

# Package ‘rYoutheria’

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**Type** Package

**Title** Access to the YouTheria Mammal Trait Database

**Description** A programmatic interface to web-services of YouTheria. YouTheria is an online database of mammalian trait data <<http://www.utheria.org/>>.

**Version** 1.0.3

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**VignetteBuilder** knitr

**URL** <https://github.com/BiologicalRecordsCentre/rYoutheria>

**BugReports** <https://github.com/biologicalrecordscentre/rYoutheria/issues>

**Depends** R (>= 3.0.0)

**Imports** plyr, RJSONIO, reshape2, RCurl

**Suggests** knitr, testthat, roxygen2

**License** MIT + file LICENSE

**RoxygenNote** 5.0.1

**NeedsCompilation** no

**Repository** CRAN

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getCountries	<i>Get country names from YouTheria</i>
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**Description**

Retrieves a data.frame of country names and IDs from YouTheria.

**Usage**

```
getCountries()
```

**Value**

A dataframe of country names and IDs. These names can be used in [getMeasurementData](#) to restrict the search to a specific country

**Examples**

```
## Not run:  
# Get a dataframe of all countries  
getCountries()  
  
## End(Not run)
```

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getLocData	<i>Get location information from YouTheria</i>
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**Description**

Retrieves location information stored on YouTheria

**Usage**

```
getLocData(country = NULL, StudyUnitId = NULL)
```

**Arguments**

country	Character specifying the country within which to search for locations. for a list of countries used <code>getCountries()</code> .
StudyUnitId	Numeric specifying the StudyUnitId to search for

**Value**

A dataframe in which each rows gives the details of a study unit

**Examples**

```
## Not run:
# Get a dataframe of Indian study units
Indian_StudyUnits <- getLocData(country = 'India')

## End(Not run)
```

---

```
getMeasurementData      Get a table of trait measurements from YouTheria
```

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**Description**

Retrieves a data.frame of trait measurements with facilities to select by location, species name and/or measurement type.

**Usage**

```
getMeasurementData(measurementType = NA, MSW93Binomial = NA,
  MSW05Binomial = NA, country = NULL, StudyUnitId = NULL,
  locationData = TRUE, locationOnly = FALSE, cast = TRUE,
  silent = FALSE)
```

**Arguments**

measurementType	Measurement types to collect data for. If NULL (default), all measurement types are returned. Can also be 'numeric' or 'character' (or a list of either type) and will filter by MeasurementTypeID and the measurement respectively. MeasurementTypeIDs and names can be found using getMeasurementTypes().
MSW93Binomial	Character giving the latin name of a species (or list of species) for which measurements are required. Naming should follow Mammal Species of the World 1993.
MSW05Binomial	Character giving the latin name of a species (or list of species) for which measurements are required. Naming should follow Mammal Species of the World 2005.
country	Character specifying the country from which you wish to collect data. If NULL all data is retrieved. If specified then locationOnly is set to TRUE
StudyUnitId	Numeric specifying the StudyUnitId from which you wish to collect data. If NULL all data is retrieved
locationData	Logical dictating whether location information should be added to the output. Default is FALSE but is set to TRUE if either StudyUnitId or country are specified.
locationOnly	If TRUE data is only be returned if it has location information.
cast	If TRUE (default) then the data is cast so that each observation is one row in the output. If false then each observation has one row for each data element recorded (i.e. range, mean, units, etc)
silent	If TRUE progress reporting is silenced

**Value**

A data.frame with each row giving a trait measurement

**Examples**

```
## Not run:
# Select measurement type by id
M14 <- getMeasurementData(14)
M22_7_2 <- getMeasurementData(c(22,7,2))

# Select measurement type by name
WM <- getMeasurementData('Wing Morphology')
WM_TN <- getMeasurementData(c('Wing Morphology', 'Teat Number'))

# Select by measurement type and species name
PpPr_bodymass <- getMeasurementData(measurementType = 1,
                                     MSW93Binomial = c('Pongo pygmaeus', 'Peroryctes raffrayana'))

#Select by measurement type, species name and location
Ob_Activity_Tanz <- getMeasurementData(measurementType = 'Activity Cycle',
                                       MSW05Binomial = 'Oryx beisa',
                                       country = 'Tanzania')

## End(Not run)
```

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getMeasurementTypes    *Get Measurement Types*

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**Description**

Retrieves a data.frame of measurement types available from YouTheria.

**Usage**

```
getMeasurementTypes(measurementType = NULL)
```

**Arguments**

measurementType

If NULL (default), then all measurement types are returned. Can also be 'numeric' or 'character' (or a list of either type) and will filter by Id and Name respectively in the resulting data.frame.

**Value**

A dataframe of measurement types giving their Id and Name

**Examples**

```
## Not run:
# Get a dataframe of all measurement types
AllMT <- getMeasurementTypes()

# Search by name
BM_MT <- getMeasurementTypes('Body Mass')
BM_LL_MT <- getMeasurementTypes(c('Body Mass', 'Limb Length'))

# Search by ID
MT1 <- getMeasurementTypes(1)
MT123 <- getMeasurementTypes(1:3)

## End(Not run)
```

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rYoutheria

*The rYoutheria package*

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**Description**

The rYoutheria package harnesses the Youtheria website's APIs to give easy access to a large amount of mammal trait data. The package allows the user to select data by species, location and measurement type. More information can be found out about the Youtheria dataset at <http://www.utheria.org/>

Click on the index link below for more information on each function

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YoutheriaToDF

*Convert data returned from API to a dataframe*

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**Description**

Takes the list returned by `fromJSON(getURL(url))`, where `url` is the `ValueByType` controller in the Youtheria API, and returns a `data.frame`. This code is faster than using `plyr`.

**Usage**

```
YoutheriaToDF(x)
```

**Arguments**

`x` a list of trait data as returned by `fromJSON(getURL(url))`.

**Value**

A `data.frame` of melted trait data

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