

# Package: srkwstatus (via r-universe)

September 29, 2026

**Type** Package

**Title** Package for processing and exploring killer whale demographic data

**Version** 1.0.5

**Date** 2026-01-29

**Description** Generates killer whale demographic data from rows (observations) and fits preliminary models.

**Depends** R (>= 4.0.0)

**Imports** dplyr, mgcv, usethis, stringr, ggridges, ggplot2, rstanarm, viridis, testthat

**Suggests** knitr, rmarkdown, gridExtra

**URL** <https://noaa-nwfsc.github.io/srkw-status/>

**BugReports** <https://github.com/noaa-nwfsc/srkw-status/issues>

**License** GPL (>=3)

**RoxygenNote** 7.3.3

**Encoding** UTF-8

**VignetteBuilder** knitr

**LazyData** true

**Roxygen** list(markdown = TRUE)

**Config/pak/sysreqs** cmake git libglpk-dev make libgit2-dev libicu-dev libuv1-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

**Repository** <https://nmfs-opensci.r-universe.dev>

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**RemoteUrl** <https://github.com/noaa-nwfsc/srkw-status>

**RemoteRef** HEAD

**RemoteSha** ba0b8c40e422aa9f5afcf845a0697b4d7d15701f

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|             |                                                                                           |
|-------------|-------------------------------------------------------------------------------------------|
| ages2stages | <i>A data frame mapping Southern Resident killer whales ages and sexes to life stages</i> |
|-------------|-------------------------------------------------------------------------------------------|

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Description

A data frame mapping Southern Resident killer whales ages and sexes to life stages

Usage

ages2stages

Format

A data frame.

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|        |                                                                                                         |
|--------|---------------------------------------------------------------------------------------------------------|
| expand | <i>Function expand expands a data frame from animals as observations to animal-years as obserations</i> |
|--------|---------------------------------------------------------------------------------------------------------|

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Description

Function expand expands a data frame from animals as observations to animal-years as obserations

Usage

```
expand(  
  filename,  
  start_year = 1976,  
  current_year = NULL,  
  fem_age_mat = 10,  
  fem_age_senesc = 43,  
  ages2stages = NULL  
)
```

**Arguments**

|                |                                                                   |
|----------------|-------------------------------------------------------------------|
| filename       | A file location (csv file) with births and deaths of each animal  |
| start_year     | Starting year for the expanded data, starts at 1976               |
| current_year   | End year for the expanded data, defaults to current calendar year |
| fem_age_mat    | Female age at maturity, 10 years of age by default                |
| fem_age_senesc | Female age at reproductive senescence, defaults to 43             |
| ages2stages    | A data frame of mapping ages and sexes to stages                  |

**Examples**

```
## Not run:
library(kwdemog)
data(orca)
data(ages2stages)
expanded_data = expand(orca, ages2stages = ages2stages)
# or use a filename
expanded_data = expand("use_this_file.csv", start_year = 1979, current_year = 2018,
  fem_age_mat = 10, fem_age_senesc = 43, ages2stages = ages2stages)

## End(Not run)
```

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orca

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*Example census for Southern Resident killer whales*


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**Description**

Example census for Southern Resident killer whales

**Usage**

```
orca
```

**Format**

A data frame.

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|         |                                                                                        |
|---------|----------------------------------------------------------------------------------------|
| project | <i>Function to project SRKW population in the future using individual based models</i> |
|---------|----------------------------------------------------------------------------------------|

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## Description

Function to project SRKW population in the future using individual based models

## Usage

```
project(
  whale_data,
  seed = 123,
  n_years = 30,
  scenarios = c("1981:2020"),
  n_iter = 200,
  verbose = FALSE,
  p_female = NA,
  n_births = NA
)
```

## Arguments

|            |                                                                                                                                                                                                                         |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| whale_data | the expanded data frame, returned by <code>expand()</code>                                                                                                                                                              |
| seed       | the random seed used to initialize simulations, defaults to 123                                                                                                                                                         |
| n_years    | the length of the time series projections, defaults to 30 time steps                                                                                                                                                    |
| scenarios  | a character string, or vector of strings describing which scenario to be run. Should be entered as a range of years separated by a colon, e.g. "1981:1985" to use rates from 1981 to 1985 or ("1981:1985", "1981:2021") |
| n_iter     | the number of iterations per scenario, defaults to 200                                                                                                                                                                  |
| verbose    | whether to print status updates to screen, defaults to FALSE                                                                                                                                                            |
| p_female   | The probability of a female birth, defaults to the empirical value since 1980                                                                                                                                           |
| n_births   | The number of births used to calculate p_female. By default, this defaults to the empirical value observed since 1980 the probability of female birth. Larger values result in more precise estimates of p_female       |

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|             |                                                                   |
|-------------|-------------------------------------------------------------------|
| projections | <i>A data frame containing future SRKW population projections</i> |
|-------------|-------------------------------------------------------------------|

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**Description**

A data frame containing future SRKW population projections

**Usage**

```
projections
```

**Format**

A data frame.

---

|           |                                                                |
|-----------|----------------------------------------------------------------|
| writedata | <i>Function takes csv file and converts is to saved object</i> |
|-----------|----------------------------------------------------------------|

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**Description**

Function takes csv file and converts is to saved object

**Usage**

```
writedata(filename)
```

**Arguments**

|          |                                                                  |
|----------|------------------------------------------------------------------|
| filename | A file location (csv file) with births and deaths of each animal |
|----------|------------------------------------------------------------------|

**Examples**

```
## Not run:  
writedata("inst/extdata/whaleData_08-06-2018.csv")  
  
## End(Not run)
```

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