

Package ‘NSBcompanion’

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Type Package

Title Functions to retrieve and manipulate data from the Neptune Database (Lazarus, 1994)

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Description Some basic functions to retrieve data from Neptune, and a couple of other functions to deal with the preliminary quality control (outliers, synonyms). Basically mimic main functionalities of <http://nsb-mfn-berlin.de>.

License MIT

URL <http://github.com/plannapus/NSB/NSBcompanion>

Depends RPostgreSQL

Imports RPostgreSQL, stats, DBI

R topics documented:

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NSBcompanion-package *Some functions to retrieve data from the Neptune Database (Lazarus, 1994).*

Description

Some basic functions to retrieve data from Neptune, and a couple of other functions to deal with the preliminary quality control (outliers, synonyms).

Details

Package: NSBcompanion
Type: Package
Version: 2.1
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License: MIT

Start with `getNeptuneData` to retrieve a dataset. Function `pacmanNeptune` will help you perform a trimming of each species range to delete potential outliers and `resolveSynonymy` will resolve the synonymies using Neptune table 'neptune_taxonomy'. Functions `findAge` and `findPaleocoordinates` will find out the ages and coordinates of samples based on their depth.

Author(s)

Johan Renaudie.

References

Lazarus, D. B. 1994. Neptune: A marine Micropaleontology Database. *Mathematical Geology*, 26(7): 817-832.

changeAgeScale	<i>Change Age Scale</i>
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Description

Switch from one GPTS to another.

Usage

```
changeAgeScale(conn, age_ma, from, to)
```

Arguments

conn	Connection object (resulting from <code>nsbConnect</code>).
age_ma	Vector of numerical ages to transform.
from	Original GPTS. One of "Berg85", "CK95", "Grad08" or "Grad12".
to	Destination GPTS. One of "Berg85", "CK95", "Grad08" or "Grad12".

Value

A vector of numerical ages on the destination GPTS.

Author(s)

Johan Renaudie

Examples

```

nsb <- nsbConnect("guest", "arm_aber_sexy")
changeAgeScale(nsb, 10:20, "Grad12", "Berg85")
#[1] 9.172756 10.353858 11.492500 12.783655 13.997523 15.096420 16.246531 17.300253 18.489331
#[10] 19.620703 20.815821
dbDisconnect(nsb)

```

findAge

Age and paleocoordinates of a sample.

Description

Find a sample age and paleocoordinates based on its depth.

Usage

```

findAge(conn, hole_id, depth_mbsf)
findPaleocoordinates(conn, hole_id, age_ma)

```

Arguments

conn	Connection object (resulting from <code>nsbConnect</code>).
hole_id	Hole name (in Leg_SiteHole format, e. g. 120_747A), as a single character string.
depth_mbsf	Depth in mbsf. Can be a single numeric value or a vector of numeric values.
age_ma	Age in million years. Can be a single numeric value or a vector of numeric values. Typocally the result of <code>findAge</code>

Details

Ages are computed by linear interpolation between tiepoints. Paleolatitude and Paleolongitude are interpolated linearly between paleocoordinates computed for each 1 Ma using Seton et al. 2012 rotation model with GPLates.

Value

`findAge` outputs a dataframe with the following columns:

hole_id	The hole identifier.
depth_mbsf	The depth provided.
age_ma	The ages in Ma, as computed from the current NSB age model for the given hole.

`findPaleocoordinates` outputs a dataframe with the following columns:

hole_id	The hole identifier.
age_ma	The ages (in Ma) provided.
paleo_latitude	The paleolatitude computed for the given age from NSB table <code>neptune_paleogeography</code> , based on Seton et al. 2012 rotation model.
paleo_longitude	The paleolongitude computed for the given age from NSB table <code>neptune_paleogeography</code> , based on Seton et al. 2012 rotation model.

Author(s)

Johan Renaudie.

References

Seton, M., Mueller, R., Zahirovic, S., Gaina, C., Torsvik, T., Shephard, G., Talsma, A., Gurnis, M., Turner, M., Maus, S., and Chandler, M. (2012). Global continental and ocean basin reconstructions since 200Ma. *Earth-Science Reviews*, 113(3):212-270.

Examples

```

nsb <- nsbConnect("guest", "arm_aberSexy")
ages <- findAge(nsb, "74_525A", seq(0, 700, 100))
findPaleocoordinates(nsb, "74_525A", ages$age_ma)
# hole_id age_ma paleo_latitude paleo_longitude
# 1 74_525A 0.000000 -29.07000 2.990000
# 2 74_525A 7.316586 -30.04432 1.9756780
# 3 74_525A 17.250107 -31.44501 0.3449808
# 4 74_525A 46.669501 -35.21729 -5.5937301
# 5 74_525A 57.047529 -36.31190 -7.2385553
# 6 74_525A 70.015133 -36.71030 -8.6612107
# 7 74_525A 74.866876 -36.79734 -9.0293501
# 8 74_525A NA NA NA
dbDisconnect(nsb)

```

getNeptuneData

Get Neptune Data

Description

Retrieve a dataset from Neptune (NSB) database.

Usage

```

getNeptuneData(conn, fossil_group, genus, species,
               age_range, lon_range, lat_range, leg, site, hole, ocean,
               resolve_syn=FALSE, filter_qi=TRUE, filter_on=TRUE, filter_rw=TRUE,
               filter_aq=FALSE, pacman, agescale="Grad12")

```

Arguments

conn	Connection object (resulting from nsbConnect).
fossil_group	Accepted values are "R" (Radiolarians), "F" (Foraminiferans), "D" (Diatoms), "DN" (Dinoflagellates) and "N" (Nanofossils), or any combinations of them.
age_range	Vector of two numeric values (min first then max) corresponding to the minimum and maximum age required (in Ma).
lon_range	Vector of two numeric values (min first then max) corresponding to the minimum and maximum longitude required (in degrees).
lat_range	Vector of two numeric values (min first then max) corresponding to the minimum and maximum latitude required (in degrees).
genus	Character string.

species	Character string.
leg	Character string.
site	Integer.
hole	Character string.
ocean	Accepted values are "ANT" (Antarctic), "ATL" (Atlantic), "PAC" (Pacific), "MED" (Mediterranean) and "IND" (Indian), or any combinations of them.
resolve_syn	Logical. Resolve taxonomy using TNL. Defaults to FALSE.
filter_qi	Logical. Filter out questionable identifications and taxa invalidly included in the fossil group. Defaults to TRUE.
filter_on	Logical. Filter out open-nomenclature taxa. Defaults to TRUE.
filter_rw	Logical. Filter out problematic samples/occurrences (reworking, ...). Defaults to TRUE.
filter_aq	Filter out sites with age quality. Defaults to FALSE. If not FALSE, set minimum quality for an age model: can be one of 'VP', 'P', 'M', 'G', 'VG', 'E'.
pacman	Perform pacman trimming. Numeric value (used for both top and bottom) or vector of 2 numeric values (top and bottom). Leave blank for no trimming.
agescale	Character string. Which age scale to use. Defaults to 'Grad12' (i. e. Gradstein et al. 2012 GPTS). Could be one of 'Berg85', 'CK95', 'Grad08' and 'Grad12'.

Value

A dataframe downloaded from NSB, similar to one that can be downloaded from the NSB website.

Author(s)

Johan Renaudie

Examples

```

nsb <- nsbConnect("guest", "arm_aber_sexy")
# Search for all Neogene siliceous microfossil occurrence in the Indian sector of the Southern Ocean:
n <- getNeptuneData(nsb, fossil_group=c("R", "D"), age_range=c(0, 23), lon_range=c(20, 120), lat_range=c(-90, -40))

# Search for all occurrences of the radiolarian species Cycladophora davisiana:
p <- getNeptuneData(nsb, fossil_group="R", genus="Cycladophora", species="davisiana")

```

makeCoreFile

Make a CORE file for NSB_ADP_wx

Description

Produce a CORE file for use with the NSB_ADP_wx software.

Usage

```
makeCoreFile(conn, site_hole)
```

Arguments

conn Connection object (resulting from `nsbConnect`).

site_hole Hole name (in SiteHole format, e.g. 747A), as a single character string.

Value

Write a tab-delimited file in the current directory.

Author(s)

Johan Renaudie.

Examples

```
nsb <- nsbConnect("guest", "arm_aberSexy")
makeCoreFile(nsb, "747A")
dbDisconnect(nsb)
```

nsbConnect	<i>Connect to NSB.</i>
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Description

Wrapper to connect to NSB database.

Usage

```
nsbConnect(username, password, intern = FALSE, local = FALSE)
```

Arguments

username Username, as character string.

password Username, as character string.

intern Are you currently running this code from inside the Museum fuer Naturkunde network? Defaults to FALSE.

local Are you trying to connect to a local, offline version of NSB? Defaults to FALSE.

Value

A connection object.

Author(s)

Johan Renaudie.

Examples

```
nsb <- nsbConnect("guest", "arm_aberSexy")
```

pacmanNeptune *Implement PacMan trimming (Lazarus et al. 2012)*

Description

Trim the top and the bottom of each species range in order to eliminate potential outliers.

Usage

```
pacmanNeptune(dataset, top, bottom)
```

Arguments

dataset	A dataframe, typically the output of getNeptuneData .
top	Percentage of occurrences to trim at the top of each species range.
bottom	Percentage of occurrences to trim at the bottom of each species range.

Value

Return a trimmed dataframe.

Author(s)

Lazarus et al. 2012 for the algorithm, Johan Renaudie for the code.

References

Lazarus et al. 2012. Pacman profiling: a simple procedure to identify stratigraphic outliers in high-density deep-sea microfossil data. *Paleobiology*, 38(1): 858-875.

Examples

```
nsb <- nsbConnect("guest", "arm_aber_sexy")
n <- getNeptuneData(nsb, fossil_group="R", age_range=c(4,6), ocean="IND")
nrow(n)
#[1] 1725
o <- pacmanNeptune(n, top=10, bottom=5)
nrow(o)
#[1] 1550
dbDisconnect(nsb)
```

resolveSynonymy	<i>Resolve synonymy.</i>
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Description

Resolve the synonymies using the result of the IODP Paleontology Coordination Group's TNL project (see Lazarus et al. 2015).

Usage

```
resolveSynonymy(conn, dataset)
```

Arguments

conn	Connection object (resulting from nsbConnect).
dataset	A dataset retrieved from NSB database using function getNeptuneData .
verbose	Logical. If TRUE print a progress bar.

Value

The function outputs a dataframe similar to the input dataset with extra columns: resolved_taxon_id, resolved_genus, resolved_species and resolved_subspecies.

Author(s)

Johan Renaudie.

References

Lazarus, D., Suzuki, N., Caulet, J.-P., Nigrini, C., Goll, I., Goll, R., Dolven, J. K., Diver, P., and Sanfilippo, A. (2015). An evaluated list of cenozoic-recent radiolarian species names (polycystinea), based on those used in the dsdp, odp and iodp deep-sea drilling programs. *Zootaxa*, 3999(3):301-333.

Examples

```
nsb <- nsbConnect("guest", "arm_aber_sexy")
data <- getNeptuneData(nsb, fossil_group="R", age_range=0:1)
res <- resolveSynonymy(nsb, data)
# Step 1 : 118 / 118
# Step 2 : 12 / 12
# 7517 rows done
length(unique(res$taxon_id))
#[1] 386
length(unique(res$resolved_taxon_id))
#[1] 299
dbDisconnect(nsb)
```

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