

# Package ‘helminthR’

December 9, 2022

**Type** Package

**Title** Access London Natural History Museum Host-Helminth Record Database

**Version** 1.0.10

**Imports** xml2, rvest, httr, magrittr, plyr, utils, taxize

**Suggests** testthat, knitr, rmarkdown

**VignetteBuilder** knitr

**URL** <https://docs.ropensci.org/helminthR/>,  
<https://github.com/rOpenSci/helminthR/>

**BugReports** <https://github.com/rOpenSci/helminthR/issues/>

**Description** Access to large host-parasite data is often hampered by the availability of data and difficulty in obtaining it in a programmatic way to encourage analyses. 'helminthR' provides a programmatic interface to the London Natural History Museum's host-parasite database, one of the largest host-parasite databases existing currently <<https://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/>>. The package allows the user to query by host species, parasite species, and geographic location.

**License** GPL-3

**LazyData** yes

**RoxygenNote** 7.1.1

**NeedsCompilation** no

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**Repository** CRAN

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helminthR-package	<i>Access London Natural History Museum host-helminth record database</i>
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### Description

'helminthR': A programmatic interface to the London Natural History Museum's host-parasite database.

The package currently allows you to query by host species, parasite species, and geographic location. No information is provided on parasite prevalence or intensity.

### Author(s)

Tad Dallas <tad.a.dallas@gmail.com>

### References

Gibson, D. I., Bray, R. A., & Harris, E. A. (Compilers) (2005). Host-Parasite Database of the Natural History Museum, London. <<http://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/>>

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cleanData	<i>Clean helminth parasite occurrence data</i>
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### Description

Given a host-parasite edgelist, this function can validate species names, provide further taxonomic information (thanks to taxize), and remove records only to genus level.

### Usage

```
cleanData(edge, speciesOnly = FALSE, validateHosts = FALSE)
```

**Arguments**

edge	Host-parasite edgelist obtained from <a href="#">findLocation</a> , <a href="#">findHost</a> , or <a href="#">findParasite</a>
speciesOnly	boolean flag to remove host and parasite species where data are only available at genus level (default = FALSE)
validateHosts	boolean flag to check host species names against Catalogue of Life information and output taxonomic information (default = FALSE)

**Details**

Use `data(locations)` for a list of possible locations.

**Value**

`cleanEdge` Host-parasite edgelist, but cleaned

**Author(s)**

Tad Dallas

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findHost	<i>Find parasite occurrence data for given host.</i>
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**Description**

Given a host genus, species, and/or location, returns a list of parasite occurrences on that host or for that location. Use `data(locations)` for a list of possible locations.

**Usage**

```
findHost(
  genus = NULL,
  species = NULL,
  location = NULL,
  citation = FALSE,
  hostState = NULL,
  speciesOnly = FALSE,
  validateHosts = FALSE,
  parGroup = NULL,
  removeDuplicates = FALSE
)
```

**Arguments**

genus	Host genus
species	Host species
location	Geographic location.
citation	Boolean. Should the output include the citation link and the number of supporting citations? default is FALSE
hostState	number corresponding to one of six different host states. The default value is NULL and includes all host states
speciesOnly	boolean flag to remove host and parasite species where data are only available at genus level (default = FALSE)
validateHosts	boolean flag to check host species names against Catalogue of Life information and output taxonomic information (default = FALSE)
parGroup	name of parasite group to query (default queries all groups)
removeDuplicates	(boolean) should duplicate host-parasite combinations be removed? (default is FALSE)

**Details**

hostState can take values 1-6 corresponding to if the recorded host was found

- (1) "In the wild"
- (2) "Zoo captivity"
- (3) "Domesticated"
- (4) "Experimental"
- (5) "Commercial source"
- (6) "Accidental infestation"

A value of NULL should be entered if you would like to include all hostStates.

parGroup can be specified as "Acanthocephalans", "Cestodes", "Monogean", "Nematodes", "Trematodes", or "Turbs" (Turbellarians etc.). The default is to query all helminth parasite taxa.

**Value**

Three (or five) column data.frame containing host species, parasite species (shortened name and full name), and citation link and number of citations (if 'citation'=TRUE), with each row corresponding to an occurrence of a parasite species on a host species.

**Author(s)**

Tad Dallas

**References**

Gibson, D. I., Bray, R. A., & Harris, E. A. (Compilers) (2005). Host-Parasite Database of the Natural History Museum, London. <<http://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/>>

**See Also**[findParasite](#)**Examples**

```
gorillaParasites <- helminthR::findHost("Gorilla", "gorilla")

# An example of how to query multiple hosts when you have a
# vector of host species names

hosts <- c("Gorilla gorilla", "Peromyscus leucopus")
plyr::ldply(hosts, function(x)
  {helminthR::findHost(unlist(strsplit(x, " ")[1], unlist(strsplit(x, " ")[2]))})
```

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 findLocation

*Find host-parasite interactions for a given location*


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**Description**

Given a location (available from `data{locations}`) this function returns all host-parasite associations in that location.

**Usage**

```
findLocation(
  location = NULL,
  group = NULL,
  citation = FALSE,
  hostState = NULL,
  speciesOnly = FALSE,
  validateHosts = FALSE,
  removeDuplicates = FALSE
)
```

**Arguments**

location	Location of host-parasite interaction.
group	Parasite group - Cestodes, Acanthocephalans, Monogeneans, Nematodes, Trematodes, or Turbellarian etc. (Turb)
citation	Boolean. Should the output include the citation link and the number of supporting citations? default is FALSE
hostState	number corresponding to one of six different host states. The default value is NULL and includes all host states.
speciesOnly	boolean flag to remove host and parasite species where data are only available at genus level (default = FALSE)

`validateHosts` boolean flag to check host species names against Catalogue of Life information and output taxonomic information (default = FALSE)

`removeDuplicates` (boolean) should duplicate host-parasite combinations be removed? (default is FALSE)

### Details

`hostState` can take values 1-6 corresponding to if the recorded host was found

- (1) "In the wild"
- (2) "Zoo captivity"
- (3) "Domesticated"
- (4) "Experimental"
- (5) "Commercial source"
- (6) "Accidental infestation"

### Value

Three (or five) column data.frame containing host species, parasite species (shortened name and full name), and citation link and number of citations (if `citation = TRUE`), with each row corresponding to an occurrence of a parasite species on a host species.

### Author(s)

Tad Dallas

### References

Gibson, D. I., Bray, R. A., & Harris, E. A. (Compilers) (2005). Host-Parasite Database of the Natural History Museum, London. <<http://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/>>

### See Also

[findHost](#)

### Examples

```
FrenchHostPars <- helminthR::findLocation(location="France")
```

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findParasite	<i>Find host-parasite interactions for a given parasite species.</i>
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### Description

Given a host genus and/or species, this function returns a matrix containing host-parasite interaction data. Search available locations using `data(locations)`.

### Usage

```
findParasite(
  genus = NULL,
  species = NULL,
  group = NULL,
  subgroup = NULL,
  location = NULL,
  citation = FALSE,
  hostState = NULL,
  speciesOnly = FALSE,
  validateHosts = FALSE,
  removeDuplicates = FALSE
)
```

### Arguments

genus	Parasite genus
species	Parasite species
group	Parasite group - Cestodes, Acanthocephalans, Monogeneans, Nematodes, Trematodes, or Turbellarian etc. (Turb)
subgroup	Parasite subgroup (family names largely)
location	Location of host-parasite interaction.
citation	Boolean. Should the output include the citation link and the number of supporting citations? default is FALSE
hostState	number corresponding to one of six different host states. The default value is NULL includes all host states
speciesOnly	boolean flag to remove host and parasite species where data are only available at genus level (default = FALSE)
validateHosts	boolean flag to check host species names against Catalogue of Life information and output taxonomic information (default = FALSE)
removeDuplicates	(boolean) should duplicate host-parasite combinations be removed? (default is FALSE)

**Details**

hostState can take values 1-6 corresponding to if the recorded host was found

- (1) "In the wild"
- (2) "Zoo captivity"
- (3) "Domesticated"
- (4) "Experimental"
- (5) "Commercial source"
- (6) "Accidental infestation"

**Value**

Three (or five) column data.frame containing host species, parasite species (shortened name and full name), and citation link and number of citations (if `citation = TRUE`), with each row corresponding to an occurrence of a parasite species on a host species.

**Author(s)**

Tad Dallas

**References**

Gibson, D. I., Bray, R. A., & Harris, E. A. (Compilers) (2005). Host-Parasite Database of the Natural History Museum, London. <<http://www.nhm.ac.uk/research-curation/scientific-resources/taxonomy-systematics/host-parasites/>>

**See Also**

[findHost](#)

**Examples**

```
strongHosts <- helminthR::findParasite(genus = "Strongyloides")

# An example of how to query multiple parasite species when
# you have a vector of parasite species names

parasites <- c("Ascaris aculeati", "Oxyuris flagellum")

plyr::ldply(parasites,
  function(x){
    helminthR::findParasite(unlist(strsplit(x, " "))[1],
      unlist(strsplit(x, " "))[2])
  }
)
```



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`locations`*Table of geographic location names, and associated coordinates*

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**Description**

Lists geographic locations that can be input to `findHost` or `findParasite` and the corresponding latitude and longitude coordinates of the country's centroid. The georeferencing was performed dynamically using the Google Maps API, but they have since restricted access. The data on locations is now provided in this data file called `locations – data(locations)` – and is based on an earlier usage of `ggmap`. The geographic coordinates may not be accurate, and users should check for accuracy (and feel free to file an issue or PR on Github with corrections).

**Usage**

```
data(locations)
```

**Format**

**Location** Name of geographic location

**Latitude** Latitude of location centroid

**Longitude** Longitude of location centroid

**References**

Gibson, D. I., Bray, R. A., & Harris, E. A. (Compilers) (2005). Host-Parasite Database of the Natural History Museum, London.

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