Package ‘santaR’

October 14, 2022

Title  Short Asynchronous Time-Series Analysis
Version 1.2.3
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Description  A graphical and automated pipeline for the analysis
of short time-series in R (‘santaR’). This approach is designed to accommodate asynchronous
time sampling (i.e. different time points for different individuals),
inter-individual variability, noisy measurements and large numbers of variables.
Based on a smoothing splines functional model, ‘santaR’ is able to detect variables
highlighting significantly different temporal trajectories between study groups.
Designed initially for metabolic phenotyping, ‘santaR’ is also suited for other Systems Biology
disciplines. Command line and graphical analysis (via a ‘shiny’ application) enable fast and
parallel automated analysis and reporting, intuitive visualisation and comprehensive plotting
options for non-specialist users.

Depends R (>= 4.0.0)
License GPL-3

BugReports https://github.com/adwolfer/santaR/issues/new
URL https://github.com/adwolfer/santaR

Encoding UTF-8

LazyData true

Imports plyr (>= 1.8.4), foreach (>= 1.4.4), doParallel (>= 1.0.11),
pcaMethods (>= 1.70.0), ggplot2 (>= 2.2.1), gridExtra (>= 2.3),
reshape2 (>= 1.4.3), iterators (>= 1.0.9), shiny (>= 1.3.2),
bslib, DT (>= 0.9)

biocViews pcaMethods (>= 1.70.0)

Suggests knitr, rmarkdown, pander, R.rsp, testthat

VignetteBuilder knitr, R.rsp

RoxygenNote 7.2.0

NeedsCompilation no

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Timothy Ebbels [ctb],
Joe Cheng [ctb] (Shiny javascript custom-input control)
**Description**

A dataset containing the concentrations of 22 mediators of inflammation over an episode of acute inflammation. The mediators have been measured at 7 time-points on 8 subjects, concentration values have been unit-variance scaled for each variable.
**AICc_smooth_spline**

**Usage**

```
acuteInflammation
```

**Format**

List of 2 data frames of 56 rows each, containing the 22 measured variables (data) and the corresponding sampling metadata (meta):

- **data:** var  mediator concentration, unit-variance scaled
- **meta:** time  time of the measurement, in hour
- **meta:** ind  subject ID for the measurement
- **meta:** group  group membership of the subject/measurement

```
AICc_smooth_spline  Calculate the Akaike Information Criterion Corrected for small observation numbers for a smooth.spline
```

**Description**

Calculate the Akaike Information Criterion Corrected for small observation numbers (AICc) for a fitted smooth.spline. The smaller the AICc, the better the spline fit.

**Usage**

```
AICc_smooth_spline(fittedSmoothSpline)
```

**Arguments**

- `fittedSmoothSpline`  A fitted smooth.spline

**Value**

The AICc value.
AIC_smooth_spline

Description
Calculate the Akaike Information Criterion (AIC) for a fitted smooth.spline. The smaller the AIC, the better the spline fit.

Usage
AIC_smooth_spline(fittedSmoothSpline)

Arguments
- fittedSmoothSpline
  A fitted smooth.spline

Value
The AIC value.

BIC_smooth_spline

Description
Calculate the Bayesian Information Criterion (BIC) for a fitted smooth.spline. The smaller the BIC, the better the spline fit.

Usage
BIC_smooth_spline(fittedSmoothSpline)

Arguments
- fittedSmoothSpline
  A fitted smooth.spline

Value
The BIC value.
get_eigen_DF

Compute the optimal df and weighted-df using 5 spline fitting metric

Description
Compute the optimal degree of freedom (df) and weighted degree of freedom (wdf) using 5 fitting metrics (CV: Cross-Validation, GCV: Generalised Cross-Validation, AIC: Akaike Information Criterion, BIC: Bayesian Information Criterion, AICc: Akaike Information Criterion Corrected for small sample size) over all eigenSplines generated by get_eigen_spline. The degree of freedom (df) is obtained by averaging the optimal df across each eigenSpline. The weighted degree of freedom (wdf) is obtained by weighting the optimal df in each eigenSpline by the percentage of variance explained by each eigenSpline, before summing the optimal dfs (variance sums to 100%).

Usage
get_eigen_DF(eigen)

Arguments
eigen A list of eigenSpline parameters as generated by get_eigen_spline, containing eigen$matrix, eigen$variance, eigen$model and eigen$countTP.

Value
A list: answer$df a vector of optimum df by CV, GCV, AIC, BIC, AICc. answer$wdf a vector of weighted optimum df by CV, GCV, AIC, BIC, AICc.

See Also
Graphical implementation with santaR_start_GUI
Other DFsearch: get_eigen_DFoverlay_list(), get_eigen_spline(), get_param_evolution(), plot_nbTP_histogram(), plot_param_evolution()

Examples
## 8 subjects, 8 time-points, 3 variables
inputData <- acuteInflammation$data[,1:3]
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
eigen <- get_eigen_spline(inputData, ind, time, nPC=NA, scaling="scaling_UV",
method="nipals", verbose=TRUE, centering=TRUE, ncores=0)
# nipals calculated PCA
# Importance of component(s):
# PC1 PC2 PC3 PC4 PC5 PC6
# R2 0.8924 0.0848 0.01055 0.006084 0.0038 0.002362
# Cumulative R2 0.8924 0.9772 0.98775 0.993838 0.9976 1.000000
get_eigen_DF(eigen)
# $df
get_eigen_DFoverlay_list

Plot for each eigenSpline the automatically fitted spline, splines for all possible df and a spline at a manually chosen df.

Description

Plot for each eigenSpline the automatically fitted spline (red), splines for all possible df (grey) and a spline at a manually chosen df (blue).

Usage

get_eigen_DFoverlay_list(
  eigen,
  manualDf = 5,
  nPC = NA,
  step = NA,
  showPt = TRUE,
  autofit = TRUE
)

Arguments

eigen A list of eigenSpline parameters as generated by get_eigen_spline, containing eigen.matrix, eigen.variance, eigen.model and eigen$countTP.

manualDf (int) A manually selected df. Default is 5.
nPC (int) The first n eigenSplines to plot. Default is NA, plot all eigenSplines.
step (float) The df increment employed to plot splines over the range of df.
showPt (bool) If True the eigenSpline data points are plotted. Default is TRUE.
autofit (bool) If True the automatically fitted splines (using CV) are plotted. Default is TRUE.

Value

A list of ggplot2 plotObjects, one plot per eigenSpline. All results can be plotted using do.call(grid.arrange, returnedResult).
get_eigen_spline

See Also

Graphical implementation with santaR_start_GUI

Other DFsearch: get_eigen_DF(), get_eigen_spline(), get_param_evolution(), plot_nbTP_histogram(), plot_param_evolution()

Examples

## 8 subjects, 4 time-points, 3 variables
inputData <- acuteInflammation$data[0:32,1:3]
ind <- acuteInflammation$meta$ind[0:32]
time <- acuteInflammation$meta$time[0:32]
eigen <- get_eigen_spline(inputData, ind, time, nPC=NA, scaling="scaling_UV",
                          method="nipals", verbose=TRUE, centering=TRUE, ncores=0)

paramSpace <- get_param_evolution(eigen, step=1)
plotList <- get_eigen_DFoverlay_list(eigen, manualDF=3, step=0.5, showPt=TRUE, autofit=TRUE)
plotList[1]
# do.call(grid.arrange, plotList)

---

get_eigen_spline  Compute eigenSplines across a dataset

Description

Compute "eigenSplines" across a dataset to discover the best df for spline fitting.

Steps:

- UV Scale the data.
- Turn each VAR in (IND x TIME) and group all VAR in (IND+VAR x TIME) using get_eigen_spline_matrix.
- Compute "eigen.splines" on the transposed table (TIME x IND+VAR).
- Returns eigen$matrix = PCprojection x TIME and eigen$variance = variance explained for each PC.

Usage

get_eigen_spline(
  inputData,     # required
  ind,            # required
  time,           # required
  nPC = NA,       # required
  scaling = "scaling_UV",  
  method = "nipals",  # required
  verbose = TRUE,  
  centering = TRUE,  # required
  ncores = 0
)


get_eigen_spline

Arguments

inputData  Matrix of measurements with observations as rows and variables as columns.
ind        Vector of subject identifier (individual) corresponding to each measurement.
time       Vector of time corresponding to each measurement.
nPC        (int) Number of Principal Components to compute, if none given (nPC=NA) compute all PC (usually number TP-1 as there is 1PC less than the smallest dimension).
scaling   "scaling_UV" or "scaling_mean" scaling across all samples for each variable. Default "scaling_UV". Note: scaling takes place outside of the pcaMethods call, therefore $model will indicate "Data was NOT scaled before running PCA".
method     PCA method "svd" doesn't accept missing value. "nipals" can handle missing values. Default "nipals".
verbose    If TRUE print the PCA summary. Default TRUE.
centering  If TRUE centering for PCA, needed to remove baseline levels of each pc (often PC1). Default TRUE.
ncores     (int) Number of cores to use for parallelisation of the grouping of all splines. Default 0 for no parallelisation.

Value

A list eigen: eigen$matrix data.frame of eigenSplines values with PCprojection as row and TIME as column. eigen$variance Vector of variance explained for each PC. eigen$model resulting pcaMethods model. eigen$countTP Matrix of number of measurements for each unique timepoint (as row).

Comments::

• CENTERING: Centering converts all the values to fluctuations around zero instead of around the mean of the variable measurements. Hereby, it adjusts for differences in the offset between high and low intensity variables. It is therefore used to focus on the fluctuating part of the data, and leaves only the relevant variation (being the variation between the observations) for analysis.

• SCALING: Scaling methods are data pretreatment approaches that divide each variable by a factor -the scaling factor- which is different for each variable. They aim to adjust for the differences in fold differences between the various variables by converting the data into differences in values relative to the scaling factor. This often results in the inflation of small values, which can have an undesirable side effect as the influence of the measurement error -that is usually relatively large for small values- is increased as well.

• UNIT VARIANCE SCALING: UV or Autoscaling, is commonly applied and uses the standard deviation as the scaling factor. After autoscaling, all variables have a standard deviation of one and therefore the data is analysed on the basis of correlations instead of covariances, as is the case with centering.

• BEFORE PCA, centering must be applied on the matrix that will be submitted to PCA to remove "baseline" levels.
get_eigen_spline

See Also

Graphical implementation with SantaR_start_GUI

Other DFsearch: get_eigen_DFoverlay_list(), get_eigen_DF(), get_param_evolution(), plot_nbTP_histogram(), plot_param_evolution()

Examples

```r
## 7 measurements, 3 subjects, 4 unique time-points, 2 variables
inputData <- matrix(c(1,2,3,4,5,6,7,8,9, 10,11,12,13,14,15,16,17,18), ncol=2)
ind <- c('ind_1', 'ind_1', 'ind_1', 'ind_2', 'ind_2', 'ind_2', 'ind_3', 'ind_3', 'ind_3')
time <- c(0,5,10,0,10,15,5,10,15)
get_eigen_spline(inputData, ind, time, nPC=NA, scaling="scaling_UV", method="nipals",
                 verbose=TRUE, centering=TRUE, ncores=0)

# nipals calculated PCA
# Importance of component(s):
#    PC1  PC2  PC3
# R2   0.7113 0.2190 0.05261
# Cumulative R2 0.7113 0.9303 0.98287
# total time: 0.12 secs
# $matrix
#     0  5 10 15
# PC1 -1.7075707 -0.7066426 0.7075708 1.7066425
# PC2 -0.3415271  0.9669724 1.0944005 -0.4297013
# PC3 -0.1764657 -0.5129981 0.5110671 0.1987611
# $variance
# [1] 0.71126702 0.21899068 0.05260949
# $model
# nipals calculated PCA
# Importance of component(s):
#    PC1  PC2  PC3
# R2   0.7113 0.2190 0.05261
# Cumulative R2 0.7113 0.9303 0.98287
# 6 Variables
# 4 Samples
# 6 NAs (25 %)
# 3 Calculated component(s)
# Data was mean centered before running PCA
# Data was NOT scaled before running PCA
# Scores structure:
# [1] 4 3
# Loadings structure:
# [1] 6 3
# $countTP
# [1,] 3 6
```
get_eigen_spline_matrix

Generate a Ind x Time + Var data.frame concatenating all variables from input variable

Description

Generate Ind x Time data.frame for each variable using `get_ind_time_matrix` and then concatenate all variables rowise. Resulting data.frame contain Time as columns and Individuals and Variables as rows. Pairs of Individual and Timepoint without a measurement are left as NA. If ncore!=0 the function is parallelised, however the parallelisation overhead cost is high if not required.

Usage

```
get_eigen_spline_matrix(inputData, ind, time, ncores = 0)
```

Arguments

- `inputData`  
data.frame of measurements with observations as rows and variables as columns
- `ind`  
Vector of subject identifier (individual) corresponding to each measurement
- `time`  
Vector of time corresponding to each measurement
- `ncores`  
(int) Number of cores to use for parallelisation. Default 0 for no parallelisation.

Value

data.frame of measurements for each IND x TIME + VAR. Rows are unique Individual IDs per variable, and columns unique measurement Time. Pairs of (IND,TIME+VAR) without a measurement are left as NA.

Examples

```
## Not run:
## 6 measurements, 3 subjects, 3 unique time-points, 2 variables
inputData <- matrix(c(1,2,3,4,5,6, 7,8,9,10,11,12), ncol=2)
ind <- c('ind_1', 'ind_1', 'ind_1', 'ind_2', 'ind_2', 'ind_3')
time <- c(0,5,10,0,10,5)
get_eigen_spline_matrix(inputData, ind, time, ncores=0)
  #   0   5  10
  # 1   1   2   3
  # 2   4   NA  5
  # 3   NA   6   NA
  # 4   7   8   9
  # 5  10   NA  11
  # 6   NA  12   NA
```

## End(Not run)
**get_grouping**

*Generate a matrix of group membership for all individuals*

**Description**

Establish the group membership of individuals based on the metadata across all observations using the vector of subject identifier and the matching vector of group membership.

**Usage**

```r
get_grouping(ind, group)
```

**Arguments**

- `ind` vector of subject identifier (individual) for each observation
- `group` vector of group membership for each observation

**Value**

data.frame with as rows each unique Individual ID and 2 columns (ind and group).

**See Also**

Other Analysis: `get_ind_time_matrix()`, `santaR_CBand()`, `santaR_auto_fit()`, `santaR_auto_summary()`, `santaR_fit()`, `santaR_plot()`, `santaR_pvalue_dist()`, `santaR_pvalue_fit()`, `santaR_start_GUI()`

**Examples**

```r
## 3 subjets in 2 groups
ind <- c('ind_1', 'ind_1', 'ind_1', 'ind_2', 'ind_2', 'ind_3')
group <- c('g1', 'g1', 'g1', 'g2', 'g2', 'g1')
get_grouping(ind, group)
# ind group
# 1 ind_1 g1
# 2 ind_2 g2
# 3 ind_3 g1

## 8 subjects in 2 groups
ind <- acuteInflammation$meta$ind
group <- acuteInflammation$meta$group
get_grouping(ind, group)
# ind group
# 1 ind_1 Group1
# 2 ind_2 Group2
# 3 ind_3 Group1
# 4 ind_4 Group2
# 5 ind_5 Group1
# 6 ind_6 Group2
# 7 ind_7 Group1
```
get_ind_time_matrix

Generate a Ind x Time DataFrame from input data

Description

Convert input data with each measurement as a row, to a data.frame of measurements with Individual as rows and Time as columns. Pairs of Individual and Timepoint without a measurement are left as NA. The resulting data.frame is employed as input for santaR_fit.

Usage

get_ind_time_matrix(Yi, ind, time, orderVect)

Arguments

Yi  
vector of measurements

ind  
vector of subject identifier (individual) corresponding to each measurement

time  
vector of time corresponding to each measurement

orderVect  
if provided, a vector of unique time to be used to order the time columns (otherwise rely on sort)

Value

data.frame of measurements for each IND x TIME. Rows are unique Individual IDs and columns unique measurement Time. Pairs of (IND,TIME) without a measurement are left as NA.

See Also

Other Analysis: get_grouping(), santaR_CBand(), santaR_auto_fit(), santaR_auto_summary(), santaR_fit(), santaR_plot(), santaR_pvalue_dist(), santaR_pvalue_fit(), santaR_start_GUI()

Examples

## 6 measurements, 3 subjects, 3 unique time-points
Yi <- c(1,2,3,4,5,6)
ind <- c('ind_1','ind_1','ind_1','ind_2','ind_2','ind_3')
time <- c(0,5,10,0,10,5)
get_ind_time_matrix(Yi, ind, time)
# 0 5 10
#  ind_1 1 2 3
#  ind_2 4 NA 5
#  ind_3 NA 6 NA

## 56 measurements, 8 subjects, 7 unique time-points
Yi <- acuteInflammation$data$var_1
get_param_evolution

get_param_evolution <- acuteInflammation$meta$ind
get_ind_time_matrix(Yi, ind, time)

get_param_evolution  Compute the value of different fitting metrics over all possible df for each eigenSpline

Description

Compute the value of 5 fitting metrics (CV: Cross-Validation, GCV: Generalised Cross-Validation, AIC: Akaike Information Criterion, BIC: Bayesian Information Criterion, AICc: Akaike Information Criterion Corrected for small sample size) over all possible df for each eigenSpline generated by get_eigen_spline. The resulting matrix of fitting parameter values can be plotted using plot_param_evolution.

Usage

get_param_evolution(eigen, step = 0.1)

Arguments

eigen A list of eigenSpline parameters as generated by get_eigen_spline, containing eigen$matrix, eigen$variance, eigen$model and eigen$countTP.

step (float) The df increment employed to cover the range of df. Default steps of 0.1

Value

A list of n matrices (n being the number of eigenSplines). Each matrix of fitting parameter values has as rows different fitting metrics, as columns different df values.

See Also

Graphical implementation with santaR_start_GUI

Other DFsearch: get_eigen_DFoverlay_list(), get_eigen_DF(), get_eigen_spline(), plot_nbTP_histogram(), plot_param_evolution()

Examples

## 8 subjects, 4 time-points, 3 variables
inputData <- acuteInflammation$data[0:32,1:3]
ind <- acuteInflammation$meta$ind[0:32]
time <- acuteInflammation$meta$time[0:32]
eigen <- get_eigen_spline(inputData, ind, time, nPC=NA, scaling="scaling_UV", method="nipals", verbose=TRUE, centering=TRUE, ncores=0)

# nipals calculated PCA
# Importance of component(s):
# loglik_smooth_spline

Calculate the penalised loglikelihood of a smooth.spline

## Description

Calculate the penalised loglikelihood of a smooth.spline using the integrated second derivative. The likelihood consists of 1) the (weighted) residuals sum of squares, 2) a penalty term (integrated second derivative = total curvature). The smaller the penalised loglikelihood, the better the fit as the residuals and penalty on roughness are minimised. Adapted from aroma.light::likelihood.smooth.spline.

## Usage

loglik_smooth_spline(fittedSmoothSpline)

## Arguments

- fittedSmoothSpline: A fitted smooth.spline
Value

The penalised loglikelihood.

Description

Plot an histogram of the number of time-trajectories with a given number of time-points. When the number of time-points is inferior to the \( df \) selected, a spline cannot be fitted. The histogram highlights the number and percentage of time-trajectories that will be rejected for a given \( df \).

Usage

\[
\text{plot_nbTP_histogram(eigen, dfCutOff = NA)}
\]

Arguments

eigen

A list of eigenSpline parameters as generated by \texttt{get_eigen_spline}, containing \texttt{eigen$matrix}, \texttt{eigen$variance}, \texttt{eigen$model} and \texttt{eigen$countTP}.

dfCutOff

(int) A number (a selected \( df \)) to highlight the portion of trajectories that would be rejected from the dataset (numberTP < \( df \)). Default is NA, with no cut-off plotted.

Value

A ggplot2 plotObject.

See Also

Graphical implementation with \texttt{santaR_start_GUI}.

Other DFsearch: \texttt{get_eigen_DFoverlay_list()}, \texttt{get_eigen_DF()}, \texttt{get_eigen_spline()}, \texttt{get_param_evolution()}, \texttt{plot_param_evolution()}

Examples

```r
## 8 subjects, 4 time-points, 3 variables, some missing values
inputData <- acuteInflammation$data[0:32,1:3]
inputData <- inputData[-1,]
inputData <- inputData[-8,]
inputData <- inputData[-30,]
inputData <- inputData[-29,]
ind <- acuteInflammation$meta$ind[0:32]
ind <- ind[-1]
ind <- ind[-8]
ind <- ind[-30]
ind <- ind[-29]
```
plot_param_evolution

Plot the evolution of different fitting parameters across all possible df for each eigenSpline

Description

Plot the evolution of 5 different fitting metrics (CV: Cross-Validation, GCV: Generalised Cross-Validation, AIC: Akaike Information Criterion, BIC: Bayesian Information Criterion, AICc: Akaike Information Criterion Corrected for small sample size) over all possible df for each eigenSpline generated by get_param_evolution.

Usage

plot_param_evolution(paramSpace, scaled = FALSE)

Arguments

paramSpace A list of n matrices (n being the number or eigenSplines) as generated by plot_param_evolution. Each matrix of fitting parameters has as rows different fitting metrics, as columns different df values.

scaled (bool) If TRUE, the value of each eigenSpline fitting parameter are scaled between 0 and 1. Default is TRUE.

Value

A list of ggplot2 plotObjects, one plot per fitting parameters. All results can be plotted using do.call(grid.arrange, returnedResult)

See Also

Graphical implementation with santaR_start_GUI

Other DFsearch: get_eigen_DFoverlay_list(), get_eigen_DF(), get_eigen_spline(), get_param_evolution(), plot_nbTP_histogram()
Examples

```r
## 8 subjects, 4 time-points, 3 variables
inputData <- acuteInflammation$data[1:32,1:3]
ind <- acuteInflammation$meta$ind[1:32]
time <- acuteInflammation$meta$time[1:32]
eigen <- get_eigen_spline(inputData, ind, time, nPC=NA, scaling="scaling_UV",
                         method="nipals", verbose=TRUE, centering=TRUE, ncores=0)
paramSpace <- get_param_evolution(eigen, step=0.25)
plotList <- plot_param_evolution(paramSpace, scaled=TRUE)
plotList[1]
#do.call(grid.arrange, plotList)
```

---

**santaR**

*santaR: A package for Short Asynchronous Time-series Analysis in R*

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Description

*santaR* provides a graphical and automated pipeline for the analysis of short time-series studies. It enables the detection of significantly altered time trajectories between study groups, while being resilient to missing values and unsynchronised measurements.

Details

The main functions of *santaR* are *santaR_start_GUI* to start the graphical user interface, as well as *santaR_auto_fit* and *santaR_auto_summary* for automated command line analysis and reporting. Refer to the vignettes for graphical user interface and command line tutorials.

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- Timothy Ebbels <t.ebbels@imperial.ac.uk> [contributor]
- Joe Cheng <joe@rstudio.com> (Shiny javascript custom-input control) [contributor]

See Also

Useful links:

- [https://github.com/adwolfer/santaR](https://github.com/adwolfer/santaR)
santaR_auto_fit

Automate all steps of santaR fitting. Confidence bands estimation and
p-values calculation for one or multiple variables

Description

santaR_auto_fit encompasses all the analytical steps for the detection of significantly altered
time trajectories (input data preparation: get_ind_time_matrix, establishing group membership: get_grouping, spline modelling of individual and group time evolutions: santaR_fit, computation of group mean curve confidence bands: santaR_CBand, identification of significantly altered time trajectories: santaR_pvalue_dist and/or santaR_pvalue_fit). As santaR is an univariate approach, multiple variables can be processed independently, which santaR_auto_fit can execute in parallel over multiple CPU cores.

Usage

santaR_auto_fit(
inputData,
ind,
time,
group = NA,
df,
ncores = 0,
CBand = TRUE,
pval.dist = TRUE,
pval.fit = FALSE,
nBoot = 1000,
alpha = 0.05,
nPerm = 1000,
nStep = 5000,
alphaPval = 0.05,
forceParIndTimeMat = FALSE
)

Arguments

inputData data.frame of measurements with observations as rows and variables as columns.
ind Vector of subject identifier (individual) corresponding to each measurement.
time Vector of the time corresponding to each measurement.
group NA or vector of group membership for each measurement. Default is NA for no groups.
df (float) Degree of freedom to employ for fitting the individual and group mean smooth.spline.
ncores (int) Number of cores to use for parallelisation. Default 0 for no parallelisation.
CBand If TRUE calculate confidence bands for group mean curves. Default is TRUE.
santaR_auto_fit

pval.dist  If TRUE calculate $p$-value based on inter-group mean curve distance. Default is TRUE.
pval.fit   If TRUE calculate $p$-value based on group mean curve improvement in fit. Default is FALSE.
nBoot     (int) Number of bootstrapping rounds for confidence band calculation. Default 1000.
alpha     (float) Confidence (0.05 for 95% Confidence Bands). Default 0.05.
nPerm     (int) Number of permutations for $p$-value calculation. Default 1000.
nStep     (int) Number of steps (granularity) employed for the calculation of the area between group mean curves ($p$-value dist). Default is 5000.
alphaPval  (float) Confidence Interval on the permuted $p$-value (0.05 for 95% Confidence Interval). Default 0.05.
forceParIndTimeMat
If TRUE parallelise the preparation of input data by get_ind_time_matrix. Default is FALSE.

Details

Note:

- The calculation of confidence bands accounts for approximately a third of the time taken by santaR_auto_fit, while the identification of significantly altered time trajectories (either santaR_pvalue_dist or santaR_pvalue_fit) accounts for two third of the total time. The time taken by these steps increases linearly with the increase of their respective parameters: nBoot for confidence bands, nPerm and nStep for identification of significantly altered trajectories using santaR_pvalue_dist, nPerm for santaR_pvalue_fit. Default values of these parameters are optimised to balance the time taken with the precision of the value estimation; increasing nPerm can tighten the $p$-value confidence intervals.

- If the parallelisation is activated (ncores>0), the fit of spline models, the calculation of confidence bands on the group mean curves and the identification of altered trajectories are executed for multiple variables simultaneously. However the preparation of input data (get_ind_time_matrix) is not parallelised by default as the parallelisation overhead cost is superior to the time potentially gained for all but the most complex datasets. The parallelisation overhead (instantiating worker nodes, duplicating and transferring inputs to the worker nodes, concatenating results) typically equals around 2 seconds, while executing get_ind_time_matrix is usually a matter of millisecond for a single variable (ex: 7 time-points, 24 individuals, 1 variable); the parallelisation overhead far exceeding the time needed to process all variables sequentially. If the number of individual trajectories (subjects), of time-points, or of variables is very large, forceParIndTimeMat enables the parallelisation of get_ind_time_matrix.

Value

A list of SANTAObj corresponding to each variable’s analysis result.
### Examples

```r
## 2 variables, 56 measurements, 8 subjects, 7 unique time-points
## Default parameter values decreased to ensure an execution < 2 seconds
inputData <- acuteInflammation$data[,1:2]
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
SANTAObjList <- santaR_auto_fit(inputData, ind, time, group, df=5, ncores=0, CBand=TRUE, pval.dist=TRUE, nBoot=100, nPerm=100)

# Input data generated: 0.02 secs
# Spline fitted: 0.03 secs
# ConfBands done: 0.53 secs
# p-val dist done: 0.79 secs
# total time: 1.37 secs
length(SANTAObjList)
# [1] 2
names(SANTAObjList)
# [1] "var_1" "var_2"
```

### Description

After multiple variables have been analysed using `santaR_auto_fit`, `santaR_auto_summary` helps identify significant results and summarise them in an interpretable fashion. Correction for multiple testing can be applied to generate Bonferroni [1], Benjamini-Hochberg [2] or Benjamini-Yekutieli [3] corrected p-values. P-values can be saved to disk in .csv files. For a given significance cut-off (plotCutOff), the number of variables significantly altered is reported and plots are automatically saved to disk by increasing p-value. The aspect of the plots can be altered such as the representation of confidence bands (showConfBand) or the generation of a mean curve across all samples (showTotalMeanCurve) to help assess difference between groups when group sizes are unbalanced.

### Usage

```r
santaR_auto_summary(
  SANTAObjList,
  targetFolder = NA,
  summaryCSV = TRUE,
  CSVName = "summary",
  savePlot = TRUE,
```
plotCutOff = 0.05,
showTotalMeanCurve = TRUE,
showConfBand = TRUE,
legend = TRUE,
fdrBH = TRUE,
fdrBY = FALSE,
fdrBonf = FALSE,
CIpval = TRUE,
plotAll = FALSE
)

Arguments

SANTAObjList          A list of SANTAObj with p-values calculated, as generated by santaR_auto_fit.
targetFolder          (NA or str) NA or the path to a folder in which to save summary.xls and plots. 
                        If NA no outputs are saved to disk. If targetFolder does not exist, folders will 
                        be created. Default is NA.
summaryCSV             If TRUE save the (corrected if applicable) p-values to 'CSVName'_summary.csv. 
                        'CSVName'_pvalue-all.csv,'CSVName'_pvalue-dist.csv,'CSVName'_pvalue-dist.csv 
                        (default summary_summary.csv,...). Default is TRUE.
CSVName                (string) Filename of the csv to save. Default is 'summary'.
savePlot               If TRUE save to targetFolder all variables with $p < $plotCutOff ordered by 
                        p-values. Default is TRUE.
plotCutOff             (float) P-value cut-off value to save summary plots to disk. Default 0.05.
showTotalMeanCurve     If TRUE add the mean curve across all groups on the plots. Default is TRUE.
showConfBand           If TRUE plot the confidence band for each group. Default is TRUE.
legend                 If TRUE add a legend to the plots. Default is TRUE.
fdrBH                  If TRUE add the Benjamini-Hochberg corrected p-value to the output. Default 
                        is TRUE.
fdrBY                  If TRUE add the Benjamini-Yekutieli corrected p-value to the output. Default 
                        is FALSE.
fdrBonf                If TRUE add the Bonferroni corrected p-value to the output. Default is FALSE.
CIpval                 If TRUE add the upper and lower confidence interval on p-value to the output. 
                        Default is TRUE.
plotAll                If TRUE override the plotCutOff parameter and plot all variables. Default is 
                        FALSE.

Value

A list: result$pval.all data.frame of p-values, with all variables as rows and different p-value 
        corrections as columns. result$pval.summary data.frame of number of variables with a p-value 
        inferior to a cut-off. Different metric and p-value correction as rows, different cut-off (Inf 0.05, Inf 
        0.01, Inf 0.001) as columns.
References


See Also

Other AutoProcess: `santaR_auto_fit()`, `santaR_plot()`, `santaR_start_GUI()`

Other Analysis: `get_grouping()`, `get_ind_time_matrix()`, `santaR_CBand()`, `santaR_auto_fit()`, `santaR_fit()`, `santaR_plot()`, `santaR_pvalue_dist()`, `santaR_pvalue_fit()`, `santaR_start_GUI()`

Examples

```r
## 2 variables, 56 measurements, 8 subjects, 7 unique time-points
## Default parameter values decreased to ensure an execution < 2 seconds
inputData <- acuteInflammation$data[,1:2]
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
SANTAObjList <- santaR_auto_fit(inputData, ind, time, group, df=5, ncores=0, CBand=TRUE, pval.dist=TRUE, nBoot=100, nPerm=100)

# Input data generated: 0.02 secs
# Spline fitted: 0.03 secs
# ConfBands done: 0.53 secs
# p-val dist done: 0.79 secs
# total time: 1.37 secs
result <- santaR_auto_summary(SANTAObjList)
print(result)
# $pval.all
#   dist  dist_upper  dist_lower  curveCorr  dist_BH
# var_1  0.03960396  0.09783202  0.01543922 3.2429725352 0.03960396
# var_2  0.00990099  0.05432519  0.00173774 0.0006572238 0.01980198
#
# $pval.summary
#     Test  Inf 0.05  Inf 0.01  Inf 0.001
# 1     dist  2    1    0
# 2     dist_BH  2    0    0
```
Description

Generate bootstrapped group mean curve Confidence Bands, by resampling of individual curves with replacement. Returns a SANTAObj with added Confidence Bands.

- Resampling whole data curves assumes less of the data than resampling of residuals.
- The resampled distribution is of same size as the original distribution (same number of individuals in each group as in the input data).
- The degree of freedom for the estimator is identical to the one employed for curve fitting in santaR_fit.

Usage

santaR_CBand(SANTAObj, nBoot = 1000, alpha = 0.05, subsampling = 250)

Arguments

- **SANTAObj**: A fitted SANTAObj as generated by santaR_fit.
- **nBoot**: (int) Number of bootstrapping rounds. Default 1000.
- **alpha**: (float) Confidence (0.05 for 95% Confidence Bands). Default 0.05.
- **subsampling**: (int) Number of points to sample in the time range (for the estimator and Confidence Bands). Default is 250.

Value

A SANTAObj with added Confidence Bands for each group.

See Also

Other Analysis: get_grouping(), get_ind_time_matrix(), santaR_auto_fit(), santaR_auto_summary(), santaR_fit(), santaR_plot(), santaR_pvalue_dist(), santaR_pvalue_fit(), santaR_start_GUI()
Generate a SANTAObj containing all the splines model for individual and group time evolutions. Once all the splines representing individual and group evolutions are fitted, all time-points are back-projected and employed in subsequent analysis in place of the input measurements (functional approach). A grouping can be provided to separate individuals and compare trajectories: any number of groups can be provided, but comparison of group trajectories can only be executed between 2 groups.

- Individual trajectories with less than 4 time-points are rejected due to constraints on `smooth.spline` fitting (number of time-points < 4).
- Individual trajectories with less time-points than `df` are rejected due to constraints on `smooth.spline` fitting (number of time-points < `df`).
- Rejected individual trajectories are not taken into account for mean curves calculations.

Usage

```r
santaR_fit(inputMatrix, df, grouping = NA, verbose = TRUE)
```

Arguments

- `inputMatrix` data.frame of measurements for each IND x TIME as generated by `get_ind_time_matrix`. Rows are unique Individual IDs and columns unique measurement Time. Pairs of (IND,TIME) without a measurement are left as NA.
- `df` (float) Degree of freedom to employ for fitting the `smooth.spline`
- `grouping` NA or a data.frame with 2 columns (ind and group) listing as rows each unique Individual ID and the corresponding group membership, as generated by `get_grouping`. Default is NA for no groups.
- `verbose` (bool) If TRUE output the progress of fitting. Default is TRUE.

Value

A SANTAObj containing all the spline models with individual and group time evolutions, for further analysis.

Details:: The returned SANTAObj is structured as follow:

- `SANTAObj` santaR object for further analysis
- `SANTAObj$properties$df` input degree of freedom
- `SANTAObj$properties$CBand$status` Confidence Bands for group mean curve calculated (TRUE or FALSE)
- `SANTAObj$properties$CBand$nBoot` parameter, number of bootstrap rounds for calculation of the group mean curve confidence bands
- `SANTAObj$properties$CBand$alpha` parameter, confidence of the group mean curve band
SANTAObj$properties$pval.dist$status  
*p*-value distance calculated (*TRUE* or *FALSE*)

SANTAObj$properties$pval.dist$nPerm  
parameter, number of permutations for calculation of distance *p*-value

SANTAObj$properties$pval.dist$alpha  
parameter, confidence on the bootstrapped *p*-value

SANTAObj$properties$pval.fit$status  
*p*-value fitting calculated (*TRUE* or *FALSE*)

SANTAObj$properties$pval.fit$nPerm  
parameter, number of permutations for calculation of fitting *p*-value

SANTAObj$properties$pval.fit$alpha  
parameter, confidence on the bootstrapped *p*-value

SANTAObj$general$inputData  
`inputMatrix`

SANTAObj$general$cleanData.in  
only kept individuals INPUT values (equivalent to `inputMatrix` - rejected)

SANTAObj$general$cleanData.pred  
only kept individuals PREDICTED values on Ind splines

SANTAObj$general$meanCurve  
`spline fit over all kept datapoint` ([`cleanData.pred`]) `smooth.spline` object

SANTAObj$general$pval.curveCorr  
Pearson correlation coefficient between the two group curves, to detect highly correlated group shapes if required.

SANTAObj$general$pval.dist  
P-value between groups based on distance between groupMeanCurves

SANTAObj$general$pval.dist$l  
lower bound confidence interval on *p*-value

SANTAObj$general$pval.dist$u  
upper bound confidence interval on *p*-value

SANTAObj$general$pval.fit  
P-value between groups based on groupMeanCurves fitting

SANTAObj$general$pval.fit$l  
lower bound confidence interval on *p*-value

SANTAObj$general$pval.fit$u  
upper bound confidence interval on *p*-value

SANTAObj$groups  
list of group information

SANTAObj$groupsrejectedInd  
list of rejected individual (#tp < 4 or df) | data

SANTAObj$groupscurveInd  
list of spline fit | `smooth.spline` object

SANTAObj$groupMeanCurve  
spline fit over groupData.pred | `smooth.spline` object

SANTAObj$groupMeanCurve[in  
all group points INPUT values (x,y) [kept individuals]

SANTAObj$groupMeanCurve[pred  
all group points PREDICTED values on Ind splines (x,y)

SANTAObj$groups$groupData.in  
only individuals from this group INPUT value (IND x TIME)

SANTAObj$groups$groupData.pred  
only individuals from this group PREDICTED values on Ind splines (x,y)

See Also

Other Analysis: `get_grouping()`, `get_ind_time_matrix()`, `santaR_CBand()`, `santaR_auto_fit()`, `santaR_auto_summary()`, `santaR_plot()`, `santaR_pvalue_dist()`, `santaR_pvalue_fit()`, `santaR_start_GUI()`

Examples

```r
## 56 measurements, 8 subjects, 7 unique time-points
Yi <- acuteInflammation$data$var_1
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
grouping <- get_grouping(ind, group)
inputMatrix <- get_ind_time_matrix(Yi, ind, time)
resultSANTAObj <- santaR_fit(inputMatrix, df=5, grouping=grouping, verbose=TRUE)
```
santaR_plot  
Plot a SANTAObj

Description
Plot a SANTAObj generated by santaR_fit. Returns a ggplot2 plotObject that can be further modified using ggplot2 grammar.

Usage
santaR_plot(
  SANTAObj,
  title = "",
  legend = TRUE,
  showIndPoint = TRUE,
  showIndCurve = TRUE,
  showGroupMeanCurve = TRUE,
  showTotalMeanCurve = FALSE,
  showConfBand = TRUE,
  colorVect = NA,
  sampling = 250,
  xlab = "x",
  ylab = "y",
  shortInd = FALSE
)

Arguments
SANTAObj  A fitted SANTAObj as generated by santaR_fit.
title     (str) A plot title. The default title is empty.
legend    (bool) If TRUE a legend panel is added to the right. Default is TRUE. Note: the legend cannot be generated if only the Confidence Bands or the Total Mean Curve are plotted.
showIndPoint (bool) If TRUE plot each input measurements (in group color). Default is TRUE.
showIndCurve (bool) If TRUE plot each individual’s curve (in group color). Default is TRUE.
showGroupMeanCurve (bool) If TRUE plot the mean curve for each group (in group color). Default is TRUE.
showTotalMeanCurve (bool) If TRUE plot the mean curve across all measurements and groups (in grey). Default is FALSE.
showConfBand If TRUE plot the confidence bands calculated with santaR_CBand.
colorVect  Vector of ggplot2 colors. The number of colors must match the number of groups (ex:colorVect=c("deepskyblue","red")).
**santaR_pvalue_dist**

- **sampling** (int) Number of data points to use when plotting each spline (sub-sampling). Default is 250.
- **xlab** (str) x-axis label. Default is 'x'.
- **ylab** (str) y-axis label. Default is 'y'.
- **shortInd** if TRUE individual trajectories are only plotted on the range on which they are defined. Default is FALSE.

**Value**

A ggplot2 plotObject.

**See Also**

Other Analysis: `get_grouping()`, `get_ind_time_matrix()`, `santaR_CBand()`, `santaR_auto_fit()`, `santaR_auto_summary()`, `santaR_fit()`, `santaR_pvalue_dist()`, `santaR_pvalue_fit()`, `santaR_start_GUI()`

Other AutoProcess: `santaR_auto_fit()`, `santaR_auto_summary()`, `santaR_start_GUI()`

**Examples**

```r
## 56 measurements, 8 subjects, 7 unique time-points
Yi <- acuteInflammation$data$var_3
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
grouping <- get_grouping(ind, group)
inputMatrix <- get_ind_time_matrix(Yi, ind, time)
SANTAObj <- santaR_fit(inputMatrix, df=5, grouping=grouping, verbose=TRUE)
SANTAObj <- santaR_CBand(SANTAObj, nBoot=100)
p <- santaR_plot(SANTAObj, title='Example')
print(p)
```

**Description**

Evaluate the difference in group trajectories based on the comparison of distance between group mean curves. Individual group membership is repeatedly randomly permuted to generate new random groups and group mean curves, then employed to compute a Null distribution of distance between group mean curves. The distance between two group mean curves is defined as the area between both curves. The distance between the real group mean curves is then compared to this Null distribution and a p-value is computed.

- The Pearson correlation coefficient between the two group mean curves is calculated to detect highly correlated group shapes if required.
• The \( p \)-value is calculated as \( (b+1)/(n\text{Perm}+1) \) as to not report a \( p \)-value=0 (which would give problem with FDR correction) and reduce type I error.

• The \( p \)-value will vary depending on the random sampling. Therefore a confidence interval can be constructed using Wilson’s interval which presents good properties for small number of trials and probabilities close to 0 or 1.

Usage

\[
\text{santaR\_pvalue\_dist(SANTAObj, nPerm = 1000, nStep = 5000, alpha = 0.05)}
\]

Arguments

- \text{SANTAObj} A fitted \text{SANTAObj} as generated by \text{santaR\_fit}.
- \text{nPerm} (int) Number of permutations. Default 1000.
- \text{nStep} (int) Number of steps employed for the calculation of the area between group mean curves. Default is 5000.
- \text{alpha} (float) Confidence Interval on the permuted \( p \)-value (0.05 for 95\% Confidence Interval). Default 0.05.

Value

A \text{SANTAObj} with added \( p \)-value dist and confidence interval on the \( p \)-value.

See Also

Comparison with constant model with \text{santaR\_pvalue\_dist\_within}

Other Analysis: \text{get\_grouping()}, \text{get\_ind\_time\_matrix()}, \text{santaR\_CBand()}, \text{santaR\_auto\_fit()}, \text{santaR\_auto\_summary()}, \text{santaR\_fit()}, \text{santaR\_plot()}, \text{santaR\_pvalue\_fit()}, \text{santaR\_start\_GUI()}

Examples

```r
## 56 measurements, 8 subjects, 7 unique time-points
## Default parameter values decreased to ensure an execution < 2 seconds
Yi <- acuteInflammation$data$var_3
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
grouping <- get_grouping(ind, group)
inputMatrix <- get_ind_time_matrix(Yi, ind, time)
SANTAObj <- santaR_fit(inputMatrix, df=5, grouping=grouping, verbose=TRUE)
SANTAObj <- santaR_pvalue_dist(SANTAObj, nPerm=100)
```
**santaR_pvalue_dist_within**

Evaluates the difference between a group mean curve and a constant model.

**Description**

Execute a t-test based on the comparison of distance between a group mean curve and a constant linear model. Generate \( n \) constant linear model. The Null distribution is generated by permuting the \( n \) group individuals and the \( n \) constant trajectories. The real distance (area) between the group trajectory and the flat trajectory is compared to the Null distribution of distances, similarly to `santaR_pvalue_dist`.

**Usage**

```r
santaR_pvalue_dist_within(SANTAGroup, nPerm = 1000, nStep = 5000)
```

**Arguments**

- **SANTAGroup**: A fitted group extracted from a `SANTAObj` generated by `santaR_fit`.
- **nPerm**: (int) Number of permutations. Default 1000.
- **nStep**: (int) Number of steps employed for the calculation of the area between group mean curves. Default is 5000.

**Value**

A \( p \)-value

**See Also**

Inter-group comparison with `santaR_pvalue_dist`

**Examples**

```r
## 56 measurements, 8 subjects, 7 unique time-points
## Default parameter values decreased to ensure an execution < 2 seconds
Yi <- acuteInflammation$data$var_3
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
grouping <- get_grouping(ind, group)
inputMatrix <- get_ind_time_matrix(Yi, ind, time)
SANTAObj <- santaR_fit(inputMatrix, df=5, grouping=grouping, verbose=TRUE)
SANTAGroup <- SANTAObj$groups[[2]]
#SANTAGroup <- SANTAObj$groups$Group2
santaR_pvalue_dist_within(SANTAGroup, nPerm=500)
# ~0.00990099
```
santaR_pvalue_fit Evaluate difference in group trajectories based on the comparison of model fit (F-test) between one and two groups

Description

Evaluate the difference in group trajectories by executing a t-test based on the comparison of improvement in model fit (F-test) between fitting one group mean curve to all individuals and fitting two group mean curves. This between-class differential evolution test, evaluates whether fitting 2 group curves decreases the residuals compared to a single group mean curve. The statistic employed is defined as a quantification of evidence for differential evolution, with the larger the statistic the more differentially evolving the variable appears to be. Individual group membership is repeated randomly permuted to generate new random groups and group mean curves, then employed to compute a Null distribution of the statistic (improvement in model fit from one to two groups). The improvement in model fit for the real group membership is then compared to this Null distribution (of no group difference) and a p-value is computed. Adapted from Storey and al. 'Significance analysis of time course microarray experiments', PNAS, 2005 [1].

- The p-value is calculated as (b+1)/(nPerm+1) as to not report a p-value=0 (which would give problem with FDR correction) and reduce type I error.
- The p-value will vary depending on the random sampling. Therefore a confidence interval can be constructed using Wilson’s interval which presents good properties for small number of trials and probabilities close to 0 or 1.

Usage

santaR_pvalue_fit(SANTAObj, nPerm = 1000, alpha = 0.05)

Arguments

SANTAObj A fitted SANTAObj as generated by santaR_fit.
nPerm (int) Number of permutations. Default 1000.
alpha (float) Confidence Interval on the permuted p-value (0.05 for 95% Confidence Interval). Default 0.05.

Value

A SANTAObj with added p-value fit and confidence interval on the p-value.

References

**santaR_pvalue_fit_within**

*Evaluate difference between a group mean curve and a constant model using the comparison of model fit (F-test)*

### Description

Execute a t-test based on the comparison of improvement of model fit from a single group mean curve to the fit of both a group mean curve and a constant linear model. This statistic identifies within-class differential evolution, and test whether the population average time curve is flat or not. 

$n$ constant linear model are generated to match the $n$ individual trajetories. The **Null** distribution is generated by permuting the $n$ group individuals and the $n$ constant trajectories. The real improvement in model fit for the real group membership versus flat trajectories is then compared to the **Null** distribution of model fit improvement, similarly to `santaR_pvalue_fit`. Adapted from Storey and al. 'Significance analysis of time course microarray experiments', PNAS, 2005 [1].

### Usage

```r
santaR_pvalue_fit_within(SANTAGroup, nPerm = 1000)
```

### Arguments

- **SANTAGroup**: A fitted group extracted from a `SANTAObj` generated by `santaR_fit`.
- **nPerm**: (int) Number of permutations. Default 1000.

### Value

A *p*-value.
References


See Also

Inter-group comparison with `santaR_pvalue_fit`

Examples

```r
# 56 measurements, 8 subjects, 7 unique time-points
# Default parameter values decreased to ensure an execution < 2 seconds
Yi <- acuteInflammation$data$var_3
ind <- acuteInflammation$meta$ind
time <- acuteInflammation$meta$time
group <- acuteInflammation$meta$group
grouping <- get_grouping(ind, group)
inputMatrix <- get_ind_time_matrix(Yi, ind, time)
SANTAObj <- santaR_fit(inputMatrix, df=5, grouping=grouping, verbose=TRUE)
SANTAGroup <- SANTAObj$groups[[1]]
#SANTAGroup <- SANTAObj$groups$Group1
santaR_pvalue_fit_within(SANTAGroup, nPerm=500)
# ~0.6726747
```

santaR start GUI

santaR Graphical User Interface

Description

santaR Graphical User Interface (GUI) implements all the functions for short asynchronous time-series analysis. To exit press ESC in the command line. Once started, the GUI presents 4 tabs corresponding to the main steps of analysis: *Import, DF search, Analysis* and *Export*.

- The *Import* tab manages input data in comma separated value (csv) format or as an *RData* file containing a SANTAObj previously generated with *santaR*. Once data is imported the *DF search* and *Analysis* tabs become available.

- *DF search* implements the tools for the selection of an optimal number of degrees of freedom (df).

- With the data imported and a pertinent df selected, *Analysis* regroups the interface to visualise and identify variables significantly altered over time. All options present in the command line version of *santaR* are available, with the added possibility to modify the class labelling of each subject (group). A plotting interface enables the interactive visualisation of the raw data points, individual trajectories, group mean curves and confidence bands for all variables, which subsequently can be saved. Finally, if inter-group differential trajectories have been characterised, all significance testing results (with correction for multiple testing) are presented in interactive tables.
The Export tab manages the saving of results and automated reporting. Fitted data is saved as a SANTAObj, which contains all inputs and outputs, and can be downloaded as an RData file for future analysis, or reproduction of results. csv files containing significance testing results can also be generated and summary plot for each significantly altered variable saved for rapid evaluation.

`santaR`'s command line procedure is the most efficient approach for very high number of variables due to the added level of automation. However the GUI can help understand the use of the methodology, select the best parameters on a subset of the data, or to visually explore the results.

Usage

```r
santaR_start_GUI(browser = TRUE)
```

Arguments

- `browser`: If TRUE open the graphical user interface in a web browser instead of a R window. Default is TRUE

Value

None, start GUI. To exit press ESC in the command line.

See Also

Other AutoProcess: `santaR_auto_fit()`, `santaR_auto_summary()`, `santaR_plot()`

Other Analysis: `get_grouping()`, `get_ind_time_matrix()`, `santaR_CBand()`, `santaR_auto_fit()`, `santaR_auto_summary()`, `santaR_fit()`, `santaR_plot()`, `santaR_pvalue_dist()`, `santaR_pvalue_fit()`

Examples

```r
## Not run:
## Start graphical interface, press 'ESC' in the command line to stop.
santaR_start_GUI()
## End(Not run)
```

---

**scaling_mean**

Mean scaling of each column

Description

Scale each variable (column) by the mean. Mean-scaling applied as (value - mean) / mean. As `scaling_UV` might give too much importance to flat trajectories due to the division by the standard deviation, by dividing by the mean, high intensity values will have a lower influence and the low intensity will be boosted.
Usage

```
scaling_mean(inputMat)
```

Arguments

- `inputMat` (Observation x Variable) data.frame of measurements, with observations as rows and different variables as columns.

Value

Matrix of measurements mean-scaled columnwise.

Examples

```R
## Not run:
inputMat <- data.frame(matrix(c(1,4,7, 8,4,0, 3,6,9), nrow=3))
scaling_mean(inputMat)
#   X1  X2  X3
# [1,] -0.75 1 -0.5
# [2,] 0.00 0 0.0
# [3,] 0.75 -1 0.5
## End(Not run)
```

---

### scaling_UV

Unit-Variance scaling of each column

Description

Unit-Variance (UV) scale each variable (column). UV-scaling applied as (value - mean) / stdev. Unit-Variance Scaling or Autoscaling, is commonly applied and uses the standard deviation as the scaling factor. After autoscaling, all metabolites have a standard deviation of one and therefore the data is analyzed on the basis of correlations instead of covariances.

Usage

```
scaling_UV(inputMat)
```

Arguments

- `inputMat` (Observation x Variable) data.frame of measurements, with observations as rows and different variables as columns.

Value

Matrix of measurements UV-scaled columnwise.
Examples

```r
## Not run:
inputMat <- data.frame(matrix(c(1,4,7, 8,4,0, 3,6,9), nrow=3))
scaling_UV(inputMat)
#      X1 X2 X3
# [1,] -1  1 -1
# [2,]  0  0  0
# [3,]  1 -1  1
## End(Not run)
```
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