

# Package ‘specieshindex’

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**Type** Package

**Title** How (scientifically) popular is a given species?

**Version** 0.4.1

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**Description** Finds the h-index of a species.

**Depends** R ( $\geq$  3.5.0)

**LazyData** true

**Imports** rscopus,

wosr,  
rbace,  
taxize,  
dplyr,  
tidyr,  
data.table,  
httr,  
XML,  
ggplot2,  
ggpubr

**Suggests** devtools,

httpptest,  
knitr,  
RefManageR,  
rmarkdown,  
roxygen2,  
testthat ( $\geq$  3.0.0)

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**URL** <https://github.com/jessicatytam/specieshindex>

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

Encoding UTF-8  
Config/testthat/edition 3

R topics documented:

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Allindices	<i>Index summary</i>
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---

Description

This function returns a dataframe of the summary of all of the indices.

Usage

```
Allindices(data, genus, species, sourcetype = 0)
```

Arguments

- data           The dataframe generated from [Fetch](#).
- genus          Genus classification from the binomial name.
- species        Species classification from the binomial name.
- sourcetype     Source type; default is 0, enter 1 to add SourceType variables.

**Value**

A datarame of all of the indices in the package.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
Allindices(Woylie,
           genus = "Bettongia", species = "penicillata",
           sourcetype = 0)
```

---

Count	<i>Search count of literature</i>
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---

**Description**

This function counts the total number of search results from Scopus, Web of Science, or BASE. A check will be conducted via [gnr\\_resolve](#) to validate the genus and species names.

**Usage**

```
Count(db, search, genus, species = NULL, synonyms, additionalkeywords)
```

**Arguments**

db	Literature database. Scopus ("scopus"), Web of Science ("wos"), or Base ("base").
search	Search fields. Title only ("t") or title, abstract, and keywords ("tak").
genus	Genus classification from the binomial name.
species	Species classification from the binomial name.
synonyms	Alternate species names.
additionalkeywords	Optional search terms.

**Value**

Search count of the genus or species with the given **genus** and/or **species**.

## Examples

```
## Not run:
Count(db = "scopus",
      search = "t",
      genus = "Osphranter", species = "rufus")

## End(Not run)
## Not run:
Count(db = "scopus",
      search = "t",
      genus = "Osphranter", species = "rufus",
      synonyms = "Macropus rufus",
      additionalkeywords = "conserv*")

## End(Not run)
```

---

Fetch

*Fetch citation records*

---

## Description

This function fetches citation information from Scopus, Web of Science, or BASE. Duplicates are to be removed by the user after fetching the data.

## Usage

```
Fetch(
  db,
  search,
  genus,
  species = NULL,
  synonyms,
  additionalkeywords,
  language = 0
)
```

## Arguments

db	Literature database. Scopus ("scopus"), Web of Science ("wos"), or Base ("base").
search	Search fields. Title only ("t") or title, abstract, and keywords ("tak").
genus	Genus classification from the binomial name.
species	Species classification from the binomial name.
synonyms	Alternate species names.
additionalkeywords	Optional search terms.
language	Language of the paper; default is 0, enter 1 to retrieve the variable. Scopus only.

**Value**

A dataframe of the genus' or species' citation records with the given **genus** and/or **species**.

**Examples**

```
## Not run:
Fetch(db = "scopus",
      search = "t",
      genus = "Osphranter", species = "rufus")

## End(Not run)
## Not run:
Fetch(db = "scopus",
      search = "t",
      genus = "Osphranter", species = "rufus",
      synonyms = "Macropus rufus",
      additionalkeywords = "conserv*")

## End(Not run)
```

---

**getYear***Extract year*

---

**Description**

Extracts the year of each publication of the output from any of the Fetch functions and counts the number of publications each year.

**Usage**

```
getYear(data, genus, species)
```

**Arguments**

<b>data</b>	Output from any of the fetch function.
<b>genus</b>	Genus classification from the binomial name.
<b>species</b>	Species classification from the binomial name.

**Value**

A dataframe with the year and frequency of the publications

Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
getYear(data = Woylie,
        genus = "Bettongia", species = "penicillata")
```

---

Koala	<i>Koala.</i>
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---

Description

A dataset with some literature on Koalas

Usage

Koala

Format

A data frame :

**citations** number of cites

**journal** journal

**authkeywords** authkeywords

**cover\_date** cover\_date

**cover\_display\_date** cover\_display\_date

**dc\_creator** dc.creator

**dc\_description** dc.description

**dc\_identifier** dc.identifier

**description** description

**doi** doi

**eid** eid

**pii** pii

**prism\_aggregationType** prism\_aggregationType

**prism\_eIssn** prism\_eIssn

**prism\_issn** prism\_issn

**prism\_pageRange** prism\_pageRange

**prism\_url** prism\_url

**source\_id** source.id

**subtype** subtype

**title** title ...

**Source**

<http://www.diamondse.info/>

---

languages	<i>languages</i>
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**Description**

A dataset with some literature on languages

**Usage**

languages

**Format**

A data frame :

**language** names of languages ...

**Source**

somewhere?

---

Platypus	<i>Platypus</i>
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---

**Description**

A dataset with some literature on Platypus

**Usage**

Platypus

**Format**

A data frame :

**citations** number of cites

**journal** journal

**authkeywords** authkeywords

**cover\_date** cover\_date

**cover\_display\_date** cover\_display\_date

**dc\_creator** dc\_creator

**dc\_description** dc\_description  
**dc\_identifier** dc\_identifier  
**description** description  
**doi** doi  
**eid** eid  
**pii** pii  
**prism\_aggregationType** prism\_aggregationType  
**prism\_eIssn** prism\_eIssn  
**prism\_issn** prism\_issn  
**prism\_pageRange** prism\_pageRange  
**prism\_url** prism\_url  
**source\_id** source\_id  
**subtype** subtype  
**title** title ...

**Source**

WOS

---

plotAllindices	<i>Index plot</i>
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---

**Description**

Plots the indices of a single species or combined.

**Usage**

plotAllindices(data)

**Arguments**

data                   The dataframe generated from [Allindices](#).

**Value**

ggplot



## Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")
Quokka <- Fetch(db = "scopus",
               search = "tak",
               genus = "Setonix", species = "brachyurus")
Platypus <- Fetch(db = "scopus",
                 search = "tak",
                 genus = "Ornithorhynchus", species = "anatinus")
Koala <- Fetch(db = "scopus",
              search = "tak",
              genus = "Phascolarctos", species = "cinereus")

## End(Not run)
W <- Allindices(Woylie,
               genus = "Bettongia", species = "penicillata")
Q <- Allindices(Quokka,
               genus = "Setonix", species = "brachyurus")
P <- Allindices(Platypus,
               genus = "Ornithorhynchus", species = "anatinus")
K <- Allindices(Koala,
               genus = "Phascolarctos", species = "cinereus")
CombineSp <- dplyr::bind_rows(W, Q, P, K)
plotAllindices(CombineSp)
```

---

plotPub

*Publication plot*


---

## Description

Plots the publication by year of a single species or combined.

## Usage

```
plotPub(data)
```

## Arguments

**data**                      The dataframe generated from [getYear](#).

## Value

ggplot

## Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")
Quokka <- Fetch(db = "scopus",
               search = "tak",
               genus = "Setonix", species = "brachyurus")
Platypus <- Fetch(db = "scopus",
                 search = "tak",
                 genus = "Ornithorhynchus", species = "anatinus")
Koala <- Fetch(db = "scopus",
               search = "tak",
               genus = "Phascolarctos", species = "cinereus")

## End(Not run)
extract_year_W <- getYear(data = Woylie,
                        genus = "Bettongia", species = "penicillata")
extract_year_Q <- getYear(data = Quokka,
                        genus = "Setonix", species = "brachyurus")
extract_year_P <- getYear(data = Platypus,
                        genus = "Ornithorhynchus", species = "anatinus")
extract_year_K <- getYear(data = Koala,
                        genus = "Phascolarctos", species = "cinereus")
Combine_pub <- rbind(extract_year_W, extract_year_Q, extract_year_P, extract_year_K)
plotPub(Combine_pub)
```

---

Quokka

*Quokka*

---

## Description

A dataset with some literature on Quokka

## Usage

Quokka

## Format

A data frame :

**citations** number of cites

**journal** journal

**authkeywords** authkeywords

**cover\_date** cover\_date

**cover\_display\_date** cover\_display\_date

**dc\_creator** dc\_creator  
**dc\_description** dc\_description  
**dc\_identifier** dc\_identifier  
**description** description  
**doi** doi  
**eid** eid  
**pii** pii  
**prism\_aggregationType** prism\_aggregationType  
**prism\_eIssn** prism\_eIssn  
**prism\_issn** prism\_issn  
**prism\_pageRange** prism\_pageRange  
**prism\_url** prism\_url  
**source\_id** source\_id  
**subtype** subtype  
**title** title ...

**Source**

WOS

---

SourceType	<i>Source type</i>
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---

**Description**

This function calculates the total number of items for each document type.

**Usage**

SourceType(data)

**Arguments**

data                    The dataframe generated from [Fetch](#).

**Value**

A dataframe with each document and their counts.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
SourceType(Woylie)
```

---

SpH5

*Species h5 index*


---

**Description**

This function calculates the h-index of a species in the past 5 years.

**Usage**

```
SpH5(data)
```

**Arguments**

`data`                      The dataframe generated from [Fetch](#).

**Value**

H5 index.

**References**

Suzuki, H. (2012). *Google Scholar Metrics for Publications*. Retrieved from <https://scholar.googleblog.com/2012/04/google-scholar-metrics-for-publications.html>.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
SpH5(Woylie)
```

---

SpHAfterdate	<i>Species h-index with a given time frame</i>
--------------	--

---

**Description**

This function calculates the h-index using a given date up till the newest record.

**Usage**

```
SpHAfterdate(data, date)
```

**Arguments**

data	The dataframe generated from <a href="#">Fetch</a> .
date	The lower limit of the timeframe.

**Value**

H-index of the given time period.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
SpHAfterdate(Woylie, "2000-01-01")
```

---

SpHindex	<i>Species h-index</i>
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---

**Description**

This function calculates the h-index of a species.

**Usage**

```
SpHindex(data)
```

**Arguments**

data	The dataframe generated from <a href="#">Fetch</a> .
------	--

**Value**

H-index.

**References**

Bertoli-Barsotti, L. & Lando, T. (2015). On a formula for the h-index. *Journal of Informetrics*, 9(4), 762-776.

Hirsch, J. (2005). An index to quantify an individual's scientific research output. *Proceedings of the National Academy of Sciences of the United States of America*, 102(46), 16569-16572.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
SpHindex(Woylie)
```

---

Spi10

*Species i10 index*

---

**Description**

This function calculates the i10 index of a species. i10 index counts all of the publications with 10 or more citations.

**Usage**

```
Spi10(data)
```

**Arguments**

**data**                      The dataframe generated from [Fetch](#).

**Value**

i10 index.

**References**

Cornell University (2019). *i10-index*. Retrieved from <https://guides.library.cornell.edu/c.php?g=32272&p=203393>.

## Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
Spi10(Woylie)
```

---

SpMindex

*Species m-index*

---

## Description

This function calculates the m-index of species. M-index uses the h-index and divides it by the number of years of activity.

## Usage

```
SpMindex(data)
```

## Arguments

**data**                      The dataframe generated from [Fetch](#).

## Value

M-index.

## References

University of Pittsburgh (2019). *Research Impact and Metrics: Author metrics*. Retrieved from <https://pitt.libguides.com/bibliometricIndicators/AuthorMetrics>.

## Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
SpMindex(Woylie)
```

---

TotalCite	<i>Total citations</i>
-----------	------------------------

---

**Description**

This function calculates the total number of citations.

**Usage**

```
TotalCite(data)
```

**Arguments**

data                      The dataframe generated from [Fetch](#).

**Value**

A numerical value of the total number of citations.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
TotalCite(Woylie)
```

---

TotalJournals	<i>Total journals</i>
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---

**Description**

This function calculates the total number of journals.

**Usage**

```
TotalJournals(data)
```

**Arguments**

data                      The dataframe generated from [Fetch](#).

**Value**

An integer of the total number of journals.



## Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
TotalJournals(Woylie)
```

---

TotalPub	<i>Total publications</i>
----------	---------------------------

---

## Description

This function calculates the total number of publications.

## Usage

```
TotalPub(data)
```

## Arguments

**data**                      The dataframe generated from [Fetch](#).

## Value

An integer of the total number of publications.

## Examples

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
TotalPub(Woylie)
```

---

Woylie	<i>Woylie</i>
--------	---------------

---

**Description**

A dataset with some literature on Woylie

**Usage**

Woylie

**Format**

A data frame :

**citations** number of cites

**journal** journal

**authkeywords** authkeywords

**cover\_date** cover\_date

**cover\_display\_date** cover\_display\_date

**dc\_creator** dc\_creator

**dc\_description** dc\_description

**dc\_identifier** dc\_identifier

**description** description

**doi** doi

**eid** eid

**pii** pii

**prism\_aggregationType** prism\_aggregationType

**prism\_eIssn** prism\_eIssn

**prism\_issn** prism\_issn

**prism\_pageRange** prism\_pageRange

**prism\_url** prism\_url

**source\_id** source\_id

**subtype** subtype

**title** title ...

**Source**

WOS

---

YearsPublishing	<i>Years since first publication</i>
-----------------	--------------------------------------

---

**Description**

The number of years since the first publication in relation to the species.

**Usage**

```
YearsPublishing(data)
```

**Arguments**

data	The dataframe generated from <a href="#">Fetch</a> .
------	--

**Value**

Number of years.

**Examples**

```
## Not run:
Woylie <- Fetch(db = "scopus",
               search = "tak",
               genus = "Bettongia", species = "penicillata")

## End(Not run)
YearsPublishing(Woylie)
```

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