

Package ‘GAOSrmark’

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Type Package

Title Huggins robust and closed capture analyses for GAOS monitoring

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Description Automated analyses of GAOS photo-resight data in R via program MARK. This package builds upon a robust design analysis written by Andy Hutcheon.

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LazyData TRUE

Depends RMark, tidyverse, lubridate, here, conflicted, scales

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amalgamate	<i>amalgamate</i>
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Description

Combines objects produced by `find_robust` and `find_closed` functions into a single object.

Usage

```
my.data <- amalgamate(a, b, ...)
```

Format

- `a, b, ...`: two or more objects to be combined.

Examples

```
a <- find_robust(period = "2012_13",
  species = "Grand",
  site = "Airport",
  average = FALSE)

b <- find_closed(period = "2015_16",
  species = "Grand",
  site = "Airport",
  average = FALSE)

my.data <- amalgamate(a, b)
```

closed_capture_analysis	<i>closed_capture_analysis</i>
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Description

Runs the Huggins variant of the closed analysis in program MARK using the RMark package. This model suite is based on 4 core models: *M0* (detection probabilities constant), *Mt* (detection probabilities time varying), *Mh* (detection probabilities constant with a two mixture heterogeneous population), and *Mht* (detection probabilities time varying with a two mixture heterogeneous population).

Usage

```
closed_capture_analysis(path, site_species, year)
```

Format

- `path`: the internal path to the folder where the results and outputs should be deposited.
- `site_species`: the site and species name corresponding to those used by the `sloop_robust_design` function.
- `year`: the year in which the closed capture monitoring occurred (required for graphs). Note: year is numeric.

Details

Note: depends upon the `closed_capture_encounters` function being run first.

The function will write the following outputs to the folder:

- a AICc model selection table labelled "`_AICctable_closed`" in .csv format.
- a table of population estimates from the top model labelled "`_estimates_closed`" in .csv format.

In addition, the function will return:

- a complete list of RMark files to the "Results" subfolder.

Note: These RMark outputs can only be opened within R. The files are not named by model, but the model name can be found in the output text. The new files will not overwrite old files, consequently, the "Results" folder should be cleared before an analysis is run.

Examples

```
closed_capture_encounters(file.name = "Extract_Grand.csv",
                          site = "Airport",
                          include1s = FALSE,
                          start_date = "2016-02-10",
                          finish_date = "2016-02-16")

closed_capture_analysis(path = "Closed_capture/2015_16/Grand/Airport",
                        site_species = "Airport_grand",
                        year = 2016)

closed_model_average(site_species = "Airport_grand", year = 2016)
```

```
closed_capture_encounters
      closed_capture_encounters
```

Description

Generates the encounter history required for a closed capture mark recapture analysis.

Usage

```
closed_capture_encounters(file.name,
                          site,
                          include1s = FALSE,
                          start_date,
                          finish_date)
```

Format

- `file.name`: the .csv extract which contains the information for the species.
- `site`: the site name (capitalised).
- `include1s`: whether or not to include or exclude size1s (young-of-the-year). Unless there is a special reason you should use `include1s = FALSE`.
- `start_date`: the start date for the sampling session in the format (YYYY-MM-DD). Note `start_date` is a string and needs to be in quotes.
- `finish_date`: the finish date for the sampling session in the format (YYYY-MM-DD). Note `start_date` is a string and needs to be in quotes.

Details

The function will save the encounter history in memory as 'encounter.his'.

Examples

```
closed_capture_encounters(file.name = "Extract_Grand.csv",
                          site = "Airport",
                          include1s = FALSE,
                          start_date = "2016-02-10",
                          finish_date = "2016-02-16")
```

`closed_model_average` *closed_model_average*

Description

Generates model averaged estimates from the outputs of `closed_capture_analysis`.

Usage

```
closed_model_average(site_species, year)
```

Format

- `site_species`: the site and species name corresponding to those used by the `sloop_robust_design` function.
- `year`: the year in which the closed capture monitoring occurred (required for graphing). Note: `year` is numeric.

Details

Note: depends upon `closed_capture_analysis` function being run first.

The function will write the following outputs to the folder:

- closed capture population estimates labelled "`_averaged_closed`" in .csv format.

Examples

```

closed_capture_encounters(file.name = "Extract_Grand.csv",
                           site = "Airport",
                           include1s = FALSE,
                           start_date = "2016-02-10",
                           finish_date = "2016-02-16")

closed_capture_analysis(path = "Closed_capture/2015_16/Grand/Airport",
                        site_species = "Airport_grand",
                        year = 2016)

closed_model_average(site_species = "Airport_grand", year = 2016)

```

find_closed

*find_closed***Description**

Retrieves estimate data from the specified closed capture analysis. This is a prerequisite for the amalgamate and the synopsis functions.

Usage

```

find_closed(period,
            species,
            site,
            average = FALSE)

```

Format

Note: these arguments are required to accurately locate the file.

- period: monitoring season (e.g. "2015_16")
- species: the species name (e.g. "Grand")
- site: the site name (e.g. "Airport")
- average: whether model averaging is require (e.g. FALSE)

Examples

```

b <- find_closed(period = "2015_16",
                 species = "Grand",
                 site = "Airport",
                 average = FALSE)

```

find_robust	<i>find_robust</i>
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Description

Retrieves estimate data from the specified robust design capture analysis. This is a prerequisite for the amalgamate and the synopsis functions.

Usage

```
find_robust(period,
            species,
            site,
            average = FALSE)
```

Format

Note: these arguments are required to accurately locate the file.

- period: monitoring season (e.g. "2015_16")
- species: the species name (e.g. "Grand")
- site: the site name (e.g. "Airport")
- average: whether model averaging is require (e.g. FALSE)

Examples

```
a <- find_robust(period = "2012_13",
                species = "Grand",
                site = "Airport",
                average = FALSE)
```

mini_capture_analysis	<i>mini_capture_analysis</i>
-----------------------	------------------------------

Description

An alternate version of the closed_capture_analysis function in which the heterogeneity models are removed. This model suite is based on just 2 models: *MO* (detection probabilities constant), and *Mt* (detection probabilities time varying).

Usage

```
mini_capture_analysis(path, site_species, year)
```

Format

- path: the internal path to the folder where the results and outputs should be deposited.
- site_species: the site and species name corresponding to those used by the sloop_robust_design function.
- year: the year in which the closed capture monitoring occurred (required for graphs). Note year is numeric.

Details

Note: depends upon the `closed_capture_encounters` function being run first.

The function will write the following outputs to the folder:

- a AICc model selection table labelled "_AICcetable_closed" in .csv format.
- a table of population estimates from the top model labelled "_estimates_closed" in .csv format.

In addition, the function will return:

- a complete list of RMark files to the "Results" subfolder.

Note: These RMark outputs can only be opened within R. The files are not named by model, but the model name can be found in the output text. The new files will not overwrite old files, consequently, the "Results" folder should be cleared before an analysis is run.

Examples

```
closed_capture_encounters(file.name = "Extract_Grand.csv",
                          site = "TopMini",
                          includeIs = FALSE,
                          start_date = "2016-02-10",
                          finish_date = "2016-02-16",
                          year_folder = "2015_16")

mini_capture_analysis(path = "Closed_capture/2015_16/Grand/TopMini",
                      site_species = "TopMini_grand",
                      year = 2016)
```

mini_robust_design	<i>mini_robust_design</i>
--------------------	---------------------------

Description

An alternate version of the `sloop_robust_design` function in which the heterogeneity models are removed. This function is useful at sites with sample sizes (e.g. mini enclosures), as under such situations the `sloop_robust_design` function can often produce nonsensical population estimates. Consequently, this function should be always be used for the mini enclosures. It can also be used for other sites if the heterogeneity models are causing spurious estimates to be produced.

Usage

```
mini_robust_design(path, site_species, start_year)
```

Format

- `path`: path within project folder to .inp and .txt files.
- `site_species`: site species name to find the correct .inp and .txt files.
- `start_year`: the year in which robust design monitoring began (typically 2006). This input is required because the .txt files derived from Sloop do not state the start year (this causes issues when graphing). Note: `start_year` is numeric.

Details

The function will write the following outputs to the folder:

- a graph labelled "_estimates_robust" in .png format.
- a AICc model selection table labelled "_AICcetable_robust" in .csv format.
- a table of population estimates from the top model labelled "_estimates_robust" in .csv format.

In addition, the function will return:

- a complete list of RMark files to the "Results" subfolder.

Note: These RMark outputs can only be opened within R. The files are not named by model, but the model name can be found in the output text. The new files will not overwrite old files, consequently, the "Results" folder should be cleared before an analysis is run.

Examples

```
mini_robust_design(path = "Sloop_robust_design/2012_13/Grand/BottomMini",
  site_species = "BottomMini_grand",
  start_year = 2006)
```

monitoring_overview	<i>monitoring_overview</i>
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Description

Gives graphic showing all monitoring since 2006 based on the .csv file.

Usage

```
monitoring_overview(file_name)
```

Format

- file_name: .csv file containing the data for the analysis.

Examples

```
monitoring_overview(file_name = "Extract_otago.csv")
```

```
sloop_folder_structure
      sloop_folder_structure
```

Description

Lists all the files contained within the named folder. Only folders within the project are considered

Usage

```
sloop_folder_structure(folder)
```

Format

- folder: the folder within the project to be mapped.

Examples

```
sloop_folder_structure(folder = "Sloop_robust_design")
```

```
sloop_model_average      sloop_model_average
```

Description

Generates model averaged estimates from the outputs of sloop_robust_design.

Usage

```
sloop_model_average(start_year)
```

Format

- start_year: the year in which robust design monitoring began (typically 2006). This input is required because the .txt files derived from Sloop does not state the start year (this causes issues when graphing). Note: start_year is numeric.

Details

The function will write the following outputs to the folder:

- a graph labelled "_average_robust" in .png format.
- a table of population estimates labelled "_average_robust" in .csv format.

Examples

```
sloop_robust_design(path = "Sloop_robust_design/2012_13/Grand/Airport",
                    site_species = "Airport_grand",
                    start_year = 2006)

sloop_model_average(start_year = 2006)
```

sloop_robust_design *sloop_robust_design*

Description

Runs the Huggins variant of the robust design through program MARK using the RMark package. It tests 12 candidate models based on the code of Andy Hutcheon. This model suite is based on 4 core models: *MO* (detection probabilities constant), *Mt* (detection probabilities time varying), *Mh* (detection probabilities constant with a two mixture heterogeneous population), and *Mht* (detection probabilities time varying with a two mixture heterogeneous population). On top of these 3 different sets of movement models are examined : (1) no movement, (2) random movement, and (3) Markovian movement (in which the the probability of the animal migrating differs according to whether it is or is not detected initially).

The function will write the following outputs to the folder:

- a graph labelled "_estimates_robust" in .png format.
- a AICc model selection table labelled "_AICcetable_robust" in .csv format.
- a table of population estimates from the top model labelled "_estimates_robust" in .csv format.

In addition, the function will return:

- a complete list of RMark files to the "Results" subfolder.

Note: These RMark outputs can only be opened within R. The files are not named by model, but the model name can be found in the output text. The new files will not overwrite old files, consequently, the "Results" folder should be cleared before an analysis is run.

Usage

```
sloop_robust_design(path, site_species, start_year)
```

Format

- path: path within project folder to .inp and .txt files.
- site_species: site species name to find the correct .inp and .txt files.
- start_year: the year in which robust design monitoring began (typically 2006). This input is required because the .txt files derived from Sloop do not state the start year (this causes issues when graphing). Note: start_year is numeric.

Examples

```
sloop_robust_design(path = "Sloop_robust_design/2012_13/Grand/Airport",
  site_species = "Airport_grand",
  start_year = 2006)
```

`synopsis`*synopsis*

Description

Combines differing analyses into a single data set and graph.

Usage

```
synopsis(folder_name, data, site_species)
```

Arguments

- `folder_name`: the folder into which the outputs of the synopsis are to be delivered.
- `data`: the name of the data object produced by the `amalgamate` function.
- `site_species`: the site and species name for naming purposes.

Details

The function will write the following outputs to the folder:

- a graph labelled "`_synopsis`" in .png format.
- a table of the estimates used to produce the graph "`_synopsis`" in .csv format.

Examples

```
synopsis(folder_name = "2018_synopsis",  
        data = my.data,  
        site_species = "Airport_grand")
```

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