

Package ‘forImage’

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Type Package

Title Foraminiferal Image Analysis and Test Measurement

Version 0.1.0

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Description The goal of this collection of functions is to provide an easy to use tool for the measurement of foraminifera and other unicellulars organisms size. With functions developed to guide foraminiferal test biovolume calculations and cell biomass estimations. The volume function includes several microalgae models geometric adaptations based on Hillebrand et al. (1999) <doi:10.1046/j.1529-8817.1999.3520403.x>, Sun and Liu (2003) <doi:10.1093/plankt/fbg096> and Vadrucchi, Cabrini and Bassett (2007) <doi:10.1285/i1825229Xv1n2p83>.

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URL <https://github.com/ThaiseRF/forImage>

BugReports <https://github.com/ThaiseRF/forImage/issues>

Encoding UTF-8

Depends R (>= 3.2.0)

LazyData true

Imports dplyr, magrittr, tibble, reticulate

RoxygenNote 7.1.0

Suggests knitr, rmarkdown, data.table, xml2, raster, testthat (>= 2.1.0)

SystemRequirements Python >=3.5, numpy (>= 1.18.1), imutils (>= 0.5.3), scipy (>= 1.4.1), pandas (>= 1.0.2), Pillow (>= 7.0.0), openv (>= 4.1.2)

VignetteBuilder knitr

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NeedsCompilation no

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ammonia	<i>Ammonia size data</i>
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Description

A ‘data.frame’ containing the size and other attributes of species from genus *Ammonia*. The variables are as follows:

Usage

```
ammonia
```

Format

A ‘data.frame’ with 867 rows and 7 variables:

species species of genus *Ammonia* from which raw data were gathered

ind number of individuals by species

h test height in um (82.05–390.65)

d_one test minor diameter in um (20–220)

d_two test major diameter in um (75.1–364.6)

area test surface area in um² (4438–107903)

pco percent cell occupancy of the test (11–100)

amphistegina *Amphistegina size data*

Description

A ‘data.frame’ containing the size and other attributes of genus *Amphistegina*. The variables are as follows:

Usage

```
amphistegina
```

Format

A ‘data.frame’ with 167 rows and 5 variables:

ind number of individuals

h test height in um (60.0–579.0)

d_one test diameter in um (111.3–1193.1)

area test surface area in um² (9722–3027282)

pco percent cell occupancy of the test (3.408–100)

angulogerina *Angulogerina size data*

Description

A ‘data.frame’ containing the size and other attributes of species from genus *Angulogerina*. The variables are as follows:

Usage

```
angulogerina
```

Format

A 'data.frame' with 100 rows and 6 variables:

ind number of individuals

h test height in um (81.75–380.91)

d_one test minor diameter in um (34–156)

d_two test major diameter in um (66.04–237.34)

area test surface area in um² (4654–41915)

pc percent cell occupancy of the test (6.818–100)

asterotrochammina	<i>Asterotrochammina size data</i>
-------------------	------------------------------------

Description

A 'data.frame' containing the size and other attributes of species from genus *Asterotrochammina*. The variables are as follows:

Usage

asterotrochammina

Format

A 'data.frame' with 335 rows and 7 variables:

species species of genus *Asterotrochammina* from which raw data were gathered

ind number of individuals by species

h test height in um (12–72)

d_one test minor diameter in um (77.86–265.50)

radius test radius in um (38.93–132.75)

area test surface area in um² (4761–57577)

pc percent cell occupancy of the test (15–100)

bio.volume	<i>Biovolume calculus</i>
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Description

This function calculates Foraminifera biovolume, through geometric approximation. To compute others organisms cell volume use [volume.total](#) function

Usage

```
bio.volume(data, pco = 0.76, genus = NULL, model = NULL)
```

Arguments

data	a numeric vector or data frame with size data. Size data parameters by model see volume details.
pco	(optional) vector informing percent of cell occupancy in the test. Default value set for specific genus in data_pco .
genus	(optional) character informing foraminifera genus to calculate individual biovolume. See all genera available in data_pco
model	(optional if genus unknown) character informing geometric model to calculate volume. See all models available in volume.total

Details

The function calculates the biovolume of different individuals from the available genera.

Value

A 'data.frame' or numeric object, consisting of calculated individual volume (if not available), biovolume and model (if genus is informed).

Author(s)

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See Also

[volume.total](#)

[biomass](#)

[measure](#)

Examples

```
# Calculate biovolume for different genera
#Ammonia size data
data("ammonia")

bio.volume(ammonia, genus= "ammonia")

# Calculate biovolume for unknown genus
df <- data.frame(h = 10, d_one = 10,
d_two = 10, area = 10, width = 10, length = 10)
bio.volume(df, model = "10h1", pco = 0.76)
```

biomass

Biomass estimative

Description

The function estimates biomass through biovolume data and applies different cell density values as conversion methods. See details ‘Details’:

Usage

```
biomass(biovolume, method = "michaels")
```

Arguments

biovolume	numeric value, object or data.frame with cell living volume values.
method	The methods of conversion from biovolume to biomass are listed below, default is 'michaels': <ul style="list-style-type: none"> • 'saidova' : adopted cell density of 1.027 g/cm³; • 'strathmann' : measured cell density of 0.110 pgC[org]/um³; • 'turley' : estimated cell density of 0.132 pgC[org]/um³; • 'putt' : estimated cell density of 0.140 pgC[org]/um³; • 'gerlach' : adopted cell density of 1.13 g/cm³ wet mass, assuming 10 percent as living organic carbon; • 'michaels' : calculated cell density of 0.089 pgC[org]/um³.

Details

For biomass estimates based on biovolume is usual the application of a cell density value, to retrieve the amount of organic carbon in the organism. The function made available distinct options of conversion factor which are based in several authors. These factors have been applied to a wide diversity of nano, micro, and macro-organisms, some applied to foraminifera and other nearby groups.

Value

An 'data.frame' or numeric object, consisting of calculated biomass in ugC[org]/ind.

Author(s)

Thaise R. Freitas <thaisericoardo.freitas@gmail.com>

References

- Saidova, K. (1966). The biomass and quantitative distribution of live foraminifera in the Kurile-Kamchatka trench area. *DOKLADY AKAD. NAUK SSSR*, 174(1), 216–217.
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See Also

[bio.volume](#), [volume.total](#)

Examples

```
#Ammonia biomass calculation
data(ammonia)

#calculate test volume and biovolume
df <- bio.volume(data = ammonia, genus = "ammonia")
df

#calculate individual biomass with choosen method
res <- biomass(df, method = 'michaels')
res
```

bolivina

Bolivina size data

Description

A 'data.frame' containing the size and other attributes of species from genus *Bolivina*. The variables are as follows:

Usage

```
bolivina
```

Format

A 'data.frame' with 628 rows and 7 variables:

species species of genus *Bolivina* from which raw data were gathered

ind number of individuals by species

d_one test minor diameter in um (72.37–502.12)

h test height (thickness) in um (12.5–83.0)

d_two test major diameter in um (60.60–226.21)

area test surface area in um² (3187–72244)

pco percent cell occupancy of the test (9.72–100)

cibicidoides

Cibicidoides size data

Description

A 'data.frame' containing the size and other attributes of species from genus *Cibicidoides*. The variables are as follows:

Usage

```
cibicidoides
```


Format

A 'data.frame' with 118 rows and 7 variables:

species species of genus Cibicidoides from which raw data were gathered

ind number of individuals by species

h test height in um (24–117)

d_one test minor diameter in um (76.46–266.85)

radius test radius in um (38.23–133.43)

area test surface area in um² (4591–55928)

pco percent cell occupancy of the test (11.87–100)

data_pco

Foraminiferal genera data for forImage examples

Description

This 'data.frame' contains protoplasm occupancy mean and standard deviation data of 72 foraminifera genera. These genera data are originally from Freitas and others (2019)

Format

A 'data.frame' with 72 rows and 3 variables:

genera foraminifera genera

mean mean protoplasm occupancy percentage (pco)

sd standard deviation of mean (pco)

n number of specimens

model fitted geometric model in Freitas and others (2019)

Details

Foraminifera genera with (pco) available:

"ammonia"	"amphistegina"	"angulogerina"
"archaias"	"asterotrochammina"	"bolivina"
"buliminella"	"cancris"	"caronia"
"cassidulina"	"cibicides"	"cibicidoides"
"cornuspira"	"cribroelphidium"	"cymbaloporetta"
"deuterammina"	"disconorbis"	"discorbia"
"discorbinella"	"discorbis"	"discorbitina"
"edentostomina"	"elphidium"	"eoeponidella"
"eponides"	"fissurina"	"fursenkoina"
"glabratella"	"globocassidulina"	"hanzawaia"
"hauerina"	"heronallenia"	"laevipeneroplis"

"lepidodeuterammina"	"loxostomina"	"miliolinella"
"mullinoides"	"mychostomina"	"neoonorbina"
"nonionella"	"nonioninoides"	"pararotalia"
"paratrochammina"	"patellina"	"planispirillina"
"planorbulina"	"planulina"	"pyrgo"
"quinqueloculina"	"rectocibicides"	"remaneicella"
"reophax"	"rosalina"	"rotaliammina"
"rotorbinella"	"rotorbis"	"sahulua"
"sigmavirgulina"	"siphonina"	"sorites"
"spirillina"	"spiroloculina"	"spirorbina"
"tetrataxiella"	"textularia"	"triloculina"
"triloculinella"	"trochammina"	"webbinella"
"wiesnerella"		

 depth.xml

Import image object depth (Z)

Description

The function retrieves the object depth information from image metadata as source.

Usage

```
## S3 method for class 'xml'
depth(x, ...)
```

Arguments

```
x          file containing metadata, if xml type: '.xml', '.tif_meta.xml'
...        other arguments.
```

Value

A 'data.frame' with the following information:

- file : filename
- z_depth : measured focus range depth (z)

Examples

```
## Not run:
#Path to example file from package
meta <- system.file("extdata", "foram.tif_meta.xml", package="forImage")

#retrieve z-depth data
depth.xml(meta)
## End(Not run)
```

discorbinella	<i>Discorbinella size data</i>
---------------	--------------------------------

Description

A 'data.frame' containing the size and other attributes of species from genus *Discorbinella*. The variables are as follows:

Usage

```
discorbinella
```

Format

A 'data.frame' with 318 rows and 7 variables:

species species of genus *Discorbinella* from which raw data were gathered

ind number of individuals by species

h test height in um (15–72)

d_one test minor diameter in um (67.69–197.43)

radius test radius in um (33.85–98.71)

area test surface area in um² (3599–30614)

pco percent cell occupancy of the test (9.673–100)

exampleImage	<i>Foraminiferal photomicrograph for forImage examples</i>
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Description

Contains image file of one foraminifer. These files are originally from previous work - Freitas and others (2019)

Format

Image objects with variable dimension and resolution.

install_measure	<i>Install python packages dependencies for measure function</i>
-----------------	--

Description

The function is a wrapper to install all python packages dependencies for measure function at once. It will install the following packages: numpy, scipy, imutils, Pillow, pandas, and opencv-python. If the latest versions of these packages are already installed, there is no need to run this function.

Usage

```
install_measure(  
    method = "auto",  
    conda = "auto",  
    envname = NULL,  
    extra_packages = NULL,  
    pip = F  
)
```

Arguments

method	Installation method. By default, "auto" automatically finds a method that will work in the local environment. Change the default to force a specific installation method. Note that the "virtualenv" method is not available on Windows.
conda	Path to conda executable (or "auto" to find conda using the PATH and other conventional install locations).
envname	Name of environment to install packages into.
extra_packages	Additional packages if needed.
pip	Install from pip, if possible.

Details

On Linux and OS X the "virtualenv" method will be used by default ("conda" will be used if virtualenv isn't available). On Windows, the "conda" method is always used. For more information check the 'reticulate' package documentation: <https://rstudio.github.io/reticulate/>

Value

No return value. The function is only called to install the required packages.

laevipeneroplis	<i>Laevipeneroplis size data</i>
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Description

A ‘data.frame‘ containing the size and other attributes of species from genus *Laevipeneroplis*. The variables are as follows:

Usage

```
laevipeneroplis
```

Format

A ‘data.frame‘ with 79 rows and 7 variables:

species species of genus *Laevipeneroplis* from which raw data were gathered

ind number of individuals by species

h test height in um (40–633.9)

d_one test minor diameter in um (47–624.2)

area test surface area in um² (8827–306012)

pc percent cell occupancy of the test (15.24–100)

d_two test major diameter in um (169.2–544.0) - The NA’s related to one species of this genus that don’t required this measure

loxostomina	<i>Loxostomina size data</i>
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Description

A ‘data.frame‘ containing the size and other attributes of species from genus *Loxostomina*. The variables are as follows:

Usage

```
loxostomina
```

Format

A 'data.frame' with 31 rows and 7 variables:

ind number of individuals by species
d_one test minor diameter in um (101.4–534.6)
h test height in um (28.0–80.0)
d_two test major diameter in um (89.76–261.17)
area test surface area in um² (6636–76089)
pco percent cell occupancy of the test (9.88–100)

measure

Foraminifera image measurement

Description

This function measures dimensions in photomicrographs.

Usage

```
measure(file, scale = NULL, ref_scale = NULL,
unit = "um", pco = FALSE, save = FALSE, path = NULL)
```

Arguments

file	image file with or without metadata.
scale	(optional) image physical pixel size (metric / pixel).
ref_scale	(optional) reference scale available on image (in micrometers or millimeters). This scale should be inserted under the main object.
unit	scale unit. Needs to agree with reference scale or metric per pixel. (Default "um")
pco	(optional) will assess proportion of cell occupancy inside the shell. Outlined proportion. This argument is still being tested and should be used with caution.
save	If TRUE save the result image in a specified folder (see path) or the working directory, if FALSE it does not save the image with measures. (Default FALSE)
path	(optional) path to save result file.

Value

A 'data.frame' containing the file name, surface area and major and minor axis. The unit is dependent on the pixel per metric scale. It also returns a PNG file with the measured dimensions if save = TRUE.

Author(s)

Thaise R. Freitas <thaisericoardo.freitas@gmail.com>

See Also

[bio.volume](#), [volume.total](#)

Examples

```
## Not run:  
#Path to example file from package  
img <- system.file("extdata", "foram.tif", package="forImage")  
  
#measure individual dimension  
measure(img)  
  
## End(Not run)
```

nonionella

Nonionella size data

Description

A ‘data.frame’ containing the size and other attributes of species from genus *Nonionella*. The variables are as follows:

Usage

```
nonionella
```

Format

A ‘data.frame’ with 208 rows and 7 variables:

species species of genus *Nonionella* from which raw data were gathered

ind number of individuals by species

d_one test minor diameter in um (93.39–564.98)

h test height in um (19.50–294.00)

d_two test major diameter in um (82.99–547.67)

area test surface area in um² (5783–222371)

pc0 percent cell occupancy of the test (15.51–100)

patellina	<i>Patellina size data</i>
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Description

A ‘data.frame’ containing the size and other attributes of species from genus *Patellina*. The variables are as follows:

Usage

```
patellina
```

Format

A ‘data.frame’ with 79 rows and 6 variables:

ind number of individuals by species

h test height in um (24–66)

d_one test minor diameter in um (84.84–247.46)

radius test radius in um (42.42–123.73)

area test surface area in um² (5653–87838)

pco percent cell occupancy of the test (9.94–100)

quineloculina	<i>Quineloculina size data</i>
---------------	--------------------------------

Description

A ‘data.frame’ containing the size and other attributes of species from genus *Quineloculina*. As this genus has a wide morphological variation, two types of models can be applied to calculate its volume. Therefore the variables are grouped by model as well as by species. It is also an example that the model argument can be a ‘data.frame’ column. The variables are as follows:

Usage

```
quineloculina
```


Format

A 'data.frame' with 688 rows and 10 variables:

species species of genus Quinqueloculina from which raw data were gathered

ind number of individuals by species

h test height in um (107.4–944.4)

d_one test minor diameter in um (26.94–389.73)

d_two test major diameter in um (18.52–662.23)

area test surface area in um² (6294–431271)

pco percent cell occupancy of the test (13.76–100)

length test length in um (44.02–609.00)

width test width in um (83.72–688.32)

model geometric model ('10hl'-'17fs')

rectocibicides

Rectocibicides size data

Description

A 'data.frame' containing the size and other attributes of genus *Rectocibicides*. The variables are as follows:

Usage

rectocibicides

Format

A 'data.frame' with 199 rows and 4 variables:

ind number of individuals

h test height in um (22.00–101.50)

area test surface area in um² (3450–674280)

pco percent cell occupancy of the test (10–100)

spirillina	<i>Spirillina size data</i>
------------	-----------------------------

Description

A ‘data.frame’ containing the size and other attributes of species from genus *Spirillina*. The variables are as follows:

Usage

```
spirillina
```

Format

A ‘data.frame’ with 42 rows and 6 variables:

ind number of individuals by species
h test height in um (12–44)
d_one test minor diameter in um (73.71–105.14)
radius test radius in um (36.86–123.73)
area test surface area in um² (4268–34730)
pc percent cell occupancy of the test (7.10–100)

textularia	<i>Textularia size data</i>
------------	-----------------------------

Description

A ‘data.frame’ containing the size and other attributes of species from genus *Textularia*. The variables are as follows:

Usage

```
textularia
```

Format

A ‘data.frame’ with 84 rows and 7 variables:

species species of genus *Textularia* from which raw data were gathered
ind number of individuals by species
h test height in um (113.6–1034.4)
d_one test minor diameter in um (40–306)
d_two test major diameter in um (103.8–552.6)
area test surface area in um² (8235–336929)
pc percent cell occupancy of the test (10.46–100)

volume.total	<i>Volumetric calculus of organisms</i>
--------------	---

Description

The function calculates organisms volume based on geometric approximation.

Usage

```
## S3 method for class 'total'
volume(data, model, ...)
```

Arguments

data	data frame containing size data. Size data parameters may vary according to chosen model, see Details.
model	character informing geometric model to calculate volume, the models options are listed below: <ul style="list-style-type: none"> • '1h1' : sphere • '2s1' : half-sphere • '3h1' : prolate spheroid • '4h1' : cone or double cone • '6fs' : paraboloid • '7fs' : dome • '8h1' : cylinder • '10h1' : ellipsoid • '11fs' : elliptic cone • '12v' : cone + half ellipsoid • '13h1s1' : gomphonemoid • '14h1' : prism on elliptic base/elliptic cylinder • '15h1' : half elliptic prism • '17fs' : triangular dypyramid • 'ahx' : area x height
...	other parameters.

Details

These geometric models applied in this function are based and adapted from microalgae models developed by Hillebrand et al. (1999) - ('.h1'), Sun and Liu (2003) - ('.s1') and Vadrucchi, Cabrini and Basset (2007) - ('.v'), plus other adapted models ('.fs'). The models can be a variable in data if specified as model. The size data parameters should follow the specified measures determined by each model, where d_{one} is minor diameter, d_{two} is major diameter and h is height.

'1h1' $V = (\pi * (d_{one}^3))/6$

'2s1'	$V = (\pi * (d_{one}^3))/12$
'3h1'	$V = (\pi * h * (d_{one}^2))/6$
'4h1'	$V = (\pi * h * (d_{one}^2))/12$
'6fs'	$V = (\pi * hx * (d_{one}^2))/8$
	where <i>hx</i> is a function of test height for trochamminids.
'7fs'	$V = (\pi * h * (4 * (h^2) + 3 * (d_{one}^2)))/24$
'8h1'	$V = (\pi * h * (d_{one}^2))/4$
'10h1'	$V = (\pi * h * d_{one} * d_{two})/6$
'11fs'	$V = (\pi * h * d_{one} * d_{two})/12$
'12v'	$V = (\pi * h * d_{one} * d_{two})/12$
'13h1s1'	$V = ((d_{one} * d_{two})/4) * (d_{one} + ((\pi/4) - 1) * d_{two}) * \text{asin}(h/(2 * d_{one}))$
'14h1'	$V = (\pi * h * d_{one} * d_{two})/4$
'15h1'	$V = \pi * h * d_{one} * d_{two}/4$
'17fs'	$V = ((length * width)/2) * h/3$

Value

A 'data.frame' or numeric object, consisting of calculated individual volume along with biovolume if the pco is informed.

Author(s)

Thaise R. Freitas <thaisericardo.freitas@gmail.com>

References

- Hillebrand, H., Dürselen, C.D., Kirschtel, D., Pollinger, U., & Zohary, T. (1999). Biovolume calculation for pelagic and benthic microalgae. *Journal of Phycology*, 35(2), 403–424. doi:10.1046/j.1529-8817.1999.3520403.x
- Sun, J., & Liu, D. (2003). Geometric models for calculating cell biovolume and surface area for phytoplankton. *Journal of Plankton Research*, 25(11), 1331–1346. doi:10.1093/plankt/fbg096
- Vadrucchi, M. R., Cabrini, M., & Basset, A. (2007). Biovolume determination of phytoplankton guilds in transitional water ecosystems of Mediterranean Ecoregion. *Transitional Waters Bulletin*, 2, 83–102. doi:10.1285/i1825229Xv1n2p83

See Also

[measure](#)
[bio.volume](#)

Examples

```
#Ammonia size data
data("ammonia")

#calculate test volume
volume.total(ammonia, model = "10h1")
```

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