

R documentation

Neotoma

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boxplotTaxon	<i>Create A Boxplot Of One Column In A Genus</i>
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Description

Creates a boxplot in a new window of one numerical column from a genus. The boxplot can aggregate over all the values of one column for the genus, or

Usage

```
boxplotTaxon(taxonname, column, byspecies=FALSE, paramnames=NA, paramvalues=NA)
```

Arguments

taxonname	is either a character literal containing the name of the genus or a data frame with data from the genus. If a character literal is provided, the optional parameters paramnames and paramvalues may also be used.
column	is a character literal with name of the column to be plotted.
byspecies	is a boolean value determining whether one boxplot or a series of boxplots comparing each species within the genus will be generated. If TRUE, a boxplot for each species will be shown. If FALSE or if no value is provided, one boxplot aggregating across all species in the genus will be created.
paramnames	is a vector of additional, optional parameter names that will be used in the URI. See http://api.neotomadb.org/doc/resources/sampleddata for a list of valid parameter names. If no vector is provided, no additional parameters will be used.

paramvalues is a vector of additional, optional parameter values that correspond to the parameter names in the **paramnames** vector, which will be used to construct the URI. Must be the same length as **paramnames**. If a **paramvalues** vector is included, a **paramnames** vector must also be included.

Examples

```
boxplotTaxon("Microtus", column="SiteLongitudeEast")
microtusdata <- getTaxon("Microtus")
boxplotTaxon(microtusdata, column="SiteLongitudeEast")
boxplotTaxon(microtusdata, column="SiteLongitudeEast", paramnames="ageold", paramvalues=1000)
```

getSampleData	<i>Transform One SampleData Taxon Into An R Data Frame</i>
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Description

Returns a dataframe based on user-entered parameters or a URI.

Usage

```
getSampleData(paramnames=NA, paramvalues=NA, uri=NA)
```

Arguments

paramnames is a vector of parameter names that will be used in the URI. At least one parameter must be given. At least one parameter must be "taxonname" or "taxonids". See <http://api.neotomadb.org/doc/resources/sampleddata> for a list of valid parameter names.

paramvalues is a vector of parameter values that correspond to the parameter names in the **paramnames** vector, which will be used to construct the URI.

uri is the URI to transform into a data frame. This parameter can be used instead of **paramnames** and **paramvalues** to select data from NeotomaDB.

Examples

```
getSampleData(paramnames="taxonname", paramvalues="Mammuthus")
getSampleData(paramnames=c("taxonname", "ageold", "ageyoung"), c("Mammuthus", 50000, 0))
#getSampleData(uri="http://api.neotomadb.org/data/sampleddata?taxonname=Smilodon")
```

getTaxon

*Transform One Genus Into An R Data Frame***Description**

Returns a data frame of one genus based on the genus name and optional additional parameters.

Usage

```
getTaxon(taxonname, paramnames=NA, paramvalues=NA)
```

Arguments

taxonname	is a character literal containing the name of the genus to be returned as a data frame.
paramnames	is a vector of additional, optional parameter names that will be used in the URI. See http://api.neotomadb.org/doc/resources/sampledata for a list of valid parameter names. If no vector is provided, no additional parameters will be used.
paramvalues	is a vector of additional, optional parameter values that correspond to the parameter names in the paramnames vector, which will be used to construct the URI. Must be the same length as paramnames. If a paramvalues vector is included, a paramnames vector must also be included.

Examples

```
getTaxon("Microtus")
getTaxon("Microtus", paramnames="ageyoung", paramvalues=1000)
```

histTaxon

*Histogram Of One Column From A Genus***Description**

Creates a histogram in a new window of one column from a genus. The number and size of bins is adjustable.

Usage

```
histTaxon(taxonname, column, species=NA, breaks="Sturges", paramnames=NA, paramvalues=NA)
```

Arguments

taxonname	is either a character literal containing the name of the genus or a data frame with data from the genus. If a character literal is provided, the optional parameters paramnames and paramvalues may also be used.
column	is a character literal with name of the column to be plotted.
species	is a character literal with the name of the species to be selected; if no value is entered, the histogram will aggregate across all species in the genus.

breaks	one of: * a vector giving the breakpoints between histogram cells, * a single number giving the number of cells for the histogram, * a character string naming an algorithm to compute the number of cells * a function to compute the number of cells. In the last three cases the number is a suggestion only.
paramnames	is a vector of additional, optional parameter names that will be used in the URI. See http://api.neotomadb.org/doc/resources/sampleddata for a list of valid parameter names. If no vector is provided, no additional parameters will be used.
paramvalues	is a vector of additional, optional parameter values that correspond to the parameter names in the paramnames vector, which will be used to construct the URI. Must be the same length as paramnames. If a paramvalues vector is included, a paramnames vector must also be included.

Examples

```
histTaxon("Microtus", column="SiteAltitude")
microtusdata <- getTaxon("Microtus")
histTaxon(microtusdata, column="SiteAltitude", species="Microtus longicaudus/M. montanus")
histTaxon(microtusdata, column="SiteAltitude", breaks=20)
```

lmTaxon

Linear Regression On Two Numeric Columns in a Genus

Description

Creates a scatterplot in a new window of two numeric columns, displays the correlation coefficient, and plots the linear regression line.

Usage

```
lmTaxon(taxonname, x, y, paramnames=NA, paramvalues=NA)
```

Arguments

taxonname	is either a character literal containing the name of the genus or a data frame with data from the genus. If a character literal is provided, the optional parameters paramnames and paramvalues may also be used.
x	is the name of the column that will be the x column of the scatterplot.
y	is the name of the column that will be the y column of the scatterplot.
paramnames	is a vector of additional, optional parameter names that will be used in the URI. See http://api.neotomadb.org/doc/resources/sampleddata for a list of valid parameter names. If no vector is provided, no additional parameters will be used.
paramvalues	is a vector of additional, optional parameter values that correspond to the parameter names in the paramnames vector, which will be used to construct the URI. Must be the same length as paramnames. If a paramvalues vector is included, a paramnames vector must also be included.

Examples

```
microtusdata <- getTaxon("Microtus")
lmTaxon(microtusdata, "SiteAltitude", "SiteLongitudeEast")
lmTaxon(microtusdata, "SiteAltitude", "SiteLongitudeEast", paramnames="ageyoung", paramvalues=1000)
```

lmTimeSeries

*Linear Time Series Model of One Column in a Genus***Description**

Creates a scatterplot in a new window of the timeseries (using the SampleAge column if available, and the mean of SampleAgeYounger and SampleAgeOlder if not), displays the correlation coefficient, and plots the linear regression line.

Usage

```
lmTimeSeries(taxonname, column, paramnames=NA, paramvalues=NA)
```

Arguments

taxonname	is either a character literal containing the name of the genus or a data frame with data from the genus. If a character literal is provided, the optional parameters paramnames and paramvalues may also be used.
column	is the name of the column that will be the y column of the scatterplot.
paramnames	is a vector of additional, optional parameter names that will be used in the URI. See http://api.neotomadb.org/doc/resources/sampledata for a list of valid parameter names. If no vector is provided, no additional parameters will be used.
paramvalues	is a vector of additional, optional parameter values that correspond to the parameter names in the paramnames vector, which will be used to construct the URI. Must be the same length as paramnames. If a paramvalues vector is included, a paramnames vector must also be included.

Examples

```
microtusdata <- getTaxon("Microtus")
lmTimeSeries(microtusdata, "SiteLatitudeNorth")
lmTimeSeries("Microtus", "SiteLatitudeNorth", paramnames="ageyoung", paramvalues=1000)
```

summarizeTaxon

*Generate A Statistical Summary Of One Genus***Description**

Returns the mean, median, and quartiles for each column of one genus. The summary can be generated on the genus as a whole or by species.

Usage

```
summarizeTaxon(taxonname, byspecies=FALSE, columns=NA, paramnames=NA, paramvalues=NA)
```

Arguments

taxonname	is either a character literal containing the name of the genus or a data frame with data from the genus. If a character literal is provided, the optional parameters paramnames and paramvalues may also be used.
byspecies	is a boolean value indicating whether the analysis should be performed by species or aggregated on all species across the taxon. If TRUE, a summary for each species will be shown. If FALSE or if no value is provided, one summary aggregating across all species in the genus will be shown.
columns	is the vector of columns to include in the summary. All columns must be numeric.
paramnames	is a vector of additional, optional parameter names that will be used in the URI. See http://api.neotomadb.org/doc/resources/sampledata for a list of valid parameter names. If no vector is provided, no additional parameters will be used.
paramvalues	is a vector of additional, optional parameter values that correspond to the parameter names in the paramnames vector, which will be used to construct the URI. Must be the same length as paramnames. If a paramvalues vector is included, a paramnames vector must also be included.

Examples

```
summarizeTaxon("Mammuthus")
mammuthus <- getSampleData(paramnames="taxonname", paramvalues="Mammuthus")
summarizeTaxon(mammuthus, byspecies=TRUE, columns=c("SiteLatitudeNorth"))
summarizeTaxon("Microtus", columns=c("SiteLatitudeNorth"))
summarizeTaxon("Mammuthus", paramnames=c("ageold", "ageyoung"),
  paramvalues=c(50000, 0), columns=c("SiteLatitudeNorth"))
```