# Package 'specieshindex'

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**Type** Package

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

**Version** 0.0.1

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

**Depends** R (>= 3.1.0)

**LazyData** true

**Imports** rscopus,
taxize,
tidyverse

**Suggests** testthat,
knitr,
roxygen2,
devtools

**License** MIT + file LICENSE

**URL** https://github.com/jessicatytam/Honours

**RoxygenNote** 7.1.1

## R topics documented:

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`Allindices` *This function returns a summary of all of the indices.*

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## Description

This function returns a summary of all of the indices.

## Usage

```
Allindices(data)
```

## Arguments

| | |
|---|---|
| `data` | The dataframe generated from `FetchSpT` or `FetchSpTAK`. |

## Value

A datarame of all of the indices in the package.

## Examples

```
Allindices(SpeciesData)
```

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`ARRatio` *This function calculates the percentage ratio of articles:rerviews.*

---

## Description

This function calculates the percentage ratio of articles:rerviews.

## Usage

```
ARRatio(data)
```

## Arguments

| | |
|---|---|
| `data` | The dataframe generated from `FetchSpT` or `FetchSpTAK`. |

## Value

A character value of the percentage ratio of the number of articles and reviews.

### Examples

```
ARRatio(SpeciesData)
```

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`extractcontent` *Extract citation data from Scopus.*

---

### Description

Extract citation data from Scopus.

### Usage

```
extractcontent(search.string, datatype = "application/xml")
```

### Arguments

| | |
|---|---|
| `search.string` | Search string with Boolean operators or Scopus advanced search. |
| `datatype` | Formats the URL to be sent to the API. The default is "application/xml". |

### Value

A list of entries of the search from Scopus.

### Examples

```
extractcontent("TITLE-ABS-KEY("bettongia penicillata") AND DOCTYPE(ar OR re)")
```

---

`extractXML` *Extract XML list into a dataframe.*

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### Description

Extract XML list into a dataframe.

### Usage

```
extractXML(theFile)
```

### Arguments

| | |
|---|---|
| `theFile` | The file to be converted. |

### Value

A converted dataframe generated from `extractcontent`.

### Examples

```
extractXML(SpeciesXML)
```

`FetchSpT` *This function fetches citation information from Scopus using genus and species name found in the title of the publications.*

## Description

This function fetches citation information from Scopus using genus and species name found in the title of the publications.

## Usage

```
FetchSpT(genus, species, APIkey)
```

## Arguments

| | |
|---|---|
| `genus` | Genus classification from the binomial name. |
| `species` | Species classification from the binomial name. |
| `APIkey` | Scopus API key needed to access and download data from their database. |

## Value

A dataframe of the species' citation records with the given `genus` and `species`.

## Examples

```
FetchSpT("Bettongia", "penicillata", "442b9048417ef20cf680a0ae26ee4d86")

#lower case letter in genus is also accepted and will return identical results

FetchSpT("bettongia", "penicillata", "442b9048417ef20cf680a0ae26ee4d86")
```

`FetchSpTAK` *This function fetches citation information from Scopus using genus and species name found in the title, abstract and keywords of the publications.*

## Description

This function fetches citation information from Scopus using genus and species name found in the title, abstract and keywords of the publications.

## Usage

```
FetchSpTAK(genus, species, APIkey)
```

## Arguments

| | |
|---|---|
| `genus` | Genus classification from the binomial name. |
| `species` | Species classification from the binomial name. |
| `APIkey` | Scopus API key needed to access and download data from their database. |

## Value

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

## Examples

```
FetchSpT("Bettongia", "penicillata", "442b9048417ef20cf680a0ae26ee4d86")

#lower case letter in genus is also accepted and will return identical results

FetchSpT("bettongia", "penicillata", "442b9048417ef20cf680a0ae26ee4d86")
```

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

---

## Description

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

## Usage

```
HAfterdate(data, date)
```

## Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |
| date | The lower limit of the timeframe. |

## Value

H-index of the given time period.

## Examples

```
HAfterdate(SpeciesData, "2000-01-01")
```

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# searchCount *This function counts the total number of search results.*

---

## Description

This function counts the total number of search results.

## Usage

```
searchCount(genus, species, APIkey, datatype = "application/xml")
```

### Arguments

| | |
|---|---|
| genus | Genus classification from the binomial name. |
| species | Species classification from the binomial name. |
| APIkey | Scopus API key needed to access and download data from their database. |
| datatype | Formats the URL to be sent to the API. The default is "application/xml". |

### Value

Search count of the species with the given genus and species.

### Examples

```
searchCount("Bettongia", "penicillata", "442b9048417ef20cf680a0ae26ee4d86")

#lower case letter in genus is also accepted and will return identical results

searchCount("bettongia", "penicillata", "442b9048417ef20cf680a0ae26ee4d86")
```

---

## SpH5 *This function calculates the h-index of a species in the past 5 years.*

---

### Description

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

### Usage

```
SpH5(data)
```

### Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |

### Value

H5 index.

### Examples

```
SpH5(SpeciesData)
```

`SpHindex` *This function calculates the h-index of a species.*

## Description

This function calculates the h-index of a species.

## Usage

```
SpHindex(data)
```

## Arguments

| | |
|---|---|
| `data` | The dataframe generated from `FetchSpT` or `FetchSpTAK`. |

## Value

H-index.

## Examples

```
SpHindex(SpeciesData)
```

`Spi10` *This function calculates the i10 index of a species. i10 index counts all of the publications with 10 or more citations.*

## 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 `FetchSpT` or `FetchSpTAK`. |

## Value

i10 index.

## Examples

```
Spi10(SpeciesData)
```

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

## 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 FetchSpT or FetchSpTAK. |

## Value

M-index.

## Examples

```
SpMindex(SpeciesData)
```

TotalArt *This function calculates the total number of articles.*

## Description

This function calculates the total number of articles.

## Usage

```
TotalArt(data)
```

## Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |

## Value

An integer of the total number of articles.

## Examples

```
TotalArt(SpeciesData)
```

## TotalCite *This function calculates the total number of citations.*

### Description

This function calculates the total number of citations.

### Usage

```
TotalCite(data)
```

### Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |

### Value

A numerical value of the total number of citations.

### Examples

```
TotalCite(SpeciesData)
```

## TotalJournals *This function calculates the total number of journals.*

### Description

This function calculates the total number of journals.

### Usage

```
TotalJournals(data)
```

### Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |

### Value

An integer of the total number of journals.

### Examples

```
TotalJournals(SpeciesData)
```

## TotalPub — *This function calculates the total number of publications.*

### Description

This function calculates the total number of publications.

### Usage

```
TotalPub(data)
```

### Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |

### Value

An integer of the total number of publications.

### Examples

```
TotalPub(SpeciesData)
```

## TotalRev — *This function calculates the total number of reviews.*

### Description

This function calculates the total number of reviews.

### Usage

```
TotalRev(data)
```

### Arguments

| | |
|---|---|
| data | The dataframe generated from FetchSpT or FetchSpTAK. |

### Value

An integer of the total number of reviews.

### Examples

```
TotalRev(SpeciesData)
```

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

## Description

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

## Usage

```
YearsPublishing(data)
```

## Arguments

| | |
|---|---|
| `data` | The dataframe generated from `FetchSpT` or `FetchSpTAK`. |

## Value

Number of years.

## Examples

```
YearsPublishing(SpeciesData)
```

# Index