

Package ‘genasis’

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computational tools

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Depends R (>= 2.0.1), Kendall, fitdistrplus

Description

genasis package contains methods for air pollution assessment. Concerned on persistent organic pollutants, the package allows to compute trends of their concentrations, compare different datasets and estimate relations between values from active and passive air samplers.

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genanaggr	<i>Computes annual aggregations from (relevant) POPs concentration data</i>
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Description

Function `genannagr` aggregates (concentration) values over time using selected aggregation function. Aggregation is made for whole years by the middle time points of measurement intervals. If assumptions on number of measurements or their (semi)equidistance are not met, the aggregation is flagged and eventually discarded.

Usage

```
genanaggr(x, y=NA, input="openair", output=NA,
          pollutant=NA, method="mean", minn=4,
          gap=3, show.flagged=FALSE)
```

Arguments

<code>x</code>	vector of concentration values or data frame of "genasis"/"openair" type. See 'Details' for more detailed description of both data types.
<code>y</code>	vector of measurement dates in the case of vector input only.
<code>input</code>	type of data.frame in the case of data.frame input. The allowed values are "openair" (default) and "genasis". In case of vector input, this argument is meaningless.
<code>output</code>	type of output data.frame. As in the input argument, both data frames "openair" and "genasis" are available, with the default value equal to input.
<code>pollutant</code>	name of the pollutant(s), for which the aggregation is made. Not necessary if only data for one pollutant is available in <code>x</code> . If not specified, the aggregation is made for all pollutants in <code>x</code> .
<code>method</code>	a function to compute the aggregation which can be applied to all pollutants data.
<code>minn</code>	the minimal number of measurements for receiving result without the flag.
<code>gap</code>	the maximal size of a time gap between two consequent measurements as a multiple of average time between measurements in given year for receiving result without the flag.
<code>show.flagged</code>	logical. If TRUE, the flagged values are allowed in result, If FALSE, these values are replaced by NAs.

Details

Function `genanaggr` computes annual aggregations of measured (concentration) values. The function recognises three different input formats: Option `input="openair"` uses `openair` format of data frame with first column of name `"date"` and type `"Date"`, optional columns of names `"date_end"`, `"temp"`, `"wind"` and `"note"` and other columns of type `"numeric"` containing concentration values and named by names of the compounds. `input="genasis"` is used for the data frame with six columns `"valu"`, `"comp"`, `"date_start"`, `"date_end"`, `"temp"` and `"wind"` where the first, fifth and sixth are of class `"numeric"`, second of class `"character"` and third and fourth columns could be both `"character"` or `"Date"` type. The names of columns in `input="genasis"` are not rigid, only their order is assumed. There is also a possibility to specify `x` and `y` as two vectors of equal length, first of type `numeric` containing concentration values, second of type `"character"` or `Date` containing measurement dates.

There is no report in a case of vector output. In a case of `output="openair"`, the problematic rows are flagged in column `"note"` with a list of problematic compound. Finally in a case of `output="genasis"`, there is a detailed description of the problem (unfulfilled criterion) in the relevant row of the data frame of `"genasis"` type.

If there is only a single date (date column in `"openair"`, `date_start` column in `"genasis"` type data frame or `y` in the case of vector input), it is used directly, whereafter if a range is available (specified by `date_end` in both data.frame formats), the middle day of the range is computed. If only the month (as `"2013-05"` or `"5.2013"`) or the year (as `"2013"`) is specified, the date is placed into the 15th day in the case of month or into a 1st July in the case of year.

An user-specified function is used for computing the aggregations for all pollutants (or another parameters), except of reserved names `"temp"` and `"wind"`, for which the arithmetic mean is used. It can be a function or a symbol or character string naming a function on a numeric vector.

There are two conditions of usability of (concentration) values inside individual years for the aggregation. First, the `minn` argument, default set up to 4, which restricts the minimal number of measurements during each year as a criteria of representativeness and second, the `gap` argument, default set up to 3, which restricts the maximal time gap between consequents measurements (and start/end of the year) in scale of average time gap between them as a criteria of equidistance. If not both conditions are met, the aggregation is flagged (by a note in column `note` in case of data frame) and according to a logical value of the `show.flagged`, the results are shown or replaced by NAs.

Value

a list containing:

<code>res</code>	Aggregated data frame of <code>"openair"/"genasis"</code> format or vector of aggregated values in case of vector input. Start and end dates are set up to 1st January and 31st December of each year. There is also the column <code>"note"</code> containing flags and brief description of their reason in both data farme output formats.
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References

Klanova, J.; Dusek, L.; Boruvkova, J.; Hulek, R.; Sebkova, K. i.; Gregor, J.; Jarkovsky, J.; Kalina, J.; Hrebicek, J. and Holoubek, I. (2012) The initial analysis of the Global Monitoring Plan (GMP) reports and a detailed proposal to develop an interactive on-line data storage, handling, and presentation module for the GMP in the framework of the GENASIS database and risk assessment tool. Masaryk University, pp. 157.

See Also

[genloq](#), [genoutlier](#), [genhistogram](#), [genpastaact](#), [genplot](#), [genstatistic](#), [gentransform](#), [genwhisker](#)

Examples

```
## Vector input.
genanaggr(c(0.123,0.158,0.087,0.252,0.211,0.154),
          c("2012-01-10","2012-08-17","2012-12-12",
            "2013-04-09","2013-08-08","2013-12-10"),
          minn=3)

## Use of example data from the package:
data(kosetice.pas.genasis)
genanaggr(kosetice.pas.genasis,input="genasis",show.flagged=TRUE)
data(kosetice.act.openair)
genanaggr(genoutlier(kosetice.act.openair[1:6],
                    plot=FALSE)$res,minn=6,gap=1.5)
```

gendate

Compile the date of measurement

Description

Function gendate compiles different types of calendar dates and returns vector of class "Date". gendate recognizes single argument x as a vector of class "character", "Date", "POSIXct" or "POSIXlt".

Usage

```
gendate(x)
```

Arguments

x vector of calendar dates of class "character", "Date", "POSIXct" or "POSIXlt".

Details

The `gendate` function rounds different types of date to single days. If more precise time point is specified by "POSIXct" or "POSIXlt" class, only the information about the day is used. In the case of character input, two formats are recognized: "2013-05-30" and "30.05.2013" also in shortened variant "2013-5-30" and "30.5.2013". Only the first 10 characters are used in both cases. If only the month (as "2013-05" or "5.2013") or the year (as "2013") is specified by the character string, the date is placed into the 15th day in the case of month or into a 1st July in the case of year.

Value

`res` vector of dates of class "Date".

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Examples

```
## Single dates:
gendate(Sys.Date())
gendate("10.6.1993")
gendate("1856")

## Date vectors:
gendate(c("2000-05-30", "2001", "4.4.98", "2003-06-01 12:30:45"))
gendate(c(as.POSIXlt("2003-06-01 12:30:45"), "2003-07-02"))
```

genhistogram

genhistogram

Description

Function `genhistogram` creates a histogram of (usually) concentrations with equidistant breaks placed in "good-looking" numbers. If `plot=TRUE`, the resulting histogram is plotted with several possibilities of graphical options.

Usage

```
genhistogram(x, breaks=7, input="openair", pollutant=NA,
             delta=0, plot=TRUE, distr="norm", gap=0.05,
             columns=2, col="#A52375", emboss=0, xlab="Concentration",
             ylab="Number of samples", main=NA)
```

Arguments

x	vector of concentration values or data frame of genesis/openair type. See 'Details' for more detailed description of both data types.
breaks	a number of breaks between individual histogram cells.
input	type of data.frame in the case of data.frame input. The allowed values are "openair" (default) and "genesis". In case of vector input, this argument is meaningless.
pollutant	name of the pollutant, for which the plot is plotted. Not necessary if only data for one pollutant is available in x. If not specified, plots for all pollutants are drawn in a multi-plot arrangement.
delta	a delta value before the lowest and after the highest value of x. Positive number or 0.
plot	logical. Should the result be plotted?
distr	a name of distribution to interlace. Values "norm" and "lnorm" are possible.
gap	the size of a gap between columns in a relative width of the column (number between 0 and 1).
columns	number of columns in the multi-plot arrangement.
col	a specification for the default plotting color. See section 'Color Specification' in par .
emboss	0,1,2 or 3 for different emboss effect of genhistogram columns.
xlab	a label for the x axis, defaults to "Concentration".
ylab	a label for the y axis, defaults to "Number of samples".
main	overall title for the histogram.

Details

Function genhistogram creates a histogram, e.g. distribution of given data values into several cells with equidistant breaks placed in "good-looking" numbers. The function considers both the magnitude of the data values and their precision (number of decimals) and choose the breaks to be interpretable well (not to have a lot of decimals). Some empty range is added before the first and behind the last data value in order to smooth the breaks numbers. The minimal size of this range could be determined by the delta parameter.

The function recognises three different input formats: Option input="openair" uses openair format of data frame with first column of name 'date' and type Date, optional columns of names "date_end", "temp", "wind" and "note" and other columns of class "numeric" containing concentration values and named by names of the compounds. input="genesis" is used for the data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first, fifth and sixth are of class "numeric", second of type character and third and fourth columns could be both "character" or "Date" class. The names of columns in "genesis" type data frame are not rigid, only their order is assumed. There is also a possibility to specify x as a numeric vector.

If plot=TRUE, the resulting histogram is plotted with several graphical possibilities. There are two options for plotting a curve of idealised distribution of concentration values. distr="lnorm"

(default) draws curve of lognormal distribution, while `distr="norm"` draws curve of normal distribution defined by central tendency and variance of concentration data.

The argument `emboss` allows to induce an impression of plasticity of the histogram columns by two different graphical effects or their combination. `emboss=0` implies flat columns without any effect, `emboss=1` makes an impression of shading, `emboss=2` bevels edges of the columns and `emboss=3` combines last two effect into one.

Value

a list containing:

<code>borders</code>	numerical vector of column cell borders
<code>distr</code>	numerical vector of counts of values in the individual column cells

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See Also

[genloq](#), [genoutlier](#), [genpactoact](#), [genanaggr](#), [genplot](#), [genstatistic](#), [gentransform](#), [genwhisker](#)

Examples

```
## Vector input.
genhistogram(rnorm(60))

## Use of example data from the package:
data(kosetice.pas.openair)
genhistogram(kosetice.pas.openair[,1:8],col="orange",emboss=3)
data(kosetice.pas.genasis)
genhistogram(kosetice.pas.genasis[1:208,],input="genasis",
             distr="lnorm",col="orange",emboss=2)
```

<code>genloq</code>	<i>Substitution of (concentration) values below a limit of quantification (LoQ)</i>
---------------------	---

Description

Function `genloq` uses given (or determines) threshold of the limit of quantification and substitutes string "LoQ" of values below it.

Usage

```
genloq(x, y=NA, input="openair", output=NA, loq=NA,
       method="mle", distr="lnorm", pollutant=NA, plot=TRUE,
       ylim=c(NA,NA), columns=2, col.points="black", pch=1,
       xlab="Date", ylab="Concentration", main=NA)
```

Arguments

x	a vector of concentration values (of class "numeric" or "character") or data frame of "genasis"/"openair" type with concentration column allowed to be of class "character". See 'Details' for more detailed description of both data types and the exceptions for genloq function.
y	a vector of measurement dates in the case of vector input only.
input	a type of data frame in the case of data frame input. The allowed values are "openair" (default) and "genasis" with an exception of the column with concentration values, which could be of class "character". In case of vector input, this argument is meaningless.
output	a type of output data frame. As in the input argument, both data frames "openair" and "genasis" are available, with the default value equal to input.
loq	a value of the limit of quantification which will be used for all pollutants.
method	method of values below LoQ substitution. Allowed values are "exc" for exclusion, "1.0", "2.0", "sq2" for substitution by constant and "mle" for modified maximum likelihood method. See 'Details' for more detailed description of methods.
distr	if method="mle" (default), specifies if normal distr="norm" or log-normal distr="lnorm" distribution will be used for likelihood maximization.
pollutant	a name(s) of the pollutant(s), for which the LoQs are substituted. Not necessary if only data for one pollutant is available in x. If not specified, results for all pollutants are computed and plots for all pollutants are drawn in a multi-plot arrangement.
plot	logical. Indicates, whether plot should be plotted.
ylim	vector of class "numeric" and length 2 setting the lower and upper border of the plot.
columns	number of columns in the multi-plot arrangement.
col.points	color of over LoQ points inside the plot.
pch	plotting 'character', i.e., symbol to use. For more details see points .
xlab	the x label of the plot.
ylab	the y label of the plot.
main	overall title for the plot.

Details

The genloq function substitutes values below the limit of quantification (LoQ) (equivalently the limit of detection (LoD)) marked as "loq", "LoQ" or "LOQ" in the x. Although both data frames of types "openair" and "genasis" are defined with columns containing concentration values of class "numeric", it is necessary to mark values below LoQ as character string - thus here is an exception from the definition and both data types "openair" and "genasis", as well as vector x could contain concentration values of class "character". See 'Examples' paragraph.

Thus the function recognises three different input formats: Option input="openair" uses "openair" format of data frame with first column of name "date" and class "Date", optional columns

of names "date_end", "temp", "wind" and "note" and other columns of class "numeric" or "character" containing concentration values and named by names of the compounds. `input="genasis"` is used for the data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first could be both "numeric" or "character" class, fifth and sixth are of class "numeric", second of class "character" and third and fourth columns could be both "character" or "Date" class. The names of columns in `input="genasis"` are not rigid, only their order is assumed. There is also a possibility to specify `x` and `y` as two vectors of equal length, first of class "numeric" or "character" containing concentration values, second of class "character" or "Date" containing measurement dates.

The output argument specifies of which type the result will be. Both types of "data.frame" class `output="openair"` and `output="genasis"` are available - now without any exceptions with all concentration values of class "numeric", the default value is equal to the input argument, therefore the vector class of output is possible only if `x` is "numeric" or "character" vector and output is not specified.

There are five available methods of LoQs treatment. The simplest method `method="exc"` is not recommended because of high bias and meaningless approach. Standard constant methods `method="1.0"`, `method="2.0"` and `method="sq2"` serve for substitution of (concentration) values below LoQ by value of LoQ divided gradually by 1, 2 and square root of 2. The most recommended is the modified maximum likelihood method `method="mle"` which will be described later.

Value

a list containing:

<code>res</code>	the data frame (or vector) according to the output argument settings with substituted (or eventually excluded) (concentration) values below limit of quantification.
<code>loq</code>	numeric value of LoQ

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See Also

[genoutlier](#), [genhistogram](#), [genpastroact](#), [genanaggr](#), [genplot](#), [genstatistic](#), [gentransform](#), [genwhisker](#)

Examples

```
## Definition of simple data sources:
c1<-rlnorm(100,0,1)
c2<-"random compound"
c3<-as.Date(as.Date("2013-01-01"):as.Date("2013-04-10"),
            origin="1970-01-01")
c4<-c3+1

# Cuts the values below the 0.5.
c1[which(c1<0.5)]<-"LoQ"
```

```

sample_genasis<-data.frame(c1,c2,c3,c4)
sample_openair<-data.frame(c4,c1)
colnames(sample_openair)=c("date",c2)

## Examples of different usages:
genloq(c1,c3,pollutant=c2,method="sq2")
genloq(sample_openair,method="mle")

```

genoutlier

Identification and exclusion of outliers

Description

Function `genoutlier` finds and excludes outlied (concentration) values according to selected method and draws plot of outliers.

Usage

```

genoutlier(x, y=NA, input="openair", output=NA, method="lm3s",
           sides=2, pollutant=NA, plot=TRUE, columns=2,
           col.points="black", pch=1, xlab="Date",
           ylab="Concentration", main=NA)

```

Arguments

<code>x</code>	a vector of concentration values or data frame of <code>genasis/openair</code> type. See 'Details' for more detailed description of both data types.
<code>y</code>	a vector of measurement dates in the case of vector input only.
<code>input</code>	a type of <code>data.frame</code> in the case of <code>data.frame</code> input. The allowed values are "openair" (default) and "genasis". In case of vector input, this argument is meaningless.
<code>output</code>	a type of output <code>data.frame</code> . As in the <code>input</code> argument, both <code>data.frames</code> "openair" and "genasis" are available, with the default value equal to <code>input</code> .
<code>method</code>	method of threshold(s) determination. Allowed values are "m2s" and "m3s" for mean \pm 3 standard deviation, "lm2s" and "lm3s" for log-transformed variant and "iqr2", "iqr4" and "iqr7" for interquatile distances. See 'Details' for more detailed description of methods.
<code>sides</code>	if <code>sides=2</code> (default), both lower and upper threshold are used. If <code>sides=1</code> , only the upper one is in charge.
<code>pollutant</code>	a name(s) of the pollutant(s), for which the outliers are find. Not necessary if only data for one pollutant is available in <code>x</code> . If not specified, plots for all pollutants are drawn in a multi-plot arrangement.
<code>plot</code>	logical. Indicates, whether plot should be plotted.
<code>columns</code>	number of columns in the multi-plot arrangement.

col.points	color of non-outlied points inside the plot.
pch	plotting 'character', i.e., symbol to use. For more details see points .
xlab	the x label of the plot.
ylab	the y label of the plot.
main	overall title for the plot.

Details

The `genoutlier` function finds outlied (concentration) values according to a criterion given by arguments `method` and `sides` and substitutes them by NAs. The function recognises three different input formats: Option `input="openair"` uses "openair" format of data frame with first column of name "date" and class "Date", optional columns of names "date_end", "temp", "wind" and "note" and other columns of class "numeric" containing concentration values and named by names of the compounds. `input="genesis"` is used for the data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first, fifth and sixth are of class "numeric", second of class "character" and third and fourth columns could be both "character" or "Date" class. The names of columns in `input="genesis"` are not rigid, only their order is assumed. There is also a possibility to specify `x` and `y` as two vectors of equal length, first of class "numeric" containing concentration values, second of class "character" or "Date" containing measurement dates.

The output argument specifies of which type the result will be. Both types of "data.frame" class `output="openair"` and `output="genesis"` are available, the default value is equal to the input argument, therefore the vector class of output is possible only if `x` is of class "numeric" and output is not specified.

There are seven available methods of outlier threshold set up: `method="m3s"` set the lower threshold equal to sample mean - 3 standard deviations and the upper threshold to the sample mean + 3 standard deviations. Variant `method="m2s"` works similarly with only doubled standard deviations. In case of log-normally distributed data, the variant `method="lm3s"` could work better, setting up the lower threshold as geometric mean / 3 geometric standard deviation and the upper threshold as geometric mean * 3 geometric standard deviation. Analogously `method="lm2s"` works with the doubled geometric standard deviation. Non-parametric variants "iqr2", "iqr4" and "iqr7" set lower threshold to 25th quantile - a * interquartile range and upper threshold to 75th quantile + a * interquartile range with parameter `a` sequentially 0.5, 1.5 and 3 (thus the whole range is 2, 4 and 7 times the interquartile range).

The argument `sides` serves to specification, whether the one-sided or two-sided exclusion of outliers will be done. In the case `sides=2` (default), both outliers under the lower and over the upper threshold are excluded, conversely if `sides=1`, only the outliers over the upper threshold are excluded.

Value

a list containing:

res	the data frame (or vector) according to the output argument settings with outlied values substituted by NAs.
lower	numeric value of lower threshold
upper	numeric value of upper threshold

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See Also

[genloq](#), [genhistogram](#), [genpactoact](#), [genanaggr](#), [genplot](#), [genstatistic](#), [gentransform](#), [genwhisker](#)

Examples

```
## Definition of simple data sources:
c1<-rnorm(100)+12
c2<-"random compound"
c3<-as.Date(as.Date("2013-01-01"):as.Date("2013-04-10"),
            origin="1970-01-01")
c4<-c3+1

sample_genasis<-data.frame(c1,c2,c3,c4)
sample_openair<-data.frame(c4,c1)
colnames(sample_openair)=c("date",c2)

## Examples of different usages:
genoutlier(sample_openair,input="openair",pollutant="random compound",
            method="m2s")
genoutlier(sample_genasis,input="genasis",method="m3s")

## Use of example data from the package:
data(kosetice.pas.openair)
genoutlier(genpactoact(kosetice.pas.openair[,1:8]),method="lm3s",
            main="Outliers",ylab="Concentration ngm-3")
genoutlier(kosetice.pas.openair[,c(1:4,23:26)],col.points="orange",
            method="lm3s")
data(kosetice.pas.genasis)
genoutlier(kosetice.pas.genasis[625:832,],input="genasis",
            method="lm2s",sides=1)
```

genpactoact

Recalculates adsorption results from passive air samplers to (active-like) concentrations

Description

Function `genpactoact` provides two different tools for recalculating POPs concentration results from passive air samplers (in mass per filter units) to concentrations (in mass per air volume) comparable with results from active air samples.

Usage

```
genpactoact(x, date_start=NA, date_end=NA, input="openair",
            output=NA, method="auto", days=28, pollutant=NA,
            temp=NA, wind=NA)
```

Arguments

x	vector of concentration values or data frame of "genasis"/"openair" type. See 'Details' for more detailed description of both data types.
date_start	vector specifying the start of the measurement of class "character", "Date", "POSIXct" or "POSIXlt", as described in gendate . Only meaningful for vector input.
date_end	vector specifying the end of the measurement of class "character", "Date", "POSIXct" or "POSIXlt", as described in gendate . Only meaningful for vector input.
input	type of data.frame in the case of data.frame input. The allowed values are "openair" (default) and "genasis". In case of vector input, this argument is meaningless.
output	type of output data frame. As in the input argument, both data frames "openair" and "genasis" are available, with the default value equal to input.
method	method used for recalculation. Available values are "const", "temp", "tempwind", "auto", "gaps4" and "gaps7". For detailed description see 'Details'.
days	the length of the measurement period, which will be used, if not specified well by date_start and date_end arguments. If date_start is specified and date_end is not, the date of end of the measurement is computed and add.
pollutant	name of the pollutant to select specific model constants. See 'Details' for a list of allowed values. It is necessary to specify pollutant argument in a case of numeric input.
temp	a numeric vector of average temperatures in Celsius degrees (if known) during the measurement period. Only meaningful in a case of vector input.
wind	a numeric vector of average wind speeds in meters per second (if known) during the measurement period. Only meaningful in a case of vector input.

Details

The `genpactoact` function enables to use two different models for recalculating values of POPs concentration (in mass per filter units) from passive air samplers (of Genasis design) to real air concentrations (in mass per air volume units) as obtained from active air samplers. The function recognises three different input formats: Option `input="openair"` uses "openair" format of data frame with first column of name 'date' and type "Date", optional columns of names "date_end", "temp", "wind" and "note" and other columns of type "numeric" containing concentration values and named by names of the compounds. `input="genasis"` is used for the data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first, fifth and sixth are of type "numeric", second of type "character" and third and fourth columns could be both "character" or "Date" type. The names of columns in `input="genasis"` are not rigid, only their order is assumed. There is also a possibility to specify x and y as two vectors of equal

length, first of type "numeric" containing concentration values, second of type "character" or "Date" containing measurement dates.

There are six possibilities of model choice. Three similar variants `method="const"`, `method="temp"` and `method="tempwind"` leads to the Genasis model taking into account gradually only the concentration, concentration and temperature and finally concentration, temperature and wind speed. If temperature and/or wind are necessary for the selected model, they need to be specified in appropriate column of data frame or as a `temp` and/or `wind` arguments in case of the vector input. The option `method="auto"` combines above mentioned three approaches, using as many variables, as possible (in such a cases NA represents not-known temperature/wind.)

Remaining two options `method="gaps4"` and `method="gaps7"` lead to use of Global Air Passive Sampling (GAPS) model with two different effective gas-phase sampling rates (4 for usual and 7 for significantly windy sites). In all cases this model uses temperature (either as `temp` argument in the vector input mode, or as column `temp` in the data frame input mode) and does not use wind speed for the recalculation.

The argument `pollutant` could take any value from the following set: "naphthalene", "acenaphtylene", "acenaphtene". For other pollutants no model constant are known and thus the concentration can not be recalculated.

Value

`res` Data frame or vector depending on the output argument, containing recalculated values of POPs air concentrations (in mass unit per cubic meter).

Author(s)

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References

Harner, T.; Su, K.; Genualdi, S.; Karpowicz, J.; Ahrens, L.; Mihele, C.; Schuster, J.; Charland, J. and Narayan, J., Calibration and application of PUF disk passive air samplers for tracking polycyclic aromatic compounds (PACs). *Atmospheric Environment* Vol. 75 (2013), pp. 123-128.

See Also

[genloq](#), [genoutlier](#), [genhistogram](#), [genanaggr](#), [genplot](#), [genstatistic](#), [gentransform](#), [genwhisker](#)

Examples

```
## Vector input
genpactoact(c(1,2,1.2,1.1,0.1),days=28,pollutant=c("pp-DDE"))

## Use of example data from the package:
data(kosetice.pas.genasis)
genpactoact(kosetice.pas.genasis,input="genasis",
            method="gaps7",pollutant=c("PCB 28"))
```

```
data(kosetice.pas.openair)
genpastaact(genoutlier(kosetice.pas.openair[,c(1:4,20)],plot=FALSE)$res,
            method="auto")
```

genplot

Plot of concentration time series

Description

Function `genplot` allows to draw points of time series of persistent organic pollutant concentration. Several parametric and non-parametric interlacing curves are available and optional (linear and exponential) and three possibilities of drawing confidence interval of the trend line (none, one-coloured and gradient).

Usage

```
genplot(x, y=NA, input="openair", pollutant=NA, plot=TRUE,
        distr="lnorm", xlim=c(NA,NA), ylim=c(NA,NA), n=NA,
        col="#A52375", col.points="black", pch=1, il="ls",
        ci=TRUE, r=0.95, columns=2, xlab="Date",
        ylab="Concentration", main=NA)
```

Arguments

<code>x</code>	vector of concentration values or data frame of <code>genasis/openair</code> type. See 'Details' for more detailed description of both data types.
<code>y</code>	vector of measurement dates in the case of vector input only.
<code>input</code>	type of <code>data.frame</code> in the case of <code>data.frame</code> input. The allowed values are "openair" (default) and "genasis". In case of vector input, this argument is meaningless.
<code>pollutant</code>	name of the pollutant(s), for which the plot is plotted. Not necessary if only data for one pollutant is available in <code>x</code> . If not specified, plots for all pollutants are drawn in a multi-plot arrangement.
<code>plot</code>	logical. Indicates, whether plot should be plotted.
<code>xlim</code>	"character" or "Date" class vector of length 2, giving the x axis coordinates ranges.
<code>ylim</code>	numeric vector of length 2, giving the y axis coordinates ranges.
<code>n</code>	number of breaks of interlacing line. If not specified, <code>n</code> is equal to the number of concentration values.
<code>col</code>	color of interlacing line and confidence interval area, if chosen.
<code>col.points</code>	color of points inside the plot.
<code>pch</code>	plotting "character", i.e., symbol to use. For more details see points .
<code>il</code>	type of the interlacing curve. Value "ls" leads to least square fitting of the curve, value "ts" leads to a non-parametric Theil-Sen curve. If the value is "", no curve is plotted.

distr	shape of the interlacing curve. Value "norm" leads to a linear interpolation, value "lnorm" to an exponential. If the value is "", no curve is plotted.
ci	indicates, whether confidence interval of interlacing curve should be plotted. The allowed values are TRUE (default), FALSE and "gradient".
r	significance level of the confidence interval as a positive number between 0 and 1.
columns	number of columns in the multi-plot arrangement.
xlab	the x label of the plot.
ylab	the y label of the plot.
main	overall title for the plot.

Details

The genplot function enables to draw a plot of concentration time series. The function recognises three different input formats: Option input="openair" uses openair format of data frame with first column of name "date" and type Date, optional columns of names "date_end", "temp", "wind" and "note" and other columns of class "numeric" containing concentration values and named by names of the compounds. input="genasis" is used for the data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first, fifth and sixth are of class "numeric", second of class "character" and third and fourth columns could be both "character" or "Date" class. The names of columns in input="genasis" are not rigid, only their order is assumed. There is also a possibility to specify x and y as two vectors of equal length, first of class "numeric" containing concentration values, second of class "character" or "Date" containing measurement dates.

In all cases of input, if both start and end date are given, the date point is plotted as a middle of measurement period, if only one date is given, it is used directly.

There are two options for plotting interlacing line of concentrations. distr="lnorm" (default) expects lognormal distribution and plots exponential trend, while distr="norm" expects roughly normal distribution of concentration data and plots linear trend.

Two methods of interlacing are available under the argument il. il="ls" (default) deploys least squares method, while il="ts" deploys the Theil-Sen linear (or log-transformed exponential) estimator.

Confidence intervals of trend lines are also available by the option ci with available values TRUE (default) for one-coloured area, "gradient" for probability gradient and FALSE for no confidence interval to be drawn. The default significance level of the confidence interval r is set up to 0.95.

Default values of col and col.points parameters to specify colours of regression line and points in the plot are set up to #A52375 and black, default shape of points pch is set up to standard circles (1).

In a case of multiple pollutants specified, the argument columns specifies the number of columns in resulting table of plots. Be careful with plotting higher numbers of plots - usual devices are not large enough to plot more than four plots at once, there is a need to set up sufficiently high and broad space for plotting inside the device settings.

Main label and axes labels could be specified in main, xlab and ylab. A name of the pollutant is added after the user-set up label. If no specification is given, the name of the pollutant is used in main and "Date" and "Concentration" in axes labels.

Value

a list containing:

slope	slope of the regression line (in the case of exponential line, it is in a form of exponent of $\exp(x)$).
intercept	slope of the regression line (in the case of exponential line, it is in a form of multiplicative constant).
belt	x-coordintaes (as "Data" class vector) of line breaks.
line	y-coordintaes (concentration as "numeric" class vector) of line breaks.
lower	y-coordintaes (as "Data" class vector) of confidence interval area lower border breaks.
upper	y-coordintaes (as "Data" class vector) of confidence interval area upper border breaks.

Author(s)

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See Also

[genloq](#), [genoutlier](#), [genhistogram](#), [genpactoact](#), [genanaggr](#), [genstatistic](#), [gentransform](#), [genwhisker](#)

Examples

```
## Definition of simple data sources:
c1<-c(0.386,0.256,0.182,0.254)
c2<-"fluorene"
c3<-c("2013-05-01", "2013-06-03", "2013-07-05", "2013-08-07")
c4<-c("2013-05-08", "2013-06-10", "2013-07-12", "2013-08-14")

sample_genasis<-data.frame(c1,c2,c3,c4)
sample_openair<-data.frame(c4,c1)
colnames(sample_openair)=c("date", "fluorene")

## Examples of different usages:
genplot(sample_openair, input="openair", pollutant="fluorene", distr="lnorm",
        n=10, ci="gradient", col="black", col.points="red", pch=15)
genplot(sample_genasis, input="genasis", n=10, col="blue")
genplot(c1, c3, ci=FALSE, pch=1, main="fluorene")

## Use of example data from the package:
data(kosetice.pas.openair)
genplot(kosetice.pas.openair[,1:8], col="orange", il="ts", ci=FALSE)
data(kosetice.pas.genasis)
## Not run: genplot(kosetice.pas.genasis[1:208,], input="genasis",
        distr="lnorm", ci="gradient", col="orange")
## End(Not run)
```

genranges	<i>Determines "smooth" range of input data</i>
-----------	--

Description

Function `genranges` determines suitable lower and upper borders of numeric range covering all values of input vector. Both borders are chosen suitable rounded not to have a lot of decimals.

Usage

```
genranges(x, delta=0)
```

Arguments

<code>x</code>	numerical vector.
<code>delta</code>	a fraction of the range before the first and after the last value.

Details

The `genranges` function determines two numbers for lower and upper border of a range, covering all the values of input vector. Both the numbers are chosen taking into account the magnitude and the accuracy of input values, such that the result is rounded by adding some space before the first and after the last value. A minimal size of this space could be defined by the argument `delta`.

Value

<code>range</code>	numerical vector of length 2: first element is the lower and second element the upper border of the range.
--------------------	--

Author(s)

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Examples

```
## Input as a pair of vectors.  
genranges(c(0.9, NA, 18.335, 8, NaN, -6.4))
```

genstatistic	<i>Computes a set of statistics on input data</i>
--------------	---

Description

Function `genstatistic` computes a set of statistic according to demands on evaluation of Genesis and GMP data.

Usage

```
genstatistic(x, y=NA, input="openair", pollutant=NA, by.years=FALSE)
```

Arguments

<code>x</code>	vector of concentration values or data frame of "genesis"/"openair" type. See 'Details' for more detailed description of both data types.
<code>y</code>	vector of measurement dates in the case of vector input only.
<code>input</code>	type of data frame in the case of data frame input. The allowed values are "openair" (default) and "genesis". In case of vector input, this argument is meaningless.
<code>pollutant</code>	name of the pollutant(s), which will be included into resulting data frame.
<code>by.years</code>	logical. Should the statistics be computed for each year separately?

Details

The `genstatistic` function provides a set of descriptive statistics, commonly used when evaluating Genesis datasets. The resulting table contains 18 columns (19 in the variant with `by.years=TRUE`):

- `pollutant` name of the compound as taken from `x`.
- `year` the year, for which the summary statistics are computed (only if `by.years=TRUE`).
- `n` number of valid results used for calculations of the summary statistics.
- `mean` arithmetic mean of concentration values.
- `sd` standard deviation of concentration values.
- `geom.` mean geometric mean of concentration values.
- `geom. sd` geometric standard deviation.
- `min` minimal value.
- `median` median of concentration values.
- `max` maximal value.
- `Pearson` Pearson correlation (product moment) to time, available if at least 3 concentration values are present.
- `Pp` p value of Pearson trend test, available if at least 3 concentration values are present.
- `Daniels` Daniels trend test, available if at least 3 concentration values are present.
- `Dp` p value of Daniels trend test, available if at least 3 concentration values are present.
- `Mann-Kendall` Mann-Kendall tau, see [MannKendall](#), available if at least 4 concentration values are present.
- `MKp` p-value of Mann-Kendall trend test, for metodic, see [MannKendall](#), available if at least 3 concentration values are present.

LS slope linear regression line (least squares fitting) slope.
 TS slope Theil-Sen linear regression line slope.
 delta difference between the final and the initial concentration value in the period.

Value

res data frame containing 18 (19 in case of `by.years=TRUE`) as described in paragraph 'Details'.

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See Also

[genloq](#), [genoutlier](#), [genhistogram](#), [genpastaact](#), [genanaggr](#), [genplot](#), [gentransform](#), [genwhisker](#)

Examples

```
## Vector input.
genstatistic(c(0.123,0.158,0.087,0.252,0.211,0.154),
             c("2012-01-10","2012-08-17","2012-12-12",
               "2013-04-09","2013-08-08","2013-12-10"),
             pollutant=c("pp-DDE"),by.years=TRUE)

## Use of example data from the package:
data(kosetice.pas.genasis)
genstatistic(kosetice.pas.genasis,input="genasis")
data(kosetice.pas.openair)
genstatistic(genpastaact(genoutlier(kosetice.pas.openair[,c(1:4,20:26)]),
                           plot=FALSE)$res,method="auto"))
```

<code>gentransform</code>	<i>Transforms data structure (vector, "genasis", "openair")</i>
---------------------------	---

Description

Function `gentransform` enables to transform different data structures used in the `genasis` package one to another.

Usage

```
gentransform(x, y=NA, input="openair", output=NA, pollutant=NA)
```

Arguments

x	vector of concentration values or data frame of genesis/openair type. See 'Details' for more detailed description of both data types.
y	vector of measurement dates in the case of vector input only.
input	type of data frame in the case of data frame input. The allowed values are "openair" (default) and "genesis". In case of vector input, this argument is meaningless.
output	type of output data frame. As in the input argument, both data frames "openair" and "genesis" are available, with the default value equal to input.
pollutant	name of the pollutant(s), which will be included into resulting data frame.

Details

The gentransform function serves from transforming data from one three different input formats to one of two formats used in genesis package: Option "openair" uses openair format of data frame with first column of name 'date' and class "Date", optional columns of names "date_end", "temp", "wind" and "note" and other columns of type "numeric" containing concentration values and named by names of the compounds. input="genesis" is used for input of a data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first, fifth and sixth are of class "numeric", second of class "character" and third and fourth columns could be both "character" or "Date" class. The names of columns in input="genesis" are not rigid, only their order is assumed. There is also a possibility to input x and y as two vectors of equal length, first of class "numeric" containing concentration values, second of class "character" or "Date" containing measurement dates.

Argument output must be specified in the case of vector input. In other cases it is set up equal to input, which leaves the data frame without significant changes (except sorting the rows by date).

Value

res	Data frame or vector depending on the output argument, containing recalculated values of POPs air concentrations (in mass unit per cubic meter).
-----	--

Author(s)

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See Also

[genloq](#), [genoutlier](#), [genhistogram](#), [genpastroact](#), [genanaggr](#), [genplot](#), [genstatistic](#), [genwhisker](#)

Examples

```
## Input as a pair of vectors.
gentransform(c(0.386,0.256,0.182,0.254),
             c("2013-05-01", "2013-06-03", "2013-07-05", "2013-08-07"),
             output="genesis")
gentransform(c(0.386,0.256,0.182,0.254),
```

```

c("2013-05-01", "2013-06-03", "2013-07-05", "2013-08-07"),
output="openair", pollutant="PeCB")

## Not run: ## Data frame inputs:
data(kosetice.act.genasis)
gentransform(kosetice.act.genasis, input="genasis", output="openair")
data(kosetice.pas.openair)
gentransform(genpastaact(genoutlier(kosetice.pas.openair, plot=FALSE)$res),
             output="genasis")
## End(Not run)

```

genwhisker

Box and whisker plot - overview of dataset

Description

Function `genwhisker` allows to draw several box & whisker plots of the dataset. Boxes and whiskers could be drawn for all the data on each pollutant or differentiated by colours over individual years.

Usage

```

genwhisker(x, y=NA, input="openair", method="mqm", pollutant=NA,
           distr="norm", by.years=FALSE, col="#A52375",
           legend=TRUE, xlab="", ylab="Concentration", main=NA)

```

Arguments

<code>x</code>	vector of concentration values or data frame of "genasis"/"openair" type. See 'Details' for more detailed description of both data types.
<code>y</code>	vector of measurement dates in the case of vector input only.
<code>input</code>	type of data.frame in the case of data.frame input. The allowed values are "openair" (default) and "genasis". In case of vector input, this argument is meaningless.
<code>method</code>	arrangement of boxes and whiskers. Default "mqm" means median-quartiles-min/max, alternative "mqq" (median-quartiles-5/95quantiles) and "tqm" (trimean-quartiles-min/max) are available.
<code>pollutant</code>	name of the pollutant(s), which will be included into the box & whisker plot. Not necessary if only data for one pollutant is available in <code>x</code> . If not specified, all pollutants are included into the box & whisker plot.
<code>distr</code>	if <code>distr="norm"</code> (default), the linear y-axis is used, if <code>distr="lnorm"</code> , the logarithmic scale is used.
<code>by.years</code>	logical. If <code>by.years=FALSE</code> , all data for each pollutant are used together, if <code>by.years=TRUE</code> , individual years are distinguished by colors specified in argument <code>col</code> .
<code>col</code>	vector of colors of the boxes & whiskers. If a length of the vector in the color-by-years version is different from the number of years in the measurement period, implicit colors are used.

legend	logical. Should a legend be drawn in a multi-color mode?
xlab	a label for the x axis.
ylab	a label for the y axis.
main	a main title for the plot.

Details

The `genwhisker` function draws a box & whisker plot of selected compounds from the dataset. The function recognises three different input formats: Option `input="openair"` uses "openair" format of data frame with first column of name 'date' and class "Date", optional columns of names "date_end", "temp", "wind" and "note" and other columns of class "numeric" containing concentration values and named by names of the compounds. `input="genasis"` is used for the data frame with six columns "valu", "comp", "date_start", "date_end", "temp" and "wind" where the first, fifth and sixth are of class "numeric", second of class "character" and third and fourth columns could be both "character" or "Date" class. The names of columns in `input="genasis"` are not rigid, only their order is assumed. There is also a possibility to specify x and y as two vectors of equal length, first of class "numeric" containing concentration values, second of class "character" or "Date" containing measurement dates.

Central tendency of the dataset for selected pollutants from x is drawn as a bold horizontal line, 25th and 75th quantiles (e.g. 1st and 3rd quartiles) as a lighter box and extremes by a light horizontal lines (whiskers) at the ends of vertical line connecting all the values. There are three possibilities of boxes & whiskers arrangement. Option `method="mqm"` (default) means that central tendency lies in median, box margins in 1st and 3rd quartiles and whiskers in min/max. Alternative `method="mqq"` means that central tendency lies in median, box margins in 1st and 3rd quartiles and whiskers in 5th and 95th quantiles, finally `method="tqm"` means that central tendency lies in trimean, box margins in 1st and 3rd quartiles and whiskers in min/max.

There are two possibilities of drawing. The default option `by.years=FALSE` plots all the values for each pollutant in one box & whisker arrangement, while `by.years=TRUE` plots a number of color-distinguished overlapping boxes & whiskers. The colors could be defined by the argument `col` as a vector of the same length as the period of measurement. If the length of the vector and the period differ, default colors are used for plotting.

If `by.years=TRUE` and `legend=TRUE`, the legend is drawn upon the plot as a colored years according to the color(s) of box(es) & whisker(s).

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See Also

[genloq](#), [genoutlier](#), [genhistogram](#), [genpastaact](#), [genanaggr](#), [genplot](#), [genstatistic](#), [gentransform](#)

Examples

```
## Definition of simple data sources:
c1<-c(0.386,0.269,0.182,0.254,0.455,0.263,0.405,0.211)
c2<-"benzo(ghi)perylene"
```

```

c3<-c("2012-02-01", "2012-05-03", "2012-08-05", "2012-11-07",
      "2013-02-15", "2013-05-10", "2013-08-02", "2013-11-06")
c4<-c("2012-02-08", "2012-05-10", "2012-08-12", "2012-11-14",
      "2013-02-22", "2013-05-17", "2013-08-09", "2013-11-13")

sample_genasis<-data.frame(c1,c2,c3,c4)
sample_openair<-data.frame(c4,c1)
colnames(sample_openair)=c("date",c2)

## Examples of different usages:
genwhisker(sample_openair,distr="lnorm",col="black")
genwhisker(sample_genasis,input="genasis",distr="norm",by.years=TRUE,
           col=c("blue","red"),legend=TRUE,main="benzo(ghi)perylene")
genwhisker(c1,c3,main="benzo(ghi)perylene")

## Use of example data from the package:
data(kosetice.pas.openair)
genwhisker(kosetice.pas.openair[,1:8],
           col=c("gold","orange","red","black"),by.years=TRUE)
data(kosetice.pas.genasis)
genwhisker(kosetice.pas.genasis[1:208,],input="genasis",distr="lnorm",
           col="orange")

```

`kosetice.act.genasis` *Data on active POPs concentration measurements on Kosetice observatory*

Description

Data on active POPs concentration measurements on Kosetice observatory in data frame of "genasis" type.

Usage

```
data(kosetice.act.genasis)
```

Format

A data frame with 6270 observations on the following 6 variables.

`valu` concentration of individual POP in ngm-3

`comp` name of the pollutant

`date_start` initial date of measurement period

`date_end` final date of measurement period

`temp` average temperature during the measurement period in Celsius degrees

`wind` average wind speed during the measurement period in ms-1

Source

Global ENvironmental ASsessment Information System (GENASIS) (<http://www.genasis.cz/data-browser/>)

References

Dusek L., Klanova J., Boruvkova J., Hulek R., Jarkovsky J., Kubasek M., Gregor J., Sebkova K., Hrebicek J., Holoubek I., Kalina J. (2010). GENASIS - Global Environmental Assessment and Information System [online].

Examples

```
data(kosetice.act.genasis)
genstatistic(kosetice.act.genasis, input="genasis", pollutant="benzo(a)pyrene")
```

`kosetice.act.openair` *Data on active POPs concentration measurements on Kosetice observatory*

Description

Data on active POPs concentration measurements on Kosetice observatory in data frame of "openair" type.

Usage

```
data(kosetice.act.openair)
```

Format

A data frame with 209 rows on the following 34 variables.

`date` initial date of measurement period

`date_end` final date of measurement period

`temp` average temperature during the measurement period in Celsius degrees

`wind` average wind speed during the measurement period in ms-1

`naphthalene` concentration of naphthalene in ngm-3

`acenaphtylene` concentration of acenaphtylene in ngm-3

`acenaphtene` concentration of acenaphtene in ngm-3

`fluorene` concentration of fluorene in ngm-3

`phenantrene` concentration of phenantrene in ngm-3

`anthracene` concentration of anthracene in ngm-3

`fluoranthene` concentration of fluoranthene in ngm-3

`pyrene` concentration of pyrene in ngm-3

benzo(a)anthracene concentration of benzo(a)anthracene in ngm-3
chrysene concentration of chrysene in ngm-3
benzo(b)fluoranthene concentration of benzo(b)fluoranthene in ngm-3
benzo(k)fluoranthene concentration of benzo(k)fluoranthene in ngm-3
benzo(a)pyrene concentration of benzo(a)pyrene in ngm-3
indeno(123cd)pyrene concentration of indeno(123cd)pyrene in ngm-3
benzo(ghi)perylene concentration of benzo(ghi)perylene in ngm-3
PCB 28 concentration of PCB 28 in ngm-3
PCB 52 concentration of PCB 52 in ngm-3
PCB 101 concentration of PCB 101 in ngm-3
PCB 118 concentration of PCB 118 in ngm-3
PCB 138 concentration of PCB 138 in ngm-3
PCB 153 concentration of PCB 153 in ngm-3
PCB 180 concentration of PCB 180 in ngm-3
alpha-HCH concentration of alpha-HCH in ngm-3
beta-HCH concentration of beta-HCH in ngm-3
gamma-HCH concentration of gamma-HCH in ngm-3
pp-DDE concentration of p,p'-DDE in ngm-3
pp-DDD concentration of p,p'-DDD in ngm-3
pp-DDT concentration of p,p'-DDT in ngm-3
PeCB concentration of PeCB in ngm-3
HCB concentration of HCB in ngm-3

Source

Global ENvironmental ASsessment Information System (GENASIS) (<http://www.genasis.cz/data-browser/>)

References

Dusek L., Klanova J., Boruvkova J., Hulek R., Jarkovsky J., Kubasek M., Gregor J., Sebkova K., Hrebicek J., Holoubek I., Kalina J. (2010). GENASIS - Global Environmental Assessment and Information System [online].

Examples

```
data(kosetice.act.openair)
## Not run: genstatistic(kosetice.act.openair)
```

`kosetice.pas.genasis` *Data on passive POPs concentration measurements on Kosetice observatory*

Description

Data on passive POPs concentration measurements on Kosetice observatory in data frame of "genasis" type.

Usage

```
data(kosetice.pas.genasis)
```

Format

A data frame with 1560 observations on the following 6 variables.

`valu` concentration of individual POP in ngfilter-1

`comp` name of the pollutant

`date_start` initial date of measurement period

`date_end` final date of measurement period

`temp` average temperature during the measurement period in Celsius degrees

`wind` average wind speed during the measurement period in ms-1

Source

Global ENvironmental ASsessment Information System (GENASIS) (<http://www.genasis.cz/data-browser/>)

References

Dusek L., Klanova J., Boruvkova J., Hulek R., Jarkovsky J., Kubasek M., Gregor J., Sebkova K., Hrebicek J., Holoubek I., Kalina J. (2010). GENASIS - Global Environmental Assessment and Information System [online].

Examples

```
data(kosetice.pas.genasis)
genstatistic(kosetice.pas.genasis, input="genasis", pollutant="benzo(a)pyrene")
```

`kosetice.pas.openair` *Data on passive POPs concentration measurements on Kosetice observatory*

Description

Data on passive POPs concentration measurements on Kosetice observatory in data frame of "openair" type.

Usage

```
data(kosetice.pas.openair)
```

Format

A data frame with 52 rows on the following 34 variables.

`date` initial date of measurement period

`date_end` final date of measurement period

`temp` average temperature during the measurement period in Celsius degrees

`wind` average wind speed during the measurement period in ms-1

`naphthalene` concentration of naphthalene in ngm-3

`acenaphtylene` concentration of acenaphtylene in ngm-3

`acenaphtene` concentration of acenaphtene in ngm-3

`fluorene` concentration of fluorene in ngm-3

`phenantrene` concentration of phenantrene in ngm-3

`anthracene` concentration of anthracene in ngm-3

`fluoranthene` concentration of fluoranthene in ngm-3

`pyrene` concentration of pyrene in ngm-3

`benzo(a)anthracene` concentration of benzo(a)anthracene in ngm-3

`chrysene` concentration of chrysene in ngm-3

`benzo(b)fluoranthene` concentration of benzo(b)fluoranthene in ngm-3

`benzo(k)fluoranthene` concentration of benzo(k)fluoranthene in ngm-3

`benzo(a)pyrene` concentration of benzo(a)pyrene in ngm-3

`indeno(123cd)pyrene` concentration of indeno(123cd)pyrene in ngm-3

`benzo(ghi)perylene` concentration of benzo(ghi)perylene in ngm-3

`PCB 28` concentration of PCB 28 in ngm-3

`PCB 52` concentration of PCB 52 in ngm-3

`PCB 101` concentration of PCB 101 in ngm-3

`PCB 118` concentration of PCB 118 in ngm-3

PCB 138 concentration of PCB 138 in ngm-3
PCB 153 concentration of PCB 153 in ngm-3
PCB 180 concentration of PCB 180 in ngm-3
alpha-HCH concentration of alpha-HCH in ngm-3
beta-HCH concentration of beta-HCH in ngm-3
gamma-HCH concentration of gamma-HCH in ngm-3
pp-DDE concentration of p,p'-DDE in ngm-3
pp-DDD concentration of p,p'-DDD in ngm-3
pp-DDT concentration of p,p'-DDT in ngm-3
PeCB concentration of PeCB in ngm-3
HCB concentration of HCB in ngm-3

Source

Global ENvironmental ASsessment Information System (GENASIS) (<http://www.genasis.cz/data-browser/>)

References

Dusek L., Klanova J., Boruvkova J., Hulek R., Jarkovsky J., Kubasek M., Gregor J., Sebkova K., Hrebicek J., Holoubek I., Kalina J. (2010). GENASIS - Global Environmental Assessment and Information System [online].

Examples

```
data(kosetice.pas.openair)  
genstatistic(kosetice.pas.openair)
```

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