Package ‘TTAinterfaceTrendAnalysis’

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Type Package

Title Temporal Trend Analysis Graphical Interface

Version 1.5.1

Date 2014-02-20

Description This interface was created to develop a standard procedure of temporal trend analysis in the framework of the OSPAR convention. It is based on four successive steps: simply manipulate your database, select the parameters you want to analyse, build your regulated time series, perform analysis and read the results all in one easy to use interface. Statistical analysis call other package function such as Kendall tests (wq package) or cusum function (Pastec package).

License GPL (>= 2)

Depends R (>= 3.0.0), base, stats, grDevices

Imports Hmisc, pastecs, reshape, wq, e1071, timeSeries, fBasics, relimp, multcomp, nlme, tcltk, lubridate, tcltk2

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**TTAinterface-package**  
*Interface Package for Temporal Trend Analysis*

**Description**

A friendly interface to perform Temporal Trend Analyses (MannKendall tests). Just follow the successive step from the data formatting to the results sorting.

**Details**

- **Package:** TTAinterface
- **Type:** Package
- **Version:** 1.5.1
- **Date:** 2014-02-20
- **License:** GPL (>=2)

**Author(s)**

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**Envir**  
*A temporary environment to stock data and objects*

**Description**

The function create an environment where the data, arguments and objects that are used between the different functions of the package will be stock for better exchange processes.

**Usage**

`Envir()`

**Details**

Objects passed through the environment 'Envir' are called in the other function as Envir$objects
fixdata

**Fixdata function**

**Description**

Simply modify your dataset through the interface.

**Usage**

```r
fixdata()
```

**Value**

The edited database that is automatically read by the interface to replace former values.

**Note**

`fixdata()` calls the function `fix()` that acts on the raw data base. The `fix()` function itself calls the function `edit()` from the package `utils`.

**See Also**

`fix`, `edit`

---

**FULLoption**

**Main function**

**Description**

This is the core function of the interface. It receives arguments from the interface (see the function `<TTAinterface()>`) and builds regularized time series, performs diagnostics and analyses.

**Usage**

```r
FULLoption(param, depth=NULL, sal = NULL, site=NULL, rawdata="NO", select="NO",
    resume.reg="NO", test.normality="NO", plotB = "NO",
    selectBox="ByYears", log.trans="NO", plotZ="NO", datashow="NO",
    help.timestep = "NO", auto.timestep = "NO", time.step = NULL,
    help.aggreg = "NO", auto.aggreg = "NO", aggreg = NULL, mix = "YES",
    outliers.re = "NO", na.replace="NO", start = NULL, end = NULL,
    months = c(1:12), norm = "NO", npsu = 30, autocorr = "NO",
    spectrum="NO", anomaly="NO", a.barplot="NO", zsmooth="NO",
    local.trend = "NO", test = "HK")
```
Arguments

**param**
The name of the parameter you want to analyse it must be the name of the column where are your data. Have to be enter like this: "yourparam".

**depth**
If existing, the depth interval where your data will be analyse. If values are different from depth max and depth min, missing value are exclude Depth column must be name as 'DEPTH'. Enter the value like this: c(a,b). For analysis at one specific depth you can enter c(a,a).

**sal**
Same thing as for the depth Salinity column must be name as 'S'.

**site**
Labels of sampling site as they appears in the database Enter the value like this c("S1", "S2").

**rawdata**
Peform desciptive statistics on raw database, can be "YES" or "NO" (the default).

**select**
Peform desciptive statistics on selected parameter and site, can be "YES" or "NO" (the default).

**resume.reg**
Peform desciptive statistics on regularized time series, can be "YES" or "NO" (the default).

**test.normality**
Perform a Shapiro-Wilk normality test on selected parameter, can be "YES" or "NO" (the default).

**plotB**
Display a boxplot of rawdata with outliers identified as cirle, can be "YES" or "NO" (the default).

**selectBox**
Options for plotB: allow to choose between boxplot by years or by months.

**log.trans**
This option transform your data in log(x+1) prior to perform analysis.

**plotZ**
Display a plot of the regularized time series, can be "YES" or "NO" (the default).

**datashow**
Show a table of the regularized data, can be "YES" or "NO" (the default).

**help.timestep**
Display an advice for time step selection, base on the mean time that separate two successive measurements. Can be "YES" or "NO" (the default).

**auto.timestep**
Autoexecute the advice without display it.

**time.step**
Choice of the time step for data aggregation during the build of the time series, can be "Fortnight", "Semi-fortnight", "Mensual", "Annual" or "Mono-mensual" for an aggregation of the data of a month of all years (e.g. all January data).

**help.aggreg**
Display an advice for method of aggregation selection, base on Wilcoxon p.value between rawdata and the different method. Can be "YES" or "NO" (the default).

**auto.aggreg**
Autoexecute the advice without display it.

**aggreg**
Choice of the method of aggregation during the build of the time series, can be "Mean", "Median", "Max" for maximal value selection or "Quantile" for selection of the quantile 90

**mix**
Allow to mix the data of all sampling site during analysis. Permanently set to "YES" and removed from the GUI since version 1.5.

**outliers.re**
Remove the outliers from the rawdata, the outliers list is save in a .csv file. (for outliers visual identification see boxplot section).
**FULLoption**

- **na.replace**: Replace missing values with median of the corresponding cycle (week, month...) for lags longer than 3 days and linear regression for shorter missed period. Can be "YES" or "NO" (the default).

- **start**: Define the first year of data analysis (by default the first of the database).

- **end**: Define the last year of data analysis (by default the last of the database).

- **months**: Define the months of data analysis (by default the twelve months).

- **norm**: Compute normalised values of nutrients at the salinity npsu for each years, can be "YES" or "NO" (the default).

- **npsu**: Compute normalised values of nutrients at the salinity npsu for each years, 30 by default.

- **autocorr**: Display the autocorrelation diagramme of the regularized time series using the acf function with arguments : lag.max = ((nrow(TimeSerie))/2), na.action = na.pass. Can be "YES" or "NO" (the default)

- **spectrum**: Display the Fourrier spectrum of the regularized time series using a Smoothed Periodogram (spec.pgram). Can be "YES" or "NO" (the default).

- **anomaly**: Display a color box (function filled.contour) plot by year each time.step (months or weeks) minus the mean of the time.step of all years. Red colors show positive anomalies and blue colors negative anomalies. Can be "YES" or "NO" (the default).

- **a.barplot**: Display an anomaly barplot as a function of the time.step. Red colors show positive anomalies and blue colors negative anomalies. Can be "YES" or "NO" (the default).

- **zsmooth**: Display a detrended plot of the time series using the stl function with arguments s.window="periodic", na.action=na.fail. Can be "YES" or "NO" (the default).

- **local.trend**: Display the interactive cusum plot of the time series (local.trend of the pastecs package) that allow to manually identify the period of change in the tendency using the function identify and perform a Kendall familly test on each identified period (see test section). Can be "YES" or "NO" (the default).

- **test**: Perform a test to evaluate the presence and the magnitude of a temporal trend on the time series. Can be "MK" for Seasonal Mann-Kendall test (the default), "SMK" for the same test with detail for each time step, "LOESS" that fit a polynomial surface determined by one or more numerical predictors, using local fitting; a MK is perform on this fitting.

**Value**

Results are return as .png figures or .txt files Results are also directly readable directly in the right part of the interface.

Savepath can be choose using the option 'Select directory' (see the function selectdirectory more informations)

Name of saved filed follow the nomenclature : Original.file.name_analysis.name_parameter.txt/.png

or for multiple period analysis (see cusum for more details) : Original.file.name_analysis.name_parameter_starting.year_ending.years.txt

analysis.names are:
Description

Allow to chose the directory where results (.txt and .png files) will be saved.

Usage

selectdirectory()

Details

It select the main save directory; the package will create appropriate sub-folder as function of selected parameters, statistics, methods etc. Then you will be able to perform successive analyses without overwriting the previous results.
SRNDunkerque

Coastal survey near the Gravelines power plant form 1995 to 2010

Description

Variation in temperature, salinity and chlorophyll-a concentration (microg/l) monthly measured between 1995 and 2010 at three different stations distributed onshore to offshore (North See) near the city of Dunkerque (north of France) for the SRN monitoring program (Ifremer). This database contain many missing values.

Usage

SRNDunkerque

Format

A data.frame (TXT) containing 1561 measurements of temperature, salinity and chlorophyll-a concentration

Source

The Ifremer QUADRIGE_2 meta-database

TTAinterface

Graphic Interface For Temporal Trend Analysis

Description

A friendly user graphic interface to perform temporal trend analysis. The interface offer multiple options to select parameters and build time series that the user can follow step by step. Some options are selected by default to let the hurry user to do really quick analysis. Some diagnostic tools are also present.

Usage

TTAinterface()

Value

Results are saved in .txt files or .png figures in the desire directory (see selectdirectory). See 'FULLoption' values for more details.

Author(s)

David Devreker
See Also

FULLoption fixdata selectdirectory
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