

# Package ‘paleopop’

May 9, 2026

**Type** Package

**Title** Pattern-Oriented Modeling Framework for Coupled Niche-Population  
Paleo-Climatic Models

**Version** 2.1.7

**Maintainer** July Pilowsky <pilowskyj@caryinstitute.org>

**URL** <https://github.com/GlobalEcologyLab/paleopop/>

**BugReports** <https://github.com/GlobalEcologyLab/paleopop/issues>

**Description** This extension of the poems pattern-oriented modeling (POM) framework provides a collection of modules and functions customized for paleontological time-scales, and optimized for single-generation transitions and large populations, across multiple generations.

**Depends** R (>= 3.6.0)

**License** GPL (>= 3)

**Encoding** UTF-8

**Language** en-AU

**LazyData** true

**RoxygenNote** 7.3.2

**Imports** poems (>= 1.0.0), R6 (>= 2.5.0), sf (>= 0.9), trend (>= 1.1.4)

**Collate** data.R PaleoPopModel.R PaleoPopResults.R PaleoRegion.R  
paleopop\_simulator.R paleopop-package.R region\_subset.R

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown, markdown, dplyr,  
raster

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**NeedsCompilation** no

**Author** Sean Haythorne [aut],  
July Pilowsky [aut, cre] (ORCID:  
<<https://orcid.org/0000-0002-6376-2585>>),  
Stuart Brown [aut] (ORCID: <<https://orcid.org/0000-0002-0669-1418>>),  
Damien Fordham [aut] (ORCID: <<https://orcid.org/0000-0003-2137-5592>>)

**Repository** CRAN

**Date/Publication** 2025-01-07 16:20:02 UTC

## Contents

bison_hs_raster . . . . .	2
paleopop . . . . .	3
PaleoPopModel . . . . .	3
PaleoPopResults . . . . .	6
paleopop_simulator . . . . .	8
PaleoRegion . . . . .	11
region_subset . . . . .	13
siberia_raster . . . . .	14

**Index** **15**

---

bison_hs_raster	<i>Bison vignette habitat suitability raster</i>
-----------------	--

---

## Description

A *raster* dataset defining estimated habitat suitability values for each grid cells of the Siberian study region of the bison example vignette.

## Usage

bison\_hs\_raster

## Format

A *raster::RasterStack* object:

**dimensions** 21 rows by 180 columns by 1001 layers

**resolution** 2 by 2 degree grid cells

**extent** longitude -180 to 180 degrees; latitude 42 to 84 degrees

**values** Estimated habitat suitability values of 0 to 1

## Source

TBA

---

paleopop	<i>paleopop: Ensemble population modeling and simulation on paleo time scales</i>
----------	---

---

## Description

The paleopop package is an extension of the [poems](#) framework of R6 classes, which simulate populations on a dynamic landscape and validate the results via pattern-oriented modeling. paleopop adds functionality for modeling populations over paleo time scales.

## Details

The new functions and R6 classes added by paleopop to the poems framework are:

[paleopop\\_simulator](#) function: Analogous to the [population\\_simulator](#) function in poems, this is the engine of simulation in paleopop, handling input parameters, simulating over long time scales, and outputting up to six different types of results.

- [PaleoRegion](#) class: Inherited from [Region](#), this class defines a geographic region that changes over time, creating a temporal mask that defines which cells are occupiable at a time step.
- [region\\_subset](#) function: a utility function for subsetting regions defined by coordinates.
- [PaleoPopModel](#) class: Inherited from [SimulationModel](#), this class encapsulates the input parameters utilized by the [paleopop\\_simulator](#).
- [PaleoPopResults](#) class: Inherited from [SimulationResults](#), this class encapsulates the results generated by the [paleopop\\_simulator](#), as well as dynamically generating additional derived results.

---

PaleoPopModel	<i>R6 class representing a population model for the paleopop simulator</i>
---------------	--

---

## Description

R6 class representing a spatially-explicit demographic-based population model. It extends the [poems](#) class with parameters for the [paleopop\\_simulator](#). It inherits functionality for creating a nested model, whereby a nested template model with fixed parameters is maintained when a model is cloned for various sampled parameters. Also provided are extensions to the methods for checking the consistency and completeness of model parameters.

## Super classes

```
poems::GenericClass -> poems::GenericModel -> poems::SpatialModel -> poems::SimulationModel
-> PaleoPopModel
```

## Public fields

attached A list of dynamically attached attributes (name-value pairs).

**Active bindings**

- `simulation_function` Name (character string) or source path of the default simulation function, which takes a model as an input and returns the simulation results.
- `model_attributes` A vector of model attribute names.
- `region` A [Region](#) (or inherited class) object specifying the study region.
- `coordinates` Data frame (or matrix) of X-Y population coordinates (WGS84) in longitude (degrees West) and latitude (degrees North).
- `random_seed` Number to seed the random number generation for stochasticity.
- `time_steps` Number of simulation time steps.
- `years_per_step` Number of years per time step.
- `populations` Number of population cells.
- `initial_abundance` Array (matrix) of initial abundance values at each population cell.
- `transition_rate` Rate (numeric) of transition between generations at each time-step.
- `standard_deviation` Standard deviation (numeric) for applying environmental stochasticity to transition rates.
- `compact_decomposition` List containing a compact transposed (Cholesky) decomposition *matrix* (`t_decomposition_compact_matrix`) and a corresponding *map* of population indices (`t_decomposition_compact_map`), as per [SpatialCorrelation](#) class attributes.
- `carrying_capacity` Array (or matrix) of carrying capacity values at each population cell (across time).
- `density_dependence` Density dependence type ("competition", "logistic", or "ceiling").
- `growth_rate_max` Maximum growth rate (utilized by density dependence processes).
- `dispersal_data` List of data frames of non-zero dispersal rates and indices for constructing a compact dispersal matrix, and optional changing rates over time, as per class [DispersalGenerator](#) *dispersal\_data* attribute.
- `dispersal_target_k` Target population carrying capacity threshold for density dependent dispersal.
- `harvest` Boolean for utilizing harvesting.
- `harvest_max` Proportion harvested per year (annual time scale - not generational).
- `harvest_g` The "G" parameter in the harvest function.
- `harvest_z` The "Z" parameter in the harvest function.
- `harvest_max_n` Maximum density per grid cell.
- `human_density` Matrix of human density (fraction) (`$populations` rows by `$time_steps` columns).
- `abundance_threshold` Abundance threshold (that needs to be exceeded) for each population to persist.
- `occupancy_threshold` Threshold for the number of populations occupied (that needs to be exceeded) for all populations to persist.
- `results_selection` List of results selection from ("abundance", "ema", "extirpation", "harvested", "occupancy", "human\_density").

`attribute_aliases` A list of alternative alias names for model attributes (form: `alias = "attribute"`) to be used with the `set` and `get` attributes methods.

`template_model` Nested template model for fixed (non-sampled) attributes for shallow cloning.

`sample_attributes` Vector of sample attribute names (only).

`required_attributes` Vector of required attribute names (only), i.e. those needed to run a simulation.

`error_messages` A vector of error messages encountered when setting model attributes.

`warning_messages` A vector of warning messages encountered when setting model attributes.

## Methods

### Public methods:

- [PaleoPopModel\\$list\\_consistency\(\)](#)
- [PaleoPopModel\\$list\\_completeness\(\)](#)
- [PaleoPopModel\\$clone\(\)](#)

**Method** `list_consistency()`: Returns a boolean to indicate if (optionally selected or all) model attributes (such as dimensions) are consistent.

*Usage:*

```
PaleoPopModel$list_consistency(params = NULL)
```

*Arguments:*

`params` Optional array of parameter/attribute names.

*Returns:* List of booleans (or NAs) to indicate consistency of selected/all attributes.

**Method** `list_completeness()`: Returns a list of booleans (or NAs) for each parameter to indicate attributes that are necessary to simulate the model have been set and are consistent/valid.

*Usage:*

```
PaleoPopModel$list_completeness()
```

*Returns:* List of booleans (or NAs) for each parameter to indicate to indicate completeness (and consistency).

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
PaleoPopModel$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

## Examples

```
library(poems)
library(raster)
# Ring Island example region
coordinates <- data.frame(x = rep(seq(-178.02, -178.06, -0.01), 5),
                          y = rep(seq(19.02, 19.06, 0.01), each = 5))
```

```

template_raster <- Region$new(coordinates = coordinates)$region_raster # full extent
sealevel_raster <- template_raster
template_raster[[c(7:9, 12:14, 17:19)]] <- NA # make Ring Island
sealevel_raster[[c(7:9, 12:14, 17:18)]] <- NA
raster_stack <- raster::stack(x = append(replicate(9, template_raster), sealevel_raster))
region <- PaleoRegion$new(template_raster = raster_stack)

# Model template
template_model <- PaleoPopModel$new(simulation_function = "paleopop_simulator", # the default
                                   region = region, years_per_step = 25, # default: 1 year
                                   time_steps = 10)
template_model$required_attributes # more requirements than the SimulationModel object in poems
template_model$is_complete() # the required attributes have not been filled in
template_model#is_consistent() # however, the attributes that are filled in are consistent

```

---

PaleoPopResults      *R6 class representing paleopop simulator results.*

---

## Description

**R6** class for encapsulating and dynamically generating spatially-explicit `paleopop_simulator` results, as well as optional re-generated `Generator` for niche carrying capacity and/or human density.

## Super classes

`poems::GenericClass` -> `poems::GenericModel` -> `poems::SpatialModel` -> `poems::SimulationResults`  
-> `PaleoPopResults`

## Public fields

`attached` A list of dynamically attached attributes (name-value pairs).

## Active bindings

`model_attributes` A vector of model attribute names.

`region` A `Region` (or inherited class) object specifying the study region.

`coordinates` Data frame (or matrix) of X-Y population coordinates (WGS84) in longitude (degrees West) and latitude (degrees North).

`time_steps` Number of simulation time steps.

`burn_in_steps` Optional number of initial 'burn-in' time steps to be ignored.

`occupancy_mask` Optional binary mask array (matrix), data frame, or raster (stack) for each cell at each time-step of the simulation including burn-in.

`trend_interval` Optional time-step range (indices) for trend calculations (assumes indices begin after the burn-in when utilized).

`abundance` Matrix of population abundance across simulation time-steps (*populations* rows by *duration* columns).

abundance\_trend Trend or average Sen's [slope](#) of total abundance (optionally across a time-step interval).

ema Matrix of population expected minimum abundance (EMA) across simulation time-steps (*populations* rows by *duration* columns).

extirpation Array of population extirpation times.

extinction\_location The weighted centroid of cells occupied in the time-step prior to the extirpation of all populations (if occurred).

harvested Matrix of the number of animals harvested from each population at each time-step (*populations* rows by *duration* columns).

occupancy Array of the number of populations occupied at each time-step.

carrying\_capacity Optional matrix of simulation input carrying capacity to be combined with results (*populations* rows by *duration* columns).

human\_density Optional matrix of simulation input human density to be combined with results (*populations* rows by *duration* columns).

all Nested simulation results for all cells.

parent Parent simulation results for individual cells.

default Default value/attribute utilized when applying primitive metric functions (e.g. `max`) to the results.

attribute\_aliases A list of alternative alias names for model attributes (form: `alias = "attribute"`) to be used with the `set` and `get` attributes methods.

error\_messages A vector of error messages encountered when setting model attributes.

warning\_messages A vector of warning messages encountered when setting model attributes.

## Methods

### Public methods:

- [PaleoPopResults\\$clone\(\)](#)

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
PaleoPopResults$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

## Examples

```
library(raster)
library(poems)
# Ring Island example region
coordinates <- data.frame(x = rep(seq(-178.02, -178.06, -0.01), 5),
                          y = rep(seq(19.02, 19.06, 0.01), each = 5))
template_raster <- Region$new(coordinates = coordinates)$region_raster # full extent
sealevel_raster <- template_raster
template_raster[][c(7:9, 12:14, 17:19)] <- NA # make Ring Island
```

```

sealevel_raster[[c(7:9, 12:14, 17:18)]] <- NA
raster_stack <- raster::stack(x = append(replicate(9, template_raster), sealevel_raster))
region <- PaleoRegion$new(template_raster = raster_stack)

# Model template
model_template <- PaleoPopModel$new(
  region = region,
  time_steps = 10,
  years_per_step = 12, # years per generational time-step
  standard_deviation = 0.1,
  growth_rate_max = 0.6,
  harvest = FALSE,
  populations = region$region_cells,
  initial_abundance = seq(9000, 0, -1000),
  transition_rate = 1.0,
  carrying_capacity = rep(1000, 17),
  dispersal = (!diag(nrow = 17, ncol = 17))*0.05,
  density_dependence = "logistic",
  dispersal_target_k = 10,
  occupancy_threshold = 1,
  abundance_threshold = 10,
  results_selection = c("abundance")
)

# Simulations
results <- paleopop_simulator(model_template)

# Results
results_model <- PaleoPopResults$new(results = results, region = region, time_steps = 10)
results_model$extirpation # cells where the population goes to zero are marked 1
results_model$occupancy # indicates with 0 and 1 which cells are occupied at each time step
results_model$ema # expected minimum abundance

```

---

paleopop\_simulator      *Runs a customized population model simulation.*

---

## Description

Simulates a population model customized for paleontological time-scales, optimized for single-generation transitions and large populations, across multiple generations and returns simulation results. Each generational time-step includes:

1. Density dependence calculations
2. Environmental stochasticity calculations
3. Generational transition calculations
4. Harvest calculations
5. Dispersal calculations
6. Results collection

**Usage**

```
paleopop_simulator(inputs)
```

**Arguments**

**inputs** Nested list/object with named elements:

- random\_seed** Number to seed the random number generation for stochasticity.
- time\_steps** Number of simulation time steps.
- years\_per\_step** Number of years per time step.
- populations** Number of populations.
- initial\_abundance** Array of initial abundances for each population.
- transition\_rate** Rate of transition (or fecundity) between generations.
- standard\_deviation** Standard deviation applied to transition rates.
- compact\_decomposition** List containing a compact transposed (Cholesky) decomposition *matrix* (`t_decomposition_compact_matrix`) and a corresponding *map* of population indices (`t_decomposition_compact_map`), as per [SpatialCorrelation](#) class attributes.
- carrying\_capacity** Matrix of carrying capacities (*populations* rows by *time\_steps* columns).
- density\_dependence** Density dependence type ("competition", "logistic", or "ceiling").
- growth\_rate\_max** Maximum growth rate (for "competition" or "logistic" density dependence).
- harvest** Boolean for utilizing harvesting.
- harvest\_max** Proportion harvested per year (note: annual time scale - not generational).
- harvest\_g** The *G* parameter in the harvest function.
- harvest\_z** The *Z* parameter in the harvest function.
- harvest\_max\_n** Maximum density per grid cell.
- human\_density** Matrix of human density (fraction) (*populations* rows by *time\_steps* columns).
- dispersal\_data** List of data frames of non-zero dispersal rates and indices for constructing a compact dispersal matrix, and optional changing rates over time, as per class [DispersalGenerator](#) *dispersal\_data* attribute.
- dispersal\_target\_k** Target population carrying capacity threshold for density dependent dispersal.
- abundance\_threshold** Abundance threshold (that needs to be exceeded) for each population to persist.
- occupancy\_threshold** Threshold for the number of populations occupied (that needs to be exceeded) for all populations to persist.
- results\_selection** List of results selection from: "abundance", "ema", "extirpation", "harvested", "occupancy", "human\_density".

**Value**

Simulation results as a nested list (as selected):

abundance Matrix of simulation abundances (*populations* rows by *time\_steps* columns).

ema Matrix of expected minimum abundances (*populations* rows by *time\_steps* columns).

extirpation Array of extirpation times for each population.

harvested Matrix of estimated individuals harvested (*populations* rows by *time\_steps* columns).

occupancy Array of number of populations occupied at each time-step.

human\_density Matrix of human densities, (*populations* rows by *time\_steps* columns).

**Examples**

```
library(raster)
library(poems)
# Ring Island example region
coordinates <- data.frame(x = rep(seq(-178.02, -178.06, -0.01), 5),
                          y = rep(seq(19.02, 19.06, 0.01), each = 5))
template_raster <- Region$new(coordinates = coordinates)$region_raster # full extent
sealevel_raster <- template_raster
template_raster[][c(7:9, 12:14, 17:19)] <- NA # make Ring Island
sealevel_raster[][c(7:9, 12:14, 17:18)] <- NA
raster_stack <- raster::stack(x = append(replicate(9, template_raster), sealevel_raster))
region <- PaleoRegion$new(template_raster = raster_stack)

# Model template
model_template <- PaleoPopModel$new(
  region = region,
  time_steps = 10,
  years_per_step = 12, # years per generational time-step
  standard_deviation = 0.1,
  growth_rate_max = 0.6,
  harvest = FALSE,
  populations = region$region_cells,
  initial_abundance = seq(9000, 0, -1000),
  transition_rate = 1.0,
  carrying_capacity = rep(1000, 17),
  dispersal = (!diag(nrow = 17, ncol = 17))*0.05,
  density_dependence = "logistic",
  dispersal_target_k = 10,
  occupancy_threshold = 1,
  abundance_threshold = 10,
  results_selection = c("abundance")
)

# Simulations
results <- paleopop_simulator(model_template) # input as PaleoPopModel object
inputs <- model_template$get_attributes()
paleopop_simulator(inputs) # input as list of attributes
```

---

PaleoRegion	<i>R6 class representing a paleontological region.</i>
-------------	--

---

### Description

**R6** class representing a study region of temporally changing spatial grid cells, defined via a *RasterLayer* object (see [raster](#)) and a temporal mask indicating which cells are included at each time step.

### Super classes

`poems::GenericClass` -> `poems::Region` -> `PaleoRegion`

### Public fields

`attached` A list of dynamically attached attributes (name-value pairs).

### Active bindings

`coordinates` Data frame (or matrix) of X-Y population (WGS84) coordinates in longitude (degrees West) and latitude (degrees North) (get and set), or distance-based coordinates dynamically returned by region raster (get only).

`region_raster` A *RasterLayer* object (see [raster](#)) defining the region with finite values (NAs elsewhere).

`use_raster` Boolean to indicate that a raster is to be used to define the region (default TRUE).

`strict_consistency` Boolean to indicate that, as well as resolution, extent and CRS, consistency checks also ensure that a raster's finite/occupiable cells are the same or a subset of those defined by the region (default TRUE).

`temporal_mask` Matrix of booleans indicating which region cells are included at each time step.

`region_cells` Dynamically calculated number of region coordinates or raster cells with finite/non-NA values.

`region_indices` Dynamically calculated region indices for raster cells with finite/non-NA values (all if not a raster).

### Methods

#### Public methods:

- `PaleoRegion$new()`
- `PaleoRegion$raster_from_values()`
- `PaleoRegion$temporal_mask_raster()`
- `PaleoRegion$clone()`

**Method** `new()`: Initialization method sets temporally changing raster layers for paleontological region.

*Usage:*

```
PaleoRegion$new(template_raster = NULL, remove_zeros = FALSE, ...)
```

*Arguments:*

`template_raster` A *RasterLayer*, *RasterBrick*, or *RasterStack* object (see [raster](#)) defining the paleontological region with example finite values (NAs elsewhere)

`remove_zeros` Boolean to indicate that cells that are zero across all layers (times) are to be removed, i.e. set to NA (default is FALSE).

... Additional parameters passed individually.

**Method** `raster_from_values()`: Converts an array (or matrix) of values into a raster (or stack) consistent with the region raster (matching extent, resolution, and finite/NA cells), and with the temporal mask (if any) applied.

*Usage:*

```
PaleoRegion$raster_from_values(values)
```

*Arguments:*

`values` An array (or matrix) of values to be placed in the raster (or stack) having dimensions consistent with the region cell number.

*Returns:* A *RasterLayer* (or *RasterStack/Brick*) object consistent with the region raster with temporal mask (if any) applied.

**Method** `temporal_mask_raster()`: Returns the temporal mask as a raster stack/brick object consistent with the region raster.

*Usage:*

```
PaleoRegion$temporal_mask_raster()
```

*Returns:* A *RasterStack/Brick* object with temporal mask values of 1 (true) and NA elsewhere.

**Method** `clone()`: The objects of this class are cloneable with this method.

*Usage:*

```
PaleoRegion$clone(deep = FALSE)
```

*Arguments:*

`deep` Whether to make a deep clone.

## Examples

```
library(poems)
library(raster)
# Ring Island example region
coordinates <- data.frame(x = rep(seq(-178.02, -178.06, -0.01), 5),
                          y = rep(seq(19.02, 19.06, 0.01), each = 5))
template_raster <- Region$new(coordinates = coordinates)$region_raster # full extent
sealevel_raster <- template_raster
template_raster[[c(7:9, 12:14, 17:19)]] <- NA # make Ring Island
sealevel_raster[[c(7:9, 12:14, 17:18)]] <- NA
raster_stack <- raster::stack(x = append(replicate(9, template_raster), sealevel_raster))
region <- PaleoRegion$new(template_raster = raster_stack)
raster::plot(region$temporal_mask_raster()[[1]], main = "Ring Island (first timestep)",
             xlab = "Longitude (degrees)", ylab = "Latitude (degrees)",
```

```

colNA = "blue", legend = FALSE)
raster::plot(region$temporal_mask_raster()[[10]], main = "Ring Island (last timestep)",
             xlab = "Longitude (degrees)", ylab = "Latitude (degrees)",
             colNA = "blue", legend = FALSE)

```

---

region_subset	<i>Function generates a region subset of matrix values based on a subset of coordinates within the original region (using nearest spatial neighbor if coordinates differ).</i>
---------------	--

---

### Description

region\_subset generates a region subset of matrix values based on a subset of coordinates within the original region (using nearest spatial neighbor if coordinates differ).

### Usage

```
region_subset(orig_coords = NULL, orig_matrix = NULL, subset_coords = NULL)
```

### Arguments

orig_coords	Data frame (or matrix) of original/full region of X-Y coordinates (WGS84) in longitude (degrees West) and latitude (degrees North).
orig_matrix	Matrix of original values with rows corresponding to the original/full region coordinates.
subset_coords	Data frame (or matrix) of X-Y subset region coordinates (WGS84) in longitude (degrees West) and latitude (degrees North).

### Value

A matrix of values corresponding to the subset region coordinates (using nearest spatial neighbor if original and subset coordinates differ).

### Examples

```

coordinates <- data.frame(x = rep(seq(-178.02, -178.06, -0.01), 5),
                          y = rep(seq(19.02, 19.06, 0.01), each = 5))
values <- matrix(seq(1, 25, 1))
subset <- data.frame(x = rep(seq(-178, -178.04, -0.005), 7),
                    y = rep(seq(19.03, 19.06, 0.005), each = 9))
region_subset(coordinates, values, subset) # nearest neighbor interpolation

```

---

siberia_raster	<i>Bison vignette Siberia raster</i>
----------------	--------------------------------------

---

**Description**

A raster dataset defining the grid cells of the Siberia study region in a temporally dynamic manner for the bison example vignette.

**Usage**

```
siberia_raster
```

**Format**

A *raster::RasterStack* object:

**dimensions** 21 rows by 180 columns by 1001 layers

**resolution** 2 by 2 degree grid cells

**crs** WGS84 latitude longitude

**extent** longitude -180 to 180 degrees; latitude 42 to 84 degrees

**values** region defined by 913 cells with value of 1, surrounded by non-region NA values

**Source**

TBA

# Index

## \* datasets

bison\_hs\_raster, 2  
siberia\_raster, 14

bison\_hs\_raster, 2

DispersalGenerator, 4, 9

Generator, 6

paleopop, 3

paleopop\_simulator, 3, 6, 8

PaleoPopModel, 3, 3

PaleoPopResults, 3, 6

PaleoRegion, 3, 11

poems, 3

poems::GenericClass, 3, 6, 11

poems::GenericModel, 3, 6

poems::Region, 11

poems::SimulationModel, 3

poems::SimulationResults, 6

poems::SpatialModel, 3, 6

population\_simulator, 3

R6, 3, 6, 11

raster, 11, 12

Region, 3, 4, 6

region\_subset, 3, 13

siberia\_raster, 14

SimulationModel, 3

SimulationResults, 3

slope, 7

SpatialCorrelation, 4, 9