

Package: NamibianHake (via r-universe)

July 23, 2026

Title Namibian Hake Stock Assessment Model

Version 0.0.0.9000

Description Runs, validates, summarizes, and reports results from the age-structured ADMB assessment model for Namibian hake.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

Suggests flextable, ggplot2, ggridges, ggthemes, htmltools, kableExtra, knitr, plotly, quarto, rema, scales, testthat (>= 3.0.0), tibble, tidyr, tidyverse, withr, xtable

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Depends R (>= 4.1.0)

Imports dplyr, here, readr

LazyData true

URL <https://jimianelli.github.io/NamibianHake/>

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Repository <https://jimianelli.r-universe.dev>

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plot_sel	<i>Plot Selectivity</i>
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Description

This function creates a plot of selectivity across years and ages.

Usage

```
plot_sel(  
  Year = M$Year,  
  sel = M[, 2:10],  
  styr = 1964,  
  fage = NULL,  
  lage = NULL,  
  alpha = 0.2,  
  scale = 3.8,  
  fill = "purple"  
)
```

Arguments

Year	A vector of years. Default is M\$Year.
sel	A matrix of selectivity values. Default is M[, 2:10].
styr	An integer specifying the start year for the plot. Default is 1964.
fage	An integer specifying the first age to include in the plot. Default is NULL.
lage	An integer specifying the last age to include in the plot. Default is NULL.
alpha	A numeric value specifying the transparency level of the fill. Default is 0.2.
scale	A numeric value specifying the scale for the density ridges. Default is 3.8.
fill	A character string specifying the fill color for the density ridges. Default is "purple".

Value

A ggplot object showing selectivity across years and ages.

Examples

```
## Not run:
plot_sel(Year = M$Year, sel = M[, 2:10], styr = 1970, fage = 1, lage = 8)

## End(Not run)
```

PlotAgeFit

Plot Age Fit

Description

This function creates a plot comparing observed and predicted age compositions for a specified type.

Usage

```
PlotAgeFit(x = bc, title = NULL, type = "fishery", fage = 2, lage = 7)
```

Arguments

x	A list containing the observed and predicted age compositions. Default is bc.
title	A character string for the plot title. Default is NULL.
type	A character string specifying the type of composition to plot. Default is "fishery".
fage	An integer specifying the first age to include in the plot. Default is 2.
lage	An integer specifying the last age to include in the plot. Default is 7.

Value

A ggplot object comparing observed and predicted age compositions.

Examples

```
## Not run:
PlotAgeFit(x = bc, title = "Age Composition", type = "survey", fage = 1, lage = 8)

## End(Not run)
```

read_admb	<i>Read ADMB output files</i>
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Description

Read ADMB output files .rep, .par, and .cor and return an R object of type 'list'

Usage

```
read_admb(repfile)
```

Arguments

repfile ADMB output files to be read (no extension needed)

Value

object of type 'list' with ADMB outputs as list elements

Author(s)

Steve Martell, Anders Nielsen, Athol Whitten, D'Arcy N. Webber

read_ctl	<i>Read ADMB .ctl file</i>
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Description

Read ADMB .ctl file and return an R object of type 'list'. DOES NOT WORK

Usage

```
read_ctl(fn)
```

Arguments

repfile name of ADMB output file to be read

Value

object of type 'list' with ADMB outputs therein

Author(s)

D'Arcy N. Webber

read_fit	<i>Read ADMB .par, .std, and .cor file and return an R object of type 'list' of estimates and correlations</i>
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Description

Read ADMB .par, .std, and .cor file and return an R object of type 'list' of estimates and correlations

Usage

```
read_fit(repfile)
```

Arguments

repfile	name of ADMB output file to be read (no extension needed)
---------	---

Value

object of type 'list' with ADMB outputs therein

Author(s)

Steve Martell, Anders Nielsen, Athol Whitten, D'Arcy N. Webber

read_psv	<i>Read ADMB .psv file</i>
----------	----------------------------

Description

Read ADMB .psv file and return an R object of type 'list'

Usage

```
read_psv(fn, nsamples = 10000)
```

Arguments

repfile	name of ADMB output file to be read (no extension needed)
---------	---

Value

object of type 'list' with ADMB outputs therein

Author(s)

Steve Martell

read_re_output	<i>Read output file from the random effects (RE) model into a data.frame</i>
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Description

Read output file from the random effects (RE) model into a data.frame

Usage

```
read_re_output(file = "rwout.rep", skip_data = FALSE, use_names = FALSE)
```

Arguments

file	A character string of the file to be read in, defaulting to 'rwout.rep' in the current working directory.
skip_data	Whether to skip returning columns representing the data inputs. If TRUE these are included and will have NA values for any missing years
use_names	Whether to use the names written by the RE model or to use more meaningful ones (default)

Value

A dataframe with columns named based on the tags in the output file

read_rep	<i>Read ADMB .rep file</i>
----------	----------------------------

Description

Read ADMB .rep file and return an R object of type 'list'

Usage

```
read_rep(fn)
```

Arguments

fn	name of ADMB output file to be read (no extension needed)
----	---

Value

object of type "list" with ADMB outputs therein

Author(s)

Steve Martell, D'Arcy N. Webber

test_re_species	<i>Test the RE on a single species. This compares a current ADMB univariate run to a previous run. It tests continuity not correctness</i>
-----------------	--

Description

Test the RE on a single species. This compares a current ADMB univariate run to a previous run. It tests *continuity* not correctness

Usage

```
test_re_species(d, test_tmb = TRUE)
```

Arguments

d The .dat file name, e.g., bigskate_t.dat, found in tests/data folder

Details

It will throw an error if the results have changed, otherwise results are consistent.

Value

A data.frame with ADMB and TMB estimates for comparing

write_re_input	<i>Write an input file for the RE model</i>
----------------	---

Description

Write an input file for the RE model

Usage

```
write_re_input(
  file,
  years,
  biomass,
  CV,
  tag = NULL,
  sp = "species",
  survey = "survey",
  yr_start = NULL,
  yr_end = NULL
)
```

Arguments

file	A path to the output file, usually ending in .dat
years	A vector of years for the observations
biomass	A vector of biomasses for the observations
CV	A vector of CV values for the observations
tag	Optional character string to print to file for bookkeeping (e.g., "EBS shelf flat-head sole")
yr_start	Optional start year for predictions
yr_end	Optional end year for predictions

Value

Nothing, a data file is written to file

See Also

read_re_output

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