

# Package: **halk** (via r-universe)

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**Type** Package

**Title** Methods to Create Hierarchical Age Length Keys for Age Assignment

**Version** 0.0.5

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**Description** Provides methods for implementing hierarchical age length keys to estimate fish ages from lengths using data borrowing. Users can create hierarchical age length keys and use them to assign ages given length.

**Depends** R (>= 2.10)

**Imports** rlang (>= 1.0.4), tibble (>= 3.1.7), dplyr (>= 1.0.9), tidyr (>= 1.2.0), purrr, tidyselect, magrittr

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adjust_ages	<i>Adjusts data to account for plus group or minimum age</i>
-------------	--

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### Description

These functions performs two tasks. It lumps all ages greater than the plus group into that age, and it filters data only to those greater than or equal to the minimum age. `adjust_plus_min_ages` works on a vector whereas `adjust_plus_min_ages_df` works on a data.frame

### Usage

```
adjust_plus_min_ages_df(data, minage = NULL, pls_grp = NULL)
```

```
adjust_plus_min_ages(age_vec, minage = NULL, pls_grp = NULL)
```

### Arguments

<code>data</code>	Data with age as a column, or a numeric vector of ages
<code>minage</code>	Numeric. The minimum age; everything else is excluded
<code>pls_grp</code>	Numeric. The plus group; all ages older will be lumped into this group
<code>age_vec</code>	A vector of ages

### Value

A data.frame similar to `data`, but with ages less than `minage` excluded and ages  $\geq$  `plus_group` aggregated into that age

---

ages_as_ordered	<i>Convert ages from/to ordered factor</i>
-----------------	--

---

**Description**

In order for the machine learning models to properly predict ages, the known ages should be converted to an ordered factor during model fitting. This will ensure that the predict.\* functions return age values that actually make sense.

**Usage**

```
ages_as_ordered_factor(data, age_col = "age")
```

```
ages_as_integer(data, age_col = "est.age")
```

**Arguments**

data	A data.frame with a column corresponding to age_col or a vector of values
age_col	Character. The name of the column that contains ages

**Value**

A data.frame with the values in age\_col converted to an ordered factor

---

assign_ages	<i>Assign ages to non-aged data based on a fitted age model</i>
-------------	---

---

**Description**

Assign ages to non-aged data based on a fitted age model

**Usage**

```
assign_ages(newdata, object, ...)
```

**Arguments**

newdata	A vector or data.frame with size/length measurements
object	An object of class "alk", "halk_fit" as produced by <a href="#">make_alk</a> or <a href="#">make_halk</a>
...	Additional parameters to pass to the S3 object methods

**Value**

A data.frame the same as newdata, but with ages assigned based on the model provided in object

**Examples**

```
spp_alk <- make_halk(spp_data, levels = "spp")
spp_est_ages <- assign_ages(spp_data, spp_alk)
```

---

`assign_alk_attributes` *Assign associated age-length key attributes to a data.frame*

---

**Description**

This is just a helper function to assign the needed attributes and classes to a data.frame that is produced by either `make_alk` or `make_halk`.

**Usage**

```
assign_alk_attributes(
  data,
  size_col = "length",
  age_col = "age",
  autobin = TRUE,
  size_bin = 1,
  min_age = NULL,
  plus_group = NULL,
  alk_n = NULL,
  classes = "alk",
  dnorm_params = NULL,
  levels = NULL
)
```

**Arguments**

<code>data</code>	A data.frame
<code>size_col</code>	Character. Name of the column representing sizes
<code>age_col</code>	Character. Name of the column representing ages
<code>autobin</code>	Logical to set the attribute of autobin
<code>size_bin</code>	Numeric. What is the width of size bins
<code>min_age</code>	Numeric. The minimum age that was included in the alk
<code>plus_group</code>	Numeric. The age that represents the plus group
<code>alk_n</code>	Numeric. The number of samples that went into creating the alk
<code>classes</code>	Character. The class that should get prepended to the data.frame class(es)
<code>dnorm_params</code>	The value of parameters that went into creating the normal distributions on the age groups
<code>levels</code>	Character vector of the levels used. This creates the "levels" attribute if present

**Value**

A data.frame with associated attributes assigned

---

assign_na_age	<i>Simple function that returns NA values</i>
---------------	---

---

**Description**

A vector of NA will be returned that is the length of x

**Usage**

```
assign_na_age(x)
```

**Arguments**

x                      Any vector of any length

**Value**

A vector the same length as x containing only NA values

---

bin_lengths	<i>Convert a vector of lengths into binned values</i>
-------------	---

---

**Description**

This will take a vector of numeric values and bin them according to the value specified in binwidth

**Usage**

```
bin_lengths(x, binwidth, include_upper = FALSE, ...)
```

**Arguments**

x                      Numeric vector of values  
binwidth              Numeric vector specifying how wide the length bins should be  
include\_upper        Logical. Append the upper value of the bin and return the length range as a character string (TRUE), or return the lower value as numeric (FALSE, default)  
...                    Additional arguments passed onto [cut](#)

**Value**

A vector of values the same length as x, but binned to the values according to binwidth

**Examples**

```
bin_lengths(length_data$length, binwidth = 2)
```

---

calc_mse	<i>Calculate mean-squared-error (MSE) and root mean-squared-error (RMSE) of estimated ages</i>
----------	--

---

### Description

These functions will calculate MSE and RMSE for estimated ages produced by [assign\\_ages](#). Output is specific to each level used by the age-length key to assign ages

### Usage

```
calc_mse(data, age_col = "age")
calc_rmse(data, age_col = "age")
```

### Arguments

data	A data.frame as created by <a href="#">assign_ages</a>
age_col	Character. Name of the age column in data

### Value

Numeric value for estimated ages with no levels or a data.frame with a MSE or RMSE value for each level used to fit ages

### Examples

```
wae_data <- spp_data[spp_data$spp == "walleye", ]
alk <- make_alk(wae_data)
wae_est_age <- assign_ages(wae_data, alk)
calc_mse(wae_est_age)
calc_rmse(wae_est_age)
```

---

calc_mse_	<i>Backend helper function to compute MSE or RMSE</i>
-----------	---

---

### Description

This function is the engine for [calc\\_mse](#) and [calc\\_rmse](#). It was only created to remove the root argument from the user in the main calc\_mse function

### Usage

```
calc_mse_(data, age_col = "age", root = FALSE)
```

**Arguments**

data	A data.frame as created by <a href="#">assign_ages</a>
age_col	Character. Name of the age column in data
root	Logical. computer MSE (FALSE, default) or RMSE (TRUE)

---

calc_stat_scores	<i>Compute test statistics for comparing actual and estimated ages</i>
------------------	--

---

**Description**

Using these functions you can compute either a Kolmogorov-Smirnov (KS) statistic or a Chi-squared test statistic to compare estimated ages to actual ages. See details for how each test works and what is reported.

**Usage**

```
calc_ks_score(
  data,
  summary_fun = mean,
  age_col = "age",
  suppress_warnings = TRUE,
  return_val = "statistic",
  ...
)
```

```
calc_chi_score(
  data,
  age_col = "age",
  suppress_warnings = TRUE,
  return_val = "statistic",
  ...
)
```

**Arguments**

data	A data.frame containing estimated ages as returned by <a href="#">assign_ages</a>
summary_fun	Function used to compute summary statistics for calc_ks_score for each age group (default is mean)
age_col	Character string specifying the name of the age column
suppress_warnings	Logical. Should any warnings from the function call to ks.test or chisq.test be suppressed (TRUE, the default)
return_val	Character. The name of the object to return from the given test
...	Additional arguments to pass to summary_fun (calc_ks_score) or chisq.test (calc_chi_score)

### Details

The KS test compares length distributions for each age class from known ages against that of estimated ages computed by the `assign_ages` function. The output is a summary value of the test statistics as specified by `summary_fun`.

The `calc_chi_score` function performs a Chi-square test (using the `chisq.test` function) on the number of estimated and actual ages for each age group.

### Value

A numeric value for each level that was used in the model to assign ages

### Examples

```
halk <- make_halk(spp_data, levels = c("spp"))
newdat <- laa_data
newdat$spp <- "bluegill"
pred_ages <- assign_ages(newdat, halk)
calc_ks_score(pred_ages)
calc_chi_score(pred_ages)
```

---

check_agelen_data	<i>Check for age/length data in the data being estimated or predicted</i>
-------------------	---

---

### Description

These are just simple helper functions used within other functions that check to make sure that ages and lengths are present in the data and stop the function call if they are missing

### Usage

```
check_age_data(data, age_col)

check_length_data(data, size_col)
```

### Arguments

data	A data.frame
age_col	Character. The column name for the age column in data
size_col	Character. The column name for the size column in data

### Value

NULL. An error will be called if age/length data is missing

---

check_model_type	<i>Check the model type and return standardized version</i>
------------------	---

---

**Description**

This is a non-exported function to check whether the model type specified is available and return a standardized version of the model name. This standardized version will then feed into a S3 method for the given model.

**Usage**

```
check_model_type(model)
```

**Arguments**

model            A character string naming the model

**Value**

A standardized version of the model name, or an error if model doesn't exist yet

---

integral_quotient	<i>Compute the quotient of integrals as a measure of percent error between two curves</i>
-------------------	---

---

**Description**

This is a method for comparing how "close" or "accurate" one curve is to another (reference) curve. The method works by dividing the area between the curves by the area under the reference curve. See Details for more information

**Usage**

```
integral_quotient(
  ref_curve_params,
  comp_curve_params,
  min_x,
  max_x,
  curve_fun = function(x, linf, k, t0) {
    out <- linf * (1 - exp(-k * (x - t0)))

    return(out)
  }
)
```

**Arguments**

ref_curve_params	A list of named parameters for the reference curve (i.e. the standard that is being compared to)
comp_curve_params	A list of named parameters for the curve that is being compared
min_x	The minimum value across which to integrate
max_x	The maximum value across which to integrate
curve_fun	The function that is being compared. Defaults to an anonymous function that is the von Bertalanffy growth function.

**Details**

The integral quotient method provides a basis for comparison between two curves by dividing the area between the curves by the area under the reference curve (i.e. the quotient of integrals)

**Value**

A value of the area between curves divided by the area under the reference curve

**Examples**

```
ref_curve_params <- list(linf = 60, k = 0.25, t0 = -0.5)
comp_curve_params <- list(linf = 62, k = 0.25, t0 = -0.4)
comp_curve2_params <- list(linf = 65, k = 0.25, t0 = -1)
comp_curve_iq <-
  integral_quotient(ref_curve_params, comp_curve_params, 0, 10)
comp_curve2_iq <-
  integral_quotient(ref_curve_params, comp_curve2_params, 0, 10)
vbgf <- function(x, linf, k, t0) {linf * (1 - exp(-k * (x - t0)))}
curve(
  vbgf(x, ref_curve_params$linf, ref_curve_params$k, ref_curve_params$t0),
  from = 0,
  to = 10,
  ylim = c(0, 60),
  xlab = "Age", ylab = "Length"
)
curve(
  vbgf(x, comp_curve_params$linf, comp_curve_params$k, comp_curve_params$t0),
  add = TRUE,
  col = "blue"
)
curve(
  vbgf(x, comp_curve2_params$linf, comp_curve2_params$k, comp_curve2_params$t0),
  add = TRUE,
  col = "red"
)
text(9, 40, labels = paste0(comp_curve_iq, "%"), col = "blue")
text(9, 43, labels = paste0(comp_curve2_iq, "%"), col = "red")
```

---

laa_data	<i>Example length-at-age data</i>
----------	-----------------------------------

---

### Description

Simple age-structured population data with age and length records for each individual. laa\_data represents a well-sampled age-length dataset, whereas laa\_data\_low\_n is one with few total samples, laa\_data\_low\_age\_n is one with few samples in some ages, and laa\_data\_few\_ages is a dataset with few age groups sampled. Species specific datasets are similar, but with the prefix laa\_ replaced by spp\_. These datasets contain species specific length-at-age data

### Usage

laa\_data

laa\_data\_low\_n

laa\_data\_low\_age\_n

laa\_data\_few\_ages

spp\_data

spp\_data\_low\_n

spp\_data\_low\_age\_n

spp\_data\_few\_ages

### Format

## 'laa\_data' A data.frame with 244 rows and 2 columns:

**spp** Species, only applicable for spp\_data\_\* data.frames

**age** Age of individual

**length** Length of individual (arbitrary units)

## 'laa\_data\_low\_n' A data.frame with 27 rows and 2 columns:

## 'laa\_data\_low\_age\_n' A data.frame with 74 rows and 2 columns:

## 'laa\_data\_few\_ages' A data.frame with 49 rows and 2 columns:

## 'spp\_data' A data.frame with 1022 rows and 3 columns:

## 'spp\_data\_low\_n' A data.frame with 87 rows and 3 columns:

## 'spp\_data\_low\_age\_n' A data.frame with 160 rows and 3 columns:

## 'spp\_data\_few\_ages' A data.frame with 261 rows and 3 columns:

---

length_data	<i>Example length data</i>
-------------	----------------------------

---

**Description**

Simple vector and data.frame containing length measurements. These are used in examples for functions that assign ages.

**Usage**

```
length_data
spp_length_data
```

**Format**

```
## length data A data.frame with one column and 244 rows
spp Species, only in spp_length_data
length Length of individual (arbitrary units)
## 'spp_length_data' A data.frame with 1022 rows and 2 columns:
```

---

make_alk	<i>Make an age-length key out of length-at-age data</i>
----------	---

---

**Description**

Make an age-length key out of length-at-age data

**Usage**

```
make_alk(
  laa_data,
  sizecol = "length",
  autobin = TRUE,
  binwidth = 1,
  agecol = "age",
  min_age = NULL,
  plus_group = NULL,
  numcol = NULL,
  min_age_sample_size = 5,
  min_total_sample_size = min_age_sample_size * min_age_groups,
  min_age_groups = 5,
  warnings = TRUE
)
```

**Arguments**

laa_data	A data.frame with length-at-age data
sizecol	Character string naming the column that holds size data
autobin	Logical. Should the function automatically assign length bins (default is TRUE)
binwidth	Numeric. If autobin = TRUE this is the width for the size bins
agecol	Character string naming the column that holds age data
min_age	Numeric. All ages less than this value will not be used in ALK
plus_group	Numeric value of the oldest age to include in the ALK. All older individuals will be included in this plus group
numcol	Character string naming the column that holds numbers data
min_age_sample_size	Only applicable to alk models. The minimum number of samples that must be in each age group in order to create an alk
min_total_sample_size	Only applicable to alk models. The minimum number of samples that must be in data in order to create an alk
min_age_groups	Only applicable to alk models. The minimum number of age groups that must be in data in order to create an alk
warnings	Logical. Display warnings (TRUE, default)

**Value**

A data.frame containing the proportions of records for each size that are at each age.

**Examples**

```
make_alk(laa_data)
```

---

make_halk	<i>Create a hierarchical age-length key (HALK)</i>
-----------	--

---

**Description**

This function creates a hierarchically nested age-length key that can be used to estimate age of an organism based on proportion of sampled organisms in each age group.

**Usage**

```
make_halk(data, levels = NULL, age_col = "age", size_col = "length", ...)
```

**Arguments**

data	A data.frame with age and size samples
levels	Character vector specifying the levels for HALK creation
age_col	Optional. String of the column name in data housing age data
size_col	Optional. String of the column name in data housing size data
...	Additional arguments passed to <code>make_alk</code>

**Value**

A `tibble` with columns for each level and a column called `alk` that houses the age-length key for that particular level

**Examples**

```
make_halk(spp_data, levels = "spp")
```

---

min_samples	<i>Count number of length-at-age samples or age groups at each level and return those with greater than equal to the minimum desired number</i>
-------------	---

---

**Description**

These are helper shortcut functions to determine if data meet the minimum desired number of age groups and/or sample sizes.

**Usage**

```
min_count_laa_data(
  data,
  sub_levels = NULL,
  min_age_sample_size = NULL,
  min_total_sample_size = NULL,
  min_age_groups = NULL
)

min_age_groups(data, sub_levels = NULL, min_age_grps)
```

**Arguments**

data	Data.frame with length-at-age data
sub_levels	The levels at which to check
min_age_sample_size	Only applicable to <code>alk</code> models. The minimum number of samples that must be in each age group in order to create an <code>alk</code>

min_total_sample_size	Only applicable to alk models. The minimum number of samples that must be in data in order to create an alk
min_age_groups	Only applicable to alk models. The minimum number of age groups that must be in data in order to create an alk
min_age_grps	The minimum number of age groups that must be present in data to create an ALK

**Value**

A data.frame just like data, but with samples excluded that don't meet the required number of samples in min\_sample\_size

---

rename_laa_cols	<i>Simple helper function to rename size and age column names to age and length</i>
-----------------	---

---

**Description**

Simple helper function to rename size and age column names to age and length

**Usage**

```
rename_laa_cols(
  data,
  size_col = "length",
  age_col = "age",
  num_col = NULL,
  goback = FALSE
)
```

**Arguments**

data	Any data.frame with some columns representing age and size
size_col	Character. The name of the column containing sizes
age_col	Character. The name of the column containing ages
num_col	Character. The name of the column containing number of individuals
goback	Logical. Reverse names once they've already been renamed

**Value**

A data.frame the same as data, but with names changed

---

spp_levels	<i>Check for species in columns and/or levels and add to levels if present</i>
------------	--

---

### Description

These helper functions just check to see if a species column exists in the data (designated as 'spp' or 'species'). If one of those columns exists, but the column name is not in the levels argument it will get added to levels.

### Usage

```
is_spp_in_levels(levels)

is_spp_in_data(data)

spp_level(levels)

rm_spp_level(levels)

add_spp_level(data, levels)
```

### Arguments

levels	The levels argument passed from <a href="#">make_halk</a>
data	A data.frame with length-at-age data

### Value

A character vector of levels possibly with 'spp' or 'species' added

---

wb_spp_data	<i>Separate species, county, waterbody example length-at-age and length data</i>
-------------	--

---

### Description

Simple age-structured population with age and/or length records, but expanded across multiple counties and waterbodies for tests and examples in [make\\_halk](#) used with levels.

### Usage

```
wb_spp_laa_data

wb_spp_length_data
```

**Format**

## 'wb\_spp\_laa\_data' A data.frame with 36,849 records and 5 columns

**spp** Species

**county** Arbitrary example county name

**waterbody** Arbitrary example waterbody name nested within county

**age** Age of individual, only in *wb\_spp\_laa\_data*

**length** Length of individual (arbitrary units)

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 9182 rows and 4 columns.

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