</code>	A <a href="#">character</a> giving the name(s) of the <a href="#">factor</a> (s) that define the subsets of response that correspond to the response values for an individual (e.g. plant, pot, cart, plot or unit) for which growth rates are to be calculated continuously. If the columns corresponding to individuals are not <a href="#">factor</a> (s) then they will be coerced to <a href="#">factor</a> (s). The subsets are formed using <a href="#">split</a> .
<code>times</code>	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used in calculating the growth rates. If a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.





```
times = "DAP",
which.rates=c("AGR", "RGR"),
avail.times.diffs = TRUE)
```

---

byIndv4Times\_SplinesGRs

*For a response in a data.frame in long format, computes, for a single set of smoothing parameters, smooths of the response, possibly along with growth rates calculated from the smooths.*

---

## Description

Uses [smoothSpline](#) to fit a spline to the values of response for each individual and stores the fitted values in data. The degree of smoothing is controlled by the tuning parameters df and lambda, related to the penalty, and by npspline.segments. The smoothing.method provides for direct and logarithmic smoothing.

The Absolute and Relative Growth Rates (AGR and RGR) can be computed either using the first derivatives of the splines or by differencing the smooths. If using the first derivative to obtain growth rates, correctBoundaries must be FALSE. Derivatives other than the first derivative can also be produced. The function [byIndv4Times\\_GRsDiff](#) is used to obtain growth rates by differencing.

The handling of missing values in the observations is controlled via na.x.action and na.y.action. If there are not at least four distinct, nonmissing x-values, a warning is issued and all smoothed values and derivatives are set to NA.

The function [probeSmoothing](#) can be used to investigate the effect the smoothing parameters (smoothing.method, df or lambda) on the smooth that results.

## Usage

```
byIndv4Times_SplinesGRs(data, response, response.smoothed = NULL,
  individuals = "Snapshot.ID.Tag", times,
  smoothing.method = "direct", smoothing.segments = NULL,
  spline.type = "NCSS", df=NULL, lambda = NULL,
  npspline.segments = NULL,
  correctBoundaries = FALSE,
  rates.method = "differences",
  which.rates = c("AGR","RGR"),
  suffices.rates = NULL, sep.rates = ".",
  avail.times.diffs = FALSE, ntimes2span = 2,
  extra.derivs = NULL, suffices.extra.derivs=NULL,
  sep.levels = ".",
  na.x.action="exclude", na.y.action = "trimx", ...)
```

## Arguments

data	A <a href="#">data.frame</a> containing the column to be smoothed.
response	A <a href="#">character</a> giving the name of the column in data that is to be smoothed.

<code>response.smoothed</code>	A <b>character</b> specifying the name of the column containing the values of the smoothed response variable, corresponding to <code>response</code> . If <code>response.smoothed</code> is <code>NULL</code> , then <code>response.smoothed</code> is set to the response to which is added the prefix <code>s</code> .
<code>individuals</code>	A <b>character</b> giving the name(s) of the <b>factor</b> (s) that define the subsets of response that correspond to the response values for an individual (e.g. plant, pot, cart, plot or unit) that are to be smoothed separately. If the columns corresponding to individuals are not <b>factor</b> (s) then they will be coerced to <b>factor</b> (s). The subsets are formed using <b>split</b> .
<code>times</code>	A <b>character</b> giving the name of the column in data containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used as the values of the predictor variable to be supplied to <b>smooth.spline</b> and in calculating growth rates. If a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
<code>smoothing.method</code>	A <b>character</b> giving the smoothing method to use. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response and then back-transforming by taking the exponential of the fitted values.
<code>smoothing.segments</code>	A named <b>list</b> , each of whose components is a numeric pair specifying the first and last values of an times-interval whose data is to be subjected as an entity to smoothing using splines. The separate smooths will be combined to form a whole smooth for each individual. If <code>get.rates</code> is <code>TRUE</code> , <code>rates.method</code> is <code>differences</code> and <code>ntimes2span</code> is 2, the smoothed growth rates will be computed over the set of segments; otherwise, they will be computed within segments. If <code>smoothing.segments</code> is <code>NULL</code> , the data is not segmented for smoothing.
<code>spline.type</code>	A <b>character</b> giving the type of spline to use. Currently, the possibilities are (i) "NCSS", for natural cubic smoothing splines, and (ii) "PS", for P-splines.
<code>df</code>	A <b>numeric</b> specifying, for natural cubic smoothing splines (NCSS), the desired equivalent number of degrees of freedom of the smooth (trace of the smoother matrix). Lower values result in more smoothing. If <code>df = NULL</code> , the amount of smoothing can be controlled by setting <code>lambda</code> . If both <code>df</code> and <code>lambda</code> are <code>NULL</code> , smoothing is controlled by the default arguments for <b>smooth.spline</b> , and any that you supply via the ellipsis (...) argument.
<code>lambda</code>	A <b>numeric</b> specifying the positive penalty to apply. The amount of smoothing decreases as <code>lambda</code> decreases.
<code>npspline.segments</code>	A <b>numeric</b> specifying, for P-splines (PS), the number of equally spaced segments between <code>min(times)</code> and <code>max(times)</code> , excluding missing values, to use in constructing the B-spline basis for the spline fitting. If <code>npspline.segments</code> is <code>NULL</code> , <code>npspline.segments</code> is set to the maximum of 10 and $\text{ceiling}((\text{nrow}(\text{data})-1)/2)$ i.e. there will be at least 10 segments and, for more than 22 times values, there will be half as many segments as there are times values. The amount of smoothing decreases as <code>npspline.segments</code> increases. When the data has been seg-

mented for smoothing (smoothing.segments is not NULL), an npspline.segments value can be supplied for each segment.

#### correctBoundaries

A **logical** indicating whether the fitted spline values are to have the method of Huang (2001) applied to them to correct for estimation bias at the end-points. Note that spline.type must be NCSS and lambda and deriv must be NULL for correctBoundaries to be set to TRUE.

#### rates.method

A **character** specifying the method to use in calculating the growth rates. The possibilities are none, differences and derivatives.

#### which.rates

A **character** giving the growth rates that are to be calculated. It should be a combination of one or more of "AGR", "PGR" and "RGR".

#### suffices.rates

A **character** giving the characters to be appended to the names of the responses to provide the names of the columns containing the calculated growth rates. The order of the suffices in suffices.rates should correspond to the order of the elements of which.rates. If NULL, the values of which.rates are used.

#### sep.rates

A **character** giving the character(s) to be used to separate the suffices.rates value from a response value in constructing the name for a new rate. For no separator, set to "".

#### avail.times.diffs

A **logical** indicating whether there is an appropriate column of times differences that can be used as the denominator in computing the growth rates. If TRUE, it will be assumed that the name of the column is the value of times with .diffs appended. If FALSE, a column, whose column name will be the value of times with .diffs appended, will be formed and saved in the result, overwriting any existing columns with the constructed name in data. It will be calculated using the values of times in data.

#### ntimes2span

A **numeric** giving the number of values in times to span in calculating growth rates by differencing. Each growth rate is calculated as the difference in the values of one of the responses for pairs of times values that are spanned by ntimes2span times values divided by the difference between this pair of times values. For ntimes2span set to 2, a growth rate is the difference between consecutive pairs of values of one of the responses divided by the difference between consecutive pairs of times values.

#### extra.derivs

A **numeric** specifying one or more orders of derivatives that are required, in addition to any required for calculating the growth rates. When rates.method is derivatives, these can be derivatives other than the first. Otherwise, any derivatives can be specified.

#### suffices.extra.derivs

A **character** giving the characters to be appended to response.method to construct the names of the derivatives. If NULL and the derivatives are to be retained, then .dv followed by the order of the derivative is appended to response.method.

.

#### sep.levels

A **character** giving the separator to use when the levels of individuals are combined. This is needed to avoid using a **character** that occurs in a **factor** to delimit levels when the levels of individuals are combined to identify subsets.

na.x.action	A <a href="#">character</a> string that specifies the action to be taken when values of x, or the times, are NA. The possible values are fail, exclude or omit. For exclude and omit, predictions and derivatives will only be obtained for nonmissing values of x. The difference between these two codes is that for exclude the returned data.frame will have as many rows as data, the missing values have been incorporated.
na.y.action	A <a href="#">character</a> string that specifies the action to be taken when values of y, or the response, are NA. The possible values are fail, exclude, omit, allx, trimx, ltrimx or rtrimx. For all options, except fail, missing values in y will be removed before smoothing. For exclude and omit, predictions and derivatives will be obtained only for nonmissing values of x that do not have missing y values. Again, the difference between these two is that, only for exclude will the missing values be incorporated into the returned data.frame. For allx, predictions and derivatives will be obtained for all nonmissing x. For trimx, they will be obtained for all nonmissing x between the first and last nonmissing y values that have been ordered for x; for ltrimx and utrimx either the lower or upper missing y values, respectively, are trimmed.
...	allows for arguments to be passed to smooth.spline.

## Value

A [data.frame](#) containing data to which has been added a column with the fitted smooth, the name of the column being the value of response.smoothed. If rates.method is not none, columns for the growth rates listed in which.rates will be added to data; the names each of these columns will be the value of response.smoothed with the elements of which.rates appended.

When rates.method is derivatives and smoothing.method is direct, the AGR is obtained from the first derivative of the spline for each value of times and the RGR is calculated as the AGR divided by the value of the response.smoothed for the corresponding time. When rates.method is derivatives and smoothing.method is logarithmic, the RGR is obtained from the first derivative of the spline and the AGR is calculated as the RGR multiplied by the corresponding value of the response.smoothed.

If extra.derivs is not NULL, the values for the nominated derivatives will also be added to data; the names each of these columns will be the value of response.smoothed with .dvf appended, where f is the order of the derivative, or the value of response.smoothed with the corresponding element of suffices.deriv appended.

Any pre-existing smoothed and growth rate columns in data will be replaced. The ordering of the data.frame for the times values will be preserved as far as is possible; the main difficulty is with the handling of missing values by the function merge. Thus, if missing values in times are retained, they will occur at the bottom of each subset of individuals and the order will be problematic when there are missing values in y and na.y.action is set to omit.

## Author(s)

Chris Brien

## References

Eilers, P.H.C and Marx, B.D. (2021) *Practical smoothing: the joys of P-splines*. Cambridge University Press, Cambridge.

Huang, C. (2001) Boundary corrected cubic smoothing splines. *Journal of Statistical Computation and Simulation*, **70**, 107-121.

## See Also

[smoothSpline](#), [probeSmoothing](#), [byIndv4Times\\_GRsDiff](#), [smooth.spline](#), [predict.smooth.spline](#), [split](#)

## Examples

```
data(exampleData)
#smoothing with growth rates calculated using derivatives
longi.dat <- byIndv4Times_SplinesGRs(data = longi.dat,
                                     response="PSA", response.smoothed = "sPSA",
                                     times="DAP",
                                     df = 4, rates.method = "deriv",
                                     suffices.rates = c("AGRdv", "RGRdv"))

#Use P-splines
longi.dat <- byIndv4Times_SplinesGRs(data = longi.dat,
                                     response="PSA", response.smoothed = "sPSA",
                                     individuals = "Snapshot.ID.Tag", times="DAP",
                                     spline.type = "PS", lambda = 0.1,
                                     npspline.segments = 10,
                                     rates.method = "deriv",
                                     suffices.rates = c("AGRdv", "RGRdv"))

#with segmented smoothing and no growth rates
longi.dat <- byIndv4Times_SplinesGRs(data = longi.dat,
                                     response="PSA", response.smoothed = "sPSA",
                                     individuals = "Snapshot.ID.Tag", times="DAP",
                                     smoothing.segments = list(c(28,34), c(35,42)),
                                     df = 5, rates.method = "none")
```

---

byIndv_ValueCalc	<i>Calculates a single value that is a function of an individual's values for a response.</i>
------------------	---

---

## Description

Applies a function to calculate a single value from an individual's values for a response in a data.frame in long format. It includes the ability to calculate the observation number that is closest to the calculated value of the function and the associated values of a [factor](#) or numeric.

**Usage**

```
byIndv_ValueCalc(data, response, individuals = "Snapshot.ID.Tag",
  FUN = "max", which.obs = FALSE, which.values = NULL,
  addFUN2name = TRUE, sep.FUNname = ".",
  weights = NULL, na.rm=TRUE, sep.levels = ".", ...)
```

**Arguments**

data	A <a href="#">data.frame</a> containing the column from which the function is to be calculated.
response	A <a href="#">character</a> giving the name of the column in data from which the values of FUN are to be calculated.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
FUN	A <a href="#">character</a> giving the name of the function that calculates the value for each subset.
which.obs	A <a href="#">logical</a> indicating whether or not to determine the observation number corresponding to the observed value that is closest to the value of the function, in addition to the value of the function itself. That is, FUN need not return an observed value of the reponse, e.g. quantile. In the case of multiple observed response values satisfying this condition, the first is returned.
which.values	A <a href="#">character</a> giving the name of the <a href="#">factor</a> or <a href="#">numeric</a> whose values are associated with the response values and whose value is to be returned for the observation number whose response value corresponds to the observed value closest to the value of the function. That is, FUN need not return an observed value of the reponse, e.g. quantile. In the case of multiple observed response values satisfying this condition, the value of the which.values vector for the first of these is returned.
addFUN2name	A <a href="#">logical</a> that, if TRUE, indicates that the FUN name is to be added to the names of the columns in the <a href="#">data.frame</a> returned by byIndv4Intvl_ValueCalc.
sep.FUNname	A <a href="#">character</a> giving the character(s) to be used to separate the name of FUN from the response value in constructing the name for a new response. For no separator, set to "".
weights	A <a href="#">character</a> giving the name of the column in data containing the weights to be supplied as w to FUN.
na.rm	A <a href="#">logical</a> indicating whether NA values should be stripped before the calculation proceeds.
sep.levels	A <a href="#">character</a> giving the separator to use when the levels of individuals are combined. This is needed to avoid using a <a href="#">character</a> that occurs in a <a href="#">factor</a> to delimit levels when the levels of individuals are combined to identify subsets.
...	allows for arguments to be passed to FUN.

**Value**

A `data.frame`, with the same number of rows as there are individuals, containing a column for the individuals and a column with the values of the function for the individuals. It is also possible to determine observation numbers or the values of another column in data for the response values that are closest to the FUN results, using either or both of `which.obs` and `which.values`. If `which.obs` is TRUE, a column with observation numbers is included in the `data.frame`. If `which.values` is set to the name of a `factor` or a `numeric`, a column containing the levels of that `factor` or the values of that `numeric` is included in the `data.frame`.

The name of the column with the values of the function will be formed by concatenating the response and FUN, separated by a full stop. If `which.obs` is TRUE, the column name for the observations numbers will have `.obs` added after FUN into the column name for the function values; if `which.values` is specified, the column name for these values will have a full stop followed by `which.values` added after FUN into the column name for the function values.

**Author(s)**

Chris Brien

**See Also**

[byIndv4Intvl\\_ValueCalc](#), [byIndv4Times\\_GRsDiff](#), [byIndv4Times\\_SplinesGRs](#)

**Examples**

```
data(exampleData)
sPSA.max.dat <- byIndv_ValueCalc(data=longi.dat, response = "PSA")
AGR.max.dat <- byIndv_ValueCalc(data=longi.dat, response = "sPSA.AGR",
                                FUN="max",
                                which.values = "DAP", which.obs = TRUE)
sPSA.dec1.dat <- byIndv_ValueCalc(data=longi.dat, response = "sPSA",
                                FUN="quantile",
                                which.values = "DAP", probs = 0.1)
```

---

calcLagged

*Replaces the values in a vector with the result of applying an operation to it and a lagged value*

---

**Description**

Replaces the values in `x` with the result of applying an operation to it and the value that is lag positions either before it or after it in `x`, depending on whether `lag` is positive or negative. For positive `lag` the first lag values will be NA, while for negative `lag` the last lag values will be NA. When operation is NULL, the values are moved lag positions down the vector.

**Usage**

```
calcLagged(x, operation = NULL, lag = 1)
```



**Arguments**

x	A <a href="#">vector</a> containing the values on which the calculations are to be made.
operation	A <a href="#">character</a> giving the operation to be performed on pairs of values in x. If operation is NULL then the values are moved lag positions down the vector.
lag	A integer specifying, for the second value in the pair to be operated on, the number positions it is ahead of or behind the current value.

**Value**

A [vector](#) containing the result of applying operation to values in x. For positive lag the first lag values will be NA, while for negative lag the last lag values will be NA.

**Author(s)**

Chris Brien

**See Also**

[Ops](#)

**Examples**

```
data(exampleData)
longi.dat$DAP.diffss <- calcLagged(longi.dat$xDAP, operation = "-")
```

---

calcTimes	<i>Calculates for a set of times, the time intervals after an origin time and the position of each within a time interval</i>
-----------	---

---

**Description**

For the column specified in imageTimes, having converted it to POSIXct if not already converted, calculates for each value the number of intervalUnits between the time and the startTime. Then the number of timePositions within the intervals is calculated for the values in imageTimes. The function difftimes is used in doing the calculations, but the results are converted to numeric. For example intervals could correspond to the number of Days after Planting (DAP) and the timePositions to the hour within each day.

**Usage**

```
calcTimes(data, imageTimes = NULL, timeFormat = "%Y-%m-%d %H:%M",
          intervals = "Time.after.Planting..d.", startTime = NULL,
          intervalUnit = "days", timePositions = NULL)
```

**Arguments**

data	A <a href="#">data.frame</a> containing any columns specified by imageTimes, intervals and timePositions.
imageTimes	A <a href="#">character</a> giving the name of the column that contains the time that each cart was imaged. Note that in importing data into R, spaces and nonalphanumeric characters in names are converted to full stops. If imageTimes is NULL then no calculations are done.
timeFormat	A character giving the POSIXct format of characters containing times, in particular imageTimes and startTime. Note that if fractions of seconds are required options(digits.secs) must be used to set the number of decimal places and timeFormat must use %OS for seconds in timeFormat.
intervals	A <a href="#">character</a> giving the name of the column in data containing, as a <a href="#">numeric</a> or a <a href="#">factor</a> , the calculated times after startTime to be plotted on the x-axis. It is given as the number of intervalUnits between the two times. If startTime is NULL then intervals is not calculated.
startTime	A character giving the time, in the POSIXct format specified by timeFormat, to be subtracted from imageTimes to calculate intervals. For example, it might be the day of planting or treatment. If startTime is NULL then intervals is not calculated.
intervalUnit	A <a href="#">character</a> giving the name of the unit in which the values of the intervals should be expressed. It must be one of "secs", "mins", "hours" or "days".
timePositions	A <a href="#">character</a> giving the name of the column in data containing, as a <a href="#">numeric</a> , the value of the time position within an interval (for example, the time of imaging during the day expressed in hours plus a fraction of an hour). If timePositions is NULL then it is not calculated.

**Value**

A data.frame, being the unchanged data data.frame when imageTimes is NULL or containing either intervals and/or timePositions depending on which is not NULL.

**Author(s)**

Chris Brien

**See Also**

[as.POSIXct](#), [imagetimesPlot](#).

**Examples**

```
data(exampleData)
raw.dat <- calcTimes(data = raw.dat,
                     imageTimes = "Snapshot.Time.Stamp", timePositions = "Hour")
```

---

cumulate	<i>Calculates the cumulative sum, ignoring the first element if exclude.1st is TRUE</i>
----------	---

---

## Description

Uses cumsum to calculate the cumulative sum, ignoring the first element if exclude.1st is TRUE.

## Usage

```
cumulate(x, exclude.1st = FALSE, na.rm = FALSE, ...)
```

## Arguments

x	A <a href="#">vector</a> containing the values to be cumulated.
exclude.1st	A <a href="#">logical</a> indicating whether or not the first value of the cumulative sum is to be NA.
na.rm	A <a href="#">logical</a> indicating whether NA values should be stripped before the computation proceeds
...	allows passing of arguments to other functions; not used at present.

## Value

A [vector](#) containing the cumulative sum.

## Author(s)

Chris Brien

## See Also

[cumsum](#)

## Examples

```
data(exampleData)
PSA.cum <- cumulate(longi.dat$PSA)
```

---

designFactors

*Adds the factors and covariates for a blocked, split-unit design*


---

## Description

Add the following **factors** and covariates to a data frame containing imaging data from the Plant Accelerator: Zone, xZone, SHZone, ZLane, ZMainunit, Subunit and xMainPosn. It checks that the numbers of levels of the **factors** are consistent with the observed numbers of carts and observations.

## Usage

```
designFactors(data, insertName = NULL, designfactorMethod = "LanePosition",
             nzones = 6, nlanesperzone = 4,
             nmainunitsperlane = 11, nsubunitspermain = 2)
```

## Arguments

- |                    |   |
|--------------------|---|
| data               | A <b>data.frame</b> to which are to be added the design <b>factors</b> and covariates and which must contain the following columns:<br>Smarthouse, Snapshot.ID.Tag, xDAP, and,<br>if designfactorMethod = "LanePosition", Lane and Position.  |
| insertName         | A <b>character</b> giving the name of the column in the data.frame after which the new <b>factors</b> and covariates are to be inserted. If NULL, they are added after the last column.   |
| designfactorMethod | A <b>character</b> giving the method to use to obtain the columns for the design <b>factors</b> Zone, ZLane, Mainunit and Subunit. For LanePosition, it is assumed that (i) Lane can be divided into Zone and ZLane, each with nzones and nlanesperzone levels, respectively, and (ii) Position can be divided into Mainunit and Subunit, each with nmainunitsperlane and nmainunitsperlane levels, respectively. The <b>factor</b> SHZone is formed by combining Smarthouse and Zone and ZMainunit is formed by combining ZLane and Mainunit. For StandardOrder, the <b>factors</b> Zone, ZLane, Mainunit, Subunit are generated in standard order, with the levels of Subunit changing for every observation and the levels of subsequent changing only after all combinations of the levels of the <b>factors</b> to its right have been cycled through. |
| nzones             | A <b>numeric</b> giving the number of zones in a smarthouse.  |
| nlanesperzone      | A <b>numeric</b> giving the number of lanes in each zone.   |
| nmainunitsperlane  | A <b>numeric</b> giving the number of mainunits in each lane.   |
| nsubunitspermain   | A <b>numeric</b> giving the number of subunits in a main plot.  |



---

exampleData	<i>A small data set to use in function examples</i>
-------------	---

---

### Description

Imaging data for 20 of the plants that were imaged over 14 days from an experiment in a Smarthouse in the Plant Accelerator. Producing these files is illustrated in the Rice vignette and the data is used as a small example in the growthPheno manual.

### Usage

```
data(exampleData)
```

### Format

Three data.frames:

1. `raw.dat` (280 rows by 33 columns) that contains the imaging data for 20 plants by 14 imaging days as produced by the image processing software;
2. `longi.dat` (280 rows by 37 columns) that contains a modified version of the imaging data for the 20 plants by 14 imaging days in `raw.dat`;
3. `cart.dat` (20 rows by 14 columns) that contains data summarizing the growth features of the 20 plants produced from the data in `longi.dat`.

---

fitSpline	<i>Fits a spline to a response in a data.frame, and growth rates can be computed using derivatives</i>
-----------	--

---

### Description

Uses `smooth.spline` to fit a natural cubic smoothing spline or JOPS to fit a P-spline to all the values of response stored in `data`.

The amount of smoothing can be controlled by tuning parameters, these being related to the penalty. For a natural cubic smoothing spline, these are `df` or `lambda` and, for a P-spline, it is `lambda`. For a P-spline, `npspline.segments` also influences the smoothness of the fit. The `smoothing.method` provides for direct and logarithmic smoothing. The method of Huang (2001) for correcting the fitted spline for estimation bias at the end-points will be applied when fitting using a natural cubic smoothing spline if `correctBoundaries` is `TRUE`.

The derivatives of the fitted spline can also be obtained, and the Absolute and Relative Growth Rates (AGR and RGR) computed using them, provided `correctBoundaries` is `FALSE`. Otherwise, growth rates can be obtained by difference using `byIndv4Times_GRsDiff`.

The handling of missing values in the observations is controlled via `na.x.action` and `na.y.action`. If there are not at least four distinct, nonmissing x-values, a warning is issued and all smoothed values and derivatives are set to NA.

The function `probeSmoothing` can be used to investigate the effect the smoothing parameters (`smoothing.method` and `df` or `lambda`) on the smooth that results.

**Usage**

```
fitSpline(data, response, response.smoothed, x,
          smoothing.method = "direct",
          spline.type = "NCSS", df = NULL, lambda = NULL,
          npspline.segments = NULL, correctBoundaries = FALSE,
          deriv = NULL, suffices.deriv = NULL, extra.rate = NULL,
          na.x.action = "exclude", na.y.action = "trimx", ...)
```

**Arguments**

- |                   |   |
|-------------------|---|
| data              | A <a href="#">data.frame</a> containing the column to be smoothed.  |
| response          | A <a href="#">character</a> giving the name of the column in data that is to be smoothed.   |
| response.smoothed | A <a href="#">character</a> specifying the name of the column containing the values of the smoothed response variable, corresponding to response.   |
| x                 | A <a href="#">character</a> giving the name of the column in data that contains the values of the predictor variable.   |
| smoothing.method  | A <a href="#">character</a> giving the smoothing method to use. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response and then back-transforming by taking the exponential of the fitted values.   |
| spline.type       | A <a href="#">character</a> giving the type of spline to use. Currently, the possibilities are (i) "NCSS", for natural cubic smoothing splines, and (ii) "PS", for P-splines.   |
| df                | A <a href="#">numeric</a> specifying, for natural cubic smoothing splines (NCSS), the desired equivalent number of degrees of freedom of the smooth (trace of the smoother matrix). Lower values result in more smoothing. If df = NULL, the amount of smoothing can be controlled by setting lambda. If both df and lambda are NULL, smoothing is controlled by the default arguments for smooth.spline, and any that you supply via the ellipsis (...) argument.  |
| lambda            | A <a href="#">numeric</a> specifying the positive penalty to apply. The amount of smoothing decreases as lambda decreases.  |
| npspline.segments | A <a href="#">numeric</a> specifying, for P-splines (PS), the number of equally spaced segments between min(x) and max(x), excluding missing values, to use in constructing the B-spline basis for the spline fitting. If npspline.segments is NULL, npspline.segments is set to the maximum of 10 and ceiling((nrow(data)-1)/2) i.e. there will be at least 10 segments and, for more than 22 x values, there will be half as many segments as there are x values. The amount of smoothing decreases as npspline.segments increases. |
| correctBoundaries | A <a href="#">logical</a> indicating whether the fitted spline values are to have the method of Huang (2001) applied to them to correct for estimation bias at the end-points. Note that spline.type must be NCSS and lambda and deriv must be NULL for correctBoundaries to be set to TRUE.  |
| deriv             | A <a href="#">numeric</a> specifying one or more orders of derivatives that are required.   |

suffices.deriv	A <b>character</b> giving the characters to be appended to <code>response.method</code> to construct the names of the derivatives. If <code>NULL</code> and the derivatives are to be retained, then <code>.dv</code> followed by the order of the derivative is appended to <code>response.method</code> .
extra.rate	A named <b>character</b> nominating a single growth rate (AGR or RGR) to be computed using the first derivative, which one being dependent on the <code>smoothing.method</code> . The name of this element will be used as a suffix to be appended to the response when naming the resulting growth rate (see Examples). If unnamed, AGR or RGR will be used, as appropriate. Note that, for the <code>smoothing.method</code> set to <code>direct</code> , the first derivative is the AGR and so <code>extra.rate</code> must be set to RGR, which is computed as the $AGR / \text{smoothed response}$ . For the <code>smoothing.method</code> set to <code>logarithmic</code> , the first derivative is the RGR and so <code>extra.rate</code> must be set to AGR, which is computed as the $RGR * \text{smoothed response}$ . Make sure that <code>deriv</code> includes one so that the first derivative is available for calculating the <code>extra.rate</code> .
na.x.action	A <b>character</b> string that specifies the action to be taken when values of <code>x</code> are <code>NA</code> . The possible values are <code>fail</code> , <code>exclude</code> or <code>omit</code> . For <code>exclude</code> and <code>omit</code> , predictions and derivatives will only be obtained for nonmissing values of <code>x</code> . The difference between these two codes is that for <code>exclude</code> the returned <code>data.frame</code> will have as many rows as <code>data</code> , the missing values have been incorporated.
na.y.action	A <b>character</b> string that specifies the action to be taken when values of <code>y</code> , or the response, are <code>NA</code> . The possible values are <code>fail</code> , <code>exclude</code> , <code>omit</code> , <code>allx</code> , <code>trimx</code> , <code>ltrimx</code> or <code>rtrimx</code> . For all options, except <code>fail</code> , missing values in <code>y</code> will be removed before smoothing. For <code>exclude</code> and <code>omit</code> , predictions and derivatives will be obtained only for nonmissing values of <code>x</code> that do not have missing <code>y</code> values. Again, the difference between these two is that, only for <code>exclude</code> will the missing values be incorporated into the returned <code>data.frame</code> . For <code>allx</code> , predictions and derivatives will be obtained for all nonmissing <code>x</code> . For <code>trimx</code> , they will be obtained for all nonmissing <code>x</code> between the first and last nonmissing <code>y</code> values that have been ordered for <code>x</code> ; for <code>ltrimx</code> and <code>utrimx</code> either the lower or upper missing <code>y</code> values, respectively, are trimmed.
...	allows for arguments to be passed to <code>smooth.spline</code> .

## Value

A **list** with two components named `predictions` and `fit.spline`.

The `predictions` component is a `data.frame` containing `x` and the fitted smooth. The names of the columns will be the value of `x` and the value of `response.smoothed`. The number of rows in the `data.frame` will be equal to the number of pairs that have neither a missing `x` or response and the order of `x` will be the same as the order in `data`. If `deriv` is not `NULL`, columns containing the values of the derivative(s) will be added to the `data.frame`; the name each of these columns will be the value of `response.smoothed` with `.dvf` appended, where `f` is the order of the derivative, or the value of `response.smoothed` and the corresponding element of `suffices.deriv` appended. If RGR is not `NULL`, the RGR is calculated as the ratio of value of the first derivative of the fitted spline and the fitted value for the spline.

The `fit.spline` component is a **list** with components



**x:** the distinct x values in increasing order;  
**y:** the fitted values, with boundary values possibly corrected, and corresponding to x;  
**lev:** leverages, the diagonal values of the smoother matrix (NCSS only);  
**lambda:** the value of lambda (corresponding to spar for NCSS - see [smooth.spline](#));  
**df:** the effective degrees of freedom;  
**npspline.segments:** the number of equally spaced segments used for smoothing method set to PS;  
**uncorrected.fit:** the object returned by [smooth.spline](#) for smoothing method set to NCSS or by `JOPS::psNormal` for PS.

### Author(s)

Chris Brien

### References

Eilers, P.H.C and Marx, B.D. (2021) *Practical smoothing: the joys of P-splines*. Cambridge University Press, Cambridge.  
 Huang, C. (2001) Boundary corrected cubic smoothing splines. *Journal of Statistical Computation and Simulation*, **70**, 107-121.

### See Also

[splitSplines](#), [probeSmoothing](#), [byIndv4Times\\_GRsDiff](#), [smooth.spline](#), [predict.smooth.spline](#), `JOPS`.

### Examples

```

data(exampleData)
fit <- fitSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP", df = 4,
  deriv=c(1,2), suffices.deriv=c("AGRdv","Acc"))
fit <- fitSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP",
  spline.type = "PS", lambda = 0.1, npspline.segments = 10,
  deriv=c(1,2), suffices.deriv=c("AGRdv","Acc"))
fit <- fitSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP", df = 4,
  deriv=c(1), suffices.deriv=c("AGRdv"),
  extra.rate = c(RGR.dv = "RGR"))

```

---

getTimesSubset	<i>Forms a subset of responses in data that contains their values for the nominated times</i>
----------------	---

---

## Description

Forms a subset of each of the responses in data that contains their values for the nominated times in a single column.

## Usage

```
getTimesSubset(data, responses,
               individuals = "Snapshot.ID.Tag", times = "DAP",
               which.times, suffix = NULL, sep.suffix.times = ".",
               include.times = FALSE, include.individuals = FALSE)
```

## Arguments

data	A <a href="#">data.frame</a> containing the column from which the growth rates are to be calculated.
responses	A <a href="#">character</a> giving the names of the columns in data whose values are to be subsetted.
individuals	A <a href="#">character</a> giving the name of the column in data containing an identifier for each individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used to identify the subset and, if a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
which.times	A <a href="#">vector</a> giving the times that are to be selected.
suffix	A <a href="#">character</a> giving the suffix to be appended to responses to form the names of the columns containing the subset.
sep.suffix.times	A <a href="#">character</a> giving the separator to use in appending a suffix for times to a trait. For no separator, set to "".
include.times	A <a href="#">logical</a> indicating whether or not to include the times in the result, the name in the result having the suffix with a separating full appended.
include.individuals	A <a href="#">logical</a> indicating whether or not to include the individuals column in the result.

## Value

A [data.frame](#) containing the subset of responses ordered by as many of the initial columns of data as are required to uniquely identify each row (see [order](#) for more information). The names of the columns for each of the responses and for times in the subset are the concatenation of their names in data and suffix, separated by a full stop.

**Author(s)**

Chris Brien

**Examples**

```
data(exampleData)
SPSALast <- getTimesSubset("sPSA", data = longi.dat, times = "DAP",
                           which.times = c(42), suffix = "last")
```

---

growthPheno-deprecated*Deprecated Functions in the Package growthPheno*

---

**Description**

These functions have been renamed and deprecated in growthPheno:

1. `getDates` -> `getTimesSubset`
2. `anomPlot` -> `plotAnom`
3. `corrPlot` -> `plotCorrmatrix`
4. `imagetimesPlot` -> `plotImagetimes`
5. `longiPlot` -> `plotProfiles`
6. `probeDF` -> `probeSmooths`

**Usage**

```
getDates(...)
anomPlot(...)
corrPlot(...)
imagetimesPlot(...)
longiPlot(...)
probeDF(...)
```

**Arguments**

...                      absorbs arguments passed from the old functions of the style `foo.bar()`.

**Author(s)**

Chris Brien

---

GrowthRates	<i>Calculates growth rates (AGR, PGR, RGRdiff) between pairs of values in a vector</i>
-------------	--

---

### Description

Calculates either the Absolute Growth Rate (AGR), Proportionate Growth Rate (PGR) or Relative Growth Rate (RGR) between pairs of time points, the second of which is lag positions before the first. in x.

### Usage

```
AGRdiff(x, time.diffs, lag=1)
PGR(x, time.diffs, lag=1)
RGRdiff(x, time.diffs, lag=1)
```

### Arguments

x	A <a href="#">numeric</a> from which the growth rates are to be calculated.
time.diffs	a numeric giving the time differences between successive values in x.
lag	A integer specifying, for the second value in the pair to be operated on, the number positions it is ahead of the current value.

### Details

The AGRdiff is calculated as the difference between a pair of values divided by the time.diffs. The PGR is calculated as the ratio of a value to a second value which is lag values ahead of the first in x and the ratio raised to the power of the reciprocal of time.diffs. The RGRdiff is calculated as the log of the PGR and so is equal to the difference between the logarithms of a pair of values divided by the time.diffs. The differences and ratios are obtained using [calcLagged](#) with lag = 1.

### Value

A [numeric](#) containing the growth rates which is the same length as x and in which the first lag values NA.

### Author(s)

Chris Brien

### See Also

[byIndv4Intvl\\_GRsAvg](#), [byIndv4Intvl\\_GRsDiff](#), [byIndv4Times\\_GRsDiff](#), [byIndv4Times\\_SplinesGRs](#), [calcLagged](#)

## Examples

```
data(exampleData)
longi.dat$PSA.AGR <- with(longi.dat, AGRdiff(PSA, time.diffs = DAP.diffs))
```

---

importExcel

---

Imports an Excel imaging file and allows some renaming of variables

---

## Description

Uses readxl to import a sheet of imaging data produced by the Lemna Tec Scanalyzer. Basically, the data consists of imaging data obtained from a set of pots or carts over time. There should be a column, which by default is called Snapshot.ID.Tag, containing a unique identifier for each cart and a column, which by default is labelled Snapshot.Time.Stamp, containing the time of imaging for each observation in a row of the sheet. Also, if startTime is not NULL, calcTimes is called to calculate, or recalculate if already present, timeAfterStart from imageTimes by subtracting a supplied startTime.

Using cameraType, keepCameraType, labsCamerasViews and prefix2suffix, some flexibility is provided for renaming the columns with imaging data. For example, if the column names are prefixed with 'RGB\_SV1', 'RGB\_SV2' or 'RGB\_TV', the 'RGB\_' can be removed and the 'SV1', 'SV2' or 'TV' become suffixes.

## Usage

```
importExcel(file, sheet="raw data", sep = ",",
            cartId = "Snapshot.ID.Tag",
            imageTimes = "Snapshot.Time.Stamp",
            timeAfterStart = "Time.after.Planting..d.",
            cameraType = "RGB", keepCameraType = FALSE,
            labsCamerasViews = NULL, prefix2suffix = TRUE,
            startTime = NULL,
            timeFormat = "%Y-%m-%d %H:%M",
            plotImagetimes = TRUE, ...)
```

## Arguments

- |       |  |
|-------|--|
| file  | A <a href="#">character</a> giving the path and name of the file containing the data.  |
| sheet | A <a href="#">character</a> giving the name of the sheet containing the data, that must include columns whose names are as specified by cartId, which uniquely indexes the carts in the experiment, and imageTimes, which reflects the time of the imaging from which a particular data value was obtained. It is also assumed that a column whose name is specified by timeAfterStart is in the sheet or that it will be calculated from imageTimes using the value of startTime supplied in the function call. |
| sep   | A <a href="#">character</a> giving the separator used in a csv file.   |

cartId	A <b>character</b> giving the name of the column that contains the unique Id for each cart. Note that in importing data into R, spaces and nonalphanumeric characters in names are converted to full stops.
imageTimes	A <b>character</b> giving the name of the column that contains the time that each cart was imaged. Note that in importing data into R, spaces and nonalphanumeric characters in names are converted to full stops.
timeAfterStart	A <b>character</b> giving the name of the column that contains or is to contain the difference between imageTimes and startTime. The function calcTimes is called to calculate the differences. For example, it might contain the number of days after planting. Note that in importing data into R, spaces and nonalphanumeric characters in names are converted to full stops.
cameraType	A <b>character</b> string nominating the abbreviation used for the cameraType. A warning will be given if no variable names include this cameraType.
keepCameraType	A logical specifying whether to retain the cameraType in the variables names. It will be the start of the prefix or suffix and separated from the remainder of the prefix or suffix by an underscore (_).
labsCamerasViews	A named <b>character</b> whose elements are new labels for the camera-view combinations and the name of each element is the old label for the camera-view combination in the data being imported. If labsCamerasViews is NULL, all column names beginning with cameraType are classed as imaging variables and the unique prefixes amongst them determined. If no imaging variables are found then no changes are made. Note that if you want to include a recognisable cameraType in a camera-view label, it should be at the start of the label in labsCamerasViews and separated from the rest of the label by an underscore (_).
prefix2suffix	A logical specifying whether the variables names with prefixed camera-view labels are to have those prefixes transferred to become suffixes. The prefix is assumed to be all the characters up to the first full stop (.) in the variable name and must contain cameraType to be moved. It is generally assumed that the characters up to the first underscore (_) are the camera type and this is removed if keepCameraType is FALSE. If there is no underscore (_), the whole prefix is moved. If labsCamerasViews is NULL, all column names beginning with cameraType are classed as imaging variables and the unique prefixes amongst them determined. If no imaging variables are found then no changes are made.
startTime	A character giving the time of planting, in the POSIXct format timeFormat, to be subtracted from imageTimes in recalculating timeAfterStart. If startTime is NULL then timeAfterStart is not recalculated.
timeFormat	A character giving the POSIXct format of characters containing times, in particular imageTimes and startTime.
plotImagetimes	A logical indicating whether a plot of the imaging times against the recalculated Time.After.Planting..d.. It aids in checking Time.After.Planting..d. and what occurred in imaging the plants.
...	allows for arguments to be passed to plotImagetimes. However, if intervals is passed an error will occur; use timeAfterStart instead.

**Value**

A `data.frame` containing the data.

**Author(s)**

Chris Brien

**See Also**

`as.POSIXct`, `calcTimes`, `plotImagetimes`

**Examples**

```
filename <- system.file("extdata/rawdata.xlsx", package = "growthPheno",
                        mustWork = TRUE)
raw.dat <- importExcel(file = filename,
                      startTime = "2015-02-11 0:00 AM")

camview.labels <- c("SF0", "SL0", "SU0", "TV0")
names(camview.labels) <- c("RGB_Side_Far_0", "RGB_Side_Lower_0",
                          "RGB_Side_Upper_0", "RGB_TV_0")
filename <- system.file("extdata/raw19datarow.csv", package = "growthPheno",
                        mustWork = TRUE)
raw.19.dat <- suppressWarnings(importExcel(file = filename,
                                           cartId = "Snapshot.ID.Tags",
                                           startTime = "06/10/2017 0:00 AM",
                                           timeFormat = "%d/%m/%Y %H:M",
                                           labsCamerasViews = camview.labels,
                                           plotImagetimes = FALSE))
```

---

intervalGRAverage	<i>Calculates the growth rates for a specified time interval by taking weighted averages of growth rates for times within the interval</i>
-------------------	--

---

**Description**

Using previously calculated growth rates over time, calculates the Absolute Growth Rates for a specified interval using the weighted averages of AGRs for each time point in the interval (AGR) and the Relative Growth Rates for a specified interval using the weighted geometric means of RGRs for each time point in the interval (RGR).

**Note: this function is soft deprecated and may be removed in future versions.**

Use `byIndv4Intvl_GRsAvg`.

**Usage**

```
intervalGRAverage(responses, individuals = "Snapshot.ID.Tag",
                  which.rates = c("AGR", "RGR"), suffices.rates=c("AGR", "RGR"),
                  times = "Days", start.time, end.time, suffix.interval,
                  data, sep=".", na.rm=TRUE)
```

## Arguments

responses	A <b>character</b> giving the names of the responses for which there are columns in data that contain the growth rates that are to be averaged. The names of the growth rates should have either AGR or RGR appended to the responses names.
individuals	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
which.rates	A <b>character</b> giving the growth rates that are to be averaged to obtain growth rates for an interval. It should be a combination of one or more of "AGR" and "RGR".
suffices.rates	A <b>character</b> giving the suffices to be appended to response to form the names of the columns containing the calculated the growth rates and in which growth rates are to be stored. Their elements will be matched with those of which.rates.
times	A <b>character</b> giving the name of the column in data containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used in calculating growth rates and, if a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
start.time	A <b>numeric</b> giving the times, in terms of values in times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the start of the interval for which the growth rate is to be calculated.
end.time	A <b>numeric</b> giving the times, in terms of values times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the end of the interval for which the growth rate is to be calculated.
suffix.interval	A <b>character</b> giving the suffix to be appended to response.suffices.rates to form the names of the columns containing the calculated the growth rates.
data	A <b>data.frame</b> containing the columns from which the growth rates are to be calculated.
sep	A <b>character</b> giving the separator to use when the levels of individuals are combined. This is needed to avoid using a <b>character</b> that occurs in a <b>factor</b> to delimit levels when the levels of individuals are combined to identify subsets.
na.rm	A <b>logical</b> indicating whether NA values should be stripped before the calculation of weighted means proceeds.

## Details

The AGR for an interval is calculated as the weighted mean of the AGRs for times within the interval. The RGR is calculated as the weighted geometric mean of the RGRs for times within the interval; in fact the exponential is taken of the weighted means of the logs of the RGRs. The weights are obtained from the times. They are taken as the sum of half the time subintervals before and after each time, except for the end points; the end points are taken to be the subintervals at the start and end of the interval.



**Value**

A `data.frame` with the growth rates. The name of each column is the concatenation of (i) one of responses, (ii) one of AGR, PGR or RGR, or the appropriate element of `suffices.rates`, and (iii) `suffix.interval`, the three components being separated by full stops.

**Author(s)**

Chris Brien

**See Also**

[intervalGRdiff](#), [intervalWUI](#), [splitValueCalculate](#), [getTimesSubset](#), [GrowthRates](#), [splitSplines](#), [splitContGRdiff](#)

**Examples**

```
data(exampleData)
longi.dat <- splitSplines(data = longi.dat,
                          response = "PSA", response.smoothed = "sPSA",
                          x="xDAP",
                          individuals = "Snapshot.ID.Tag",
                          df = 4, deriv=1, suffices.deriv = "AGRdv",
                          extra.rate = c(RGRdv = "RGR"))
sPSA.GR <- intervalGRAverage(data = longi.dat,
                             responses = "sPSA", times = "DAP",
                             which.rates = c("AGR", "RGR"),
                             suffices.rates = c("AGRdv", "RGRdv"),
                             start.time = 31, end.time = 35,
                             suffix.interval = "31to35")
```

---

intervalGRdiff

*Calculates the growth rates for a specified time interval*

---

**Description**

Using the values of the responses, calculates the specified combination of the Absolute Growth Rates using differences (AGR), the Proportionate Growth Rates (PGR) and Relative Growth Rates using log differences (RGR) between two nominated time points.

**Note:** this function is soft deprecated and may be removed in future versions.

Use [byIndv4Intvl\\_GRsDiff](#).

**Usage**

```
intervalGRdiff(responses, individuals = "Snapshot.ID.Tag",
               which.rates = c("AGR", "PGR", "RGR"), suffices.rates=NULL,
               times = "Days", start.time, end.time, suffix.interval,
               data)
```

## Arguments

responses	A <b>character</b> giving the names of the columns in data from which the growth rates are to be calculated.
individuals	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
which.rates	A <b>character</b> giving the growth rates that are to be calculated. It should be a combination of one or more of "AGR", "PGR" and "RGR".
suffices.rates	A <b>character</b> giving the characters to be appended to the names of the responses in constructing the names of the columns containing the calculated growth rates. The order of the suffices in suffices.rates should correspond to the order of the elements of which.rates.
times	A <b>character</b> giving the name of the column in data containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used in calculating growth rates and, if a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
start.time	A <b>numeric</b> giving the times, in terms of values in times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the start of the interval for which the growth rate is to be calculated.
end.time	A <b>numeric</b> giving the times, in terms of values times, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the end of the interval for which the growth rate is to be calculated.
suffix.interval	A <b>character</b> giving the suffix to be appended to response to form the names of the columns containing the calculated the growth rates.
data	A <b>data.frame</b> containing the column from which the growth rates are to be calculated.

## Details

The AGR is calculated as the difference between the values of response at the end.time and start.time divided by the difference between end.time and start.time. The PGR is calculated as the ratio of response at the end.time to that at start.time and the ratio raised to the power of the reciprocal of the difference between end.time and start.time. The RGR is calculated as the log of the PGR and so is equal to the difference between the logarithms of response at the end.time and start.time divided by the difference between end.time and start.time.

## Value

A **data.frame** with the growth rates. The name of each column is the concatenation of (i) one of responses, (ii) one of AGR, PGR or RGR, or the appropriate element of suffices.rates, and (iii) suffix.interval, the three components being separated by full stops.

## Author(s)

Chris Brien

**See Also**

[intervalGRaverage](#), [intervalWUI](#), [getTimesSubset](#), [GrowthRates](#),  
[splitSplines](#), [splitContGRdiff](#)

**Examples**

```
data(exampleData)
sPSA.GR <- intervalGRdiff(responses = "sPSA", times = "DAP",
  which.rates = c("AGR", "RGR"),
  start.time = 31, end.time = 35,
  suffix.interval = "31to35",
  data = longi.dat)
```

---

```
intervalPVA.data.frame
```

*Selects a subset of variables using Principal Variable Analysis (PVA),  
based on the observed values within a specified time interval*

---

**Description**

Principal Variable Analysis (PVA) (Cumming and Wooff, 2007) selects a subset from a set of the variables such that the variables in the subset are as uncorrelated as possible, in an effort to ensure that all aspects of the variation in the data are covered. Here, all observations in a specified time interval are used for calculation the correlations on which the selection is based.

**Usage**

```
## S3 method for class 'data.frame'
intervalPVA(obj, responses, times = "Days", start.time, end.time,
  nvarselect = NULL, p.variance = 1, include = NULL,
  plot = TRUE, ...)
```

**Arguments**

<code>obj</code>	A <a href="#">data.frame</a> containing the columns of variables from which the selection is to be made.
<code>responses</code>	A <a href="#">character</a> giving the names of the columns in data from which the variables are to be selected.
<code>times</code>	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used to identify the subset and, if a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
<code>start.time</code>	A numeric giving the time, in terms of values in times, at which the time interval begins; observations at this time and up to and including <code>end.time</code> will be included.

end.time	A numeric giving the time, in terms of values in times, at the end of the interval; observations after this time will not be included.
nvarselect	A <a href="#">numeric</a> specifying the number of variables to be selected, which includes those listed in include. If nvarselect = 1, as many variables are selected as is need to satisfy p.variance.
p.variance	A <a href="#">numeric</a> specifying the minimum proportion of the variance that the selected variables must account for,
include	A <a href="#">character</a> giving the names of the columns in data for the variables whose selection is mandatory.
plot	A <a href="#">logical</a> indicating whether a plot of the cumulative proportion of the variance explained is to be produced.
...	allows passing of arguments to other functions.

### Details

The variable that is most correlated with the other variables is selected first for inclusion. The partial correlation for each of the remaining variables, given the first selected variable, is calculated and the most correlated of these variables is selects for inclusion next. Then the partial correlations are adjust for the second included variables. This process is repeated until the specified criteria have been satisfied. The possibilities are to:

1. the default (nvarselect = NULL and p.variance = 1) select all variables in increasing order of amount of information they provide;
2. select exactly nvarselect variables;
3. select just enough variables, up to a maximum of nvarselect variables, to explain at least p.variance\*100 per cent of the total variance.

### Value

A [data.frame](#) giving the results of the variable selection. It will contain the columns Variable, Selected, h.partial, Added.Propn and Cumulative.Propn.

### Author(s)

Chris Brien

### References

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

### See Also

[PVA](#), [rcontrib](#)

**Examples**

```

data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)
longi.dat <- within(longi.dat,
  {
    Max.Height <- pmax(Max.Dist.Above.Horizon.Line.SV1,
                      Max.Dist.Above.Horizon.Line.SV2)
    Density <- PSA/Max.Height
    PSA.SV = (PSA.SV1 + PSA.SV2) / 2
    Image.Biomass = PSA.SV * (PSA.TV^0.5)
    Centre.Mass <- (Center.Of.Mass.Y.SV1 + Center.Of.Mass.Y.SV2) / 2
    Compactness.SV = (Compactness.SV1 + Compactness.SV2) / 2
  })
responses <- c("PSA", "PSA.SV", "PSA.TV", "Image.Biomass", "Max.Height", "Centre.Mass",
              "Density", "Compactness.TV", "Compactness.SV")
results <- intervalPVA(longi.dat, responses, times = "DAP",
                      start.time = "31", end.time = "31",
                      p.variance=0.9, plot = FALSE)

```

---

**intervalValueCalculate**

*Calculates a single value that is a function of an individual's values for a response over a specified time interval*

---

**Description**

Splits the values of a response into subsets corresponding individuals and applies a function that calculates a single value from each individual's observations during a specified time interval. It includes the ability to calculate the observation number that is closest to the calculated value of the function and the associated values of a [factor](#) or numeric.

**Note:** this function is soft deprecated and may be removed in future versions.

Use by [Indv4Intvl\\_ValueCalc](#).

**Usage**

```

intervalValueCalculate(response, weights=NULL, individuals = "Snapshot.ID.Tag",
                      FUN = "max", which.obs = FALSE, which.values = NULL,
                      times = "Days", start.time=NULL, end.time=NULL,
                      suffix.interval=NULL, data, sep=".", na.rm=TRUE, ...)

```

**Arguments**

response	A <a href="#">character</a> giving the name of the column in data from which the values of FUN are to be calculated.
weights	A <a href="#">character</a> giving the name of the column in data containing the weights to be supplied as w to FUN.

individuals	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
FUN	A <b>character</b> giving the name of the function that calculates the value for each subset.
which.obs	A <b>logical</b> indicating whether or not to determine the observation number corresponding to the observed value that is closest to the value of the function, in addition to the value of the function itself. That is, FUN need not return an observed value of the response, e.g. quantile.
which.values	A <b>character</b> giving the name of the <b>factor</b> or <b>numeric</b> whose values are associated with the response values and whose value is to be returned for the observation number whose response value corresponds to the observed value closest to the value of the function. That is, FUN need not return an observed value of the response, e.g. quantile. In the case of multiple observed response values satisfying this condition, the value of the which.values vector for the first of these is returned.
times	A <b>character</b> giving the name of the column in data containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used in calculating growth rates and, if a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
start.time	A <b>numeric</b> giving the times, in terms of levels of times.factor, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the start of the interval for which a value is to be calculated. If start.time is NULL, the interval will start with the first observation. In the case of multiple observed response values satisfying this condition, the first is returned.
end.time	A <b>numeric</b> giving the times, in terms of levels of times.factor, that will give a single value for each Snapshot.ID.Tag and that will be taken as the observation at the end of the interval for which a value is to be calculated. If end.time is NULL, the interval will end with the last observation.
suffix.interval	A <b>character</b> giving the suffix to be appended to response to form the name of the column containing the calculated values. If it is NULL then nothing will be appended.
data	A <b>data.frame</b> containing the column from which the function is to be calculated.
na.rm	A <b>logical</b> indicating whether NA values should be stripped before the calculation proceeds.
sep	A <b>character</b> giving the separator to use when the levels of individuals are combined. This is needed to avoid using a <b>character</b> that occurs in a <b>factor</b> to delimit levels when the levels of individuals are combined to identify subsets.
...	allows for arguments to be passed to FUN.

### Value

A **data.frame**, with the same number of rows as there are individuals, containing a column for the individuals and a column with the values of the function for the individuals. It is also possible to determine observation numbers or the values of another column in data for the response

values that are closest to the FUN results, using either or both of `which.obs` and `which.values`. If `which.obs` is TRUE, a column with observation numbers is included in the `data.frame`. If `which.values` is set to the name of a `factor` or a `numeric`, a column containing the levels of that `factor` or the values of that `numeric` is included in the `data.frame`.

The name of the column with the values of the function will be result of concatenating the response, FUN and, if it is not NULL, `suffix.interval`, each separated by a full stop. If `which.obs` is TRUE, the column name for the observations numbers will have `.obs` added after FUN into the column name for the function values; if `which.values` is specified, the column name for these values will have a full stop followed by `which.values` added after FUN into the column name for the function values.

### Author(s)

Chris Brien

### See Also

[intervalGRaverage](#), [intervalGRdiff](#), [intervalWUI](#), [splitValueCalculate](#), [getTimesSubset](#)

### Examples

```
data(exampleData)
sPSA.max <- intervalValueCalculate(response = "sPSA", times = "DAP",
                                   start.time = 31, end.time = 35,
                                   suffix.interval = "31to35",
                                   data = longi.dat)
AGR.max.dat <- intervalValueCalculate(response = "sPSA.AGR", times = "DAP",
                                       FUN="max",
                                       start.time = 31, end.time = 35,
                                       suffix.interval = "31to35",
                                       which.values = "DAP", which.obs = TRUE,
                                       data=longi.dat)
```

---

intervalWUI	<i>Calculates water use indices (WUI) over a specified time interval to a data.frame</i>
-------------	--

---

### Description

Calculates the Water Use Index (WUI) between two time points for a set of responses.

**Note: this function is soft deprecated and may be removed in future versions.**

Use by [Indv4Intvl\\_WaterUse](#).

### Usage

```
intervalWUI(responses, water.use = "Water.Use",
            individuals = "Snapshot.ID.Tag", times = "Days",
            start.time, end.time, suffix.interval = NULL,
            data, include.total.water = FALSE, na.rm = FALSE)
```

### Arguments

<code>responses</code>	A <b>character</b> giving the names of the columns in data from which the growth rates are to be calculated.
<code>water.use</code>	A <b>character</b> giving the names of the column in data which contains the water use values.
<code>individuals</code>	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
<code>times</code>	A <b>character</b> giving the name of the column in data containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used identifying the intervals and, if a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
<code>start.time</code>	A <b>numeric</b> giving the times, in terms of values in <code>times</code> , that will give a single value for each <code>Snapshot.ID.Tag</code> and that will be taken as the observation at the start of the interval for which the WUI is to be calculated.
<code>end.time</code>	A <b>numeric</b> giving the times, in terms of values <code>times</code> , that will give a single value for each <code>Snapshot.ID.Tag</code> and that will be taken as the observation at the end of the interval for which the WUI is to be calculated.
<code>suffix.interval</code>	A <b>character</b> giving the suffix to be appended to response to form the names of the columns containing the calculated the growth rates.
<code>data</code>	A <b>data.frame</b> containing the column from which the growth rates are to be calculated.
<code>include.total.water</code>	A <b>logical</b> indicating whether or not to include a column in the results for the total of <code>water.use</code> for the interval for each individual.
<code>na.rm</code>	A <b>logical</b> indicating whether NA values should be stripped before the calculation proceeds.

### Details

The WUI is calculated as the difference between the values of a response at the `end.time` and `start.time` divided by the sum of the water use after `start.time` until `end.time`. Thus, the water use up to `start.time` is not included.

### Value

A **data.frame** containing the WUIs, the name of each column being the concatenation of one of `responses`, WUI and, if not NULL, `suffix.interval`, the three components being separated by a full stop. If the total water is to be included, the name of the column will be the concatenation of `water.use`, Total and the suffix, each separated by a full stop(' ').

### Author(s)

Chris Brien



**See Also**

[intervalGRaverage](#), [intervalGRdiff](#), [splitValueCalculate](#), [getTimesSubset](#), [GrowthRates](#)

**Examples**

```
data(exampleData)
PSA.WUI <- intervalWUI(response = "PSA", water.use = "WU",
  times = "DAP", start.time = 31, end.time = 35,
  suffix = "31to35",
  data = longi.dat, include.total.water = TRUE)
```

---

is.smooths.frame

*Tests whether an object is of class smooths.frame*


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**Description**

A single-line function that tests whether an object is of class [smooths.frame](#).

**Usage**

```
is.smooths.frame(object)
```

**Arguments**

object            An object to be tested.

**Value**

A logical.

**Author(s)**

Chris Brien

**See Also**

[validSmoothsFrame](#), [as.smooths.frame](#)

**Examples**

```
dat <- read.table(header = TRUE, text = "
Type TunePar TuneVal Tuning Method ID DAP PSA sPSA
NCSS df 4 df-4 direct 045451-C 28 57.446 51.18456
NCSS df 4 df-4 direct 045451-C 30 89.306 87.67343
NCSS df 7 df-7 direct 045451-C 28 57.446 57.01589
NCSS df 7 df-7 direct 045451-C 30 89.306 87.01316
")
dat[1:7] <- lapply(dat[1:7], factor)
dat <- as.smooths.frame(dat, individuals = "ID", times = "DAP")
```

```
is.smooths.frame(dat)
validSmoothsFrame(dat)
```

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longitudinalPrime	<i>Selects a set variables to be retained in a data frame of longitudinal data</i>
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## Description

Forms the prime traits by selecting a subset of the traits in a data.frame of imaging data produced by the Lemna Tec Scanalyzer. The imaging traits to be retained are specified using the `traits` and `labsCamerasViews` arguments. Some imaging traits are divided by 1000 to convert them from pixels to kilopixels. Also added are [factors](#) and explanatory variates that might be of use in an analysis.

## Usage

```
longitudinalPrime(data, cartId = "Snapshot.ID.Tag",
  imageTimes = "Snapshot.Time.Stamp",
  timeAfterStart = "Time.after.Planting..d.",
  PSAColumn = "Projected.Shoot.Area..pixels.",
  idcolumns = c("Genotype.ID", "Treatment.1"),
  traits = list(all = c("Area",
    "Boundary.Points.To.Area.Ratio",
    "Caliper.Length", "Compactness",
    "Convex.Hull.Area"),
    side = c("Center.Of.Mass.Y",
    "Max.Dist.Above.Horizon.Line")),
  labsCamerasViews = list(all = c("SV1", "SV2", "TV"),
    side = c("SV1", "SV2")),
  smarthouse.lev = NULL,
  calcWaterLoss = TRUE, pixelsPERcm)
```

## Arguments

data	<p>A <a href="#">data.frame</a> containing the columns specified by <code>cartId</code>, <code>imageTimes</code>, <code>timeAfterStart</code>, <code>PSAColumn</code> <code>idcolumns</code>, <code>traits</code> and <code>cameras</code> along with the following columns: <code>Smarthouse</code>, <code>Lane</code>, <code>Position</code>, <code>Weight.Before</code>, <code>Weight.After</code>, <code>Water.Amount</code>, <code>Projected.Shoot.Area..pixels</code>.</p> <p>The defaults for the arguments to <code>longitudinalPrime</code> requires a <a href="#">data.frame</a> containing the following columns, although not necessarily in the order given here:</p> <p><code>Smarthouse</code>, <code>Lane</code>, <code>Position</code>, <code>Weight.Before</code>, <code>Weight.After</code>, <code>Water.Amount</code>, <code>Projected.Shoot.Area..pixels</code>, <code>Area.SV1</code>, <code>Area.SV2</code>, <code>Area.TV</code>, <code>Boundary.Points.To.Area.Ratio.SV1</code>, <code>Boundary.Points.To.Area.Ratio.SV2</code>, <code>Boundary.Points.To.Area.Ratio.TV</code>, <code>Caliper.Length.SV1</code>,</p>
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	Caliper.Length.SV2, Caliper.Length.TV, Compactness.SV1, Compactness.SV2, Compactness.TV, Convex.Hull.Area.SV1, Convex.Hull.Area.SV2, Convex.Hull.Area.TV, Center.Of.Mass.Y.SV1, Center.Of.Mass.Y.SV2, Max.Dist.Above.Horizon.Line.SV1, Max.Dist.Above.Horizon.Line.SV2.
cartId	A <a href="#">character</a> giving the name of the column that contains the unique Id for each cart.
imageTimes	A <a href="#">character</a> giving the name of the column that contains the time that each cart was imaged.
timeAfterStart	A <a href="#">character</a> giving the name of the column that contains the time after some nominated starting time e.g. the number of days after planting.
PSAcolumn	A <a href="#">character</a> giving the name of the column that contains the projected shoot area.
idcolumns	A <a href="#">character</a> vector giving the names of the columns that identify differences between the plants or carts e.g. Genotype.ID, Treatment.1, Treatment.2.
traits	A <a href="#">character</a> or a <a href="#">list</a> whose components are <a href="#">characters</a> . Each <a href="#">character</a> gives the names of the columns for imaging traits whose values are required for each of the camera-view combinations given in the corresponding <a href="#">list</a> component of labsCamerasViews. If labsCamerasViews or a component of labsCamerasViews is NULL, then the contents of traits or the corresponding component of traits are merely treated as the names of columns to be retained.
labsCamerasViews	A <a href="#">character</a> or a <a href="#">list</a> whose components are <a href="#">characters</a> . Each <a href="#">character</a> gives the labels of the camera-view combinations for which is required values of each of the imaging traits in the corresponding <a href="#">character</a> of traits. It is assumed that the camera-view labels are appended to the trait names and separated from the trait names by a full stop (.). If labsCamerasViews or a component of labsCamerasViews is NULL, then the contents of the traits or the corresponding component of traits are merely treated as the names of columns to be retained.
smarthouse.lev	A <a href="#">character</a> vector giving the levels to use for the Smarthouse <a href="#">factor</a> . If NULL then the unique values in Smarthouse will be used.
calcWaterLoss	A <a href="#">logical</a> indicating whether to calculate the Water.Loss. If it is FALSE, Water.Before, Water.After and Water.Amount will not be in the returned <a href="#">data.frame</a> . They can be copied across by listing them in a component of traits and set the corresponding component of cameras to NULL.
pixelsPERcm	A <a href="#">numeric</a> giving the number of pixels per cm for the images. <i>No longer used.</i>

## Details

The columns are copied from data, except for those columns in the list under **Value** that have '(calculated)' appended.

**Value**

A `data.frame` containing the columns specified by `cartId`, `imageTimes`, `timeAfterStart`, `idcolumns`, `traits` and `cameras`. The defaults will result in the following columns:

1. Smarthouse: `factor` with levels for the Smarthouse
2. Lane: `factor` for lane number in a smarthouse
3. Position: `factor` for east/west position in a lane
4. Days: `factor` for the number of Days After Planting (DAP)
5. `cartId`: unique code for each cart
6. `imageTimes`: time at which an image was taken in POSIXct format
7. `Reps`: `factor` indexing the replicates for each combination of the `factors` in `idcolumns` (calculated)
8. `xPosn`: numeric for the Positions within a Lane (calculated)
9. `Hour`: hour of the day, to 2 decimal places, at which the image was taken (calculated)
10. `xDays`: numeric for the DAP that is centred by subtracting the mean of the unique days (calculated)
11. `idcolumns`: the columns listed in `idcolumns` that have been converted to `factors`
12. `Weight.Before`: weight of the pot before watering (only if `calcWaterLoss` is TRUE)
13. `Weight.After`: weight of the pot after watering (only if `calcWaterLoss` is TRUE)
14. `Water.Amount`: the weight of the water added (= `Weight.After` - `Weight.Before`) (calculated)
15. `Water.Loss`: the difference between `Weight.Before` for the current imaging and the `Weight.After` for the previous imaging (calculated unless `calcWaterLoss` is FALSE)
16. `Area`: the `Projected.Shoot.Area..pixels.` divided by 1000 (calculated)
17. `Area.SV1`: the `Projected.Shoot.Area` from Side View 1 divided by 1000 (calculated)
18. `Area.SV2`: the `Projected.Shoot.Area` from Side View 2 divided by 1000 (calculated)
19. `Area.TV`: the `Projected.Shoot.Area` from Top View divided by 1000 (calculated)
20. `Boundary.To.Area.Ratio.SV1`
21. `Boundary.To.Area.Ratio.SV2`
22. `Boundary.To.Area.Ratio.TV`
23. `Caliper.Length.SV1`
24. `Caliper.Length.SV2`
25. `Caliper.Length.TV`
26. `Compactness.SV1` from Side View 1
27. `Compactness.SV2` from Side View 2
28. `Compactness.TV`: from Top View
29. `Convex.Hull.Area.SV1`: area of Side View 1 Convex Hull divided by 1000 (calculated)
30. `Convex.Hull.Area.SV2`: area of Side View 2 Convex Hull divided by 1000 (calculated)
31. `Convex.Hull.TV`: `Convex.Hull.Area.TV` divided by 1000 (calculated)
32. `Center.Of.Mass.Y.SV1`: Centre of Mass from Side View 1

33. Center.Of.Mass.Y.SV2: Centre of Mass from Side View 2
34. Max.Distance.Above.Horizon.Line.SV1: the Max.Distance.Above.Horizon.Line.SV1 converted to cm using pixelsPERcm (calculated)
35. Max.Distance.Above.Horizon.Line.SV2: the Max.Distance.Above.Horizon.Line.SV2 converted to cm using pixelsPERcm (calculated)

### Author(s)

Chris Brien

### Examples

```
data(exampleData)
longiPrime.dat <- longitudinalPrime(data=raw.dat, smarthouse.lev=1)

longiPrime.dat <- longitudinalPrime(data=raw.dat, smarthouse.lev=1,
                                   traits = list(a = "Area", c = "Compactness"),
                                   labsCamerasViews = list(all = c("SV1", "SV2", "TV"),
                                                            t = "TV"))

longiPrime.dat <- longitudinalPrime(data=raw.dat, smarthouse.lev=1,
                                   traits = c("Area.SV1", "Area.SV2", "Area.TV",
                                              "Compactness.TV"),
                                   labsCamerasViews = NULL)

longiPrime.dat <- longitudinalPrime(data=raw.dat, smarthouse.lev=1,
                                   calcWaterLoss = FALSE,
                                   traits = list(img = c("Area", "Compactness"),
                                                  H2O = c("Weight.Before", "Weight.After",
                                                         "Water.Amount")),
                                   labsCamerasViews = list(all = c("SV1", "SV2", "TV"),
                                                            H2O = NULL))
```

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plotAnom

*Identifies anomalous individuals and produces profile plots without them and with just them*

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### Description

Uses [byIndv4Intvl\\_ValueCalc](#) and the function [anom](#) to identify anomalous individuals in longitudinal data. The user can elect to print the anomalous individuals, a profile plot without the anomalous individuals and/or a profile plot with only the anomalous individuals. The plots are produced using ggplot. The plot can be faceted so that a grid of plots is produced.

**Usage**

```
plotAnom(data, response="sPSA",
          individuals="Snapshot.ID.Tag",
          times = "DAP", x = NULL,
          breaks.spacing.x = -2, angle.x = 0,
          vertical.line=NULL,
          groupsFactor=NULL, lower=NULL, upper=NULL,
          start.time=NULL, end.time=NULL,
          suffix.interval=NULL,
          columns.retained=c("Snapshot.ID.Tag", "Smarthouse", "Lane",
                             "Position", "Treatment.1", "Genotype.ID"),
          whichPrint=c("anomalous","innerPlot","outerPlot"), na.rm=TRUE, ...)
```

**Arguments**

data	A <a href="#">data.frame</a> containing the data to be tested and plotted.
response	A character specifying the response variable that is to be tested and plotted on the y-axis.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . If not a <a href="#">numeric</a> , it will be converted to a <a href="#">numeric</a> and used to provide the values to be plotted on the x-axis. If a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
x	A <a href="#">character</a> specifying a variable, or a function of variables, to be plotted on the x-axis. If NULL, it will be set to the value of times, which it can be assumed will be converted to a <a href="#">numeric</a> .
breaks.spacing.x	A <a href="#">numeric</a> whose absolute values specifies the distance between major breaks for the x-axis in a sequence beginning with the minimum x value and continuing up to the maximum x value. If it is negative, the breaks that do not have x values in data will be omitted. Minor breaks will be at half major break value or, if these do not correspond to x-values in data when breaks.spacing.x is negative, have a spacing of one. Thus, when breaks.spacing.x is negative, grid lines will only be included for x-values that occur in data. These settings can be overwritten by supplying, in ggplotFuncs, a scale_x_continuous function from ggplot2.
angle.x	A <a href="#">numeric</a> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in ggplotFuncs, a theme function from ggplot2.
vertical.line	A <a href="#">numeric</a> giving position on the x-axis at which a vertical line is to be drawn. If NULL, no line is drawn.
groupsFactor	A <a href="#">factor</a> giving the name of a <a href="#">factor</a> that defines groups of individuals between which the test for anomalous individuals can be varied by setting values

	for one or more of lower, upper, start.time and end.time to be NULL, a single value or a set of values whose number equals the number of levels of groupsFactor. If NULL or only a dingle value is supplied, the test is the same for all individuals.
lower	A <a href="#">numeric</a> such that values in response below it are considered to be anomalous. If NULL, there is no testing for values below the lower bound.
upper	A <a href="#">numeric</a> such that values in response above it are considered to be anomalous. If NULL, there is no testing for values above the upper bound.
start.time	A <a href="#">numeric</a> giving the start of the time interval, in terms of a level of times, during which testing for anomalous values is to occur. If NULL, the interval will start with the first observation.
end.time	A <a href="#">numeric</a> giving the end of the time interval, in terms of a level of times, during which testing for anomalous values is to occur. If NULL, the interval will end with the last observation.
suffix.interval	A <a href="#">character</a> giving the suffix to be appended to response to form the name of the column containing the calculated values. If it is NULL then nothing will be appended.
columns.retained	A <a href="#">character</a> giving the names of the columns in data that are to be retained in the data.frame of anomalous individuals.
whichPrint	A <a href="#">character</a> indicating what is to be printed. If anomalous is included, the columns.retained are printed for the anomalous individuals.
na.rm	A <a href="#">logical</a> indicating whether NA values should be stripped before the testing proceeds.
...	allows for arguments to be passed to <a href="#">plotLongitudinal</a> .

## Value

A [list](#) with three components:

1. data, a data frame resulting from the [merge](#) of data and the [logical](#) identifying whether or not an individual is anomalous;
2. innerPlot, an object of class ggplot storing the profile plot of the individuals that are not anomalous;
3. outerPlot, an object of class ggplot storing the profile plot of only the individuals that are anomalous.

The name of the column indicating anomalous individuals will be result of concatenating the response, [anom](#) and, if it is not NULL, suffix.interval, each separated by a full stop. The ggplot objects can be plotted using print and can be modified by adding ggplot functions before printing. If there are no observations to plot, NULL will be returned for the plot.

## Author(s)

Chris Brien

**See Also**

[anom](#), [byIndv4Intvl\\_ValueCalc](#), [ggplot2](#).

**Examples**

```
data(exampleData)
anomalous <- plotAnom(longi.dat, response="sPSA.AGR",
                      times = "xDAP",
                      lower=2.5, start.time=40,
                      vertical.line=29,
                      breaks.spacing.x = 2,
                      whichPrint=c("innerPlot"),
                      y.title="sPSA AGR")
```

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plotCorrmatrix

*Calculates and plots correlation matrices for a set of responses*

---

**Description**

Having calculated the correlations a heat map indicating the magnitude of the correlations is produced using ggplot. In this heat map, the darker the red in a cell then the closer the correlation is to -1, while the deeper the blue in the cell, then the closer the correlation is to 1. A matrix plot of all pairwise combinations of the variables can be produced. The matrix plot contains a scatter diagram for each pair, as well as the value of the correlation coefficient. The argument `pairs.sets` can be used to restrict the pairs in the matrix plot to those combinations within each set.

**Usage**

```
plotCorrmatrix(data, responses, which.plots = c("heatmap","matrixplot"),
               title = NULL, labels = NULL, labelSize = 4, pairs.sets = NULL,
               show.sig = FALSE, axis.text.size = 20, ggplotFuncs = NULL,
               printPlot = TRUE, ...)
```

**Arguments**

<code>data</code>	A <a href="#">data.frame</a> containing the columns of variables to be correlated.
<code>responses</code>	A <a href="#">character</a> giving the names of the columns in data containing the variables to be correlated.
<code>which.plots</code>	A <a href="#">character</a> specifying the plots of the correlations to be produced. The possibilities are one or both of heatmap and matrixplot.
<code>title</code>	Title for the plots.
<code>labels</code>	A <a href="#">character</a> specifying the labels to be used in the plots. If labels is NULL, responses is used for the labels.
<code>labelSize</code>	A <a href="#">numeric</a> giving the size of the labels in the matrixplot.



<code>pairs.sets</code>	A <b>list</b> each of whose components is a <b>numeric</b> giving the position of the variable names in responses that are to be included in the set. All pairs of variables in this <code>pairs.set</code> will be included in a <code>matrixplot</code> .
<code>show.sig</code>	A <b>logical</b> indicating whether or not to give asterisks on the heatmap indicating the correlations are significantly different from zero.
<code>axis.text.size</code>	A <b>numeric</b> giving the size of the labels on the axes of the heatmap.
<code>ggplotFuncs</code>	A <b>list</b> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied in creating the <code>ggplot</code> object.
<code>printPlot</code>	A <b>logical</b> indicating whether or not to print the plot.
<code>...</code>	allows passing of arguments to other functions; not used at present.

### Details

The correlations and their p-values are produced using `rcorr` from the `Hmisc` package. The heatmap is produced using `ggplot` and the `matrixplot` is produced using `GGally`.

### Value

The heatmap plot, if produced, as an object of class "ggplot", which can be plotted using `print`; otherwise `NULL` is returned.

### Author(s)

Chris Brien

### See Also

`rcorr`, `GGally`, `ggplot`.

### Examples

```
data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)
longi.dat <- within(longi.dat,
  {
    Max.Height <- pmax(Max.Dist.Above.Horizon.Line.SV1,
                      Max.Dist.Above.Horizon.Line.SV2)
    Density <- PSA/Max.Height
    PSA.SV = (PSA.SV1 + PSA.SV2) / 2
    Image.Biomass = PSA.SV * (PSA.TV^0.5)
    Centre.Mass <- (Center.Of.Mass.Y.SV1 + Center.Of.Mass.Y.SV2) / 2
    Compactness.SV = (Compactness.SV1 + Compactness.SV2) / 2
  })
responses <- c("PSA", "PSA.SV", "PSA.TV", "Image.Biomass", "Max.Height", "Centre.Mass",
              "Density", "Compactness.TV", "Compactness.SV")
plotCorrmatrix(longi.dat, responses, pairs.sets=list(c(1:4),c(5:7)))
```

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plotDeviationsBoxes	<i>Produces boxplots of the deviations of the observed values from the smoothed values over values of x.</i>
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## Description

Produces boxplots of the deviations of the observed values from the smoothed values over values of x.

## Usage

```
plotDeviationsBoxes(data, observed, smoothed, x.factor,
                     x.title = NULL, y.titles = NULL,
                     facet.x = ".", facet.y = ".",
                     facet.labeller = NULL,
                     facet.scales = "fixed",
                     angle.x = 0,
                     deviations.plots = "absolute",
                     ggplotFuncs = NULL, printPlot = TRUE, ...)
```

## Arguments

data	A <a href="#">data.frame</a> containing the observed and smoothed values from which the deviations are to be computed.
observed	A character specifying the response variable for which the observed values are supplied.
smoothed	A character specifying the smoothed response variable, corresponding to observed, for which values are supplied.
x.factor	A <a href="#">character</a> giving the <a href="#">factor</a> to be plotted on the x-axis.
x.title	Title for the x-axis. If NULL then set to x.
y.titles	A <a href="#">character</a> giving the titles for the y-axis, one for each plot specified deviations.plots.
facet.x	A <a href="#">data.frame</a> giving the variable to be used to form subsets to be plotted in separate columns of plots. Use "." if a split into columns is not wanted. For which.plots set to methodcompare or dfcompare facet.x.pf is ignored.
facet.y	A <a href="#">data.frame</a> giving the variable to be used to form subsets to be plotted in separate rows of plots. Use "." if a split into columns is not wanted.
facet.labeller	A ggplot function for labelling the facets of a plot produced using the ggplot function. For more information see ggplot.
facet.scales	A <a href="#">character</a> specifying whether the scales are shared across all facets of a plot ("fixed"), or do they vary across rows (the default, "free_x"), columns ("free_y"), or both rows and columns ("free")?
angle.x	A <a href="#">numeric</a> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in ggplotFuncs, a theme function from ggplot2.

deviations.plots	A <a href="#">character</a> specifying whether absolute and/or relative deviations are to be plotted.
ggplotFuncs	A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the <code>list</code> function with a ggplot function call for each element. These functions are applied in creating the ggplot object for plotting.
printPlot	A <a href="#">logical</a> indicating whether or not to print the plots.
...	allows passing of arguments to ggplot.

**Value**

A list whose components are named `absolute` and `relative`; a component will contain an object of class "ggplot" when the plot has been requested using the `deviations.plots` argument and a `NULL` otherwise. The objects can be plotted using `print`.

**Author(s)**

Chris Brien

**See Also**

[plotMedianDeviations](#), [probeSmoothing](#), [ggplot](#).

**Examples**

```
data(exampleData)

plotDeviationsBoxes(longi.dat, observed = "PSA", smoothed = "sPSA",
  x.factor="DAP", facet.x.pf = ".", facet.y= ".", df =5)
```

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plotImagetimes	<i>Plots the position of a time within an interval against the interval for each cart</i>
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**Description**

Uses `ggplot` to produce a plot of the time position within an interval against the interval. For example, one might plot the hour of the day carts are imaged against the days after planting (or some other number of days after an event). A line is produced for each value of `groupVariable` and the colour is varied according to the value of the `colourVariable`. Each Smarthouse is plotted separately. It aids in checking whether delays occurred in imaging the plants.

**Usage**

```
plotImagetimes(data, intervals = "Time.after.Planting..d.", timePositions = "Hour",
  groupVariable = "Snapshot.ID.Tag", colourVariable = "Lane",
  ggplotFuncs = NULL, printPlot = TRUE)
```

**Arguments**

data	A <a href="#">data.frame</a> containing any columns specified by intervals, timePositions, groupVariable and colourVariable.
intervals	A <a href="#">character</a> giving the name of the column in data containing, as a <a href="#">numeric</a> or a <a href="#">factor</a> , the calculated times to be plotted on the x-axis. For example, it could be the days after planting or treatment.
timePositions	A <a href="#">character</a> giving the name of the column in data containing, as a <a href="#">numeric</a> , the value of the time position within an interval (for example, the time of imaging during the day expressed in hours plus a fraction of an hour).
groupVariable	A <a href="#">character</a> giving the name of the column in data containing the variable to be used to group the plotting.
colourVariable	A <a href="#">character</a> giving the name of the column in data containing the variable to be used to colour the plotting.
ggplotFuncs	A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the list function with a ggplot function call for each element. These functions are applied in creating the ggplot object.
printPlot	A <a href="#">logical</a> indicating whether or not to print the plot.

**Value**

An object of class "ggplot", which can be plotted using print.

**Author(s)**

Chris Brien

**See Also**

ggplot, [calcTimes](#).

**Examples**

```
data(exampleData)
library(ggplot2)
longi.dat <- calcTimes(longi.dat, imageTimes = "Snapshot.Time.Stamp",
                      timePositions = "Hour")
plotImagetimes(data = longi.dat, intervals = "DAP", timePositions = "Hour",
               ggplotFuncs=list(scale_colour_gradient(low="grey20", high="black"),
                               geom_line(aes(group=Snapshot.ID.Tag, colour=Lane))))
```

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plotLongitudinal	<i>Produces profile plots of longitudinal data for a set of individuals</i>
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## Description

Produce profile plots of longitudinal data for a response using ggplot. A line is drawn for the data for each individual and the plot can be faceted so that a grid of plots is produced. For each facet a line for the medians over time can be added, along with the value of the outer whiskers (median  $\pm 1.5 * IQR$ ).

## Usage

```
plotLongitudinal(data, x = "xDays+44.5", response = "Area",
                 individuals = "Snapshot.ID.Tag", title = NULL,
                 x.title = "Days", y.title = "Area (kpixels)",
                 facet.x = ".", facet.y = ".",
                 labeller = NULL, colour = "black",
                 colour.column = NULL, colour.values = NULL,
                 alpha = 0.1, addMediansWhiskers = FALSE,
                 xname = "xDays", ggplotFuncs = NULL,
                 printPlot = TRUE)
```

## Arguments

data	A <a href="#">data.frame</a> containing the data to be plotted.
x	A <a href="#">character</a> giving the variable to be plotted on the x-axis.
response	A character specifying the response variable that is to be plotted on the y-axis.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
x.title	Title for the x-axis.
y.title	Title for the y-axis.
title	Title for the plot.
facet.x	A <a href="#">data.frame</a> giving the variable to be used to form subsets to be plotted in separate columns of plots. Use "." if a split into columns is not wanted.
facet.y	A <a href="#">data.frame</a> giving the variable to be used to form subsets to be plotted in separate rows of plots. Use "." if a split into rows is not wanted.
labeller	A ggplot function for labelling the facets of a plot produced using the ggplot function. For more information see ggplot.
colour	A <a href="#">character</a> specifying a single colour to use in drawing the lines for the profiles. If colouring according to the values of a variable is required then use colour.column.
colour.column	A <a href="#">character</a> giving the name of a column in data over whose values the colours of the lines are to be varied. The colours can be specified using colour.values.

<code>colour.values</code>	A <b>character</b> vector specifying the values of the colours to use in drawing the lines for the profiles. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) with the limits of the scale.
<code>alpha</code>	A <b>numeric</b> specifying the degrees of transparency to be used in plotting. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
<code>addMediansWhiskers</code>	A <b>logical</b> indicating whether plots over time of the medians and outer whiskers are to be added to the plot. The outer whiskers are related to the whiskers on a box-and-whisker and are defined as the median plus (and minus) 1.5 times the interquartile range (IQR). Points lying outside the whiskers are considered to be potential outliers.
<code>xname</code>	A <b>character</b> giving the name of the <b>numeric</b> that contains the values of the predictor variable from which x is derived, it being that x may incorporate an expression.
<code>ggplotFuncs</code>	A list, each element of which contains the results of evaluating a ggplot function. It is created by calling the <code>list</code> function with a ggplot function call for each element. These functions are applied in creating the ggplot object.
<code>printPlot</code>	A <b>logical</b> indicating whether or not to print the plot.

**Value**

An object of class "ggplot", which can be plotted using `print`.

**Author(s)**

Chris Brien

**See Also**

`ggplot`, `labeller`.

**Examples**

```
data(exampleData)
plotLongitudinal(data = longi.dat, x = "xDAP", response = "sPSA")

plt <- plotLongitudinal(data = longi.dat, x = "xDAP", response = "sPSA",
  x.title = "DAP", y.title = "sPSA (kpixels)",
  facet.x = "Treatment.1", facet.y = "Smarthouse",
  printPlot=FALSE)
plt <- plt + ggplot2::geom_vline(xintercept=29, linetype="longdash", size=1) +
  ggplot2::scale_x_continuous(breaks=seq(28, 42, by=2)) +
  ggplot2::scale_y_continuous(limits=c(0,750))
print(plt)

plotLongitudinal(data = longi.dat, x="xDAP", response = "sPSA",
  x.title = "DAP", y.title = "sPSA (kpixels)",
```

```

facet.x = "Treatment.1", facet.y = "Smarthouse",
ggplotFuncs = list(ggplot2::geom_vline(xintercept=29,
                                     linetype="longdash",
                                     size=1),
                  ggplot2::scale_x_continuous(breaks=seq(28, 42,
                                                         by=2)),
                  ggplot2::scale_y_continuous(limits=c(0,750)))

```

---

plotMedianDeviations	<i>Calculates and plots the median of the deviations of the smoothed values from the observed values.</i>
----------------------	---

---

## Description

Calculates and plots the median of the deviations of the supplied smoothed values from the supplied observed values for traits and combinations of different smoothing methods and smoothing degrees of freedom, possibly for subsets of [factor](#) combinations. The requisite values can be generated using [probeSmoothing](#) with which.plots set to none. The results of smoothing methods applied externally to growthPheno can be included via the extra.smooths argument. Envelopes of the median value of a trait for each [factor](#) combination can be added.

**Note: this function is soft deprecated and may be removed in future versions.**

Use [plotSmoothsMedianDevns](#).

## Usage

```

plotMedianDeviations(data, response, response.smoothed,
                     x = NULL, xname="xDays",
                     individuals = "Snapshot.ID.Tag",
                     x.title = NULL, y.titles = NULL,
                     facet.x = "Treatment.1", facet.y = "Smarthouse",
                     labeller = NULL,
                     trait.types = c("response", "AGR", "RGR"),
                     propn.types = c(0.1, 0.5, 0.75), propn.note = TRUE,
                     alpha.med.devn = 0.5,
                     smoothing.methods = "direct", df, extra.smooths = NULL,
                     ggplotFuncsMedDevn = NULL, printPlot = TRUE, ...)

```

## Arguments

data	A <a href="#">data.frame</a> containing the observed and smoothed values from which the deviations are to be computed. There should be a column of smoothed values for each combination of smoothing.methods, df and the types specified by trait.types. In addition, there should be a column of values for each element of extra.smooths in combination with the elements of trait.types. Also, there should be a column of observed values for each of the types specified by trait.types
------	--

. The naming of the columns for smoothed traits should follow the convention that a name is made up, in the order specified, of (i) a `response.smoothed`, (ii) the `trait.types` if not just a response trait type, a `smoothing.method` or an `extra.smooths` and, (iii) if a `smoothing.method`, a `df`. Each component should be separated by a period (.).

<code>response</code>	A <b>character</b> specifying the response variable for which the observed values are supplied. Depending on the setting of <code>trait.types</code> , the observed values of related <code>trait.types</code> may also need to be supplied.
<code>response.smoothed</code>	A <b>character</b> specifying the name of the column containing the values of the smoothed response variable, corresponding to <code>response</code> and obtained for the combinations of <code>smoothing.methods</code> and <code>df</code> , usually using smoothing splines. If <code>response.smoothed</code> is <code>NULL</code> , then <code>response.smoothed</code> is set to the <code>response</code> to which <code>.smooth</code> is added. Depending on the setting of <code>trait.types</code> , the smoothed values of related <code>trait.types</code> may also need to be supplied.
<code>x</code>	A <b>character</b> giving the variable to be plotted on the x-axis; it may incorporate an expression. If <code>x</code> is <code>NULL</code> then <code>xname</code> is used.
<code>xname</code>	A <b>character</b> giving the name of the <b>numeric</b> that contains the values from which <code>x</code> is derived, it being that <code>x</code> may incorporate an expression.
<code>individuals</code>	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
<code>x.title</code>	A <b>character</b> giving the title for the x-axis. If <code>NULL</code> then set to <code>xname</code> .
<code>y.titles</code>	A <b>character</b> giving the titles for the y-axis, one for each trait specified by <code>trait.types</code> . If <code>NULL</code> then set to the traits derived for response from <code>trait.types</code> .
<code>facet.x</code>	A <b>data.frame</b> giving the variable to be used to form subsets to be plotted in separate columns of plots. Use "." if a split into columns is not wanted. For which <code>plots</code> set to <code>methodcompare</code> or <code>dfcompare</code> <code>facet.x</code> is ignored.
<code>facet.y</code>	A <b>data.frame</b> giving the variable to be used to form subsets to be plotted in separate rows of plots. Use "." if a split into columns is not wanted.
<code>labeller</code>	A ggplot function for labelling the facets of a plot produced using the ggplot function. For more information see ggplot.
<code>trait.types</code>	A <b>character</b> giving the traits types that are to be plotted. While AGR and RGR are commonly used, the names can be arbitrary, except that <code>response</code> is a special case that indicates that the original response is to be plotted.
<code>propn.types</code>	A <b>numeric</b> giving the proportion of the medians values of each of the <code>trait.types</code> that are to be plotted in the median deviations plots. If set to <code>NULL</code> , the plots of the proportions are omitted.
<code>propn.note</code>	A <b>logical</b> indicating whether a note giving the proportion of the median values plotted in the <code>compare.medians</code> plots.
<code>alpha.med.dev</code>	A <b>numeric</b> specifying the degrees of transparency to be used in plotting a median deviations plot. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
<code>smoothing.methods</code>	A <b>character</b> giving the smoothing method used in producing the <code>response.smoothed</code> and which is to be used in labelling the plot.



<code>df</code>	A <a href="#">numeric</a> specifying the smoothing degrees of freedom used in producing the response. <code>smoothed</code> and which is to be used in labelling the plot.
<code>extra.smooths</code>	A <a href="#">character</a> specifying one or more smoothing.method labels that have been used in naming of columns of smooths of the response obtained by methods other than the smoothing spline methods provided by <code>growthPheno</code> . Depending on the setting of <code>trait.types</code> , the smoothed values of related trait types must also be supplied, with names constructed according to the convention described under <code>data</code> .
<code>ggplotFuncsMedDevn</code>	A <a href="#">list</a> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied in creating the <code>ggplot</code> object.
<code>printPlot</code>	A <a href="#">logical</a> indicating whether or not to print any plots.
<code>...</code>	allows passing of arguments to <a href="#">plotLongitudinal</a> .

### Value

A [list](#) that consists of two components: (i) a component named `plots` that stores a [list](#) of the median deviations plots, one for each `trait.types`; (ii) a component named `med.dev.dat` that stores the [data.frame](#) containing the median deviations that have been plotted. Each plot in the `plots list` is in an object of class "ggplot", which can be plotted using `print`.

### Author(s)

Chris Brien

### See Also

[plotDeviationsBoxes](#), [probeSmoothing](#), `ggplot`.

### Examples

```
data(exampleData)
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", size=1),
             ggplot2::scale_x_continuous(breaks=seq(28, 42, by=2)))
traits <- probeSmoothing(data = longi.dat, xname = "xDAP", times.factor = "DAP",
                        response = "PSA", response.smoothed = "sPSA",
                        df = c(4:7),
                        facet.x = ".", facet.y = ".",
                        which.plots = "none",
                        propn.types = NULL)
med <- plotMedianDeviations(data = traits,
                          response = "PSA", response.smoothed = "sPSA",
                          x="xDAP", xname = "xDAP",
                          df = c(4,7), x.title = "DAP",
                          facet.x = ".", facet.y = ".",
                          trait.types = "response", propn.types = 0.05,
                          ggplotFuncsMedDevn = vline)
```

---

plotProfiles	<i>Produces profile plots of longitudinal data for a set of individuals</i>
--------------	---

---

## Description

Produce profile plots of longitudinal data for a response using ggplot. A line is drawn for the data for each individual and the plot can be faceted so that a grid of plots is produced. For each facet a line for the medians over time can be added, along with the value of the outer whiskers (median  $\pm 1.5 * IQR$ ).

## Usage

```
plotProfiles(data, response = "PSA",
             individuals = "Snapshot.ID.Tag", times = "DAP",
             x = NULL, title = NULL,
             x.title = "DAP", y.title = "PSA (kpixels)",
             facet.x = ".", facet.y = ".",
             labeller = NULL, scales = "fixed",
             breaks.spacing.x = -2, angle.x = 0,
             colour = "black",
             colour.column = NULL, colour.values = NULL,
             alpha = 0.1, addMediansWhiskers = FALSE,
             ggplotFuncs = NULL,
             printPlot = TRUE)
```

## Arguments

data	A <a href="#">data.frame</a> containing the data to be plotted.
response	A character specifying the response variable that is to be plotted on the y-axis.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . If not a <a href="#">numeric</a> , it will be converted to a <a href="#">numeric</a> and used to provide the values to be plotted on the x-axis. If a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
x	A <a href="#">character</a> specifying a variable, or a function of variables, to be plotted on the x-axis. If NULL, it will be set to the value of times, which it can be assumed will be converted to a <a href="#">numeric</a> .
x.title	Title for the x-axis.
y.title	Title for the y-axis.
title	Title for the plot.
facet.x	A <a href="#">data.frame</a> giving the variable to be used to form subsets to be plotted in separate columns of plots. Use "." if a split into columns is not wanted.

facet.y	A <a href="#">data.frame</a> giving the variable to be used to form subsets to be plotted in separate rows of plots. Use "." if a split into rows is not wanted.
labeller	A <a href="#">ggplot</a> function for labelling the facets of a plot produced using the <a href="#">ggplot</a> function. For more information see <a href="#">ggplot</a> .
scales	A <a href="#">character</a> specifying whether the scales are shared across all facets of a plot (the default, "fixed"), or do they vary across rows ("free_x"), columns ("free_y"), or both rows and columns ("free")?
breaks.spacing.x	A <a href="#">numeric</a> whose absolute values specifies the distance between major breaks for the x-axis in a sequence beginning with the minimum x value and continuing up to the maximum x value. If it is negative, the breaks that do not have x values in data will be omitted. Minor breaks will be at half major break value or, if these do not correspond to x-values in data when <code>breaks.spacing.x</code> is negative, have a spacing of one. Thus, when <code>breaks.spacing.x</code> is negative, grid lines will only be included for x-values that occur in data. These settings can be overwritten by supplying, in <code>ggplotFuncs</code> , a <code>scale_x_continuous</code> function from <a href="#">ggplot2</a> .
angle.x	A <a href="#">numeric</a> between 0 and 360 that gives the angle of the x-axis text to the x-axis. It can also be set by supplying, in <code>ggplotFuncs</code> , a theme function from <a href="#">ggplot2</a> .
colour	A <a href="#">character</a> specifying a single colour to use in drawing the lines for the profiles. If colouring according to the values of a variable is required then use <code>colour.column</code> .
colour.column	A <a href="#">character</a> giving the name of a column in data over whose values the colours of the lines are to be varied. The colours can be specified using <code>colour.values</code> .
colour.values	A <a href="#">character</a> vector specifying the values of the colours to use in drawing the lines for the profiles. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) with the limits of the scale.
alpha	A <a href="#">numeric</a> specifying the degrees of transparency to be used in plotting. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
addMediansWhiskers	A <a href="#">logical</a> indicating whether plots over time of the medians and outer whiskers are to be added to the plot. The outer whiskers are related to the whiskers on a box-and-whisker and are defined as the median plus (and minus) 1.5 times the interquartile range (IQR). Points lying outside the whiskers are considered to be potential outliers.
ggplotFuncs	A list, each element of which contains the results of evaluating a <a href="#">ggplot</a> function. It is created by calling the <code>list</code> function with a <a href="#">ggplot</a> function call for each element. These functions are applied in creating the <a href="#">ggplot</a> object.
printPlot	A <a href="#">logical</a> indicating whether or not to print the plot.

## Value

An object of class "ggplot", which can be plotted using `print`.

**Author(s)**

Chris Brien

**See Also**

ggplot, labeller.

**Examples**

```

data(exampleData)
plotProfiles(data = longi.dat, response = "sPSA", times = "DAP")

plt <- plotProfiles(data = longi.dat, response = "sPSA",
                    y.title = "sPSA (kpixels)",
                    facet.x = "Treatment.1", facet.y = "Smarthouse",
                    breaks.spacing.x = 2,
                    printPlot=FALSE)
plt <- plt + ggplot2::geom_vline(xintercept=29, linetype="longdash", linewidth=1) +
  ggplot2::scale_y_continuous(limits=c(0,750))
print(plt)

plotProfiles(data = longi.dat, response = "sPSA", times = "DAP",
             x.title = "DAP", y.title = "sPSA (kpixels)",
             facet.x = "Treatment.1", facet.y = "Smarthouse",
             ggplotFuns = list(ggplot2::geom_vline(xintercept=29,
                                                    linetype="longdash",
                                                    size=1),
                              ggplot2::scale_x_continuous(breaks=seq(28, 42,
                                                                    by=2)),
                              ggplot2::scale_y_continuous(limits=c(0,750))))

```

---

plotSmoothsComparison *Plots several sets of smoothed values for a response, possibly along with growth rates and optionally including the unsmoothed values, as well as deviations boxplots.*

---

**Description**

Plots the smoothed values for an observed response and, optionally, the unsmoothed observed response using [plotProfiles](#). Depending on the setting of `trait.types` (response, AGR or RGR), the computed traits of the Absolute Growth Rates (AGR) and/or the Relative Growth Rates (RGR) are plotted. This function will also calculate and produce, using [plotDeviationsBoxes](#), boxplots of the deviations of the supplied smoothed values from the observed response values for the traits and for combinations of the different smoothing parameters and for subsets of non-smoothing-[factor](#) combinations. The observed and smoothed values are supplied in long format i.e. with the values for each set of smoothing parameters stacked one under the other in the supplied [smooths.frame](#). Such data can be generated using [probeSmooths](#); to prevent [probeSmooths](#) producing the plots, which it does using [plotSmoothsComparison](#), [plotDeviationsBoxes](#) and

`plotSmoothsMedianDevns`, set `which.plots` to `none`. The smoothing parameters include `spline.types`, `df`, `lambdas` and `smoothing.methods` (see `probeSmooths`).

Multiple plots, possibly each having multiple facets, are produced using `ggplot2`. The layout of these plots is controlled via the arguments `plots.by`, `facet.x` and `facet.y`. The basic principle is that the number of levels combinations of the smoothing-parameter `factors` `Type`, `TunePar`, `TuneVal`, `Tuning` (the combination of `TunePar` and `TuneVal`), and `Method` that are included in `plots.by`, `facet.x` and `facet.y` must be the same as those covered by the combinations of the values supplied to `spline.types`, `df`, `lambdas` and `Method` and incorporated into the `smooths.frame` input to `plotSmoothsComparison` via the `data` argument. This ensures that smooths from different parameter sets are not pooled into the same plot. The `factors` other than the smoothing-parameter `factors` can be supplied to the `plots.by` and `facet` arguments.

The following profiles plots can be produced: (i) separate plots of the smoothed traits for each combination of the smoothing parameters (include `Type`, `Tuning` and `Method` in `plots.by`); (ii) as for (i), with the corresponding plot for the unsmoothed trait preceeding the plots for the smoothed trait (also set `include.raw` to `alone`); (iii) profiles plots that compare a smoothed trait for all combinations of the values of the smoothing parameters, arranging the plots side-by-side or one above the other (include `Type`, `Tuning` and `Method` in `facet.x` and/or `facet.y` - to include the unsmoothed trait set `include.raw` to one of `facet.x` or `facet.y`); (iv) as for (iii), except that separate plots are produced for each combination of the levels of the `factors` in `plot.by` and each plot compares the smoothed traits for the smoothing-parameter `factors` included in `facet.x` and/or `facet.y` (set both `plots.by` and one or more of `facet.x` and `facet.y`).

## Usage

```
plotSmoothsComparison(data, response, response.smoothed = NULL,
                      individuals = "Snapshot.ID.Tag", times = "DAP",
                      trait.types = c("response", "AGR", "RGR"),
                      x.title = NULL, y.titles = NULL,
                      profile.plot.args =
                        args4profile_plot(plots.by = NULL,
                                         facet.x = ".", facet.y = ".",
                                         include.raw = "no"),
                      printPlot = TRUE, ...)
```

## Arguments

**data** A `smooths.frame`, such as is produced by `probeSmooths` and that contains the data resulting from smoothing a response over time for a set of individuals, the data being arranged in long format both with respect to the times and the smoothing-parameter values used in the smoothing. That is, each response occupies a single column. The unsmoothed response and the `response.smoothed` are to be plotted for different sets of values for the smoothing parameters. The `smooths.frame` must include the columns `Type`, `TunePar`, `TuneVal`, `Tuning` and `Method`, and the columns nominated using the arguments `individuals`, `times`, `plots.by`, `facet.x`, `facet.y`, `response`, `response.smoothed`, and, if requested, the `AGR` and the `RGR` of the response and `response.smoothed`. The names of the growth rates should be formed from `response` and `response.smoothed` by adding `.AGR` and `.RGR` to both of them.

response	A <a href="#">character</a> specifying the response variable for which the observed values are supplied.
response.smoothed	A <a href="#">character</a> specifying the name of the column containing the values of the smoothed response variable, corresponding to response and obtained for the combinations of smoothing.methods and df, usually using smoothing splines. If response.smoothed is NULL, then response.smoothed is set to the response to which is added the prefix s.
times	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used to provide the values to be plotted on the x-axis. If a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
trait.types	A <a href="#">character</a> giving the trait.types that are to be plotted when which.plots is profiles. Irrespective of the setting of get.rates, the nominated traits are plotted. If all, each of response, AGR and RGR is plotted.
x.title	Title for the x-axis, used for all plots. If NULL then set to times.
y.titles	A <a href="#">character</a> giving the titles for the y-axis, one for each trait specified by trait.types and used for all plots. If NULL, then set to the traits derived for response from trait.types.
profile.plot.args	A named <a href="#">list</a> that is most easily generated using <a href="#">args4profile_plot</a> , it documenting the options available for varying profile plots and boxplots. <i>Note that if <a href="#">args4profile_plot</a> is to be called to change from the default settings given in the default plotSmoothsComparison call and some of those settings are to be retained, then the arguments whose settings are to be retained must also be included in the call to <a href="#">args4profile_plot</a>; be aware that if you call <a href="#">args4profile_plot</a>, then the defaults for this call are those for <a href="#">args4profile_plot</a>, <b>NOT</b> the call to <a href="#">args4profile_plot</a> shown as the default for plotSmoothsComparison.</i>
printPlot	A <a href="#">logical</a> indicating whether or not to print any plots.
...	allows passing of arguments to <a href="#">plotProfiles</a> .

### Value

A multilevel [list](#) that contains the ggplot objects for the plots produced. The first-level list has a component for each trait.types and each of these is a second-level list that contains the trait profile plots and for a trait. It may contain components labelled Unsmoothed, all or for one of the levels of the factors in plots.by; each of these third-level lists contains a ggplot object that can be plotted using print.

### Author(s)

Chris Brien

**See Also**

[traitSmooth](#), [probeSmooths](#), [args4profile\\_plot](#), [plotDeviationsBoxes](#), [plotSmoothsMedianDevns](#), [ggplot2](#).

**Examples**

```
data(exampleData)
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", size=1))
traits <- probeSmooths(data = longi.dat,
  response = "PSA", response.smoothed = "sPSA",
  times = "DAP",
  #only df is changed from the probeSmooth default
  smoothing.args =
    args4smoothing(smoothing.methods = "direct",
      spline.types = "NCSS",
      df = c(4,7), lambdas = NULL),
  which.plots = "none")
plotSmoothsComparison(data = traits,
  response = "PSA", response.smoothed = "sPSA",
  times = "DAP", x.title = "DAP",
  #only facet.x is changed from the probeSmooth default
  profile.plot.args =
    args4profile_plot(plots.by = NULL,
      facet.x = "Tuning", facet.y = ".",
      include.raw = "no",
      ggplotFuncs = vline))
```

---

plotSmoothsDevnBoxplots

*Produces boxplots for several sets of deviations of the smoothed values from a response, possibly along with growth rates.*

---

**Description**

Calculates and produces, using [plotDeviationsBoxes](#), boxplots of the deviations of the supplied smoothed values from the observed response values for the traits and for combinations of the different smoothing parameters and for subsets of non-smoothing-[factor](#) combinations. Which traits are plotted is controlled by `trait.types` and may include the (response and the computed traits of the Absolute Growth Rates (AGR) and/or the Relative Growth Rates (RGR). The observed and smoothed values are supplied in long format i.e. with the values for each set of smoothing parameters stacked one under the other in the supplied [smooths.frame](#). Such data can be generated using [probeSmooths](#).

Multiple plots, possibly each having multiple facets, are produced using [ggplot2](#). The layout of these plots is controlled via the arguments `plots.by`, `facet.x` and `facet.y`. The basic principle is that the number of levels combinations of the smoothing-parameter [factors](#) Type, TunePar, TuneVal, Tuning (the combination of (TunePar and TuneVal), and Method that are included in `plots.by`, `facet.x` and `facet.y` must be the same as those covered by the combinations of the values incorporated into the [smooths.frame](#) input to `plotSmoothsDevnBoxplots` via the data

argument. This ensures that smooths from different parameter sets are not pooled into the same plot. The **factors** other than the smoothing-parameter **factors** can be supplied to the `plots.by` and `facet` arguments.

## Usage

```
plotSmoothsDevnBoxplots(data, response, response.smoothed = NULL,
                        individuals = "Snapshot.ID.Tag", times = "DAP",
                        trait.types = c("response", "AGR", "RGR"),
                        which.plots = "absolute.boxplots",
                        x.title = NULL, y.titles = NULL,
                        devnboxes.plot.args =
                          args4devnboxes_plot(plots.by = NULL,
                                                facet.x = ".", facet.y = "."),
                        printPlot = TRUE, ...)
```

## Arguments

<code>data</code>	A <b>smooths.frame</b> , such as is produced by <b>probeSmooths</b> and that contains the data resulting from smoothing a response over time for a set of individuals, the data being arranged in long format both with respect to the times and the smoothing-parameter values used in the smoothing. That is, each response occupies a single column. The unsmoothed response and the <code>response.smoothed</code> are to be plotted for different sets of values for the smoothing parameters. The <b>smooths.frame</b> must include the columns <code>Type</code> , <code>TunePar</code> , <code>TuneVal</code> , <code>Tuning</code> and <code>Method</code> , and the columns nominated using the arguments <code>individuals</code> , <code>times</code> , <code>plots.by</code> , <code>facet.x</code> , <code>facet.y</code> , <code>response</code> , <code>response.smoothed</code> , and, if requested, the <code>AGR</code> and the <code>RGR</code> of the response and <code>response.smoothed</code> . The names of the growth rates should be formed from <code>response</code> and <code>response.smoothed</code> by adding <code>.AGR</code> and <code>.RGR</code> to both of them.
<code>response</code>	A <b>character</b> specifying the response variable for which the observed values are supplied.
<code>response.smoothed</code>	A <b>character</b> specifying the name of the column containing the values of the smoothed response variable, corresponding to <code>response</code> and obtained for the combinations of <code>smoothing.methods</code> and <code>df</code> , usually using smoothing splines. If <code>response.smoothed</code> is <code>NULL</code> , then <code>response.smoothed</code> is set to the <code>response</code> to which is added the prefix <code>s</code> .
<code>times</code>	A <b>character</b> giving the name of the column in <code>data</code> containing the times at which the data was collected, either as a <b>numeric</b> , <b>factor</b> , or <b>character</b> . It will be used to provide the values to be plotted on the x-axis. If a <b>factor</b> or <b>character</b> , the values should be numerics stored as characters.
<code>individuals</code>	A <b>character</b> giving the name of the <b>factor</b> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. <code>plant</code> , <code>pot</code> , <code>cart</code> , <code>plot</code> or <code>unit</code> ).
<code>trait.types</code>	A <b>character</b> giving the <code>trait.types</code> that are to be plotted. If all, each of <code>response</code> , <code>AGR</code> and <code>RGR</code> is plotted.



which.plots	A <a href="#">logical</a> indicating which plots are to be produced. The options are either none or absolute.deviations and/or relative.deviations. Boxplots of the absolute deviations are specified by absolute.boxplots, the absolute deviations being the values of a trait minus their smoothed values (observed - smoothed). Boxplots of the relative deviations are specified by relative.boxplots, the relative deviations being the absolute deviations divided by the smoothed values of the trait.
x.title	Title for the x-axis, used for all plots. If NULL then set to times.
y.titles	A <a href="#">character</a> giving the titles for the y-axis, one for each trait specified by trait.types and used for all plots. If NULL, then set to the traits derived for response from trait.types.
devnboxes.plot.args	A named <a href="#">list</a> that is most easily generated using <a href="#">args4devnboxes_plot</a> , it documenting the options available for varying the boxplots. <i>Note that if <a href="#">args4devnboxes_plot</a> is to be called to change from the default settings given in the default probeSmooths call and some of those settings are to be retained, then the arguments whose settings are to be retained must also be included in the call to <a href="#">args4devnboxes_plot</a>; be aware that if you call <a href="#">args4devnboxes_plot</a>, then the defaults for this call are those for <a href="#">args4devnboxes_plot</a>, <b>NOT</b> the call to <a href="#">args4devnboxes_plot</a> shown as the default for probeSmooths.</i>
printPlot	A <a href="#">logical</a> indicating whether or not to print any plots.
...	allows passing of arguments to <a href="#">plotProfiles</a> .

### Value

A multilevel [list](#) that contains the ggplot objects for the plots produced. The first-level list has a component for each trait.types and each of these is a second-level list with contains the deviations boxplots for a response. Each plot is in an object of class ggplot, which can be plotted using print.

### Author(s)

Chris Brien

### See Also

[traitSmooth](#), [probeSmooths](#), [args4profile\\_plot](#), [plotDeviationsBoxes](#), [plotSmoothsMedianDevns](#), [ggplot](#).

### Examples

```
data(exampleData)
traits <- probeSmooths(data = longi.dat,
  response = "PSA", response.smoothed = "sPSA",
  times = "DAP",
  #only df is changed from the probeSmooth default
  smoothing.args =
    args4smoothing(smoothing.methods = "direct",
      spline.types = "NCSS",
```



```

propn.note = TRUE,
propn.types = c(0.1, 0.5, 0.75)),
printPlot = TRUE, ...)

```

## Arguments

data	A <a href="#">smooths.frame</a> , such as is produced by <a href="#">probeSmooths</a> and that contains the data resulting from smoothing a response over time for a set of individuals, the data being arranged in long format both with respect to the times and the smoothing-parameter values used in the smoothing. That is, each response occupies a single column. The <a href="#">smooths.frame</a> must include the columns Type, TunePar, TuneVal, Tuning and Method, and the columns nominated using the arguments individuals, times, plots.by, facet.x, facet.y, plots.group, response, response.smoothed, and, if requested, the AGR and the RGR of the response and response.smoothed. The names of the growth rates should be formed from response and response.smoothed by adding .AGR and .RGR to both of them.
response	A <a href="#">character</a> specifying the response variable for which the observed values are supplied. Depending on the setting of trait.types, the observed values of related trait.types may also need to be supplied.
response.smoothed	A <a href="#">character</a> specifying the name of the column containing the values of the smoothed response variable, corresponding to response and obtained for the combinations of smoothing.methods and df, usually using smoothing splines. If response.smoothed is NULL, then response.smoothed is set to the response to which is added the prefix s. Depending on the setting of trait.types, the smoothed values of related trait.types may also need to be supplied.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used to provide the values to be plotted on the x-axis. If a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.
trait.types	A <a href="#">character</a> giving the traits types that are to be plotted. While AGR and RGR are commonly used, the names can be arbitrary, except that response is a special case that indicates that the original response is to be plotted. If all, each of response, AGR and RGR is plotted.
x.title	Title for the x-axis. If NULL then set to times.
y.titles	A <a href="#">character</a> giving the titles for the y-axis, one for each trait specified by trait.types. If NULL, then set to the traits derived for response from trait.types.
meddevn.plot.args	A named <a href="#">list</a> that is most easily generated using <a href="#">args4meddevn_plot</a> , it documenting the options available for varying median deviations plots. <i>Note that if <a href="#">args4meddevn_plot</a> is to be called to change from the default settings given in the default plotSmoothsMedianDevns call and some of those settings are to be</i>

*retained, then the arguments whose settings are to be retained must also be included in the call to `args4meddevn_plot`; be aware that if you call `args4meddevn_plot`, then the defaults for this call are those for `args4meddevn_plot`, **NOT** the call to `args4meddevn_plot` shown as the default for `plotSmoothsMedianDevns`.*

`printPlot` A **logical** indicating whether or not to print the plot.

`...` allows passing of arguments to other functions; not used at present.

## Value

A **list** that consists of two components: (i) a component named `plots` that stores a two-level **list** of the median deviations plots; the first-level **list** has a component for each `trait.types` and each of these **list**(s) is a second-level **list** that contains the set of plots specified by `plots.by` (if `plots.by` is `NULL`, a single plot is stored); (ii) a component named `med.dev.dat` that stores the **data.frame** containing the median deviations that have been plotted. Each plot in the `plots` **list** is in an object of class `ggplot`, which can be plotted using `print`.

## Author(s)

Chris Brien

## See Also

`traitSmooth`, `probeSmooths`, `args4meddevn_plot`, `plotSmoothsComparison`, `plotDeviationsBoxes`, `ggplot`.

## Examples

```
data(exampleData)
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", size=1))
traits <- probeSmooths(data = longi.dat,
  response = "PSA", response.smoothed = "sPSA",
  times = "DAP",
  get.rates = FALSE, trait.types = "response",
  smoothing.args =
    args4smoothing(smoothing.methods = "direct",
      spline.types = "NCSS",
      df = c(4,7), lambdas = NULL),
  which.plots = "none")
med <- plotSmoothsMedianDevns(data = traits,
  response = "PSA", response.smoothed = "sPSA",
  times = "DAP", trait.types = "response",
  meddevn.plot.args =
    args4meddevn_plot(plots.by = NULL,
      plots.group = "Tuning",
      facet.x = ".", facet.y = ".",
      propn.types = 0.02,
      ggplotFuncs = vline))
```

---

prepImageData	<i>Prepares raw imaging data for further processing</i>
---------------	---

---

## Description

Forms the prime traits by selecting a subset of the traits in a data.frame of imaging data produced by the Lemna Tec Scanalyzer. The imaging traits to be retained are specified using the traits and labsCamerasViews arguments. Some imaging traits are divided by 1000 to convert them from pixels to kilopixels. Also added are [factors](#) and explanatory variates that might be of use in an analysis of the data.

## Usage

```
prepImageData(data, cartId = "Snapshot.ID.Tag",
              imageTimes = "Snapshot.Time.Stamp",
              timeAfterStart = "Time.after.Planting..d.",
              PSAColumn = "Projected.Shoot.Area..pixels.",
              idcolumns = c("Genotype.ID", "Treatment.1"),
              traits = list(all = c("Area",
                                   "Boundary.Points.To.Area.Ratio",
                                   "Caliper.Length", "Compactness",
                                   "Convex.Hull.Area"),
                           side = c("Center.Of.Mass.Y",
                                   "Max.Dist.Above.Horizon.Line")),
              labsCamerasViews = list(all = c("SV1", "SV2", "TV"),
                                       side = c("SV1", "SV2")),
              smarthouse.lev = NULL,
              calcWaterUse = TRUE)
```

## Arguments

data	<p>A <a href="#">data.frame</a> containing the columns specified by cartId, imageTimes, timeAfterStart, PSAColumn idcolumns, traits and cameras along with the following columns: Smarthouse, Lane, Position, Weight.Before, Weight.After, Water.Amount, Projected.Shoot.Area..pixels.</p> <p>The defaults for the arguments to prepImageData requires a <a href="#">data.frame</a> containing the following columns, although not necessarily in the order given here: Smarthouse, Lane, Position, Weight.Before, Weight.After, Water.Amount, Projected.Shoot.Area..pixels., Area.SV1, Area.SV2, Area.TV, Boundary.Points.To.Area.Ratio.SV1, Boundary.Points.To.Area.Ratio.SV2, Boundary.Points.To.Area.Ratio.TV, Caliper.Length.SV1, Caliper.Length.SV2, Caliper.Length.TV, Compactness.SV1, Compactness.SV2, Compactness.TV, Convex.Hull.Area.SV1, Convex.Hull.Area.SV2, Convex.Hull.Area.TV, Center.Of.Mass.Y.SV1, Center.Of.Mass.Y.SV2, Max.Dist.Above.Horizon.Line.SV1, Max.Dist.Above.Horizon.Line.SV2.</p>
------	--

cartId	A <b>character</b> giving the name of the column that contains the unique Id for each cart.
imageTimes	A <b>character</b> giving the name of the column that contains the time that each cart was imaged.
timeAfterStart	A <b>character</b> giving the name of the column that contains the time after some nominated starting time e.g. the number of days after planting.
PSAcolumn	A <b>character</b> giving the name of the column that contains the projected shoot area.
idcolumns	A <b>character</b> vector giving the names of the columns that identify differences between the plants or carts e.g. Genotype.ID, Treatment.1, Treatment.2.
traits	A <b>character</b> or a <b>list</b> whose components are <b>characters</b> . Each <b>character</b> gives the names of the columns for imaging traits whose values are required for each of the camera-view combinations given in the corresponding <b>list</b> component of labsCamerasViews. If labsCamerasViews or a component of labsCamerasViews is NULL, then the contents of traits or the corresponding component of traits are merely treated as the names of columns to be retained.
labsCamerasViews	A <b>character</b> or a <b>list</b> whose components are <b>characters</b> . Each <b>character</b> gives the labels of the camera-view combinations for which is required values of each of the imaging traits in the corresponding <b>character</b> of traits. It is assumed that the camera-view labels are appended to the trait names and separated from the trait names by a full stop (.). If labsCamerasViews or a component of labsCamerasViews is NULL, then the contents of the traits or the corresponding component of traits are merely treated as the names of columns to be retained.
smarthouse.lev	A <b>character</b> vector giving the levels to use for the Smarthouse <b>factor</b> . If NULL then the unique values in Smarthouse will be used.
calcWaterUse	A <b>logical</b> indicating whether to calculate the Water.Loss. If it is FALSE, Water.Before, Water.After and Water.Amount will not be in the returned <b>data.frame</b> . They can be copied across by listing them in a component of traits and set the corresponding component of cameras to NULL.

## Details

The columns are copied from data, except for those columns that are calculated from the columns in data; those columns that are calculated have '(calculated)' appended in the list under **Value**.

## Value

A **data.frame** containing the columns specified by cartId, imageTimes, timeAfterStart, idcolumns, traits and cameras. The defaults will result in the following columns:

1. Smarthouse: **factor** with levels for the Smarthouse
2. Lane: **factor** for lane number in a smarthouse
3. Position: **factor** for east/west position in a lane
4. DAP: **factor** for the number of Days After Planting

5. xDAP: numeric for the DAP (calculated)
6. cartId: unique code for each cart
7. imageTimes: time at which an image was taken in POSIXct format
8. Hour: hour of the day, to 2 decimal places, at which the image was taken (calculated)
9. Reps: **factor** indexing the replicates for each combination of the **factors** in idcolumns (calculated)
10. idcolumns: the columns listed in idcolumns that have been converted to **factors**
11. Weight.Before: weight of the pot before watering (only if calcWaterUse is TRUE)
12. Weight.After: weight of the pot after watering (only if calcWaterUse is TRUE)
13. Water.Amount: the weight of the water added (= Water.After - Water.Before) (calculated)
14. WU: the water use calculated as the difference between Weight.Before for the current imaging and the Weight.After for the previous imaging (calculated unless calcWaterUse is FALSE)
15. PSA: the Projected.Shoot.Area..pixels. divided by 1000 (calculated)
16. PSA.SV1: the Projected.Shoot.Area from Side View 1 divided by 1000 (calculated)
17. PSA.SV2: the Projected.Shoot.Area from Side View 2 divided by 1000 (calculated)
18. PSA.TV: the Projected.Shoot.Area from Top View divided by 1000 (calculated)
19. Boundary.To.PSA.Ratio.SV1
20. Boundary.To.PSA.Ratio.SV2
21. Boundary.To.PSA.Ratio.TV
22. Caliper.Length.SV1
23. Caliper.Length.SV2
24. Caliper.Length.TV
25. Compactness.SV1 from Side View 1
26. Compactness.SV2 from Side View 2
27. Compactness.TV: from Top View
28. Convex.Hull.PSA.SV1: area of Side View 1 Convex Hull divided by 1000 (calculated)
29. Convex.Hull.PSA.SV2: area of Side View 2 Convex Hull divided by 1000 (calculated)
30. Convex.Hull.PSA.TV: Convex.Hull.Area.TV divided by 1000 (calculated)
31. Center.Of.Mass.Y.SV1: Centre of Mass from Side View 1
32. Center.Of.Mass.Y.SV2: Centre of Mass from Side View 2
33. Max.Dist.Above.Horizon.Line.SV1: the Max.Dist.Above.Horizon.Line.SV1 divided by 1000 (calculated)
34. Max.Dist.Above.Horizon.Line.SV2: the Max.Dist.Above.Horizon.Line.SV2 divided by 1000 (calculated)

#### Author(s)

Chris Brien

## Examples

```
data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)

longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1,
  traits = list(a = "Area", c = "Compactness"),
  labsCamerasViews = list(all = c("SV1", "SV2", "TV"),
    t = "TV"))

longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1,
  traits = c("Area.SV1", "Area.SV2", "Area.TV",
    "Compactness.TV"),
  labsCamerasViews = NULL)

longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1,
  calcWaterUse = FALSE,
  traits = list(img = c("Area", "Compactness"),
    H2O = c("Weight.Before", "Weight.After",
      "Water.Amount")),
  labsCamerasViews = list(all = c("SV1", "SV2", "TV"),
    H2O = NULL))
```

---

probeSmoothing	<i>Compares, for a set of specified values of df and different smoothing methods, a response and the smooths of it, possibly along with growth rates calculated from the smooths</i>
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---

## Description

Takes a response and, for each individual, uses [splitSplines](#) to smooth its values for each individual using the degrees of freedom values in df. Provided get.rates is TRUE, both the Absolute Growth Rates (AGR) and the Relative Growth Rates (RGR) are calculated for each smooth, either using differences or first derivatives. A combination of the unsmoothed and smoothed values, as well as the AGR and RGR, can be plotted for each value in smoothing methods in combination with df. Note that the arguments that modify the plots apply to all plots that are produced. The handling of missing values is controlled via na.x.action and na.y.action

**Note: this function is soft deprecated and may be removed in future versions.**

Use [probeSmooths](#).

## Usage

```
probeSmoothing(data, response = "Area", response.smoothed = NULL,
  x = NULL, xname="xDays",
  times.factor = "Days", individuals="Snapshot.ID.Tag",
  na.x.action="exclude", na.y.action = "exclude",
  df, smoothing.methods = "direct", correctBoundaries = FALSE,
  get.rates = TRUE, rates.method="differences",
  facet.x = "Treatment.1", facet.y = "Smarthouse",
```



```

labeller = NULL, x.title = NULL,
colour = "black", colour.column=NULL,
colour.values=NULL, alpha = 0.1,
trait.types = c("response", "AGR", "RGR"),
propn.types = c(0.1, 0.5, 0.75), propn.note = TRUE,
which.plots = "smoothedonly",
deviations.plots = "none", alpha.med.devn = 0.5,
ggplotFuncs = NULL, ggplotFuncsMedDevn = NULL,
...)

```

## Arguments

data	A <a href="#">data.frame</a> containing the data.
response	A character specifying the response variable to be supplied to <a href="#">smooth.spline</a> and that is to be plotted on the y-axis.
response.smoothed	A <a href="#">character</a> specifying the name of the column containing the values of the smoothed response variable, corresponding to response. If response.smoothed is NULL, then response.smoothed is set to the response to which .smooth is added.
x	A <a href="#">character</a> giving the variable to be plotted on the x-axis; it may incorporate an expression. If x is NULL then xname is used.
xname	A <a href="#">character</a> giving the name of the <a href="#">numeric</a> that contains the values of the predictor variable to be supplied to <a href="#">smooth.spline</a> and from which x is derived.
times.factor	A <a href="#">character</a> giving the name of the column in data containing the <a href="#">factor</a> for times at which the data was collected. Its levels will be used in calculating growth rates and should be numeric values stored as characters.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
na.x.action	A character string that specifies the action to be taken when values of x are NA. The possible values are fail, exclude or omit. For exclude and omit, predictions and derivatives will only be obtained for nonmissing values of x. The difference between these two codes is that for exclude the returned data.frame will have as many rows as data, the missing values have been incorporated.
na.y.action	A character string that specifies the action to be taken when values of y, or the response, are NA. The possible values are fail, exclude, omit, allx, trimx, ltrimx or rtrimx. For all options, except fail, missing values in y will be removed before smoothing. For exclude and omit, predictions and derivatives will be obtained only for nonmissing values of x that do not have missing y values. Again, the difference between these two is that, only for exclude will the missing values be incorporated into the returned data.frame. For allx, predictions and derivatives will be obtained for all nonmissing x. For trimx, they will be obtained for all nonmissing x between the first and last nonmissing y values that have been ordered for x; for ltrimx and utrimx either the lower or upper missing y values, respectively, are trimmed.

<code>df</code>	A <b>numeric</b> specifying the set of degrees of freedom to be probed.
<code>smoothing.methods</code>	A <b>character</b> giving the smoothing method to use. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response and then back-transforming by taking the exponential of the fitted values.
<code>correctBoundaries</code>	A <b>logical</b> indicating whether the fitted spline values are to have the method of Huang (2001) applied to them to correct for estimation bias at the end-points. Note that <code>spline.type</code> must be <code>NCSS</code> and <code>lambda</code> and <code>deriv</code> must be <code>NULL</code> for <code>correctBoundaries</code> to be set to <code>TRUE</code> .
<code>get.rates</code>	A <b>logical</b> specifying whether or not the growth rates (AGR and RGR) are to be computed and stored.
<code>rates.method</code>	A <b>character</b> specifying the method to use in calculating the growth rates. The two possibilities are "differences" and "derivates".
<code>facet.x</code>	A <b>data.frame</b> giving the variable to be used to form subsets to be plotted in separate columns of plots. Use "." if a split into columns is not wanted. For which <code>plots</code> set to <code>methodscompare</code> or <code>dfcompare</code> , <code>facet.x</code> is ignored.
<code>facet.y</code>	A <b>data.frame</b> giving the variable to be used to form subsets to be plotted in separate rows of plots. Use "." if a split into columns is not wanted.
<code>labeller</code>	A <code>ggplot</code> function for labelling the facets of a plot produced using the <code>ggplot</code> function. For more information see <code>ggplot</code> .
<code>x.title</code>	Title for the x-axis. If <code>NULL</code> then set to <code>times.factor</code> .
<code>colour</code>	A <b>character</b> specifying a single colour to use in drawing the lines for the profiles. If colouring according to the values of a variable is required then use <code>colour.column</code> .
<code>colour.column</code>	A <b>character</b> giving the name of a column in data over whose values the colours of the lines are to be varied. The colours can be specified using <code>colour.values</code> .
<code>colour.values</code>	A <b>character</b> vector specifying the values of the colours to use in drawing the lines for the profiles. If this is a named vector, then the values will be matched based on the names. If unnamed, values will be matched in order (usually alphabetical) with the limits of the scale.
<code>alpha</code>	A <b>numeric</b> specifying the degrees of transparency to be used in plotting. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
<code>trait.types</code>	A <b>character</b> giving the <code>trait.types</code> that are to be produced, and potentially plotted. One of more of response, AGR and RGR. If all, all three traits are produced.
<code>propn.types</code>	A <b>numeric</b> giving the proportion of the median values of each of the <code>trait.types</code> that are to be plotted in the <code>compare.medians</code> plots of the deviations of the observed values from the smoothed values. If set to <code>NULL</code> , the plots of the proportions of the median values of the traits are omitted.
<code>propn.note</code>	A <b>logical</b> indicating whether a note giving the proportion of the median values plotted in the <code>compare.medians</code> plots.

<code>which.plots</code>	A <a href="#">character</a> giving the plots that are to be produced. If none, no plots are produced. If <code>smoothedonly</code> , plots of the smoothed traits are plotted. If <code>bothseparately</code> , plots of the unsmoothed trait followed by the smoothed traits are produced for each trait. If <code>methodscompare</code> , a combined plot of the smoothed traits for each <code>smoothing.methods</code> is produced, for each value of <code>df</code> . If <code>methods+rawcompare</code> , the unsmoothed trait is added to the combined plot. If <code>dfcompare</code> , a combined plot of the smoothed trait for each <code>df</code> is produced, for each <code>smoothing.methods</code> . If <code>df+rawcompare</code> , the unsmoothed trait is added to the combined plot.
<code>deviations.plots</code>	A <a href="#">character</a> is either none or any combination of <code>absolute.boxplots</code> , <code>relative.boxplots</code> and <code>compare.medians</code> . If none, no plots are produced. Boxplots of the absolute and relative deviations are specified by <code>absolute.boxplots</code> and <code>relative.boxplots</code> . The absolute deviations are the values of a trait minus their smoothed values (observed - smoothed); the relative deviations are the absolute deviations divided by the smoothed values of the trait. The option <code>compare.medians</code> results in a plot that compares the medians of the deviations over the <code>times.factor</code> for each combination of the <code>smoothing.methods</code> and the <code>df</code> . The argument <code>trait.types</code> controls the traits for which boxplots are produced.
<code>alpha.med.devn</code>	A <a href="#">numeric</a> specifying the degrees of transparency to be used in plotting a median deviations plot. It is a ratio in which the denominator specifies the number of points (or lines) that must be overplotted to give a solid cover.
<code>ggplotFuncs</code>	A <a href="#">list</a> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. These functions are applied to all three plots produced.
<code>ggplotFuncsMedDevn</code>	A <a href="#">list</a> , each element of which contains the results of evaluating a <code>ggplot</code> function. It is created by calling the <code>list</code> function with a <code>ggplot</code> function call for each element. Note that these functions are applied to the <code>compare.median</code> deviations plots only.
<code>...</code>	allows passing of arguments to <a href="#">plotLongitudinal</a> .

### Value

A [data.frame](#) containing `individuals`, `times.factor`, `facet.x`, `facet.y`, `xname`, `response`, and, for each `df`, the smoothed response, the AGR and the RGR. It is returned invisibly. The names of the new data are constructed by joining elements separated by full stops (.). In all cases, the last element is the value of `df`. For the smoothed response, the other elements are `response` and `"smooth"`; for AGR and RGR, the other elements are the name of the smoothed response and either `"AGR"` or `"RGR"`.

### Author(s)

Chris Brien

### See Also

[splitSplines](#), [splitContGRdiff](#), [smooth.spline](#), [ggplot](#).

## Examples

```
data(exampleData)
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", size=1),
             ggplot2::scale_x_continuous(breaks=seq(28, 42, by=2)))
probeSmoothing(data = longi.dat, response = "PSA", df = c(4,7),
               xname = "xDAP", times = "DAP",
               ggplotFncs=vline)
```

---

probeSmooths

*For a response in a data.frame in long format, computes and compares, for sets of smoothing parameters, smooths of the response, possibly along with growth rates calculated from the smooths.*

---

## Description

Takes an observed response and, for each individual, uses `byIndv4Times_SplinesGRs` to smooth its values employing the smoothing parameters specified by (i) `spline.types`, (ii) the tuning parameters, being the degrees of freedom values in `df` or the smoothing penalties in `lambdas`, and (iii) the `smoothing.methods`. The values of these, and other, smoothing arguments are set using the helper function [args4smoothing](#).

Provided `get.rates` is TRUE or includes raw and/or smoothed and depending on the setting of `trait.types`, the Absolute Growth Rates (AGR) and/or the Relative Growth Rates (RGR) are calculated for each individual from the unsmoothed, observed response and from the smooths of the response, using either differences or first derivatives, as specified by `rates.method`.

Generally, profile plots for the traits (a response, an AGR or an RGR) specified in `traits.types` are produced if `which.plots` is `profiles`; if `which.plots` specifies one or more deviations plots, then those deviations plots will also be produced, these being based on the unsmoothed data from which the smoothed data has been subtracted. The layout of the plots is controlled via combinations of one or more of the smoothing-parameter [factors](#) `Type`, `TunePar`, `TuneVal`, `Tuning` (the combination of `TunePar` and `TuneVal`) and `Method`, as well as other [factors](#) associated with the data. The [factors](#) that are to be used for the profile plots are supplied via the argument `profile.plot.args` using the helper function [args4profile\\_plot](#) and for the and deviations boxplots using the helper function [args4devnboxes\\_plot](#). These helper functions set `plots.by`, `facet.x`, and `facet.y`. For the plots of the medians of the deviations, the [factors](#) are supplied via the argument `meddevn.plot.args` using the helper function [args4meddevn\\_plot](#) to set `plots.by`, `facet.x`, `facet.y` and `plots.group`. Here, the basic principle is that the number of levels combinations of the smoothing-parameter [factors](#) included in the set of plots and facets arguments to one of these helper functions must be the same as those covered by the combinations of the values supplied to `spline.types`, `df`, `lambdas` and `smoothing.methods` and incorporated into the [smooths.frame](#), such as is returned by `probeSmooths`. This ensures that smooths from different parameter sets are not pooled together in a single plot. It is also possible to include [factors](#) that are not smoothing-parameter [factors](#) in the plots and facets arguments.

The following profiles plots can be produced using [args4profile\\_plot](#): (i) separate plots of the smoothed traits for each combination of the smoothing parameters (include `Type`, `Tuning` and `Method` in `plots.by`); (ii) as for (i), with the corresponding plot for the unsmoothed trait preceeding the plots for the smoothed trait (also set `include.raw` to `alone`); (iii) profiles plots that

compare a smoothed trait for all combinations of the values of the smoothing parameters, arranging the plots side-by-side or one above the other (include Type, Tuning and Method in facet.x and/or facet.y - to include the unsmoothed trait set include.raw to one of facet.x or facet.y; (iv) as for (iii), except that separate plots are produced for each combination of the levels of the **factors** in plot.by and each plot compares the smoothed traits for the smoothing-parameter **factors** included in facet.x and/or facet.y (set both plots.by and one or more of facet.x and facet.y).

Deviation plots that can be produced are the absolute and relative deviations boxplots and plots of medians deviations (see which.plots).

The handling of missing values is controlled via na.x.action and na.y.action supplied to the helper function [args4smoothing](#).

The probeSmooths arguments are grouped according to function in the following order:

1. **Data description arguments:** data, response, response.smoothed, individuals, times, keep.columns, trait.types, get.rates, rates.method, ntimes2span.
2. **Smoothing arguments:** smoothing.args (see [args4smoothing](#)).
3. **General plot control:** x.title, y.titles, facet.labeller, which.plots.
4. **Profile plots (pf) features:** profile.plot.args (see [args4profile\\_plot](#))
5. **Median-deviations (med) plots features:** meddevn.plot.args (see [args4meddevn\\_plot](#))
6. **Deviations boxplots (box) features:** devnboxes.plot.args (see [args4devnboxes\\_plot](#))

## Usage

```
probeSmooths(data, response = "PSA", response.smoothed = NULL,
  individuals="Snapshot.ID.Tag", times = "DAP",
  keep.columns = NULL,
  get.rates = TRUE,
  rates.method="differences", ntimes2span = NULL,
  trait.types = c("response", "AGR", "RGR"),
  smoothing.args =
    args4smoothing(smoothing.methods = "direct",
      spline.types = "NCSS",
      df = NULL, lambdas = NULL),
  x.title = NULL, y.titles = NULL,
  which.plots = "profiles",
  profile.plot.args =
    args4profile_plot(plots.by = NULL,
      facet.x = ".", facet.y = ".",
      include.raw = "no"),
  meddevn.plot.args =
    args4meddevn_plot(plots.by = NULL, plots.group = NULL,
      facet.x = ".", facet.y = ".",
      propn.note = TRUE,
      propn.types = c(0.1, 0.5, 0.75)),
  devnboxes.plot.args =
    args4devnboxes_plot(plots.by = NULL,
      facet.x = ".", facet.y = ".",
      which.plots = "none"),
  ...)
```

**Arguments**

data	A <code>data.frame</code> containing the data or a <code>smooths.frame</code> as is produced by <code>probeSmooths</code> . If data is not a <code>smooths.frame</code> , then smoothing will be performed. If data is a <code>smooths.frame</code> , then the plotting and selection of smooths will be performed as specified by <code>smoothing.args</code> and <code>which.plots</code> .
response	A <code>character</code> specifying the response variable to be supplied to <code>smoothSpline</code> and that is to be plotted on the y-axis.
response.smoothed	A <code>character</code> specifying the name of the column containing the values of the smoothed response variable, corresponding to response. If <code>response.smoothed</code> is NULL, then <code>response.smoothed</code> is set to the response to which is added the prefix <code>s</code> .
individuals	A <code>character</code> giving the name of the <code>factor</code> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <code>character</code> giving the name of the column in data containing the times at which the data was collected, either as a <code>numeric</code> , <code>factor</code> , or <code>character</code> . It will be used as the values of the predictor variable to be supplied to <code>smooth.spline</code> and to be plotted on the x-axis. If a <code>factor</code> or <code>character</code> , the values should be numerics stored as characters.
keep.columns	A <code>character</code> vector giving the names of columns from data that are to be included in the <code>smooths.frame</code> that will be returned. Its main use is when no plots are being produced by <code>probeSmooths</code> , but there are columns in the supplied <code>data.frame</code> that are likely to be needed for the plots and facets arguments when producing plots subsequently.
get.rates	A <code>logical</code> or a <code>character</code> specifying which of the response and the <code>response.smoothed</code> are to have growth rates (AGR and/or RGR) computed and stored. If set to TRUE or <code>c("raw", "smoothed")</code> , growth rates will be obtained for both. Setting to only one of raw or smoothed, results in the growth rates for either the response or the <code>response.smoothed</code> being computed. If set to none or FALSE, no growth rates are computed. Which growth rates are computed can be changed using the arguments <code>traits.types</code> and the method used for computing them for the <code>response.smooth</code> by <code>rates.method</code> . The growth rates for the response can only be computed by differencing.
rates.method	A <code>character</code> specifying the method to use in calculating the growth rates for <code>response.smoothed</code> . The two possibilities are "differences" and "derivatives".
ntimes2span	A <code>numeric</code> giving the number of values in times to span in calculating growth rates by differencing. For <code>ntimes2span</code> set to NULL, if <code>rates.method</code> is set to differences then <code>ntimes2span</code> is set to 2; if <code>rates.method</code> is set to derivatives then <code>ntimes2span</code> is set to 3. Note that when <code>get.rates</code> includes raw or is TRUE, the growth rates for the unsmoothed response must be calculated by differencing, even if the growth rates for the smoothed response are computed using derivatives. When differencing, each growth rate is calculated as the difference in the values of one of the responses for pairs of times values that are spanned by <code>ntimes2span</code> times values divided by the difference between this pair of times values. For <code>ntimes2span</code> set to 2, a growth rate is the difference

between consecutive pairs of values of one of the responses divided by the difference between consecutive pairs of times values.

trait.types	A <a href="#">character</a> giving the trait.types that are to be plotted. If growth rates are included in trait.types, then they will be computed for either the response and/or the response.smoothed, depending on the setting of get.rates. Any growth rates included in trait.types for the response that are available in data, but have not been specified for computation in get.rates, will be retained in the returned smooths.frame. If all, the response.smoothed, its AGR and RGR, will be plotted. The response, and its AGR and RGR, will be plotted as the plotting options require it.
smoothing.args	A <a href="#">list</a> that is most easily generated using <a href="#">args4smoothing</a> , it documenting the options available for smoothing the data. It gives the settings of smoothing.methods, spline.types, df, lambdas, smoothing.segments, npspline.segments, na.x.action, na.y.action, external.smooths, and correctBoundaries, to be used in smoothing the response or in selecting a subset of the smooths in data, depending on whether data is a <a href="#">data.frame</a> or a <a href="#">smooths.frame</a> , respectively. Set smoothing.args to NULL if data is a <a href="#">smooths.frame</a> and only plotting or extraction of a chosen smooth is required.
x.title	Title for the x-axis, used for all plots. If NULL then set to times.
y.titles	A <a href="#">character</a> giving the titles for the y-axis, one for each trait specified by trait.types and used for all plots. If NULL then set to the traits derived for response from trait.types.
which.plots	<p>A <a href="#">logical</a> indicating which plots are to be produced. The options are either none or some combination of profiles, absolute.boxplots, relative.boxplots and medians.deviations. The various profiles plots that can be produced are described in the introduction to this function.</p> <p>Boxplots of the absolute deviations are specified by absolute.boxplots, the absolute deviations being the values of a trait minus their smoothed values (observed - smoothed). Boxplots of the relative deviations are specified by relative.boxplots, the relative deviations being the absolute deviations divided by the smoothed values of the trait.</p> <p>The option medians.deviations results in a plot that compares the medians of the absolute deviations over the values of times for each combination of the smoothing-parameter values. The arguments to probeSmooths that apply to medians.deviations plots have the suffix med.</p>
profile.plot.args	A named <a href="#">list</a> that is most easily generated using <a href="#">args4profile_plot</a> , it documenting the options available for varying profile plots and boxplots. <i>Note that if <a href="#">args4profile_plot</a> is to be called to change from the default settings given in the default probeSmooths call and some of those settings are to be retained, then the arguments whose settings are to be retained must also be included in the call to <a href="#">args4profile_plot</a>; be aware that if you call <a href="#">args4profile_plot</a>, then the defaults for this call are those for <a href="#">args4profile_plot</a>, <b>NOT</b> the call to <a href="#">args4profile_plot</a> shown as the default for probeSmooths.</i>
meddevn.plot.args	A named <a href="#">list</a> that is most easily generated using <a href="#">args4meddevn_plot</a> , it documenting the options available for varying median deviations plots. <i>Note that</i>



*if `args4meddevn_plot` is to be called to change from the default settings given in the default `probeSmooths` call and some of those settings are to be retained, then the arguments whose settings are to be retained must also be included in the call to `args4meddevn_plot`; be aware that if you call `args4meddevn_plot`, then the defaults for this call are those for `args4meddevn_plot`, **NOT** the call to `args4meddevn_plot` shown as the default for `probeSmooths`.*

`devnboxes.plot.args`

A named `list` that is most easily generated using `args4devnboxes_plot`, it documenting the options available for varying the boxplots. *Note that if `args4devnboxes_plot` is to be called to change from the default settings given in the default `probeSmooths` call and some of those settings are to be retained, then the arguments whose settings are to be retained must also be included in the call to `args4devnboxes_plot`; be aware that if you call `args4devnboxes_plot`, then the defaults for this call are those for `args4devnboxes_plot`, **NOT** the call to `args4devnboxes_plot` shown as the default for `probeSmooths`.*

...

allows passing of arguments to `plotProfiles`.

## Value

A `smooths.frame` that contains the unsmoothed and smoothed data in long format. That is, all the values for either an unsmoothed or a smoothed trait are in a single column. The smooths for a trait for the different combinations of the smoothing parameters are placed in rows one below the other. The columns that are included in the `smooths.frame` are `Type`, `TunePar`, `TuneVal`, `Tuning` and `Method`, as well as those specified by `individuals`, `times`, `response`, and `response.smoothed`. and any included in the `keep.columns`, `plots` and `facet` arguments. If `trait.types` includes `AGR` or `RGR`, then the included growth rate(s) of the response and `response.smoothed` must be present, unless `get.rates` is `TRUE` or includes `raw` and/or `smoothed`. In this case, the growth rates specified by `trait.types` will be calculated for the responses nominated by `get.rates` and the differences between the times used in calculating the rates will be computed and added. Then, the names of the growth rates are formed from `response` and `response.smoothed` by appending `.AGR` and `.RGR` as appropriate; the name of the column with the times differences will be formed by appending `.diffs` to the value of `times`. The external `smooths` will also be included. A `smooths.frame` has the attributes described in `smooths.frame`.

Columns in the supplied `data.frame` that have not been used in `probeSmooths` will not be included in the returned `smooths.frame`. If they might be needed subsequently, such as when extra plots are produced, they can be included in the `smooths.frame` by listing them in a `character` vector for the `keep.columns` argument.

The `smooths.frame` is returned invisibly.

## Author(s)

Chris Brien

## See Also

`args4smoothing`, `args4meddevn_plot`, `args4profile_plot`, `traitSmooth`, `smoothSpline`, `byIndv4Times_SplinesGRs`, `byIndv4Times_GRsDiff`, `smooth.spline`, `psNormal`, `plotSmoothsComparison`, `plotSmoothsMedianDevns`, `ggplot`.



## Examples

```

data(exampleData)
longi.dat <- longi.dat[1:140,] #reduce to a smaller data set
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", linewidth=1))
yfacets <- c("Smarthouse", "Treatment.1")
probeSmooths(data = longi.dat,
  response = "PSA", response.smoothed = "sPSA",
  individuals = "Snapshot.ID.Tag", times = "DAP",
  smoothing.args =
    args4smoothing(df = c(4,7),
      lambda = list(PS = c(0.316,10))),
  profile.plot.args =
    args4profile_plot(plots.by = NULL,
      facet.x = "Tuning",
      facet.y = c("Smarthouse", "Treatment.1"),
      include.raw = "no",
      alpha = 0.4,
      colour.column = "Method",
      colour.values = c("orange", "olivedrab"),
      ggplotFncs = vline))

#An example that supplies three smoothing schemes to be compared
data(tomato.dat)
probeSmooths(data = tomato.dat,
  response = "PSA", response.smoothed = "sPSA",
  times = "DAP",
  smoothing.args =
    args4smoothing(spline.types = c("N", "NCS", "P"),
      df = c(4, 6, NA),
      lambdas = c(NA, NA, 1),
      smoothing.methods = c("dir", "log", "log"),
      combinations = "parallel"),
  which.plots = "medians.deviations",
  meddevn.plot.args =
    args4meddevn_plot(plots.by = NULL,
      plots.group = c("Type", "Tuning", "Method"),
      facet.x = ".", facet.y = ".",
      propn.note = FALSE, propn.types = NULL))

```

## Description

Principal Variable Analysis (PVA) (Cumming and Wooff, 2007) selects a subset from a set of the variables such that the variables in the subset are as uncorrelated as possible, in an effort to ensure that all aspects of the variation in the data are covered.

Usage

PVA(obj, ...)

Arguments

- obj                   A [data.frame](#) containing the columns of variables from which the selection is to be made.
- ...                   allows passing of arguments to other functions

Details

PVA is the generic function for the PVA method. Use `methods("PVA")` to get all the methods for the PVA generic.

[PVA.data.frame](#) is a method for a [data.frame](#).

[PVA.matrix](#) is a method for a [matrix](#).

Value

A [data.frame](#) giving the results of the variable selection. It will contain the columns `Variable`, `Selected`, `h.partial`, `Added.Propn` and `Cumulative.Propn`.

Author(s)

Chris Brien

References

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

See Also

[PVA.data.frame](#), [PVA.matrix](#), [intervalPVA](#), [rcontrib](#)

---

PVA.data.frame	Selects a subset of variables stored in a <i>data.frame</i> using Principal Variable Analysis (PVA)
----------------	---

---

Description

Principal Variable Analysis (PVA) (Cumming and Wooff, 2007) selects a subset from a set of the variables such that the variables in the subset are as uncorrelated as possible, in an effort to ensure that all aspects of the variation in the data are covered.

**Usage**

```
## S3 method for class 'data.frame'
PVA(obj, responses, nvarselect = NULL, p.variance = 1, include = NULL,
     plot = TRUE, ...)
```

**Arguments**

obj	A <a href="#">data.frame</a> containing the columns of variables from which the selection is to be made.
responses	A <a href="#">character</a> giving the names of the columns in data from which the variables are to be selected.
nvarselect	A <a href="#">numeric</a> specifying the number of variables to be selected, which includes those listed in include. If nvarselect = 1, as many variables are selected as is need to satisfy p.variance.
p.variance	A <a href="#">numeric</a> specifying the minimum proportion of the variance that the selected variables must account for,
include	A <a href="#">character</a> giving the names of the columns in data for the variables whose selection is mandatory.
plot	A <a href="#">logical</a> indicating whether a plot of the cumulative proportion of the variance explained is to be produced.
...	allows passing of arguments to other functions

**Details**

The variable that is most correlated with the other variables is selected first for inclusion. The partial correlation for each of the remaining variables, given the first selected variable, is calculated and the most correlated of these variables is selects for inclusion next. Then the partial correlations are adjust for the second included variables. This process is repeated until the specified criteria have been satisfied. The possibilities are:

1. the default (nvarselect = NULL and p.variance = 1), which selects all variables in increasing order of amount of information they provide;
2. to select exactly nvarselect variables;
3. to select just enough variables, up to a maximum of nvarselect variables, to explain at least p.variance\*100 per cent of the total variance.

**Value**

A [data.frame](#) giving the results of the variable selection. It will contain the columns Variable, Selected, h.partial, Added.Propn and Cumulative.Propn.

**Author(s)**

Chris Brien

## References

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

## See Also

[PVA](#), [PVA.matrix](#), [intervalPVA.data.frame](#), [rcontrib](#)

## Examples

```
data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)
longi.dat <- within(longi.dat,
  {
    Max.Height <- pmax(Max.Dist.Above.Horizon.Line.SV1,
                      Max.Dist.Above.Horizon.Line.SV2)
    Density <- PSA/Max.Height
    PSA.SV = (PSA.SV1 + PSA.SV2) / 2
    Image.Biomass = PSA.SV * (PSA.TV^0.5)
    Centre.Mass <- (Center.Of.Mass.Y.SV1 + Center.Of.Mass.Y.SV2) / 2
    Compactness.SV = (Compactness.SV1 + Compactness.SV2) / 2
  })
responses <- c("PSA", "PSA.SV", "PSA.TV", "Image.Biomass", "Max.Height", "Centre.Mass",
              "Density", "Compactness.TV", "Compactness.SV")
results <- PVA(longi.dat, responses, p.variance=0.9, plot = FALSE)
```

---

PVA.matrix	<i>Selects a subset of variables using Principal Variable Analysis (PVA) based on a correlation matrix</i>
------------	--

---

## Description

Principal Variable Analysis (PVA) (Cumming and Wooff, 2007) selects a subset from a set of the variables such that the variables in the subset are as uncorrelated as possible, in an effort to ensure that all aspects of the variation in the data are covered.

## Usage

```
## S3 method for class 'matrix'
PVA(obj, responses, nvarselect = NULL, p.variance = 1, include = NULL,
    plot = TRUE, ...)
```

## Arguments

obj	A <a href="#">matrix</a> containing the correlation matrix for the variables from which the selection is to be made.
responses	A <a href="#">character</a> giving the names of the rows and columns in obj, being the names of the variables from which the selection is to be made.

nvarselect	A <b>numeric</b> specifying the number of variables to be selected, which includes those listed in include. If nvarselect = 1, as many variables are selected as is need to satisfy p.variance.
p.variance	A <b>numeric</b> specifying the minimum proportion of the variance that the selected variables must account for,
include	A <b>character</b> giving the names of the columns in data for the variables whose selection is mandatory.
plot	A <b>logical</b> indicating whether a plot of the cumulative proportion of the variance explained is to be produced.
...	allows passing of arguments to other functions

### Details

The variable that is most correlated with the other variables is selected first for inclusion. The partial correlation for each of the remaining variables, given the first selected variable, is calculated and the most correlated of these variables is selects for inclusion next. Then the partial correlations are adjust for the second included variables. This process is repeated until the specified criteria have been satisfied. The possibilities are:

1. the default (nvarselect = NULL and p.variance = 1), which selects all variables in increasing order of amount of information they provide;
2. to select exactly nvarselect variables;
3. to select just enough variables, up to a maximum of nvarselect variables, to explain at least p.variance\*100 per cent of the total variance.

### Value

A **data.frame** giving the results of the variable selection. It will contain the columns Variable, Selected, h.partial, Added.Propn and Cumulative.Propn.

### Author(s)

Chris Brien

### References

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

### See Also

PVA, PVA.data.frame, intervalPVA.data.frame, rcontrib

## Examples

```
data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)
longi.dat <- within(longi.dat,
  {
    Max.Height <- pmax(Max.Dist.Above.Horizon.Line.SV1,
                      Max.Dist.Above.Horizon.Line.SV2)
    Density <- PSA/Max.Height
    PSA.SV = (PSA.SV1 + PSA.SV2) / 2
    Image.Biomass = PSA.SV * (PSA.TV^0.5)
    Centre.Mass <- (Center.Of.Mass.Y.SV1 + Center.Of.Mass.Y.SV2) / 2
    Compactness.SV = (Compactness.SV1 + Compactness.SV2) / 2
  })
responses <- c("PSA", "PSA.SV", "PSA.TV", "Image.Biomass", "Max.Height", "Centre.Mass",
              "Density", "Compactness.TV", "Compactness.SV")
R <- Hmisc::rcorr(as.matrix(longi.dat[responses]))$r
results <- PVA(R, responses, p.variance=0.9, plot = FALSE)
```

---

rcontrib

*Computes a measure of how correlated each variable in a set is with the other variable, conditional on a nominated subset of them*

---

## Description

A measure of how correlated a variable is with those in a set is given by the square root of the sum of squares of the correlation coefficients between the variables and the other variables in the set (Cumming and Wooff, 2007). Here, the partial correlation between the subset of the variables listed in response that are not listed in include is calculated from the partial correlation matrix for the subset, adjusting for those variables in include. This is useful for manually deciding which of the variables not in include should next be added to it.

## Usage

```
rcontrib(obj, ...)
```

## Arguments

obj	A <a href="#">data.frame</a> containing the columns of variables from which the correlation measure is to be calculated.
...	allows passing of arguments to other functions

## Details

rcontrib is the generic function for the rcontrib method. Use methods("rcontrib") to get all the methods for the rcontrib generic.

[rcontrib.data.frame](#) is a method for a [data.frame](#).

[rcontrib.matrix](#) is a method for a [matrix](#).

**Value**

A [numeric](#) giving the correlation measures.

**Author(s)**

Chris Brien

**References**

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

**See Also**

[PVA](#), [intervalPVA](#)

---

rcontrib.data.frame	<i>Computes a measure of how correlated each variable in a set is with the other variable, conditional on a nominated subset of them</i>
---------------------	--

---

**Description**

A measure of how correlated a variable is with those in a set is given by the square root of the sum of squares of the correlation coefficients between the variables and the other variables in the set (Cumming and Wooff, 2007). Here, the partial correlation between the subset of the variables listed in `response` that are not listed in `include` is calculated from the partial correlation matrix for the subset, adjusting for those variables in `include`. This is useful for manually deciding which of the variables not in `include` should next be added to it.

**Usage**

```
## S3 method for class 'data.frame'
rcontrib(obj, responses, include = NULL, ...)
```

**Arguments**

<code>obj</code>	A <a href="#">data.frame</a> containing the columns of variables from which the correlation measure is to be calculated.
<code>responses</code>	A <a href="#">character</a> giving the names of the columns in data from which the correlation measure is to be calculated.
<code>include</code>	A <a href="#">character</a> giving the names of the columns in data for the variables for which other variables are to be adjusted.
<code>...</code>	allows passing of arguments to other functions.

**Value**

A [numeric](#) giving the correlation measures.

**Author(s)**

Chris Brien

**References**

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

**See Also**

[rcontrib](#), [rcontrib.matrix](#), [PVA](#), [intervalPVA.data.frame](#)

**Examples**

```
data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)
longi.dat <- within(longi.dat,
  {
    Max.Height <- pmax(Max.Dist.Above.Horizon.Line.SV1,
                      Max.Dist.Above.Horizon.Line.SV2)
    Density <- PSA/Max.Height
    PSA.SV = (PSA.SV1 + PSA.SV2) / 2
    Image.Biomass = PSA.SV * (PSA.TV^0.5)
    Centre.Mass <- (Center.Of.Mass.Y.SV1 + Center.Of.Mass.Y.SV2) / 2
    Compactness.SV = (Compactness.SV1 + Compactness.SV2) / 2
  })
responses <- c("PSA", "PSA.SV", "PSA.TV", "Image.Biomass", "Max.Height", "Centre.Mass",
              "Density", "Compactness.TV", "Compactness.SV")
h <- rcontrib(longi.dat, responses, include = "PSA")
```

---

rcontrib.matrix

---

*Computes a measure of how correlated each variable in a set is with the other variable, conditional on a nominated subset of them*


---

**Description**

A measure of how correlated a variable is with those in a set is given by the square root of the sum of squares of the correlation coefficients between the variables and the other variables in the set (Cumming and Wooff, 2007). Here, the partial correlation between the subset of the variables listed in response that are not listed in include is calculated from the partial correlation matrix for the subset, adjusting for those variables in include. This is useful for manually deciding which of the variables not in include should next be added to it.

**Usage**

```
## S3 method for class 'matrix'
rcontrib(obj, responses, include = NULL, ...)
```



**Arguments**

obj	A <a href="#">matrix</a> containing the correlations of the variables from which the correlation measure is to be calculated.
responses	A <a href="#">character</a> giving the names of the columns in data from which the correlation measure is to be calculated.
include	A <a href="#">character</a> giving the names of the columns in data for the variables for which other variables are to be adjusted.
...	allows passing of arguments to other functions.

**Value**

A [numeric](#) giving the correlation measures.

**Author(s)**

Chris Brien

**References**

Cumming, J. A. and D. A. Wooff (2007) Dimension reduction via principal variables. *Computational Statistics and Data Analysis*, **52**, 550–565.

**See Also**

[rcontrib](#), [rcontrib.data.frame](#), [PVA](#), [intervalPVA.data.frame](#)

**Examples**

```
data(exampleData)
longi.dat <- prepImageData(data=raw.dat, smarthouse.lev=1)
longi.dat <- within(longi.dat,
  {
    Max.Height <- pmax(Max.Dist.Above.Horizon.Line.SV1,
                      Max.Dist.Above.Horizon.Line.SV2)
    Density <- PSA/Max.Height
    PSA.SV = (PSA.SV1 + PSA.SV2) / 2
    Image.Biomass = PSA.SV * (PSA.TV^0.5)
    Centre.Mass <- (Center.Of.Mass.Y.SV1 + Center.Of.Mass.Y.SV2) / 2
    Compactness.SV = (Compactness.SV1 + Compactness.SV2) / 2
  })
responses <- c("PSA", "PSA.SV", "PSA.TV", "Image.Biomass", "Max.Height", "Centre.Mass",
              "Density", "Compactness.TV", "Compactness.SV")
R <- Hmisc::rcorr(as.matrix(longi.dat[responses]))$r
h <- rcontrib(R, responses, include = "PSA")
```

---

RicePrepped.dat	<i>Prepped data from an experiment to investigate a rice germplasm panel.</i>
-----------------	---

---

## Description

The data is the full set of Lanes and Positions from an experiment in a Smarthouse at the Plant Accelerator in Adelaide. It is used in the [growthPheno-package](#) as an executable example to illustrate the use of growthPheno. The experiment and data collection are described in Al-Tamimi et al. (2016) and the data is derived from the [data.frame](#) in the file `00-raw.0254.dat.rda` that is available from Al-Tamimi et al. (2017); half of the unprepped data is in [RiceRaw.dat](#).

## Usage

```
data(RicePrepped.dat)
```

## Format

A data.frame containing 14784 observations on 32 variables. The names of the columns in the data.frame are:

Column	Name	Class	Description
1	Smarthouse	factor	the Smarthouse in which a cart occurs.
2	Snapshot.ID.Tag	character	a unique identifier for each cart in the experiment.
3	xDAP	numeric	the numbers of days after planting on which the current data was observed.
4	DAST	factor	the numbers of days after the salting treatment on which the current data was observed.
5	xDAST	numeric	the numbers of days after the salting treatment on which the current data was observed.
6	cDAST	numeric	a centered numeric covariate for DAST.
7	DAST.diff	numeric	the number of days between this and the previous observations (all one for this experiment).
8	Lane	factor	the Lane in the 24 Lane x 24 Positions grid.
9	Position	factor	the Position in the 24 Lane x 24 Positions grid.
10	cPosn	numeric	a centered numeric covariate for Positions.
11	cMainPosn	numeric	a centered numeric covariate for Main plots.
12	Zone	factor	the Zone of 4 Lanes to which the current cart belonged.
13	cZone	numeric	a centered numeric covariate for Zone.
14	SHZone	factor	the Zone numbered across the two Smarthouses.
15	ZLane	factor	the number of the Lane within a Zone.
16	ZMainunit	factor	the number of the Main plot within a Zone.
17	Subunit	factor	the number of a Cart within a Main plot.
18	Reps	numeric	the replicate number of each Genotype-Salinity combination.
19	Genotype	factor	the number assigned to the 298 Genotypes in the experiment.
20	Salinity	factor	the Salinity treatment (Control, Salt) allocated to a Cart.

21	PSA	numeric	the Projected shoot area (kpixels).
22	PSA.AGR	numeric	the Absolute Growth Rate for the Projected shoot area (kpixels/day).
23	PSA.RGR	numeric	the Relative Growth Rate for the Projected shoot area (per day).
24	Tr	numeric	the amount of water (g) transpired by a plant.
25	TrR	numeric	the rate of water transpiration (g/day) for a plant.
26	PSA.TUE	numeric	the Transpiration Use Efficiency for PSA (kpixels / day) for a plant.
27	sPSA	numeric	the smoothed Projected shoot area (kpixels).
29	sPSA.AGR	numeric	the smoothed Absolute Growth Rate for the Projected shoot area (kpixels/day).
29	sPSA.RGR	numeric	the smoothed Relative Growth Rate for the Projected shoot area (per day).
30	sTr	numeric	the smoothed amount of water (g) transpired by a plant.
31	sTrR	numeric	the smoothed rate of water transpiration (g/day) for a plant.
32	sPSA.TUE	numeric	the smoothed Transpiration Use Efficiency for PSA (kpixels / day) for a plant.

## Source

Al-Tamimi N, Brien C, Oakey H, Berger B, Saade S, Ho YS, Schmockel SM, Tester M, Negrao S. (2017) Data from: Salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. Retrieved from: [doi:10.5061/dryad.3118j](https://doi.org/10.5061/dryad.3118j).

## References

Al-Tamimi, N, Brien, C.J., Oakey, H., Berger, B., Saade, S., Ho, Y. S., Schmockel, S. M., Tester, M. and Negrao, S. (2016) New salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. *Nature Communications*, **7**, 13342. Retrieved from [doi:10.1038/ncomms13342](https://doi.org/10.1038/ncomms13342).

---

RiceRaw.dat

*Data for an experiment to investigate a rice germplasm panel*

---

## Description

The data is half (the first 12 of 24 Lanes) of that from an experiment in a Smarthouse at the Plant Accelerator in Adelaide. It is used in the [growthPheno-package](#) as an executable example to illustrate the use of growthPheno. The experiment and data collection are described in Al-Tamimi et al. (2016) and the data is derived from the [data.frame](#) in the file `00-raw.0255.dat.rda` that is available from Al-Tamimi et al. (2017).

## Usage

```
data(RiceRaw.dat)
```

## Format

A data.frame containing 7392 observations on 33 variables.

## Source

Al-Tamimi N, Brien C, Oakey H, Berger B, Saade S, Ho YS, Schmockel SM, Tester M, Negrao S: Data from: Salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. Retrieved from: [doi:10.5061/dryad.3118j](https://doi.org/10.5061/dryad.3118j).

## References

Al-Tamimi, N, Brien, C.J., Oakey, H., Berger, B., Saade, S., Ho, Y. S., Schmockel, S. M., Tester, M. and Negrao, S. (2016) New salinity tolerance loci revealed in rice using high-throughput non-invasive phenotyping. *Nature Communications*, **7**, 13342. Retrieved from [doi:10.1038/ncomms13342](https://doi.org/10.1038/ncomms13342).

---

smooths.frame	<i>Description of a smooths.frame object</i>
---------------	--

---

## Description

A data.frame of S3-class smooths.frame that stores the smooths of one or more responses for several sets of smoothing parameters.

`as.smooths.frame` is function that converts a `data.frame` to an object of this class.

`is.smooths.frame` is the membership function for this class; it tests that an object has class smooths.frame.

`validSmoothsFrame` can be used to test the validity of a smooths.frame.

## Value

A `data.frame` that is also inherits the S3-class `smooths.frame`. It contains the results of smoothing a response over time from a set of individuals, the data being arranged in long format both with respect to the times and the smoothing-parameter values used in the smoothing. That is, each response occupies a single column. The `smooths.frame` must include the columns `Type`, `TunePar`, `TuneVal`, `Tuning` (the combination of `TunePar` and `TuneVal`) and `Method`, and the columns that would be nominated using the `probeSmooths` arguments `individuals`, the `plots` and `facet` arguments, `times`, `response`, `response.smoothed`, and, if requested, the `AGR` and the `RGR` of the response and `response.smoothed`. The names of the growth rates should be formed from `response` and `response.smoothed` by adding `.AGR` and `.RGR` to both of them. The function `probeSmooths` produces a `smooths.frame` for a response.

A `smooths.frame` has the following attributes:

1. `individuals`, the `character` giving the name of the `factor` that define the subsets of the data for which each subset corresponds to the response values for an individual;
2. `n`, the number of unique individuals;
3. `times`, the `character` giving the name of the `numeric`, or `factor` with numeric levels, that contains the values of the predictor variable plotted on the x-axis;
4. `t`, the number of unique values in the times;
5. `nschemes`, the number of unique combinations of the smoothing-parameter values in the smoothsframe.

**Author(s)**

Chris Brien

**See Also**[probeSmooths](#), [is.smooths.frame](#), [as.smooths.frame](#), [validSmoothsFrame](#), [args4smoothing](#)**Examples**

```

dat <- read.table(header = TRUE, text = "
Type TunePar TuneVal Tuning Method      ID  DAP   PSA      sPSA
NCSS      df      4   df-4 direct 045451-C  28 57.446 51.18456
NCSS      df      4   df-4 direct 045451-C  30 89.306 87.67343
NCSS      df      7   df-7 direct 045451-C  28 57.446 57.01589
NCSS      df      7   df-7 direct 045451-C  30 89.306 87.01316
")
dat[1:7] <- lapply(dat[1:6], factor)
dat <- as.smooths.frame(dat, individuals = "ID", times = "DAP")
is.smooths.frame(dat)
validSmoothsFrame(dat)

data(exampleData)
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", size=1))
smths <- probeSmooths(data = longi.dat,
                      response = "PSA", response.smoothed = "sPSA",
                      times = "DAP",
                      smoothing.args =
                        args4smoothing(smoothing.methods = "direct",
                                       spline.types = "NCSS",
                                       df = c(4,7), lambdas = NULL),
                      profile.plot.args =
                        args4profile_plot(plots.by = NULL,
                                       facet.x = "Tuning",
                                       facet.y = "Treatment.1",
                                       include.raw = "no",
                                       ggplotFuncs = vline))

is.smooths.frame(smths)
validSmoothsFrame(smths)

```

smoothSpline

---

*Fit a spline to smooth the relationship between a response and an x in a data.frame, optionally computing growth rates using derivatives.*

---

**Description**

Uses `smooth.spline` to fit a natural cubic smoothing spline or JOPS to fit a P-spline to all the values of response stored in data.

The amount of smoothing can be controlled by tuning parameters, these being related to the penalty. For a natural cubic smoothing spline, these are `df` or `lambda` and, for a P-spline, it is `lambda`. For

a P-spline, `npspline.segments` also influences the smoothness of the fit. The `smoothing.method` provides for direct and logarithmic smoothing. The method of Huang (2001) for correcting the fitted spline for estimation bias at the end-points will be applied when fitting using a natural cubic smoothing spline if `correctBoundaries` is TRUE.

The derivatives of the fitted spline can also be obtained, and the Absolute and Relative Growth Rates (AGR and RGR) computed using them, provided `correctBoundaries` is FALSE. Otherwise, growth rates can be obtained by difference using `byIndv4Times_GRsDiff`.

The handling of missing values in the observations is controlled via `na.x.action` and `na.y.action`. If there are not at least four distinct, nonmissing x-values, a warning is issued and all smoothed values and derivatives are set to NA.

The function `probeSmooths` can be used to investigate the effect the smoothing parameters (`smoothing.method` and `df` or `lambda`) on the smooth that results.

## Usage

```
smoothSpline(data, response, response.smoothed = NULL, x,
             smoothing.method = "direct",
             spline.type = "NCSS", df = NULL, lambda = NULL,
             npspline.segments = NULL, correctBoundaries = FALSE,
             rates = NULL, suffices.rates = NULL, sep.rates = ".",
             extra.derivs = NULL, suffices.extra.derivs=NULL,
             na.x.action = "exclude", na.y.action = "trimx", ...)
```

## Arguments

- |                                |  |
|--------------------------------|--|
| <code>data</code>              | A <a href="#">data.frame</a> containing the column to be smoothed.   |
| <code>response</code>          | A <a href="#">character</a> giving the name of the column in data that is to be smoothed.  |
| <code>response.smoothed</code> | A <a href="#">character</a> specifying the name of the column containing the values of the smoothed response variable, corresponding to <code>response</code> . If <code>response.smoothed</code> is NULL, then <code>response.smoothed</code> is set to the response to which is added the prefix <code>s</code> .  |
| <code>x</code>                 | A <a href="#">character</a> giving the name of the column in data that contains the values of the predictor variable.  |
| <code>smoothing.method</code>  | A <a href="#">character</a> giving the smoothing method to use. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response and then back-transforming by taking the exponential of the fitted values.  |
| <code>spline.type</code>       | A <a href="#">character</a> giving the type of spline to use. Currently, the possibilities are (i) "NCSS", for natural cubic smoothing splines, and (ii) "PS", for P-splines.  |
| <code>df</code>                | A <a href="#">numeric</a> specifying, for natural cubic smoothing splines (NCSS), the desired equivalent number of degrees of freedom of the smooth (trace of the smoother matrix). Lower values result in more smoothing. If <code>df = NULL</code> , the amount of smoothing can be controlled by setting <code>lambda</code> . If both <code>df</code> and <code>lambda</code> are NULL, smoothing is controlled by the default arguments for <code>smooth.spline</code> , and any that you supply via the ellipsis (...) argument. |

lambda	A <b>numeric</b> specifying the positive penalty to apply. The amount of smoothing decreases as lamda decreases.
npspline.segments	A <b>numeric</b> specifying, for P-splines (PS), the number of equally spaced segments between $\min(x)$ and $\max(x)$ , excluding missing values, to use in constructing the B-spline basis for the spline fitting. If npspline.segments is NULL, npspline.segments is set to the maximum of 10 and $\text{ceiling}((\text{nrow}(\text{data})-1)/2)$ i.e. there will be at least 10 segments and, for more than 22 x values, there will be half as many segments as there are x values. The amount of smoothing decreases as npspline.segments increases.
correctBoundaries	A <b>logical</b> indicating whether the fitted spline values are to have the method of Huang (2001) applied to them to correct for estimation bias at the end-points. Note that spline.type must be NCSS and lambda and deriv must be NULL for correctBoundaries to be set to TRUE.
rates	A <b>character</b> giving the growth rates that are to be calculated using derivative. It should be a combination of one or more of "AGR", "PGR" and "RGR". If NULL, then growth rates are not computed.
suffices.rates	A <b>character</b> giving the characters to be appended to the names of the responses to provide the names of the columns containing the calculated growth rates. The order of the suffices in suffices.rates should correspond to the order of the elements of which.rates. If NULL, the values of rates are used.
sep.rates	A <b>character</b> giving the character(s) to be used to separate the suffices.rates value from a response value in constructing the name for a new rate. For no separator, set to "".
extra.derivs	A <b>numeric</b> specifying one or more orders of derivatives that are required, in addition to any required for calculating the growth rates. When rates.method is derivatives, these can be derivatives other than the first. Otherwise, any derivatives can be specified.
suffices.extra.derivs	A <b>character</b> giving the characters to be appended to response.method to construct the names of the derivatives. If NULL and the derivatives are to be retained, then .dv followed by the order of the derivative is appended to response.method.
.	.
na.x.action	A <b>character</b> string that specifies the action to be taken when values of x are NA. The possible values are fail, exclude or omit. For exclude and omit, predictions and derivatives will only be obtained for nonmissing values of x. The difference between these two codes is that for exclude the returned data.frame will have as many rows as data, the missing values have been incorporated.
na.y.action	A <b>character</b> string that specifies the action to be taken when values of y, or the response, are NA. The possible values are fail, exclude, omit, allx, trimx, ltrimx or rtrimx. For all options, except fail, missing values in y will be removed before smoothing. For exclude and omit, predictions and derivatives will be obtained only for nonmissing values of x that do not have missing y values. Again, the difference between these two is that, only for exclude will the missing values be incorporated into the returned data.frame. For allx,

predictions and derivatives will be obtained for all nonmissing  $x$ . For `trimx`, they will be obtained for all nonmissing  $x$  between the first and last nonmissing  $y$  values that have been ordered for  $x$ ; for `ltrimx` and `utrimx` either the lower or upper missing  $y$  values, respectively, are trimmed.

... allows for arguments to be passed to `smooth.spline`.

## Value

A `list` with two components named `predictions` and `fit.spline`.

The `predictions` component is a `data.frame` containing  $x$  and the fitted smooth. The names of the columns will be the value of  $x$  and the value of `response.smoothed`. The number of rows in the `data.frame` will be equal to the number of pairs that have neither a missing  $x$  or response and the order of  $x$  will be the same as the order in `data`. If `deriv` is not `NULL`, columns containing the values of the derivative(s) will be added to the `data.frame`; the name each of these columns will be the value of `response.smoothed` with `.dvf` appended, where  $f$  is the order of the derivative, or the value of `response.smoothed` and the corresponding element of `suffices.deriv` appended. If `RGR` is not `NULL`, the `RGR` is calculated as the ratio of value of the first derivative of the fitted spline and the fitted value for the spline.

The `fit.spline` component is a `list` with components

**x:** the distinct  $x$  values in increasing order;

**y:** the fitted values, with boundary values possibly corrected, and corresponding to  $x$ ;

**lev:** leverages, the diagonal values of the smoother matrix (NCSS only);

**lambda:** the value of  $\lambda$  (corresponding to `spar` for NCSS - see [smooth.spline](#));

**df:** the effective degrees of freedom;

**npspline.segments:** the number of equally spaced segments used for smoothing method set to PS;

**uncorrected.fit:** the object returned by [smooth.spline](#) for smoothing method set to NCSS or by `JOPS::psNormal` for PS.

## Author(s)

Chris Brien

## References

Eilers, P.H.C and Marx, B.D. (2021) *Practical smoothing: the joys of P-splines*. Cambridge University Press, Cambridge.

Huang, C. (2001) Boundary corrected cubic smoothing splines. *Journal of Statistical Computation and Simulation*, **70**, 107-121.

## See Also

[byIndv4Times\\_SplinesGRs](#), [probeSmoothing](#), [byIndv4Times\\_GRsDiff](#), [smooth.spline](#), [predict.smooth.spline](#), `JOPS`.



## Examples

```
data(exampleData)
fit <- smoothSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP", df = 4,
  rates = c("AGR", "RGR"))
fit <- smoothSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP", df = 4,
  rates = "AGR", suffices.rates = "AGRdv",
  extra.derivs = 2, suffices.extra.derivs = "Acc")
fit <- smoothSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP",
  spline.type = "PS", lambda = 0.1, npspline.segments = 10,
  rates = "AGR", suffices.rates = "AGRdv",
  extra.derivs = 2, suffices.extra.derivs = "Acc")
fit <- smoothSpline(longi.dat, response="PSA", response.smoothed = "sPSA",
  x="xDAP", df = 4,
  rates = "AGR", suffices.rates = "AGRdv")
```

---

splitContGRdiff	<i>Adds, to a data.frame, the growth rates for individuals calculated continuously over time by differencing response values.</i>
-----------------	---

---

## Description

Uses [AGRdiff](#), [PGR](#) and [RGRdiff](#) to calculate growth rates continuously over time for the response by differencing pairs of pairs of response values and stores the results in data. The subsets are those values with the same levels combinations of the [factors](#) listed in individuals.

**Note: this function is soft deprecated and may be removed in future versions.**

Use [byIndv4Times\\_GRsDiff](#).

## Usage

```
splitContGRdiff(data, responses,
  individuals = "Snapshot.ID.Tag", INDICES = NULL,
  which.rates = c("AGR", "PGR", "RGR"), suffices.rates=NULL,
  times.factor = "Days", avail.times.diffs = FALSE,
  ntimes2span = 2)
```

## Arguments

data	A <a href="#">data.frame</a> containing the columns for which growth rates are to be calculated.
responses	A <a href="#">character</a> giving the names of the columns in data for which growth rates are to be calculated.
individuals	A <a href="#">character</a> giving the name(s) of the <a href="#">factor</a> (s) that define the subsets of response that correspond to the response values for an individual (e.g. plant, pot, cart, plot or unit) for which growth rates are to be calculated continuously.

	If the columns corresponding to individuals are not <a href="#">factor</a> (s) then they will be coerced to <a href="#">factor</a> (s). The subsets are formed using <a href="#">split</a> .
INDICES	A pseudonym for individuals.
which.rates	A <a href="#">character</a> giving the growth rates that are to be calculated. It should be a combination of one or more of "AGR", "PGR" and "RGR".
times.factor	A <a href="#">character</a> giving the name of the column in data containing the <a href="#">factor</a> for times at which the data was collected. Its levels will be used in calculating growth rates and should be numeric values stored as characters.
avail.times.diffs	A <a href="#">logical</a> indicating whether there is an appropriate column of times differences that can be used as the denominator in computing the growth rates. If TRUE, it will be assumed that the name of the column is the value of times with .diffs appended. If FALSE, a column, whose column name will be the value of times with .diffs appended, will be formed and saved in the result, overwriting any existing columns with the constructed name in data. It will be calculated using the values of times in data.
ntimes2span	A <a href="#">numeric</a> giving the number of values in times to span in calculating growth rates by differencing. Each growth rate is calculated as the difference in the values of one of the responses for pairs of times values that are spanned by ntimes2span times values divided by the difference between this pair of times values. For ntimes2span set to 2, a growth rate is the difference between consecutive pairs of values of one of the responses divided by the difference between consecutive pairs of times values.
suffices.rates	A <a href="#">character</a> giving the characters to be appended to the names of the responses to provide the names of the columns containing the calculated growth rates. The order of the suffices in suffices.rates should correspond to the order of the elements of which.rates. If NULL, the values of which.rates are used.

## Value

A [data.frame](#) containing data to which has been added 9i) a column for the differences between the times, if it is not already in data, and (ii) columns with growth rates. The name of the column for times differences will be the times with ".diffs" appended. The name for each of the growth-rate columns will be either the value of response with one of ".AGR", ".PGR" or "RGR", or the corresponding value from suffices.rates appended. Each growth rate will be positioned at observation ceiling( $\text{ntimes2span} + 1$ ) / 2 relative to the two times from which the growth rate is calculated.

## Author(s)

Chris Brien

## See Also

[fitSpline](#), [splitSplines](#)

## Examples

```
data(exampleData)
longi.dat <- splitContGRdiff(data = longi.dat,
                             response="sPSA", times.factor = "DAP",
                             individuals = "Snapshot.ID.Tag",
                             which.rates=c("AGR", "RGR"),
                             avail.times.diffs = TRUE)
```

---

splitSplines	<i>Adds the fits, and optionally growth rates computed from derivatives, after fitting splines to a response for an individual stored in a data.frame in long format</i>
--------------	--

---

## Description

Uses [fitSpline](#) to fit a spline to a subset of the values of response and stores the fitted values in data. The subsets are those values with the same levels combinations of the [factors](#) listed in individuals. The degree of smoothing is controlled by the tuning parameters df and lambda, related to the penalty, and by npspline.segments. The smoothing.method provides for direct and logarithmic smoothing.

The derivatives of the fitted spline can also be obtained, and the Absolute and Relative Growth Rates (AGR and RGR) computed using them, provided correctBoundaries is FALSE. Otherwise, growth rates can be obtained by difference using [splitContGRdiff](#).

The handling of missing values in the observations is controlled via na.x.action and na.y.action. If there are not at least four distinct, nonmissing x-values, a warning is issued and all smoothed values and derivatives are set to NA.

The function [probeSmoothing](#) can be used to investigate the effect the smoothing parameters (smoothing.method, df or lambda) on the smooth that results.

**Note: this function is soft deprecated and may be removed in future versions.**

Use [byIndv4Times\\_SplinesGRs](#).

## Usage

```
splitSplines(data, response, response.smoothed = NULL, x,
              individuals = "Snapshot.ID.Tag", INDICES = NULL,
              smoothing.method = "direct", smoothing.segments = NULL,
              spline.type = "NCSS", df=NULL, lambda = NULL,
              npspline.segments = NULL,
              correctBoundaries = FALSE,
              deriv = NULL, suffices.deriv = NULL, extra.rate = NULL,
              sep = ".",
              na.x.action="exclude", na.y.action = "exclude", ...)
```

**Arguments**

<code>data</code>	A <code>data.frame</code> containing the column to be smoothed.
<code>response</code>	A <code>character</code> giving the name of the column in <code>data</code> that is to be smoothed.
<code>response.smoothed</code>	A <code>character</code> specifying the name of the column containing the values of the smoothed response variable, corresponding to <code>response</code> . If <code>response.smoothed</code> is <code>NULL</code> , then <code>response.smoothed</code> is set to the <code>response</code> to which <code>.smooth</code> is added.
<code>x</code>	A <code>character</code> giving the name of the column in <code>data</code> that contains the values of the predictor variable.
<code>individuals</code>	A <code>character</code> giving the name(s) of the <code>factor</code> (s) that define the subsets of <code>response</code> that correspond to the response values for an individual (e.g. plant, pot, cart, plot or unit) that are to be smoothed separately. If the columns corresponding to <code>individuals</code> are not <code>factor</code> (s) then they will be coerced to <code>factor</code> (s). The subsets are formed using <code>split</code> .
<code>INDICES</code>	A pseudonym for <code>individuals</code> .
<code>smoothing.method</code>	A <code>character</code> giving the smoothing method to use. The two possibilities are (i) "direct", for directly smoothing the observed response, and (ii) "logarithmic", for smoothing the log-transformed response and then back-transforming by taking the exponential of the fitted values.
<code>smoothing.segments</code>	A named <code>list</code> , each of whose components is a numeric pair specifying the first and last values of an x-interval whose data is to be subjected as an entity to smoothing using splines. The separate smooths will be combined to form a whole smooth for each individual. If <code>smoothing.segments</code> is <code>NULL</code> , the data is not segmented for smoothing.
<code>spline.type</code>	A <code>character</code> giving the type of spline to use. Currently, the possibilities are (i) "NCSS", for natural cubic smoothing splines, and (ii) "PS", for P-splines.
<code>df</code>	A <code>numeric</code> specifying, for natural cubic smoothing splines (NCSS), the desired equivalent number of degrees of freedom of the smooth (trace of the smoother matrix). Lower values result in more smoothing. If <code>df = NULL</code> , the amount of smoothing can be controlled by setting <code>lambda</code> . If both <code>df</code> and <code>lambda</code> are <code>NULL</code> , smoothing is controlled by the default arguments for <code>smooth.spline</code> , and any that you supply via the ellipsis (...) argument.
<code>lambda</code>	A <code>numeric</code> specifying the positive penalty to apply. The amount of smoothing decreases as <code>lambda</code> decreases.
<code>npspline.segments</code>	A <code>numeric</code> specifying, for P-splines (PS), the number of equally spaced segments between <code>min(x)</code> and <code>max(x)</code> , excluding missing values, to use in constructing the B-spline basis for the spline fitting. If <code>npspline.segments</code> is <code>NULL</code> , <code>npspline.segments</code> is set to the maximum of 10 and <code>ceiling((nrow(data)-1)/2)</code> i.e. there will be at least 10 segments and, for more than 22 x values, there will be half as many segments as there are x values. The amount of smoothing decreases as <code>npspline.segments</code> increases. When the data has been segmented

for smoothing (smoothing.segments is not NULL), an npspline.segments value can be supplied for each segment.

correctBoundaries	A <a href="#">logical</a> indicating whether the fitted spline values are to have the method of Huang (2001) applied to them to correct for estimation bias at the end-points. Note that spline.type must be NCSS and lambda and deriv must be NULL for correctBoundaries to be set to TRUE.
deriv	A numeric specifying one or more orders of derivatives that are required.
suffices.deriv	A <a href="#">character</a> giving the characters to be appended to the names of the derivatives. If NULL and the derivative is to be retained then smooth.dv is appended.
extra.rate	A named <a href="#">character</a> nominating a single growth rate (AGR or RGR) to be computed using the first derivative, which one being dependent on the smoothing.method. The name of this element will be used as a suffix to be appended to the response when naming the resulting growth rate (see Examples). If unnamed, AGR or RGR will be used, as appropriate. Note that, for the smoothing.method set to direct, the first derivative is the AGR and so extra.rate must be set to RGR, which is computed as the AGR / smoothed response. For the smoothing.method set to logarithmic, the first derivative is the RGR and so extra.rate must be set to AGR, which is computed as the RGR * smoothed response. Make sure that deriv includes one so that the first derivative is available for calculating the extra.rate.
sep	A <a href="#">character</a> giving the separator to use when the levels of individuals are combined. This is needed to avoid using a <a href="#">character</a> that occurs in a <a href="#">factor</a> to delimit levels when the levels of individuals are combined to identify subsets.
na.x.action	A <a href="#">character</a> string that specifies the action to be taken when values of x are NA. The possible values are fail, exclude or omit. For exclude and omit, predictions and derivatives will only be obtained for nonmissing values of x. The difference between these two codes is that for exclude the returned data.frame will have as many rows as data, the missing values have been incorporated.
na.y.action	A <a href="#">character</a> string that specifies the action to be taken when values of y, or the response, are NA. The possible values are fail, exclude, omit, allx, trimx, ltrimx or rtrimx. For all options, except fail, missing values in y will be removed before smoothing. For exclude and omit, predictions and derivatives will be obtained only for nonmissing values of x that do not have missing y values. Again, the difference between these two is that, only for exclude will the missing values be incorporated into the returned data.frame. For allx, predictions and derivatives will be obtained for all nonmissing x. For trimx, they will be obtained for all nonmissing x between the first and last nonmissing y values that have been ordered for x; for ltrimx and rtrimx either the lower or upper missing y values, respectively, are trimmed.
...	allows for arguments to be passed to smooth.spline.

### Value

A [data.frame](#) containing data to which has been added a column with the fitted smooth, the name of the column being response.smoothed. If deriv is not NULL, columns containing the values

of the derivative(s) will be added to data; the name each of these columns will be the value of response.smoothed with .dvf appended, where f is the order of the derivative, or the value of response.smoothed with the corresponding element of suffices.deriv appended. If RGR is not NULL, the RGR is calculated as the ratio of value of the first derivative of the fitted spline and the fitted value for the spline. Any pre-existing smoothed and derivative columns in data will be replaced. The ordering of the data.frame for the x values will be preserved as far as is possible; the main difficulty is with the handling of missing values by the function merge. Thus, if missing values in x are retained, they will occur at the bottom of each subset of individuals and the order will be problematic when there are missing values in y and na.y.action is set to omit.

### Author(s)

Chris Brien

### References

- Eilers, P.H.C and Marx, B.D. (2021) *Practical smoothing: the joys of P-splines*. Cambridge University Press, Cambridge.
- Huang, C. (2001) Boundary corrected cubic smoothing splines. *Journal of Statistical Computation and Simulation*, **70**, 107-121.

### See Also

[fitSpline](#), [probeSmoothing](#), [splitContGRdiff](#), [smooth.spline](#), [predict.smooth.spline](#), [split](#)

### Examples

```
data(exampleData)
#smoothing with growth rates calculated using derivatives
longi.dat <- splitSplines(longi.dat, response="PSA", x="xDAP",
                        individuals = "Snapshot.ID.Tag",
                        df = 4, deriv=1, suffices.deriv="AGRdv",
                        extra.rate = c(RGRdv = "RGR"))

#Use P-splines
longi.dat <- splitSplines(longi.dat, response="PSA", x="xDAP",
                        individuals = "Snapshot.ID.Tag",
                        spline.type = "PS", lambda = 0.1, npspline.segments = 10,
                        deriv=1, suffices.deriv="AGRdv",
                        extra.rate = c(RGRdv = "RGR"))

#with segmented smoothing
longi.dat <- splitSplines(longi.dat, response="PSA", x="xDAP",
                        individuals = "Snapshot.ID.Tag",
                        smoothing.segments = list(c(28,34), c(35,42)), df = 5)
```

---

splitValueCalculate	<i>Calculates a single value that is a function of an individual's values for a response</i>
---------------------	--

---

## Description

Splits the values of a response into subsets corresponding individuals and applies a function that calculates a single value from each individual's observations. It includes the ability to calculate the observation number that is closest to the calculated value of the function and the associated values of a [factor](#) or numeric.

**Note: this function is soft deprecated and may be removed in future versions.**

Use [byIndv\\_ValueCalc](#).

## Usage

```
splitValueCalculate(response, weights=NULL, individuals = "Snapshot.ID.Tag",
  FUN = "max", which.obs = FALSE, which.values = NULL,
  data, na.rm=TRUE, sep=".", ...)
```

## Arguments

response	A <a href="#">character</a> giving the name of the column in data from which the values of FUN are to be calculated.
weights	A <a href="#">character</a> giving the name of the column in data containing the weights to be supplied as w to FUN.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
FUN	A <a href="#">character</a> giving the name of the function that calculates the value for each subset.
which.obs	A <a href="#">logical</a> indicating whether or not to determine the observation number corresponding to the observed value that is closest to the value of the function, in addition to the value of the function itself. That is, FUN need not return an observed value of the reponse, e.g. quantile. In the case of multiple observed response values satisfying this condition, the first is returned.
which.values	A <a href="#">character</a> giving the name of the <a href="#">factor</a> or <a href="#">numeric</a> whose values are associated with the response values and whose value is to be returned for the observation number whose response value corresponds to the observed value closest to the value of the function. That is, FUN need not return an observed value of the reponse, e.g. quantile. In the case of multiple observed response values satisfying this condition, the value of the which.values vector for the first of these is returned.
data	A <a href="#">data.frame</a> containing the column from which the function is to be calculated.

na.rm	A <a href="#">logical</a> indicating whether NA values should be stripped before the calculation proceeds.
sep	A <a href="#">character</a> giving the separator to use when the levels of individuals are combined. This is needed to avoid using a <a href="#">character</a> that occurs in a <a href="#">factor</a> to delimit levels when the levels of individuals are combined to identify subsets.
...	allows for arguments to be passed to FUN.

**Value**

A [data.frame](#), with the same number of rows as there are individuals, containing a column for the individuals and a column with the values of the function for the individuals. It is also possible to determine observation numbers or the values of another column in data for the response values that are closest to the FUN results, using either or both of `which.obs` and `which.values`. If `which.obs` is TRUE, a column with observation numbers is included in the [data.frame](#). If `which.values` is set to the name of a [factor](#) or a [numeric](#), a column containing the levels of that [factor](#) or the values of that [numeric](#) is included in the [data.frame](#).

The name of the column with the values of the function will be formed by concatenating the response and FUN, separated by a full stop. If `which.obs` is TRUE, the column name for the observations numbers will have `.obs` added after FUN into the column name for the function values; if `which.values` is specified, the column name for these values will have a full stop followed by `which.values` added after FUN into the column name for the function values.

**Author(s)**

Chris Brien

**See Also**

[intervalValueCalculate](#), [splitContGRdiff](#), [splitSplines](#)

**Examples**

```
data(exampleData)
sPSA.max.dat <- splitValueCalculate("sPSA", data = longi.dat)
AGR.max.dat <- splitValueCalculate("sPSA.AGR", FUN="max", data=longi.dat,
                                which.values = "DAP", which.obs = TRUE)
sPSA.dec1.dat <- splitValueCalculate("sPSA", FUN="quantile", data=longi.dat,
                                which.values = "DAP", probs = 0.1)
```

---

tomato.dat	<i>Longitudinal data for an experiment to investigate tomato response to mycorrhizal fungi and zinc</i>
------------	---

---



## Description

The data is from an experiment in a Smarthouse in the Plant Accelerator and is described by Watts-Williams et al. (2019). The experiment involves 32 plants, each placed in a pot in a cart, and the carts were assigned 8 treatments using a randomized complete-block design. The main response is Projected Shoot Area (PSA for short), being the sum of the plant pixels from three images. The eight treatments were the combinations of 4 Zinc (Zn) levels by two Arbuscular Mycorrhiza Fungi (AMF) levels. Each plant was imaged on 35 different days after planting (DAPs). It is used to explore the analysis of growth dynamics.

## Usage

```
data(tomato.dat)
```

## Format

A data.frame containing 1120 observations on 16 variables. The names of the columns in the data.frame are:

Column	Name	Class	Description
1	Lane	factor	the Lane in the 2 Lane x 16 Positions grid.
2	Position	factor	the Position in the 2 Lane x 16 Positions grid.
3	DAP	factor	the numbers of days after planting on which the current data was observed.
4	Snapshot.ID.Tag	character	a unique identifier for each cart in the experiment.
5	cDAP	numeric	a centered numeric covariate for DAP.
6	DAP.diffs	numeric	the number of days between this and the previous observations (all one for this experiment).
7	cPosn	numeric	a centered numeric covariate for Positions.
8	Block	factor	the block of the randomized complete-block design to which the current cart belonged.
9	Cart	factor	the number of the cart within a block.
10	AMF	factor	the AMF treatment (- AMF, +AMF) assigned to the cart.
11	Zn	factor	the Zinc level (0, 10, 40, 90) assigned to the cart.
12	Treatments	factor	the combined factor formed from AMF and Zn with levels: (-,0; -,10; -,40; -,90; +,0; +,10; +,40; +,90).
12	Weight.After	numeric	the weight of the cart after watering.
13	Water.Amount	numeric	the weight of the water added to the cart.
14	WU	numeric	the weight of the water used since the previous watering.
15	PSA	numeric	the Projected Shoot Area, being the total number of plant pixels in three plant images.

## References

Watts-Williams SJ, Jewell N, Brien C, Berger B, Garnett T, Cavagnaro TR (2019) Using high-throughput phenotyping to explore growth responses to mycorrhizal fungi and zinc in three plant species. *Plant Phenomics*, **2019**, 12.

---

traitExtractFeatures	<i>Extract features, that are single-valued for each individual, from traits observed over time.</i>
----------------------	--

---

## Description

Extract one or more sets of features from traits observed over time, the result being traits that have a single value for each individual. The sets of features are:

1. **single times** – the value for each individual for a single time. (uses `getTimesSubset`)
2. **growth rates for a time interval** – the average growth rate (AGR and/or RGR) over a time interval for each individual. (uses `byIndv4Intvl_GRsDiff` or `byIndv4Intvl_GRsAvg`)
3. **water use traits for a time interval** – the total water use (WU), the water use rate (WUR) and the water use index (WUI) over a time interval for each individual. (uses `byIndv4Intvl_WaterUse`)
4. **growth rates for the imaging period overall** – the average growth rate (AGR and/or RGR) over the whole imaging period for each individual. (uses `byIndv4Intvl_GRsDiff` or `byIndv4Intvl_GRsAvg`)
5. **water use traits for the imaging period overall** – the total water use (WU), the water use rate (WUR) and the water use index (WUI) for the whole imaging period for each individual. (uses `byIndv4Intvl_WaterUse`)
6. **totals for the imaging period overall** – the total over the whole imaging period of a trait for each individual. (uses `byIndv4Intvl_ValueCalc`)
7. **maximum for the imaging period overall** – the maximum value over the whole imaging period, and the time at which it occurred, for each individual. (uses `byIndv4Intvl_ValueCalc`)

The Tomato vignette illustrates the use of `traitSmooth` and `traitExtractFeatures` to carry out the SET procedure for the example presented in Brien et al. (2020). Use `vignette("Tomato", package = "growthPheno")` to access it.

## Usage

```
traitExtractFeatures(data, individuals = "Snapshot.ID.Tag", times = "DAP",
  starts.intvl = NULL, stops.intvl = NULL,
  suffices.intvl = NULL,
  responses4intvl.rates = NULL,
  growth.rates = NULL,
  growth.rates.method = "differences",
  suffices.growth.rates = NULL,
  water.use4intvl.traits = NULL,
  responses4water = NULL,
  water.trait.types = c("WU", "WUR", "WUI"),
  suffix.water.rate = "R", suffix.water.index = "I",
  responses4singletimes = NULL, times.single = NULL,
  responses4overall.rates = NULL,
  water.use4overall.water = NULL,
  responses4overall.water = NULL,
  responses4overall.totals = NULL,
```

```

responses4overall.max = NULL,
intvl.overall = NULL, suffix.overall = NULL,
sep.times.intvl = "to", sep.suffix.times = ".",
sep.growth.rates = ".", sep.water.traits = "",
mergedata = NULL, ...)

```

## Arguments

- |                       |  |
|-----------------------|--|
| data                  | A <a href="#">data.frame</a> containing the columns specified by individuals, times, the various responses arguments and the water.use argument.   |
| individuals           | A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).   |
| times                 | A <a href="#">character</a> giving the name of the column in data containing the times at which the data was collected, either as a <a href="#">numeric</a> , <a href="#">factor</a> , or <a href="#">character</a> . It will be used identifying the intervals and, if a <a href="#">factor</a> or <a href="#">character</a> , the values should be numerics stored as characters.  |
| starts.intvl          | A <a href="#">numeric</a> giving the times, in terms of values in times, that are the initial times for a set of intervals for which growth.rates and water.use traits are to be obtained. These times may also be used to obtain values for single-time traits (see responses4singletimes).   |
| stops.intvl           | A <a href="#">numeric</a> giving the times, in terms of values in times, that are the end times for a set of intervals for which growth.rates and water.use traits are to be obtained. These times may also be used to obtain values for single-time traits (see responses4singletimes).   |
| suffices.intvl        | A <a href="#">character</a> giving the suffices for intervals specified using starts.intvl and stops.intvl. If NULL, the suffices are automatically generated using starts.intvl, stops.intvl and sep.times.intvl.   |
| responses4intvl.rates | A <a href="#">character</a> specifying the names of the columns containing responses for which growth rates are to be obtained for the intervals specified by starts.intvl and stops.intvl. For growth.rates.method set to differences, the growth rates will be computed from the column of the response values whose name is listed in responses4intvl.rates. For growth.rates.method set to derivatives, the growth rates will be computed from a column with the growth rates computed for each time. The name of the column should be a response listed in responses4intvl.rates to which is appended an element of suffices.growth.rates.  |
| growth.rates.method   | A <a href="#">character</a> specifying the method to use in calculating the growth rates over an interval for the responses specified by responses4intvl.rates. The two possibilities are "differences" and "ratesaverages". For differences, the growth rate for an interval is computed by taking differences between the values of a response for pairs of times. For ratesaverage, the growth rate for an interval is computed by taking weighted averages of growth rates for times within the interval. That is, differences operates on the response and ratesaverage operates on the growth rates previously calculated from the response, so that the appropriate one of these must be in data. The ratesaverage option is most |

appropriate when the growth rates are calculated using the derivatives of a fitted curve. Note that, for responses for which the AGR has been calculated using differences, both methods will give the same result, but the differences option will be more efficient than ratesaverages.

- `growth.rates` A [character](#) specifying which growth rates are to be obtained for the intervals specified by `starts.intvl` and `stops.intvl`. It should contain one of both of "AGR" and "RGR".
- `suffices.growth.rates` A [character](#) giving the suffices appended to `responses4intvl.rates` in constructing the column names for the storing the growth rates specified by `growth.rates`. If `suffices.growth.rates` is NULL, then "AGR" and "RGR" will be used.
- `water.use4intvl.traits` A [character](#) giving the names of the columns in data that contain the water use values that are to be used in computing the water use traits (WU, WUR, WUI) for the intervals specified by `starts.intvl` and `stops.intvl`. If there is only one column name, then the WUI will be calculated using this name for all column names in `responses4water`. If there are several column names in `water.use4intvl.traits`, then there must be either one or the same number of names in `responses4water`. If both have same number of names, then the two lists of column names will be processed in parallel, so that a single WUI will be produced for each pair of `responses4water` and `water.use4intvl.traits` values.
- `responses4water` A [character](#) giving the names of the columns in data that are to provide the numerator in calculating a WUI for the intervals specified using `starts.intvl` and `stops.intvl`. The denominator will be the values in the columns in data whose names are those given by `water.use4intvl.traits`. If there is only one column name in `responses4water`, then the WUI will be calculated using this name for all column names in `responses4water`. If there are several column names in `responses4water`, then there must be either one or the same number of names in `water.use4intvl.traits`. If both have same number of names, then the two lists of column names will be processed in parallel, so that a single WUI will be produced for each pair of `responses4water` and `water.use4intvl.traits` values.
- See the Value section for a description of how `responses4water` is incorporated into the names constructed for the water use traits.
- `water.trait.types` A [character](#) listing the trait types to compute and return. It should be some combination of WU, WUR and WUI. See Details in [byIndv4Intvl\\_WaterUse](#) for how each is calculated.
- `suffix.water.rate` A [character](#) giving the label to be appended to the value of `water.use4intvl.traits` to form the name of the WUR.
- `suffix.water.index` A [character](#) giving the label to be appended to the value of `water.use4intvl.traits` to form the name of the WUI.
- `responses4singletimes` A [character](#) specifying the names of the columns containing responses for which a column of the values is to be formed for each response for each of the

- times values specified in `times.single`. If `times.single` is NULL, then the unique values in the combined `starts.intvl` and `stops.intvl` will be used.
- `times.single` A [numeric](#) giving the times of imaging, for each of which, the values of each `responses4single` times will be stored in a column of the resulting [data.frame](#). If NULL, then the unique values in the combined `starts.intvl` and `stops.intvl` will be used.
- `responses4overall.rates` A [character](#) specifying the names of the columns containing responses for which growth rates are to be obtained for the whole imaging period i.e. the interval specified by `intvl.overall`. The settings of `growth.rates.method`, `growth.rates`, `suffices.growth.rates`, `sep.growth.rates`, `suffix.overall` and `intvl.overall` will be used in producing the growth rates. See `responses4intvl.rates` for more information about how these arguments are used.
- `water.use4overall.water` A [logical](#) indicating whether the overall `water.traits` are to be obtained. The settings of `water.trait.types`, `suffix.water.rate`, `suffix.water.index`, `sep.water.traits`, `suffix.overall` and `intvl.overall` will be used in producing the overall water traits. See `water.use4intvl.traits` for more information about how these arguments are used.
- `responses4overall.water` A [character](#) giving the names of the columns in data that are to provide the numerator in calculating a WUI for the interval corresponding to the whole imaging period. See `response.water` for further details. See `responses4water` for more information about how this argument is processed.
- `responses4overall.totals` A [character](#) specifying the names of the columns containing responses for which a column of the values is to be formed by summing the response for each individual over the whole of the imaging period.
- `responses4overall.max` A [character](#) specifying the names of the columns containing responses for which columns of the values are to be formed for the maximum of the response for each individual over the whole of the imaging period and the times value at which the maximum occurred.
- `intvl.overall` A [numeric](#) giving the starts and stop times of imaging. If NULL, the start time will be the minimum of `starts.intvl` and the stop time will be the maximum of `stops.intvl`.
- `suffix.overall` A [character](#) giving the suffix to be appended to the names of traits that apply to the whole imaging period. It applies to `overall.growth.rates`, `water.use4overall.water`, `responses4overall.water` and `responses4overall.totals`. If NULL, then nothing will be added.
- `sep.times.intvl` A [character](#) giving the separator to use in combining a `starts.intvl` with a `stops.intvl` in constructing the suffix to be appended to an interval trait. If set to NULL and there is only one value for each of `starts.intvl` and `stops.intvl`, then no suffix will be added; otherwise `sep.times.intvl` set to NULL will result in an error.

sep.suffix.times	A <a href="#">character</a> giving the separator to use in appending a suffix for times to a trait. For no separator, set to "".
sep.growth.rates	A <a href="#">character</a> giving the character(s) to be used to separate the suffices.growth.rates value from the responses4intvl.rates values in constructing the name for a new rate. It is also used for separating responses4water values from the suffix.water.index. For no separator, set to "".
sep.water.traits	A <a href="#">character</a> giving the character(s) to be used to separate the suffix.rate and suffix.index values from the response value in constructing the name for a new rate/index. The default of "" results in no separator.
mergedata	A <a href="#">data.frame</a> containing a column with the name given in individuals and for which there is only one row for each value given in this column. In general, it will be that the number of rows in mergedata is equal to the number of unique values in the column in data labelled by the value of individuals, but this is not mandatory. If mergedata is not NULL, the values extracted by traitExtractFeatures will be <a href="#">merged</a> with it.
...	allows passing of arguments to other functions; not used at present.

## Value

A [data.frame](#) that contains an individuals column and a column for each extracted trait, in addition to any columns in mergedata. The number of rows in the [data.frame](#) will equal the number of unique element of the individuals column in data, except when there are extra values in the individuals column in data. If the latter applies, then the number of rows will equal the number of unique values in the combined individuals columns from mergedata and data.

The names of the columns produced by the function are constructed as follows:

1. **single times** – A name for a single-time trait is formed by appending a full stop to an element of responses4singletimes, followed by the value of times at which the values were observed.
2. **growth rates for a time interval** – The name for an interval growth rate is constructed by concatenating the relevant element of responses4intvl.rates, growth.rates and a suffix for the time interval, each separated by a full stop. The interval suffix is formed by joining its starts.intvl and stops.intvl values, separating them by the value of sep.times.intvl.
3. **growth rates for the whole imaging period** – The name for an interval growth rate is constructed by concatenating the relevant element of responses4intvl.rates, growth.rates and suffix.overall, each separated by a full stop.
4. **water use traits for a time interval** – Construction of the names for the three water traits begins with the value of water.use4intvl.traits. The rate (WUR) has either R or the value of suffix.water.rate added to the value of water.use4intvl.traits. Similarly the index (WUI) has either I or the value of suffix.water.index added to it. The WUI also has the element of responses4water used in calculating the WUI prefixed to its name. All three water use traits have a suffix for the interval appended to their names. This suffix is constructed by joining its starts.intvl and stops.intvl, separated by the value of sep.times.intvl.

- The `data.frame` is returned invisibly.

## Chris Brien

Brien, C., Jewell, N., Garnett, T., Watts-Williams, S. J., & Berger, B. (2020). Smoothing and extraction of traits in the growth analysis of noninvasive phenotypic data. *Plant Methods*, **16**, 36. doi:10.1186/s13007020005776.

```
getTimesSubset, byIndv4Intvl_GrSAvg, byIndv4Intvl_GrSDiff, byIndv4Intvl_WaterUse,
byIndv_ValueCalc.
```

[illegible]

```

#Smooth WU
tom.dat <- byIndv4Times_SplinesGRs(data = tom.dat,
                                   response = "WU", response.smoothed = "sWU",
                                   rates.method = "none",
                                   times = "DAP",
                                   smoothing.method = "direct",
                                   spline.type = "PS", lambda = 10^(-0.5),
                                   smoothing.segments = DAP.segs)

#Extract single-valued traits for each individual
indv.cols <- c("Snapshot.ID.Tag", "Lane", "Position", "Block", "Cart", "AMF", "Zn")
indv.dat <- subset(tom.dat, subset = DAP == DAP.endpts[1],
                  select = indv.cols)
indv.dat <- traitExtractFeatures(data = tom.dat,
                                starts.intvl = DAP.starts, stops.intvl = DAP.stops,
                                responses4singletimes = "sPSA",
                                responses4intvl.rates = "sPSA",
                                growth.rates = c("AGR", "RGR"),
                                water.use4intvl.traits = "sWU",
                                responses4water = "sPSA",
                                responses4overall.totals = "sWU",
                                responses4overall.max = "sPSA.AGR",
                                mergedata = indv.dat)

```

---

traitSmooth

*Obtain smooths for a trait by fitting spline functions and, having compared several smooths, allows one of them to be chosen and returned in a data.frame.*

---

## Description

Takes a response that has been observed for a set of individuals over a number times and carries out one or more of the following steps:

**Smooth:** Produces `response.smoothed` using splines for a set of smoothing parameter settings and, optionally, computes growth rates either as differences or derivatives. (see `smoothing.args` below and [args4smoothing](#)) This step is bypassed if a `data.frame` that is also of class `smooths.frame` is supplied to `data`.

**Profile plots:** Produces profile plots of `response.smoothed` and its growth rates that compare the smooths; also, boxplots of the deviations of the observed from smoothed data can be obtained. (see `profile.plot.args` below and [args4profile\\_plot](#)) Whether these plots are produced is controlled via `which.plots` or whether `profile.plot.args` is set to `NULL`.

**Median deviations plots:** Produces plots of the medians of the deviations of the observed response, and its growth rates, from `response.smoothed`, and its growth rates. These aid in the assessment of the different smooths. (see `meddevn.plot.args` below and [args4meddevn\\_plot](#)) Whether these plots are produced is controlled via `which.plots` or whether `meddevn.plot.args` is set to `NULL`.



**Deviations boxplots:** Produces boxplots of the absolute or relative deviations of the observed response, and its growth rates, from `response.smoothed`, and its growth rates. These aid in the assessment of the different smooths. (see `devnboxes.plot.args` below and [args4devnboxes\\_plot](#)) Whether these plots are produced is controlled via `which.plots` or whether `devnboxes.plot.args` is set to `NULL`.

**Choose a smooth:** Extract a single, favoured `response.smoothed`, and its growth rates, for a chosen set of smoothing parameter settings. (see `chosen.smooth.args` below and [args4chosen\\_smooth](#)) This step will be omitted if `chosen.smooth.args` is `NULL`.

**Chosen smooth plot:** Produces profile plots of the chosen smooth and its growth rates. (see `chosen.plot.args` below and [args4chosen\\_plot](#)) Whether these plots are produced is controlled by whether `chosen.plot.args` is set to `NULL`.

Each of the ‘args4’ functions has a set of defaults that will be used if the corresponding argument, ending in ‘.args’, is omitted. The defaults have been optimized for `traitSmooth`.

Input to the function can be either a `data.frame`, that contains data to be smoothed, or a `smooths.frame`, that contains data that has been smoothed. The function can be run (i) without saving any output, (ii) saving the complete set of smooths in a `data.frame` that is also of class `smooths.frame`, (iii) saving a subset of the smooths in a supplied `smooths.frame`, or (iv) saving a single smooth in a `data.frame`, which can be merged with a pre-existing `data.frame` such as the `data.frame` that contains the unsmoothed data.

The Tomato vignette illustrates the use of `traitSmooth` and [traitExtractFeatures](#) to carry out the SET procedure for the example presented in Brien et al. (2020). Use `vignette("Tomato", package = "growthPheno")` to access it.

## Usage

```
traitSmooth(data, response, response.smoothed, individuals, times,
            keep.columns = NULL,
            get.rates = TRUE,
            rates.method="differences", ntimes2span = NULL,
            trait.types = c("response", "AGR", "RGR"),
            smoothing.args = args4smoothing(),
            x.title = NULL, y.titles = NULL,
            which.plots = c("profiles", "medians.deviations"),
            profile.plot.args = args4profile_plot(),
            meddevn.plot.args = args4meddevn_plot(),
            devnboxes.plot.args = args4devnboxes_plot(),
            chosen.smooth.args = args4chosen_smooth(),
            chosen.plot.args = args4chosen_plot(),
            mergedata = NULL,
            ...)
```

## Arguments

data	A <code>data.frame</code> containing the data or a <code>smooths.frame</code> as is produced by <code>probeSmooths</code> . If data is not a <code>smooths.frame</code> , then smoothing will be performed. If data is a <code>smooths.frame</code> , then the plotting and selection of smooths will be performed as specified by <code>smoothing.args</code> , <code>which.plots</code> , <code>chosen.smooth.args</code> and <code>chosen.plot.args</code> .
------	---

response	A <a href="#">character</a> specifying the response variable to be smoothed.
response.smoothed	A <a href="#">character</a> specifying the name of the column to contain the values of the smoothed response variable, corresponding to response.
individuals	A <a href="#">character</a> giving the name of the <a href="#">factor</a> that defines the subsets of the data for which each subset corresponds to the response values for an individual (e.g. plant, pot, cart, plot or unit).
times	A <a href="#">character</a> giving the name of the <a href="#">numeric</a> , or <a href="#">factor</a> with numeric levels, that contains the values of the predictor variable to be supplied to <a href="#">smooth.spline</a> and to be plotted on the x-axis.
keep.columns	A <a href="#">character</a> vector giving the names of columns from data that are to be included in the <a href="#">smooths.frame</a> that will be returned.
get.rates	A <a href="#">logical</a> or a <a href="#">character</a> specifying which of the response and the response.smoothed are to have growth rates (AGR and/or RGR) computed and stored. If set to TRUE or c("raw", "smoothed"), growth rates will be obtained for both. Setting to only one of raw or smoothed, results in the growth rates for either the response or the response.smoothed being computed. If set to none or FALSE, no growth rates are computed. Which growth rates are computed can be changed using the arguments <a href="#">traits.types</a> and the method used for computing them for the response.smooth by <a href="#">rates.method</a> . The growth rates for the response can only be computed by differencing.
rates.method	A <a href="#">character</a> specifying the method to use in calculating the growth rates for response.smoothed. The two possibilities are "differences" and "derivatives".
ntimes2span	A <a href="#">numeric</a> giving the number of values in times to span in calculating growth rates by differencing. For ntimes2span set to NULL, if rates.method is set to differences then ntimes2span is set to 2; if rates.method is set to derivatives then ntimes2span is set to 3. Note that when get.rates includes raw or is TRUE, the growth rates for the unsmoothed response must be calculated by differencing, even if the growth rates for the smoothed response are computed using derivatives. When differencing, each growth rate is calculated as the difference in the values of one of the responses for pairs of times values that are spanned by ntimes2span times values divided by the difference between this pair of times values. For ntimes2span set to 2, a growth rate is the difference between consecutive pairs of values of one of the responses divided by the difference between consecutive pairs of times values.
trait.types	A <a href="#">character</a> giving the trait.types that are to be plotted. If growth rates are included in trait.types, then they will be computed for either the response and/or the response.smoothed, depending on the setting of get.rates. Any growth rates included in trait.types for the response that are available in data, but have not been specified for computation in get.rates, will be retained in the returned smooths.frame. If all, the response.smoothed, its AGR and RGR, will be plotted. The response, and its AGR and RGR, will be plotted as the plotting options require it.
smoothing.args	A <a href="#">list</a> that is most easily generated using <a href="#">args4smoothing</a> , it documenting the options available for smoothing the data. It gives the settings of smoothing.methods, spline.types, df, lambdas, smoothing.segments, npspline.segments, na.x.action,

na.y.action, external.smooths, and correctBoundaries, to be used in smoothing the response or in selecting a subset of the smooths in data, depending on whether data is a `data.frame` or a `smooths.frame`, respectively. If data is a `data.frame`, then smoothing will be performed. If data is a `smooths.frame`, no smoothing will be carried out. If `smoothing.args` is NULL then a `smooths.frame` will only be used for plotting. Otherwise, the setting of `smoothing.args` will specify the smooths that are to be extracted from the `smooths.frame`, in which case `smoothing.args` must specify a subset of the smooths in data.

<code>x.title</code>	Title for the x-axis, used for all plots. If NULL then set to times.
<code>y.titles</code>	A <code>character</code> giving the titles for the y-axis, one for each the response, the AGE and the RGR. They are used for all plots. If NULL then they are set to the response and the response with .AGR and .RGR appended.
<code>which.plots</code>	A <code>logical</code> indicating which plots of the smooths specified by <code>smoothing.args</code> are to be produced. The options are either none or some combination of profiles, absolute.boxplots, relative.boxplots and medians.deviations. The various profiles plots that can be produced are described in the introduction to this function. The plot of a chosen smooth is dealt with separately by the argument <code>chosen.plot.args</code> .
<code>profile.plot.args</code>	A named <code>list</code> that is most easily generated using <code>args4profile_plot</code> , it documenting the options available for varying the profile plots. <i>Note that if <code>args4profile_plot</code> is being called from traitSmooth to change some arguments from the default settings, then it is safest to set all of the following arguments in the call: <code>plots.by</code>, <code>facet.x</code> <code>facet.y</code> and <code>include.raw</code>. If this argument is set to NULL, these plots will not be produced.</i>
<code>meddevn.plot.args</code>	A named <code>list</code> that is most easily generated using <code>args4meddevn_plot</code> , it documenting the options available for varying median deviations plots. <i>Note that if <code>args4meddevn_plot</code> is being called from traitSmooth to change some arguments from the default settings, then it is safest to set all of the following arguments in the call: <code>plots.by</code>, <code>plots.group</code>, <code>facet.x</code> and <code>facet.y</code>. If this argument is set to NULL, these plots will not be produced.</i>
<code>devnboxes.plot.args</code>	A named <code>list</code> that is most easily generated using <code>args4devnboxes_plot</code> , it documenting the options available for varying the boxplots. <i>Note that if <code>args4devnboxes_plot</code> is being called from traitSmooth to change some arguments from the default settings, then it is safest to set all of the following arguments in the call: <code>plots.by</code>, <code>facet.x</code> and <code>facet.y</code>. If this argument is set to NULL, these plots will not be produced.</i>
<code>chosen.smooth.args</code>	A named <code>list</code> with just one element or NULL for each component. It is most easily generated using <code>args4chosen_smooth</code> with combinations set to single. The call to <code>args4smoothing</code> should give the settings of <code>smoothing.methods</code> , <code>spline.types</code> , <code>df</code> and <code>lambdas</code> for a single smooth that is to be extracted and that is amongst the smooths that have been produced for the settings specified in <code>smoothing.methods</code> . If both <code>df</code> and <code>lambda</code> in <code>chosen.smooth.args</code> are NULL, then, depending on the settings for <code>spline.type</code> and <code>smoothing.method</code> ,

the value of either `df` or `lambdas` that is the median value or the observed value immediately below the median value will be added to `chosen.smooth.args`. Otherwise, one of `df` and `lambda` should be `NULL` and the other should be a single numeric value. If a value in `chosen.smooth.args` is not amongst those investigated, a value that was investigated will be substituted.

`chosen.plot.args`

A named `list` that is most easily generated using `args4chosen_plot`, it documenting the options available for varying profile plots. Because this plot includes only a single smooth, the `chosen.smooth.args`, the smoothing-parameter `factors` are unnecessary and an error will be given if any are included. *Note that if `args4chosen_plot` is to be called to change from the default settings given in the default `traitSmooth` call, then it is safest to set all of the following arguments in the call: `plots.by`, `facet.x`, `facet.y` and `include.raw`. If set to `NULL`, then no chosen-smooth plot will be produced.*

`mergedata`

A `data.frame` that is to have the values for the `trait.types` for the smooth specified by `chosen.smooth.args` merged with it. It must contain columns with the names given in `individuals` and `times`, and for which there is only one row for each combination of unique values in these columns. In general, it will be that the number of rows in `mergedata` is equal to the number of unique combinations of the values in the columns of the `chosen.smooth.args` whose names are given by `individuals` and `times`, but this is not mandatory. If only one smooth has been produced, then it will be merged with data provided `mergedata` is `NULL` and data is not a `smooths.frame`. Otherwise, a single smooth will be merged with `mergedata`.

...

allows arguments to be passed to `plotProfiles`.

## Details

This function is a wrapper function for `probeSmooths`, `plotSmoothsComparison`, `plotSmoothsComparison` and `plotDeviationsBoxes`. It uses the helper functions `args4smoothing`, `args4profile_plot` and `args4meddevn_plot` to set arguments that control the smoothing and plotting.

It takes a response that has been observed for a set of individuals over a number times and produces `response.smoothed`, using `probeSmooths`, for a default set of smoothing parameter settings (see `args4smoothing` for the defaults). The settings can be varied from the defaults by specifying alternate values for the smoothing parameters, the parameters being the type of spline (`spline.types`), the degrees of freedom (`df`) or smoothing penalty (`lambdas`) and `smoothing.methods`. There are also several other smoothing arguments that can be manipulated to affect the smooth (for details see `args4smoothing`). The secondary traits of the absolute growth rate (AGR) and relative growth rate (RGR) are calculated from the two primary traits, the response and `response.smoothed`.

Generally, profile plots for the traits (a response, an AGR or an RGR) specified in `traits.types` are produced if `which.plots` is `profiles`; if `which.plots` specifies one or more deviations plots, then those deviations plots will also be produced, these being based on the unsmoothed data from which the smoothed data has been subtracted. The layout of the plots is controlled via combinations of one or more of the smoothing-parameter `factors` `Type`, `TunePar`, `TuneVal`, `Tuning` (the combination of `TunePar` and `TuneVal`) and `Method`, as well as other `factors` associated with the data. The `factors` that are to be used for the profile plots and deviations boxplots are supplied via the argument `profile.plot.args` using the helper function `args4profile_plot` to set `plots.by`,

facet.x, and facet.y; for the plots of the medians of the deviations, the `factors` are supplied via the argument `meddevn.plot.args` using the helper function `args4meddevn_plot` to set `plots.by`, `facet.x`, `facet.y` and `plots.group`. Here, the basic principle is that the number of levels combinations of the smoothing-parameter `factors` included in the set of `plots` and `facets` arguments to one of these helper functions must be the same as those covered by the combinations of the values supplied to `spline.types`, `df`, `lambdas` and `smoothing.methods` and incorporated into the `smooths.frame`, such as is returned by `probeSmooths`. This ensures that smooths from different parameter sets are not pooled together in a single plot. It is also possible to include `factors` that are not smoothing-parameter `factors` in the `plots` and `facets` arguments.

The following profiles plots can be produced using `args4profile_plot`: (i) separate plots of the smoothed traits for each combination of the smoothing parameters (include `Type`, `Tuning` and `Method` in `plots.by`); (ii) as for (i), with the corresponding plot for the unsmoothed trait preceding the plots for the smoothed trait (also set `include.raw` to `alone`); (iii) profiles plots that compare a smoothed trait for all combinations of the values of the smoothing parameters, arranging the plots side-by-side or one above the other (include `Type`, `Tuning` and `Method` in `facet.x` and/or `facet.y` - to include the unsmoothed trait set `include.raw` to one of `facet.x` or `facet.y`); (iv) as for (iii), except that separate plots are produced for each combination of the levels of the `factors` in `plot.by` and each plot compares the smoothed traits for the smoothing-parameter `factors` included in `facet.x` and/or `facet.y` (set both `plots.by` and one or more of `facet.x` and `facet.y`).

Deviation plots that can be produced are the absolute and relative deviations boxplots and plots of medians deviations (see `which.plots`).

By default, the single smooth for an arbitrarily chosen combination of the smoothing parameters is returned by the function. The smooth for a single combination other than default combination can be nominated for return using the `chosen.smooth.args` argument. This combination must involve only the supplied values of the smoothing parameters. The values for `response`, the `response.smoothed` and their `AGRs` and `RGRs` are added to data, after any pre-existing columns of these have been removed from data. Profile plots of the three smoothed traits are produced using `plotProfiles`. However, if `chosen.smooth.args` is `NULL`, all of the smooths will be returned in a `smooths.frame`, and plots for the single combination of the smoothing parameters will not be produced.

## Value

A `smooths.frame` or a `data.frame` that contains the unsmoothed and smoothed data in long format. That is, all the values for either an unsmoothed or a smoothed trait are in a single column.

A `smooths.frame` will be returned when (i) `chosen.smooth.args` is `NULL` and there is more than one smooth specified by the smoothing parameter arguments, or (ii) `chosen.smooth.args` is not `NULL` but `mergedata` is `NULL`. It will contain the smooths for a trait for the different combinations of the smoothing parameters, the values for the different smooths being placed in rows one below the other. The columns that are included in the `smooths.frame` are `Type`, `TunePar`, `TuneVal`, `Tuning` and `Method`, as well as those specified by `individuals`, `times`, `response`, and `response.smoothed`, and any included in the `keep.columns`, `plots` and `facet` arguments when the smooths were produced. The `AGR` or `RGR` for the `response` and `response.smoothed`, if obtained, will also be included. A `smooths.frame` has the attributes described in `smooths.frame`.

A `data.frame` will be returned when (i) `chosen.smooth.args` and `mergedata` are not `NULL` or (ii) `chosen.smooth.args` is `NULL`, `data` is not a `smooths.frame` and there is only one smooth specified by the smoothing parameter arguments. In either case, if `mergedata` is not `NULL`, the chosen smooth

or the single smooth will be merged with the `data.frame` specified by `mergedata`. When there is a single smooth and both `mergedata` and `chosen.smooth.args` are `NULL`, the `data.frame` will include the columns `individuals`, `times`, `response`, and `response.smoothed`, and any included in the `keep.columns`, `plots` and `facet` arguments, as well as any growth rates calculated as a result of `get.rates` and `trait.type`.

The `smooths.frame/data.frame` is returned invisibly.

## Author(s)

Chris Brien

## References

Brien, C., Jewell, N., Garnett, T., Watts-Williams, S. J., & Berger, B. (2020). Smoothing and extraction of traits in the growth analysis of noninvasive phenotypic data. *Plant Methods*, **16**, 36. doi:10.1186/s13007020005776.

## See Also

`args4smoothing`, `args4meddevn_plot`, `args4profile_plot`, `args4chosen_smooth`, `args4chosen_plot`, `probeSmooths` `plotSmoothsComparison` and `plotSmoothsMedianDevns`, `ggplot`.

## Examples

```
data(exampleData)
longi.dat <- longi.dat[1:140,] #reduce to a smaller data set
vline <- list(ggplot2::geom_vline(xintercept=29, linetype="longdash", linewidth=1))
yfacets <- c("Smarthouse", "Treatment.1")
smth.dat <- traitSmooth(data = longi.dat,
  response = "PSA", response.smoothed = "sPSA",
  individuals = "Snapshot.ID.Tag", times = "DAP",
  keep.columns = yfacets,
  smoothing.args =
    args4smoothing(df = c(5,7),
      lambda = list(PS = c(0.316,10))),
  profile.plot.args =
    args4profile_plot(facet.y = yfacets,
      ggplotFuncs = vline),
  chosen.plot.args =
    args4chosen_plot(facet.y = yfacets,
      ggplotFuncs = vline))
```

---

twoLevelOpcreate

*Creates a data.frame formed by applying, for each response, a binary operation to the paired values of two different treatments*

---

## Description

Takes pairs of values for a set of responses indexed by a two-level `treatment.factor` and calculates, for each of pair, the result of applying a binary operation to their values for the two levels of the `treatment.factor`. The level of the `treatment.factor` designated the control will be on the right of the binary operator and the value for the other level will be on the left.

## Usage

```
twoLevelOpcreate(data, responses, treatment.factor = "Treatment.1",
  suffices.treatment = c("Cont", "Salt"), control = 1,
  columns.suffixed = NULL,
  operations = "/", suffices.results="OST",
  columns.retained = c("Snapshot.ID.Tag", "Smarthouse", "Lane",
    "Zone", "cZone", "SHZone", "ZLane",
    "ZMainunit", "cMainPosn", "Genotype.ID"),
  by = c("Smarthouse", "Zone", "ZMainunit"))
```

## Arguments

- |                    |   |
|--------------------|---|
| data               | A <a href="#">data.frame</a> containing the columns specified by <code>treatment.factor</code> , <code>columns.retained</code> and responses.   |
| responses          | A <a href="#">character</a> giving the names of the columns in data that contain the responses to which the binary operations are to be applied.  |
| treatment.factor   | A <a href="#">factor</a> with two levels corresponding to what is to be designated the control and treated observations .   |
| suffices.treatment | A <a href="#">character</a> giving the characters to be appended to the names of the responses and <code>columns.suffixed</code> in constructing the names of the columns containing the responses and <code>columns.suffixed</code> for each level of the <code>treatment.factor</code> . The order of the suffices in <code>suffices.treatment</code> should correspond to the order of the levels of <code>treatment.factor</code> . |
| control            | A <a href="#">numeric</a> , equal to either 1 or 2, that specifies the level of <code>treatment.factor</code> that is the control treatment. The value for the control level will be on the right of the binary operator.   |
| columns.suffixed   | A <a href="#">character</a> giving the names of the <code>columns.retained</code> in data that are to be have the values for each treatment retained and whose names are to be suffixed using <code>suffices.treatment</code> . Generally, this is done when <code>columns.retained</code> has different values for different levels of the <code>treatment.factor</code> .   |
| operations         | A <a href="#">character</a> giving the binary operations to perform on the values for the two different levels of the <code>treatment.factor</code> . It should be either of length one, in which case the same operation will be performed for all columns specified in <code>response.GR</code> , or equal in length to <code>response.GR</code> so its elements correspond to those of <code>response.GR</code> .                    |



suffices.results

A **character** giving the characters to be appended to the names of the responses in constructing the names of the columns containing the results of applying the operations. The order of the suffices in `suffices.results` should correspond to the order of the operators in operations.

columns.retained

A **character** giving the names of the columns in data that are to be retained in the `data.frame` being created. These are usually **factors** that index the results of applying the operations and that might be used subsequently.

by

A **character** giving the names of the columns in data whose combinations will be unique for the observation for each treatment. It is used by **merge** when combining the values of the two treatments in separate columns in the `data.frame` to be returned.

## Value

A **data.frame** containing the following columns and the values of the :

1. those from data nominated in `columns.retained`;
2. those containing the treated values of the columns whose names are specified in responses; the treated values are those having the other level of `treatment.factor` to that specified by `control`;
3. those containing the control values of the columns whose names are specified in responses; the control values are those having the level of `treatment.factor` specified by `control`;
4. those containing the values calculated using the binary operations; the names of these columns will be constructed from responses by appending `suffices.results` to them.

## Author(s)

Chris Brien

## Examples

```
data(exampleData)
responses <- c("sPSA.AGR", "sPSA.RGR")
cols.retained <- c("Snapshot.ID.Tag", "Smarthouse", "Lane", "Position",
                  "DAP", "Snapshot.Time.Stamp", "Hour", "xDAP",
                  "Zone", "cZone", "SHZone", "ZLane", "ZMainunit",
                  "cMainPosn", "Genotype.ID")
longi.SIIT.dat <-
  twoLevelOpcreate(data = longi.dat, responses = responses,
                  suffices.treatment=c("C", "S"),
                  operations = c("-", "/"),
                  suffices.results = c("diff", "SIIT"),
                  columns.retained = cols.retained,
                  by = c("Smarthouse", "Zone", "ZMainunit", "DAP"))
longi.SIIT.dat <- with(longi.SIIT.dat,
                      longi.SIIT.dat[order(Smarthouse, Zone, ZMainunit, DAP),])
```



---

validSmoothsFrame	<i>Checks that an object is a valid <a href="#">smooths.frame</a>.</i>
-------------------	--

---

## Description

Checks that an object is a [smooths.frame](#) of S3-class data.frame that contains the columns Type, TunePar, TuneVal, Tuning, Method, as well as the columns specified by the attributes of the object, namely individuals and times.

## Usage

```
validSmoothsFrame(object)
```

## Arguments

object            a [smooths.frame](#).

## Value

TRUE or a character describing why the object is not a valid [smooths.frame](#).

## Author(s)

Chris Brien

## See Also

[is.smooths.frame](#), [as.smooths.frame](#)

## Examples

```
dat <- read.table(header = TRUE, text = "
Type TunePar TuneVal Tuning Method ID DAP PSA sPSA
NCSS df 4 df-4 direct 045451-C 28 57.446 51.18456
NCSS df 4 df-4 direct 045451-C 30 89.306 87.67343
NCSS df 7 df-7 direct 045451-C 28 57.446 57.01589
NCSS df 7 df-7 direct 045451-C 30 89.306 87.01316
")
dat[1:7] <- lapply(dat[1:6], factor)
dat <- as.smooths.frame(dat, individuals = "ID", times = "DAP")
is.smooths.frame(dat)
validSmoothsFrame(dat)
```

---

WUI*Calculates the Water Use Index (WUI)*

---

**Description**

Calculates the Water Use Index, returning NA if the water use is zero.

**Usage**

```
WUI(response, water)
```

**Arguments**

response	A <b>numeric</b> giving the value of the response achieved.
water	A <b>numeric</b> giving the amount of water used.

**Value**

A **numeric** containing the response divided by the water, unless water is zero in which case NA is returned.

**Author(s)**

Chris Brien

**Examples**

```
data(exampleData)
PSA.WUE <- with(longi.dat, WUI(PSA.AGR, WU))
```

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