A Eastern Grey Kangaroo population simulation example

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2019-03-10

Below is an example using the eastern grey kangaroo (EGK) - a large marsupial native to Australia. The required packages can be loaded using the following:

```
library(steps)
library(raster)
library(viridisLite)
library(future)
```

First we setup a stage based transition matrix, also known as a Leslie matrix. The first matrix represents survival and fecundity (transition) probabilities for each of the life stages in our kangaroo model. In this matrix, fecundities - or numbers of offspring per contributing stage - are in the first row. These are always represented as positive numbers. Survival probabilities are shown in the remaining rows and are expressed as positive numbers between zero and one. The second matrix describes the uncertainty around these transition probabilities (as standard deviations) and is used to simulate environmental stochasticity - zeros indicate that we will not account for this stochasticity, i.e. there is no uncertainty about environmental fluctuations in our system. Note, there are three life-stages and the matrices are symmetrical in the number of columns and rows (three columns, three rows). Also, names are added to the columns and rows to identify the different life-stages of the kangaroo. These example transition matrix and stochasticity matrix objects are available in the steps package ("egk_mat" and "egk_mat_stoch").

```
egk_mat <- matrix(c(0.00,0.00,1.00,
                    0.50,0.00,0.00,
                    0.00,0.85,0.85),
                  nrow = 3,
                  ncol = 3,
                  byrow = TRUE)
colnames(egk_mat) <- rownames(egk_mat) <- c('juvenile','subadult','adult')

egk_mat_stoch <- matrix(c(0.00,0.00,0.20,
                          0.05,0.00,0.00,
                          0.00,0.10,0.05),
                        nrow = 3,
                        ncol = 3,
                        byrow = TRUE)
colnames(egk_mat_stoch) <- rownames(egk_mat_stoch) <- c('juvenile','subadult','adult')
```

Read in spatial inputs to be used for the simulations. A 17.5km x 18km spatial grid with a pixel resolution of 500m x 500m is used as the landscape for the meta-population of kangaroos. Each cell represents a population that kangaroos can move to and from - dependent upon its unique attributes.

A habitat suitability layer describes the relative likelihood of the species (the kangaroo in this example) occurring in each cell and should contain values between 0 (not inhabited) and 1 (inhabited). If the original values are not in this range, they should be rescaled accordingly. This example habitat suitability layer is available in the steps package ("egk_hab"), however, any raster can be used in its place.

```
egk_hab
```

```
## class      : RasterLayer
## dimensions : 35, 36, 1260  (nrow, ncol, ncell)
## resolution : 500, 500  (x, y)
## extent     : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## data source : in memory
```

```
## names       : EGK_habitat_500
## values      : 0.003082677, 0.9678264  (min, max)
```

```
par(mar=c(0,0,0,0), oma=c(0,0,0,0))
plot(egk_hab, box = FALSE, axes = FALSE, col = viridis(100), main = "Habitat Suitability")
```
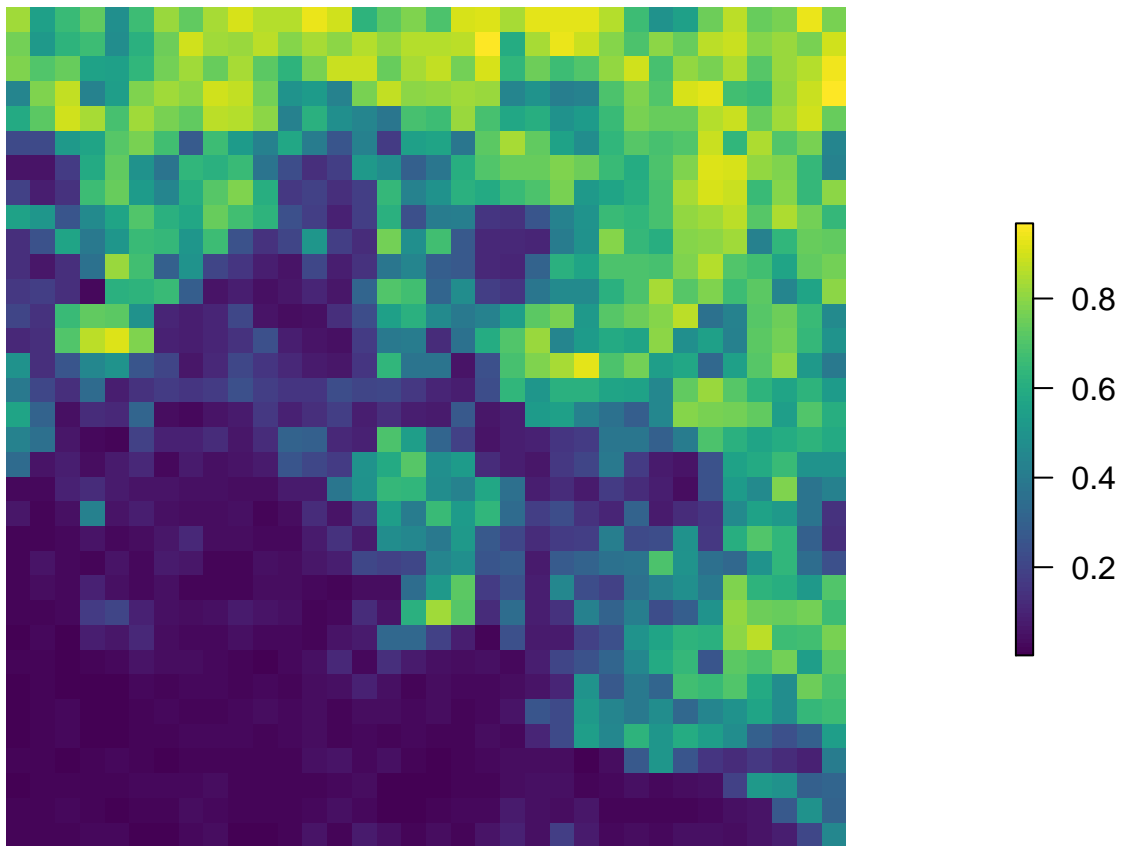

The carrying capacity layer describes the total number of organisms (here, kangaroos) that may occur in each cell and contains either zeros or positive integer values. This example carrying capacity raster is available in the steps package ("egk_k"), however, any raster can be used in its place. The example carrying capactiy is directly based on the example habitat suitability, which is why the rasters look similar, but this won't always be the case. Note, all rasters in the simulations need to have the same projection, extent, and resolution.

```
egk_k
```

```
## class       : RasterLayer
## dimensions  : 35, 36, 1260  (nrow, ncol, ncell)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## data source : in memory
## names       : layer
## values      : 1, 73  (min, max)
```

```
par(mar=c(0,0,0,0), oma=c(0,0,0,0))
plot(egk_k, box = FALSE, axes = FALSE, col = viridis(100))
```
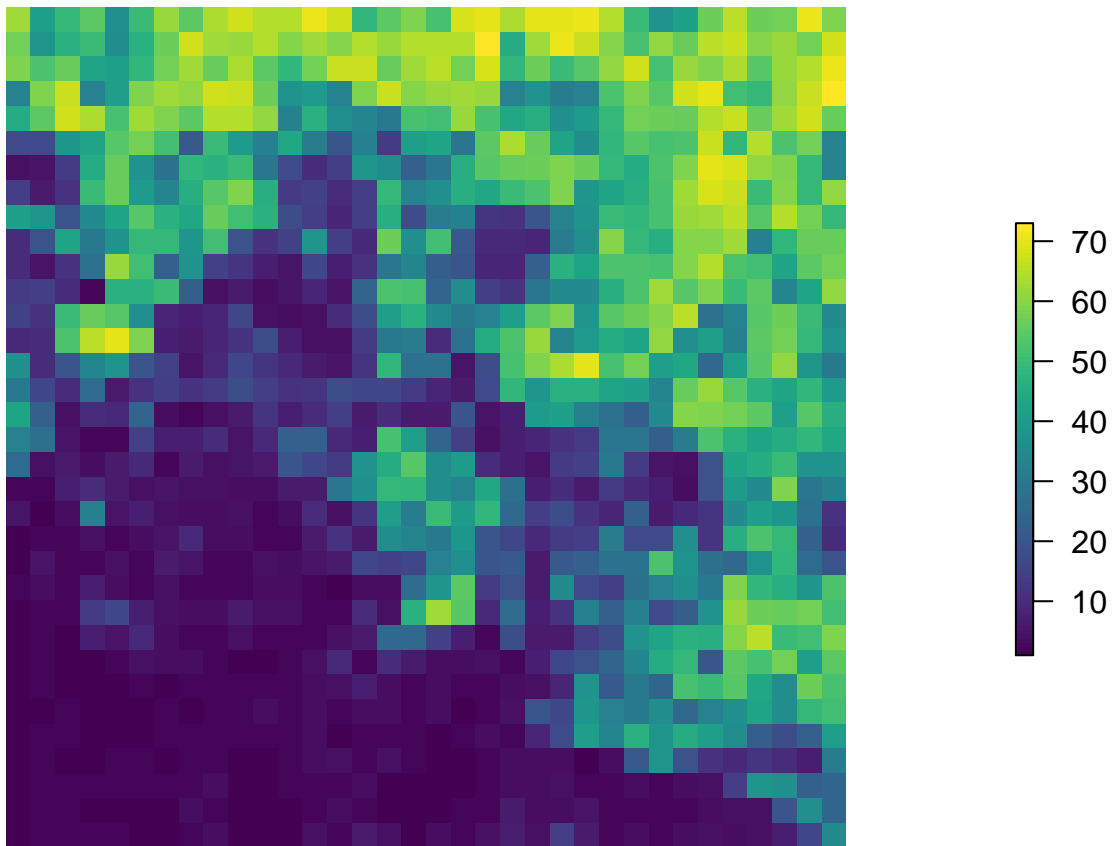
Populations are represented as a stack of rasters that describes the total number of individuals that occur in each cell for each life-stage at the beginning of the simulations (initial populations). In the kangaroo example data, there are three life-stages and thus three individual raster layers in the stack. The values are either zeros or positive integers. This example population abundance stack is available in the steps package ("egk_pop"), however, any raster stack can be used in its place.

```
egk_pop
```

```
## class       : RasterStack
## dimensions  : 35, 36, 1260, 3  (nrow, ncol, ncell, nlayers)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## names       : juvenile, subadult, adult
## min values  :        1,        1,     1
## max values  :       20,       20,    20
```

```r
par(mar=c(0,0,0,0), oma=c(0,0,0,0))
spplot(egk_pop, col.regions = viridis(100))
```
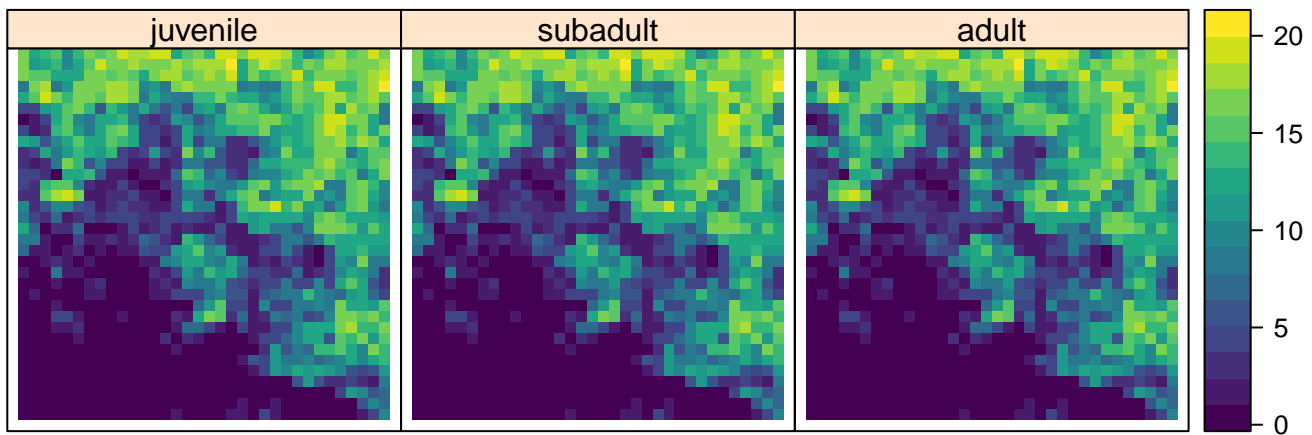
For this example, we have used equal numbers of kangaroos in each cell for each life-stage. This, of course, will not always be the case. For example, a user may derive initial population abundances by using stable state age distributions multiplied by the carrying_capacity of the landscape, and then drawn from a multinomial distribution to return whole integers:

```
library(foreach)
stable_states <- abs( eigen(egk_mat)$vectors[,1] / sum(eigen(egk_mat)$vectors[,1]))
popN <- stack(replicate(ncol(egk_mat), egk_k)) * stable_states
idx <- which(!is.na(getValues(popN[[1]])))
pop <- stack(
  foreach(i = 1:nlayers(popN)) %do% {
    max_pop <- ceiling(cellStats(popN[[i]], max, na.rm = T))
    pop_values <- popN[[i]][idx]
    popN[[i]][idx] <- rbinom(prob = (pop_values/max_pop), size = max_pop, n = length(pop_values))
    popN[[i]]
  })
names(pop) <- colnames(egk_mat)
pop
```

```
## class       : RasterStack
## dimensions  : 35, 36, 1260, 3  (nrow, ncol, ncell, nlayers)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## names       : juvenile, subadult, adult
## min values  :        0,        0,     0
## max values  :       29,       13,    33
```

All three of these spatial components (habitat suitability, carrying capacity, and initial stage abundances) define a "landscape" object, however, only the population abundance stack (egk_pop) is required to complete a simulation. The landscape object is modified at each timestep in a single simulation based on habitat and population dynamics (described in subsequent sections below).

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = NULL,
                           carrying_capacity = NULL)
```

These are the only data input requirements for a simple population simulation, however, we also need to specify population dynamics. Dynamic functions are used to modify populations or habitats in a landscape at each timestep in a simulation. They can be selected as 'off-the-shelf' functions - i.e. those included in the 'steps' package - or custom defined functions created by the user. In its most basic form, only population growth will be applied to the landscape. As shown in the following code, we use the growth() function, which uses the probabilities in the transition matrix - and leave all of the other parameters at their default values (NULL).

```r
egk_pop_dynamics <- population_dynamics(change = growth(transition_matrix = egk_mat),
                                        dispersal = NULL,
                                        modification = NULL,
                                        density_dependence = NULL)
```
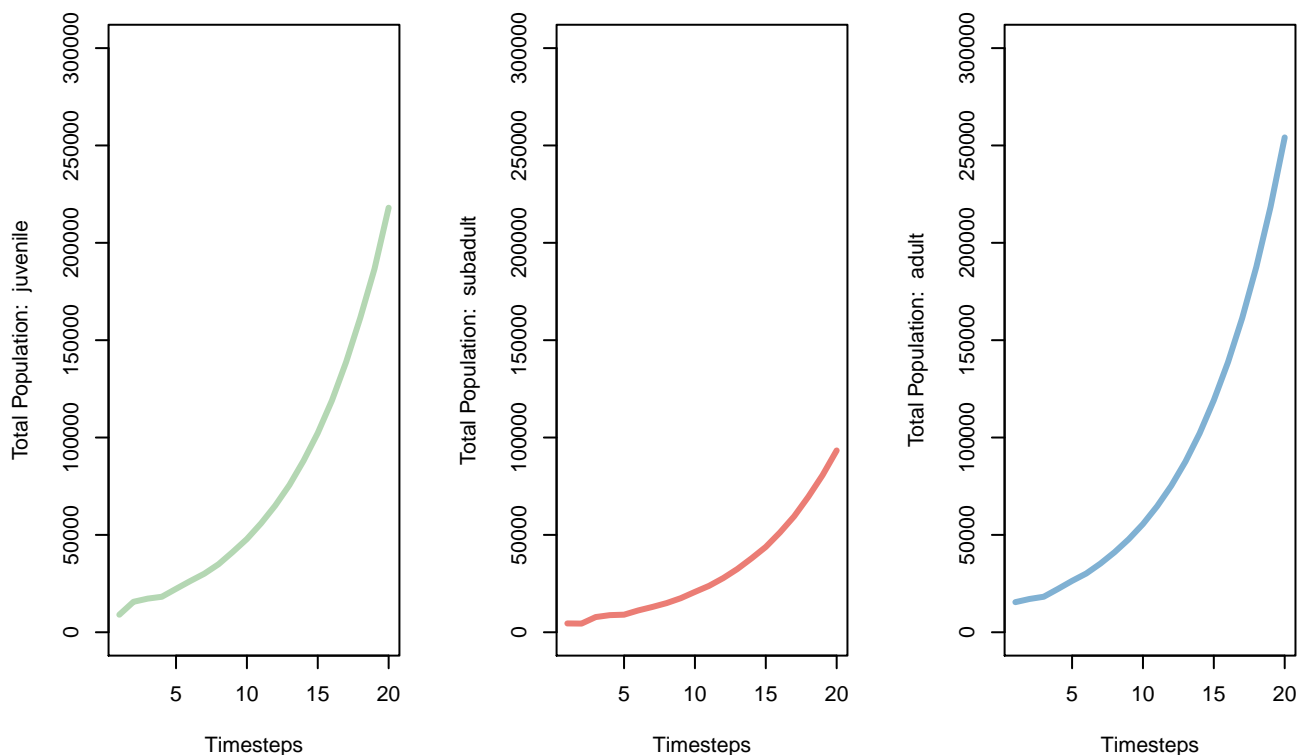
Now that we have constructed the landscape object and defined a dynamic object, we can run a single simulation (i.e replicates = 1, default). We simulate changes to the kangaroo population over twenty timesteps. Runtime will depend on the complexity of the landscape object and the configuration of the dynamic object(s). The "verbose = FALSE" suppresses information printed to the console during a simulation; if omitted or set to TRUE (default) the simulation progress bars are shown.

```r
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 1,
                          verbose = FALSE)
```

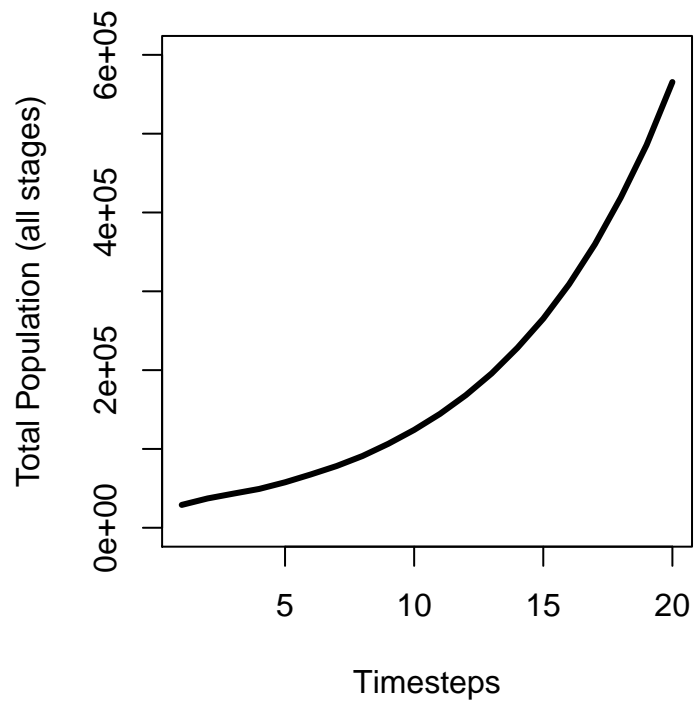Once a simulation has been run, we can plot spatially-explicit and temporally-explicit information.

For this example, we can view the kangaroo population trajectories of each life-stage:
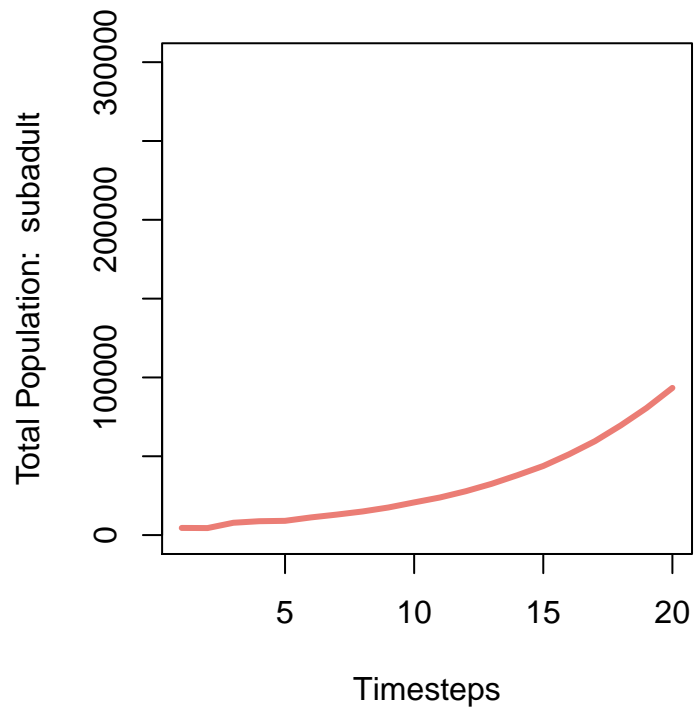
```r
plot(egk_results)
```


Or the total kangaroo population trajectory:
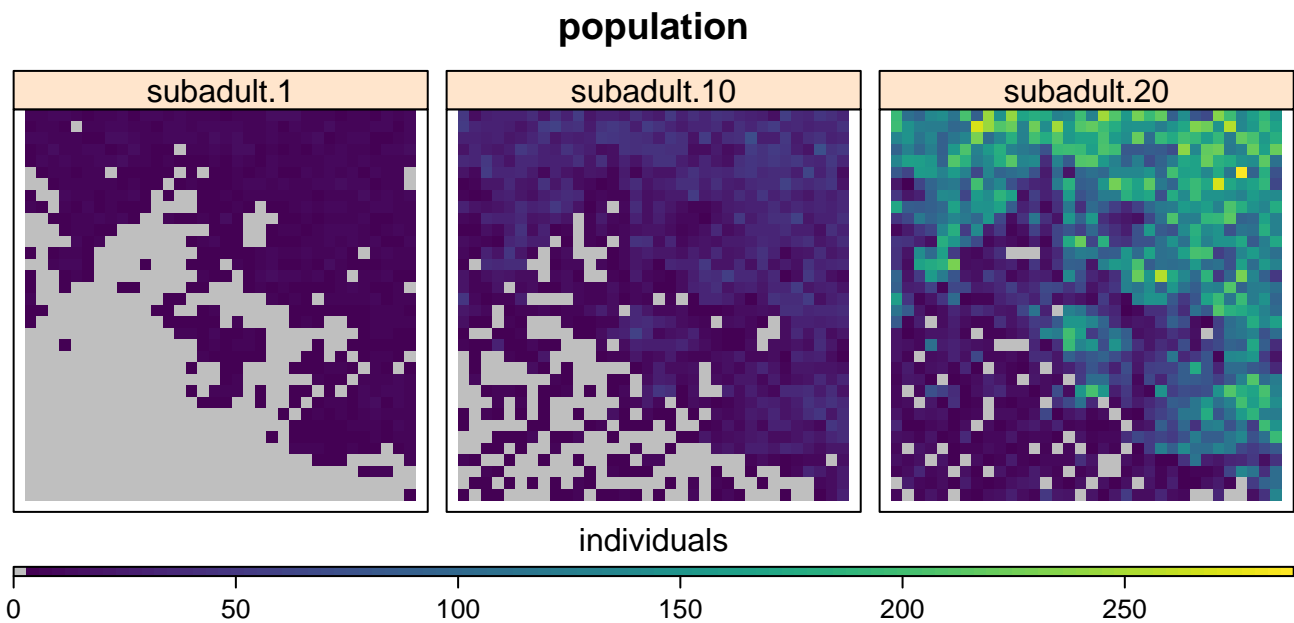
```r
plot(egk_results, stage = 0)
```

Or the kangaroo population trajectory for a single life-stage:

```
plot(egk_results, stage = 2, newplot = TRUE)
```


We can also view the population distribution over the landscape for a single life-stage (only timesteps one, ten, and twenty shown):

```
plot(egk_results, type = "raster", stage = 2, timesteps = c(1, 10, 20), panels = c(3, 1))
```

population

To view the changes in population distribution over time, all of the rasters may also be plotted as animations. Here is code to animate the the population rasters of subadults for timesteps one, ten and twenty (omit these to show all timesteps of the simulation) - note only the static images used to make the animation are shown:

```
plot(egk_results, type = "raster", stage = 2, timesteps = c(1, 10, 20), animate = TRUE)
```

We can also perform multiple simulations. For the kangaroo, we specify three replicates of a twenty timestep simulation. The replicates are run sequentially by default, however, to improve computation time, we have included the ability to run all three replicates in parallel - each on a different processor. See ?plan for more information on how to operate in parallel. Note plan() is only required to be called once at the beginning of a script.

```
plan(multiprocess, workers = 3) # This is how we specify to simulate replicates on separate processors in

egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results)
```
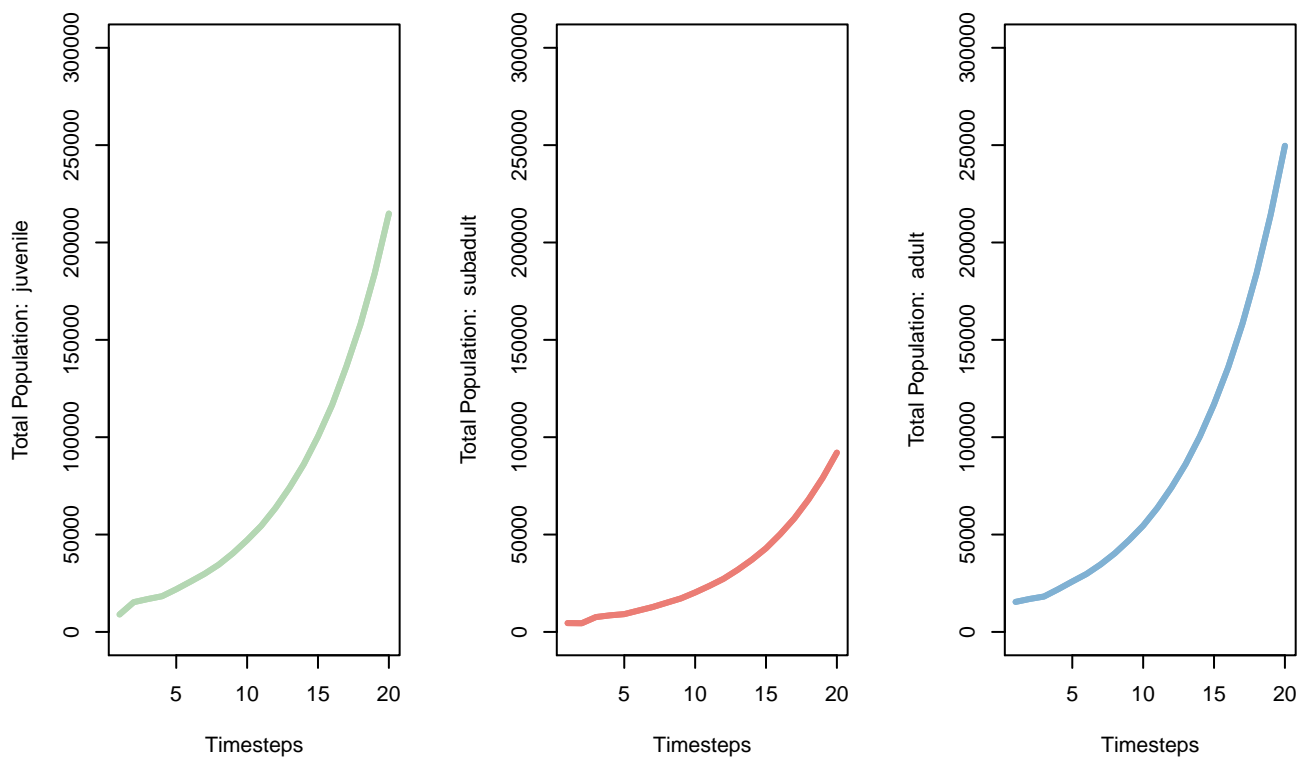
Note that the plot above looks very similar to the single replicate simulation. This is because we have not added any major stochastic dynamics to the landscape. However, demographic stochasticity IS on by default because it's incorporated into the transition probabilities that the growth function uses - this behaviour can be disabled by setting 'demo_stochasticity = "none"' in the simulation. Let's try adding some globally acting environmental stochasticity to the growth function:

```
egk_pop_dynamics <- population_dynamics(change = growth(transition_matrix = egk_mat,
                                              global_stochasticity = egk_mat_stoch),
                                   dispersal = NULL,
                                   modification = NULL,
                                   density_dependence = NULL)


egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          demo_stochasticity = "none",
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)


plot(egk_results)
```
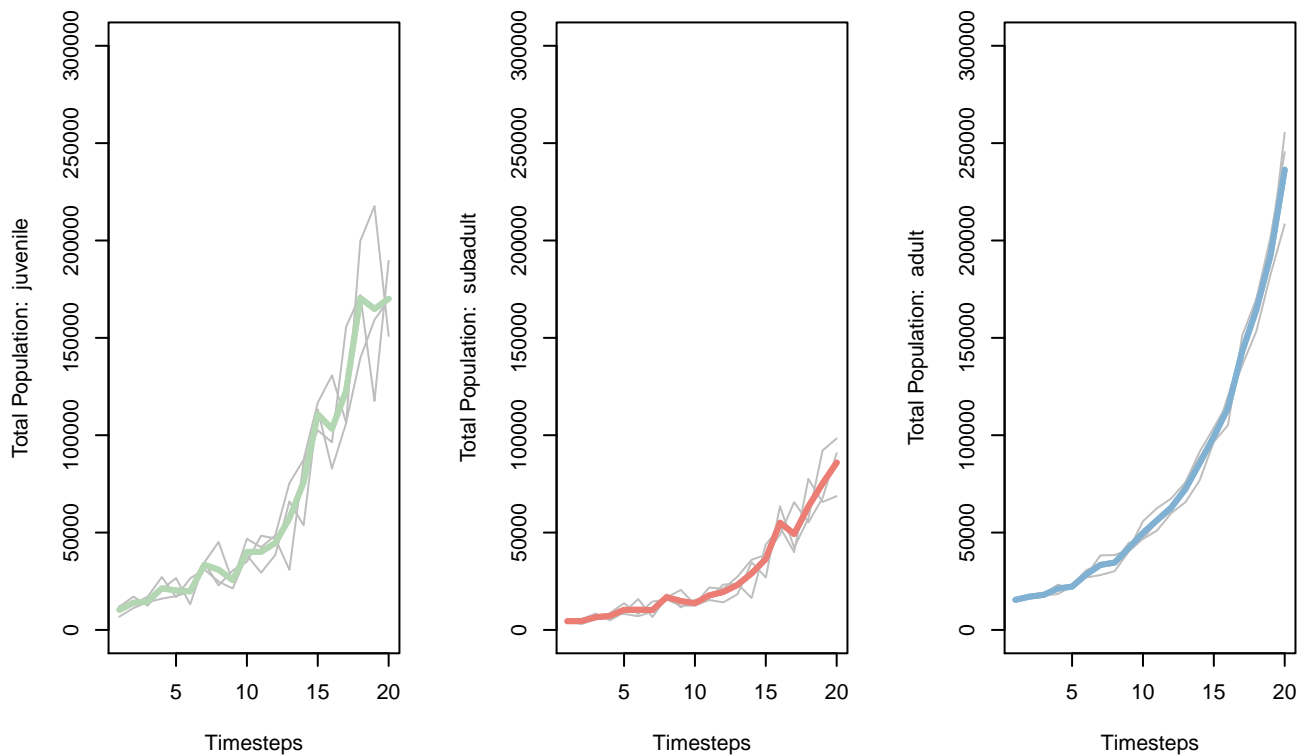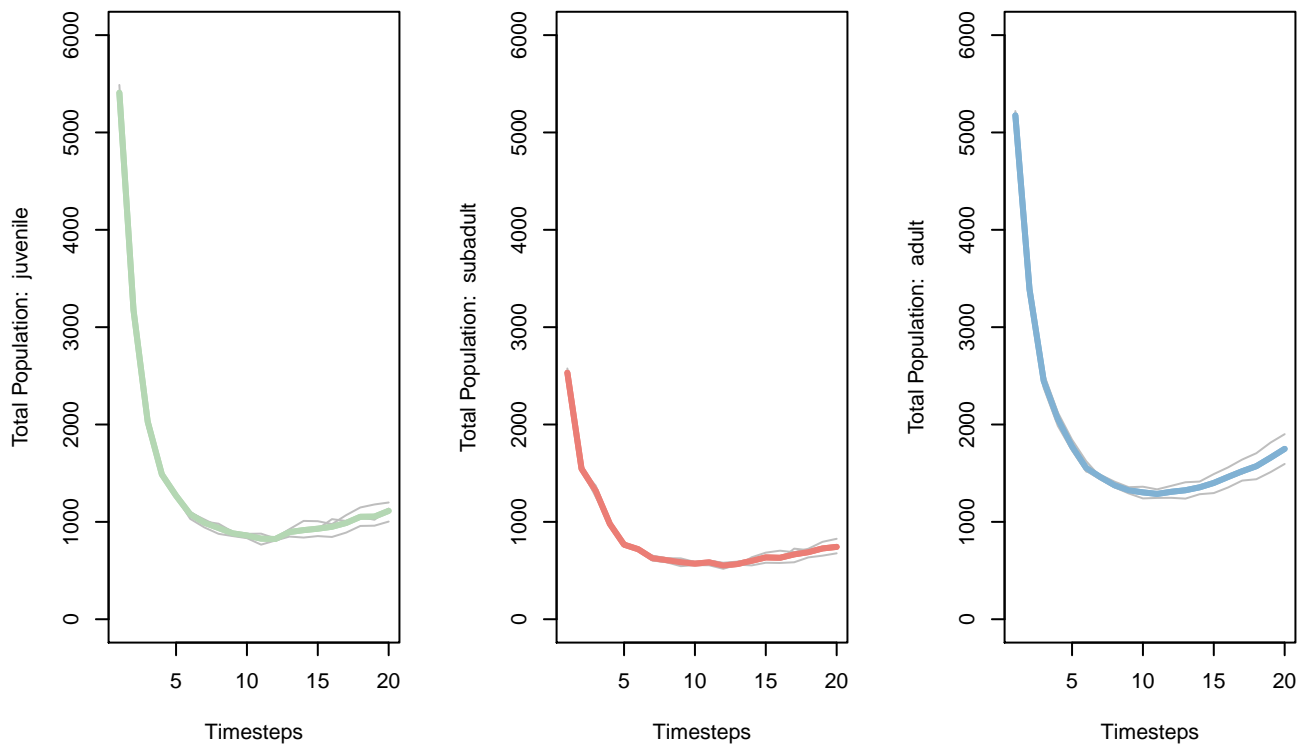
We can also specify how survival and fecundity values are influenced by spatial layers in the landscape object (e.g. habitat suitability or carrying capacity). Here, we modify the survival and fecundity values in the transition matrix at each time step according to habitat suitability by specifying a transition function within the growth function. This is done by multiplying values in the spatial layers (in this case habitat suitability) by the survival and fecundity values in the transition matrix. This produces new survival and fecundity values for each grid cell in the landscape. A user may add any spatial layer to the landscape to modify the transition matrices; here, we add a habitat suitabilty layer to the landscape for the transition function to work:

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = NULL)


egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  transition_function = modified_transition(egk_mat,
                                                  survival_layer = "suitability",
                                                  fecundity_layer = "suitability")),
  dispersal = NULL,
  modification = NULL,
  density_dependence = NULL)

egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results)
```

A user may also specify a custom function that operates on or defines survival and fecundity in the transition matrix at each timestep. The function requires a transition matrix, the landscape object, and a timestep as input parameters, and must return an array of transition matrices that matches the dimensions of the original transition matrix and number of cells in the landscape. As an example (will not work as coded due to pathing and missing fiels), we have created a custom function below that reads in spatial data to define the survival and fecundities at each timestep:

```r
deterministic_transitions <- function(transition_matrix) {

  dim <- nrow(transition_matrix)

  function (landscape, timestep) {

    #### This assumes that the files are named with a particular convention
    #### and will not work for all cases. User must change code below accordingly.

      # get metrics and constructor info
      cell_idx <- which(!is.na(raster::getValues(landscape$population[[1]])))
      current_timestep <- sprintf("%02i", timestep)
      n_cells <- length(which(!is.na(raster::getValues(landscape$population[[1]]))))

      # get relevant rasters - note, your working directory will be different
      files <- list.files("../working/rasters", pattern = paste0("_", current_timestep, "_"))

      #initialise array
      transition_array <- array(0, dim = c(dim, dim, n_cells))

      # populate array:
      for (file in files) {
        r <- as.integer(substr(substr(file, nchar(file) - (8-1), nchar(file)), 1, 2))
        c <- as.integer(substr(substr(file, nchar(file) - (6-1), nchar(file)), 1, 2))
        #note, your working directory will be different
        transition_array[r, c, ] <- raster::raster(paste0("../working/rasters/",
```

10

```
                                                                  file))[cell_idx]
    }

    #### Return array with required dimensions
    transition_array
  }
}

egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  transition_function = deterministic_transitions(transition_matrix)),
  dispersal = NULL,
  modification = NULL,
  density_dependence = NULL)
```

Now let's add some other population dynamics. We can specify ceiling density dependence with the ceiling_density function (i.e., the population will grow according to the transition matrix until it reaches a ceiling carrying capacity, at which point it will stop) but must provide a carrying capacity layer in the landscape for this to work. By default all life-stages contribute to density dependence, however, here we specify that it is based on the number of adults only (stage = 3 in the ceiling_density function). Type '?ceiling_density' for more information.

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k)

egk_pop_dynamics <- population_dynamics(change = growth(transition_matrix = egk_mat,
                                                        global_stochasticity = egk_mat_stoch),
                                        dispersal = NULL,
                                        modification = NULL,
                                        density_dependence = ceiling_density(stages = 3))

egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results)
```
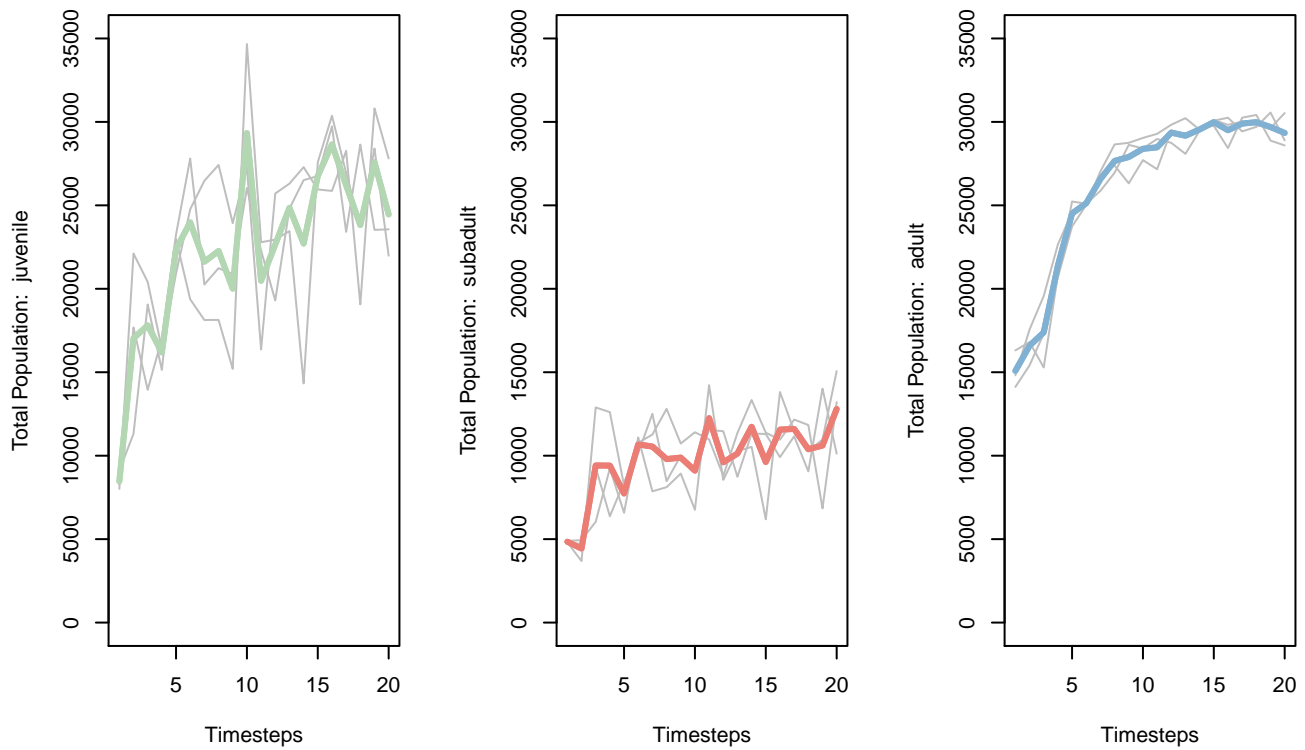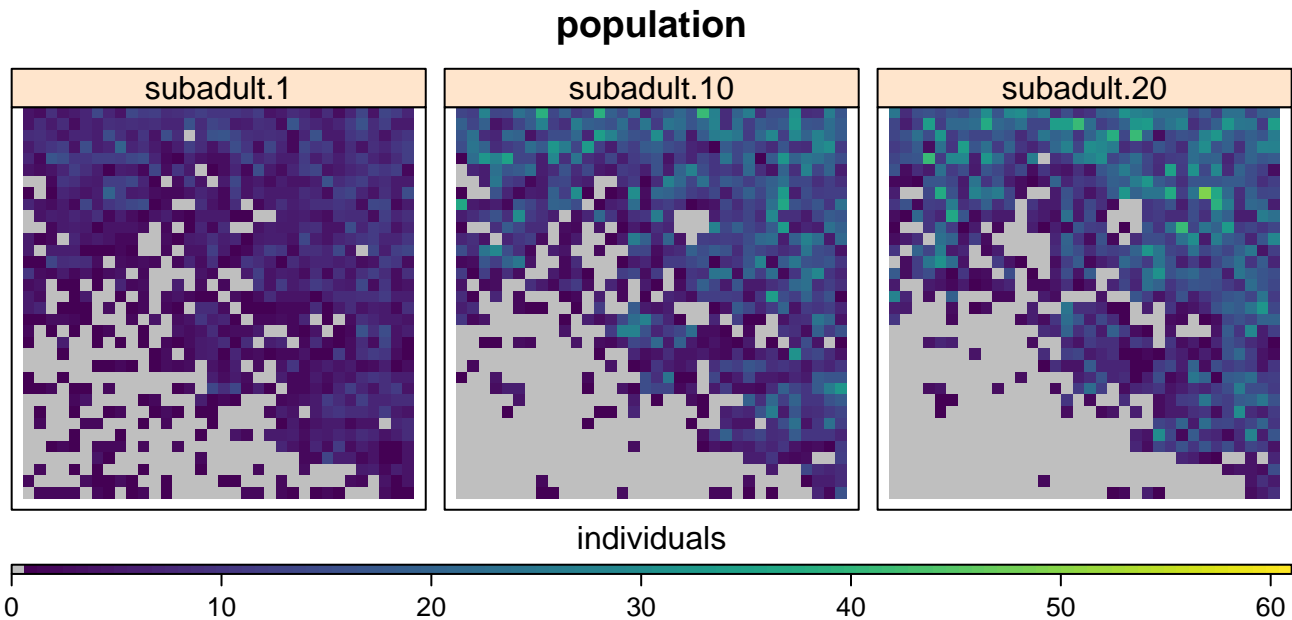
Note, if several replicates of a simulation are run, you must explicitly specify which one to plot for rasters (i.e. egk_results[1]):

```
plot(egk_results[1], type = "raster", stage = 2, timesteps = c(1, 10, 20), panels = c(3, 1))
```

population

The components of the landscape object are stored for each timestep (if they are specified) so it is possible to also view the carrying capacity throughout a single simulation (i.e. egk_results[1]). Note, only timesteps one, ten, and twenty are shown - this is controlled by specifying the 'panels' parameter in the plot call:

```
plot(egk_results[1], object = "carrying_capacity", type = "raster", timesteps = c(1, 10, 20), panels = c(3
```

k
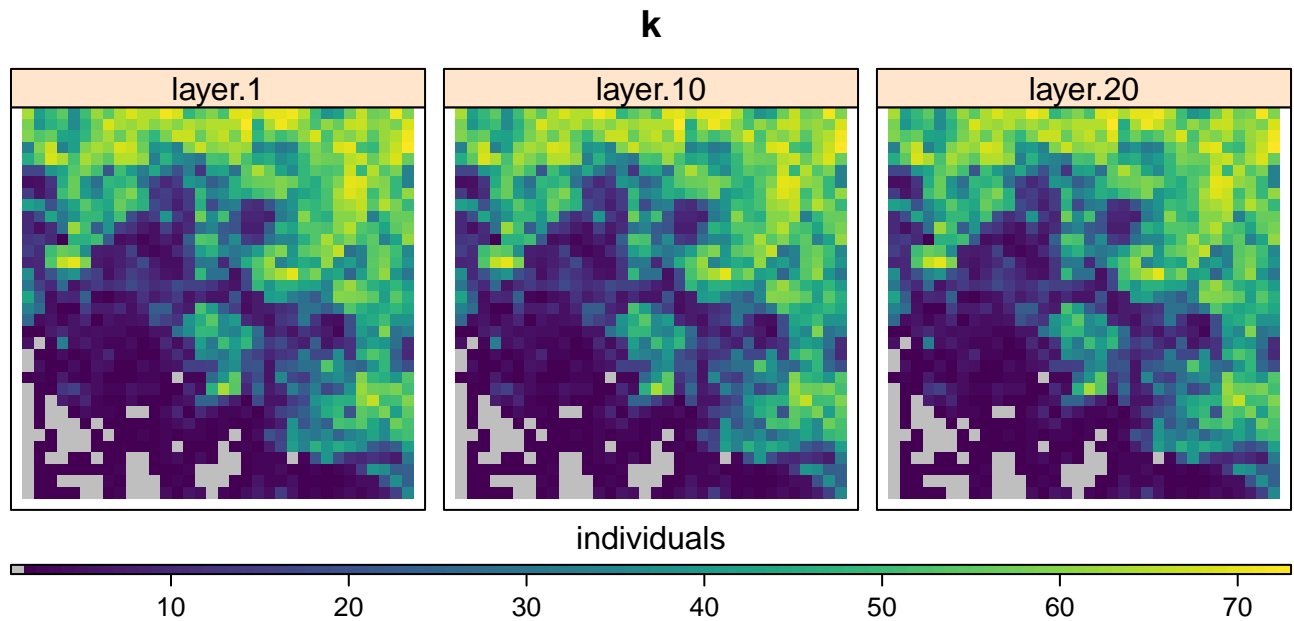
The simulation results object (egk_results in our example) is a list of lists containing spatial objects and is depicted by the following tree diagram:

- Replicate (**a**)
  - Timestep (**b**)
    * Population Raster Stack (**c**)
      · Life-Stage Raster (**d**)
    * Habitat Suitability Raster (**c**)
    * Carrying Capacity Raster (**c**)
    * Other Raster Stack (**c**)
      · Raster (**d**)

To access the different components from the results object the following syntax is used:

result_object[[**a**]][[**b**]][[**c**]][[**d**]]

where **a** through **d** represent numbers denoting replicate, timestep, or object indices. All values will equal one or a larger positive integer depending on the simulation setup. The landscape object (denoted by **c**) will always be structured in the same order where position 1 is the population, position 2 is the habitat suitability, and position 3 is the carrying capacity. Positions beyond these are reserved for additional spatial data added to the initial landscape object.

For example, to return the population raster for the first life-stage in timestep five of the second replicate the following syntax would be used:

```
egk_results[[2]][[5]][[1]][[1]]
```

```
## class       : RasterLayer
## dimensions  : 35, 36, 1260  (nrow, ncol, ncell)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## data source : in memory
## names       : juvenile
## values      : 0, 79  (min, max)
```

To return the habitat suitability for the third timestep of the second replicate (note d is not used in this case):

```
egk_results[[2]][[3]][[2]]
```

```
## class       : RasterLayer
```

```
## dimensions  : 35, 36, 1260  (nrow, ncol, ncell)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## data source : in memory
## names       : EGK_habitat_500
## values      : 0.003082677, 0.9678264  (min, max)
```

Alternatively, the names of the raster objects can be used:

```
egk_results[[2]][[3]][["carrying_capacity"]]
```

```
## class       : RasterLayer
## dimensions  : 35, 36, 1260  (nrow, ncol, ncell)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## data source : in memory
## names       : layer
## values      : 1, 73  (min, max)
```

Based on this structure, we have also provided an extraction function to return components of a simulation results object. For example, to return the same object as in the previous example:

```
extract_spatial(egk_results, replicate = 2, timestep = 3, landscape_object = "carrying_capacity")
```

```
## class       : RasterLayer
## dimensions  : 35, 36, 1260  (nrow, ncol, ncell)
## resolution  : 500, 500  (x, y)
## extent      : 319000, 337000, 5817000, 5834500  (xmin, xmax, ymin, ymax)
## coord. ref. : +proj=utm +zone=55 +south +ellps=GRS80 +towgs84=0,0,0,0,0,0,0 +units=m +no_defs
## data source : in memory
## names       : layer
## values      : 1, 73  (min, max)
```

By default, the extract function will return a population raster (landscape object = 1 or landscape object = "population"), for the first life-stage (stage = 1), for the first iteration (timestep = 1), for the first simulation run (replicate = 1). These values can be specified accordingly to return the spatial object of your choosing. Here, we plot the default object from the extract function:

```
par(mar = c(0.1, 0.1, 0.1, 0.1))
plot(extract_spatial(egk_results), box = FALSE, axes = FALSE, col = viridis(100))
```
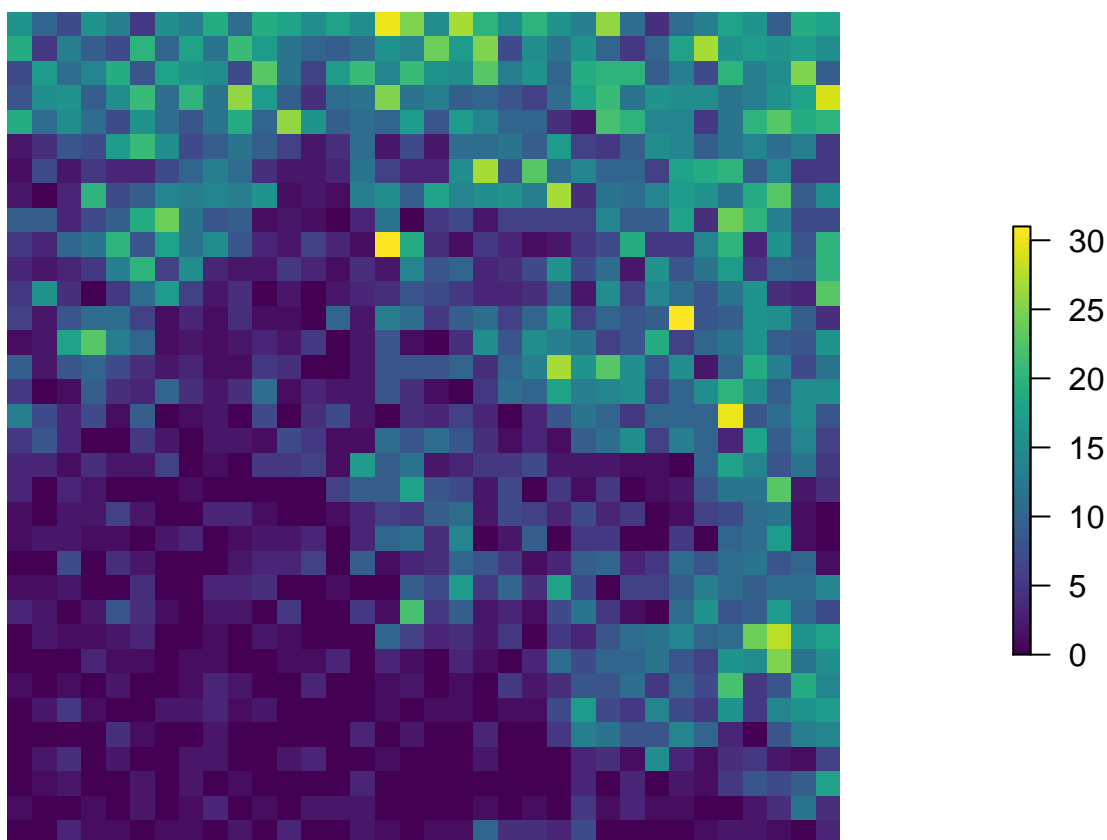
So far, the populations are only changing within their cells without any movement between cells. We can either specify assisted species movements (i.e. translocations or reintroductions) or natural species movements (dispersal) in the model simulations.

To characterise a translocation, we specify two raster layers that map the locations of where we will take individuals from and where we will place individuals in the landscape. Cell values (integers) specify how many individuals will be added/removed. Source and sink spatial layers are stored in the landscape object and referenced by name. We use a built-in translocation function to modify the population(s) in a simulation at each specified timestep. The function requires the name of source and sink layers stored in the landscape object ("source" and "sink"), the life-stages to modify, and the timesteps at which to modify the population. In this example, we provide the kangaroo source ("egk_source") and sink ("egk_sink") layers, a life-stage of 3 (only adults affected), and timesteps one, five, ten and fifteen - meaning each translocation will occur every five years in each simulation replicate. Note, if the number of individuals is not available in the landscape when the translocation is applied, a warning will be generated and only the maximum available individuals will be used.

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k,
                           source = egk_source,
                           sink = egk_sink)


egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  modification = translocation(source_layer = "source",
                               sink_layer = "sink",
                               stages = 3,
                               effect_timesteps = c(1, 5, 10, 15)),
  density_dependence = NULL)
```
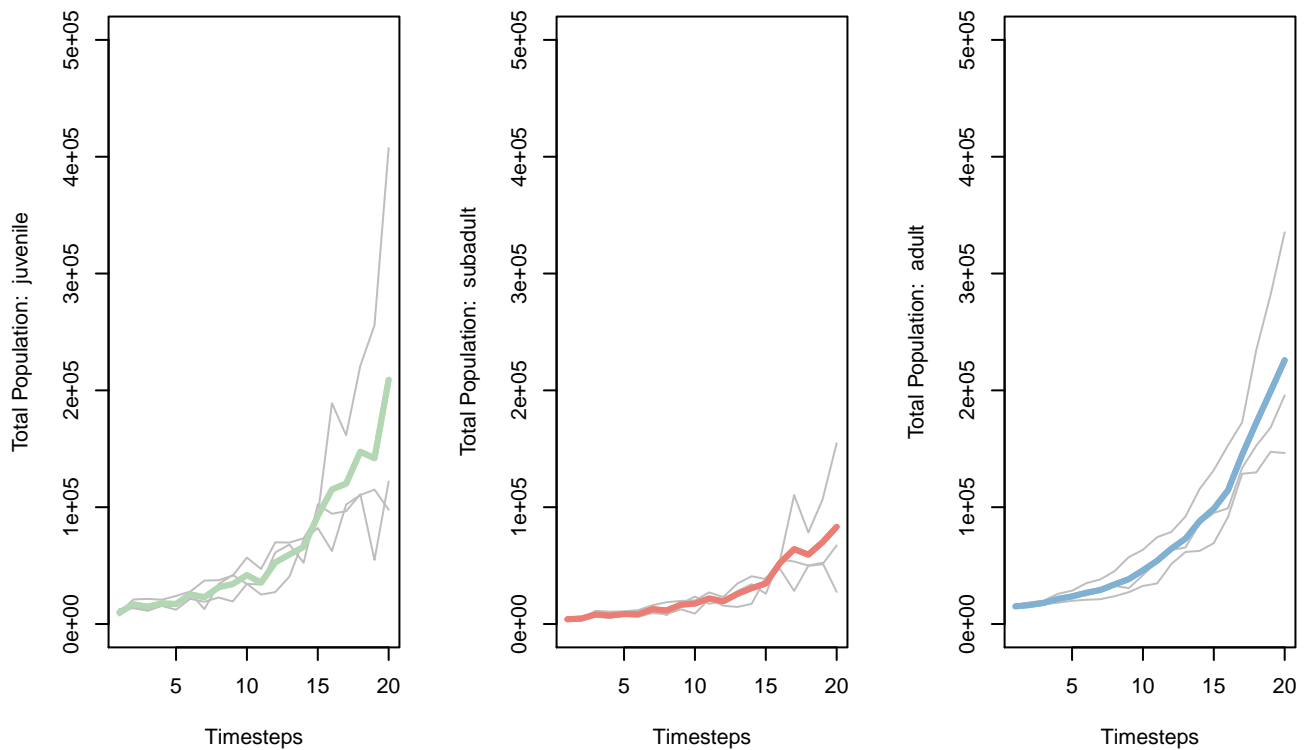
```
## [1] "source"
## [1] "sink"
```

```
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)
```

```
plot(egk_results)
```


We can also add dispersal to allow kangaroos to move throughout the landscape. There are several built-in dispersal functions and most of them utilise habitat suitability, carrying capacity, or both to determine arrival probabilities - see package help for more information by typing '?population_dispersal_functions'. Thus we will need to provide the appropriate habitat layer in the intial landscape. Below, we use kernel-based dispersal (with a maximum dispersal distance of 5000 meters) and habitat suitability to determine the arrival probabilities:

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k)
```

```
egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = kernel_dispersal(arrival_probability = "suitability",
                               dispersal_distance = 5000,
                               dispersal_kernel = exponential_dispersal_kernel(distance_decay = 5000)),
  density_dependence = ceiling_density(stages = 3))
```

```
## distance_decay:
##
## [1] 5000
##
```
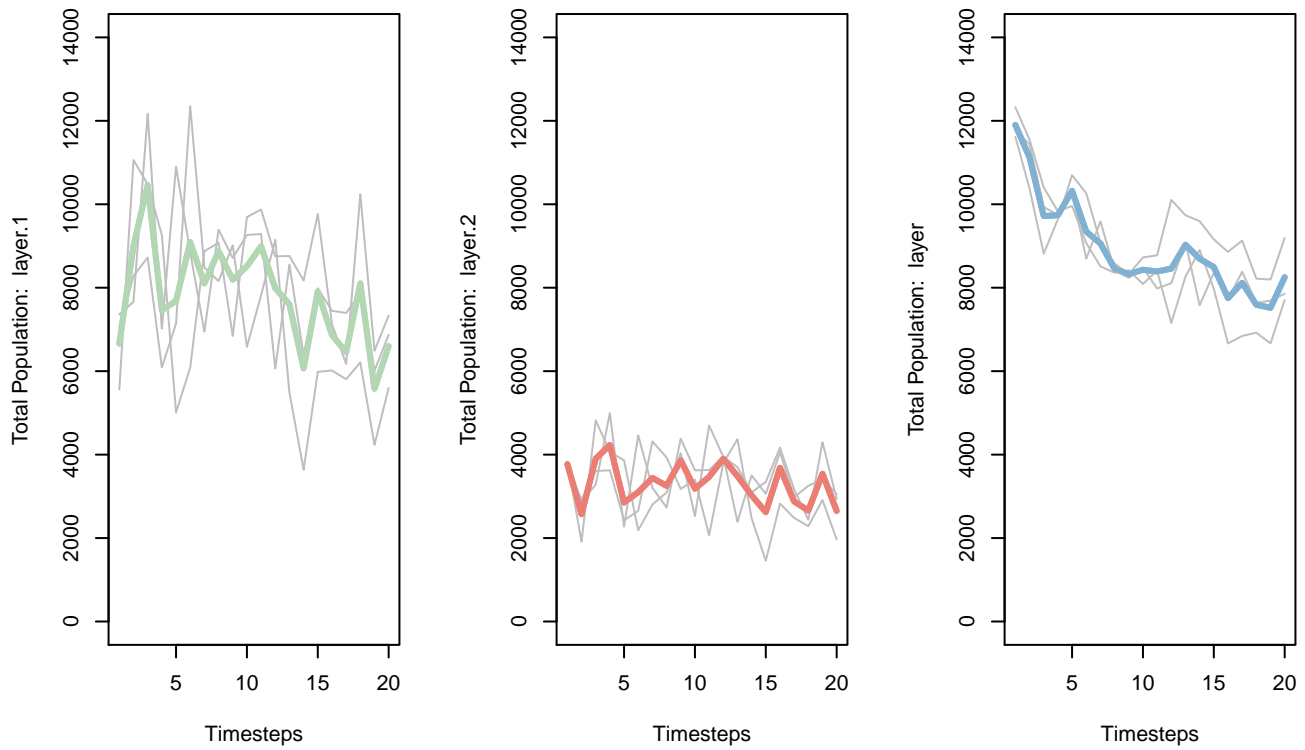
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```
## normalize:
##
## [1] FALSE
```

```
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)
```

```
##        3 life stages exist but 1 dispersal proportion(s) of 1 were specified. Is this what was intended?
```

```
plot(egk_results)
```


Let's have a look at how the adult population is changing in the first replicate of the simulation:

```
plot(egk_results[1], type = "raster", stage = 3, timesteps = c(1, 10, 20), panels = c(3, 1))
```

population
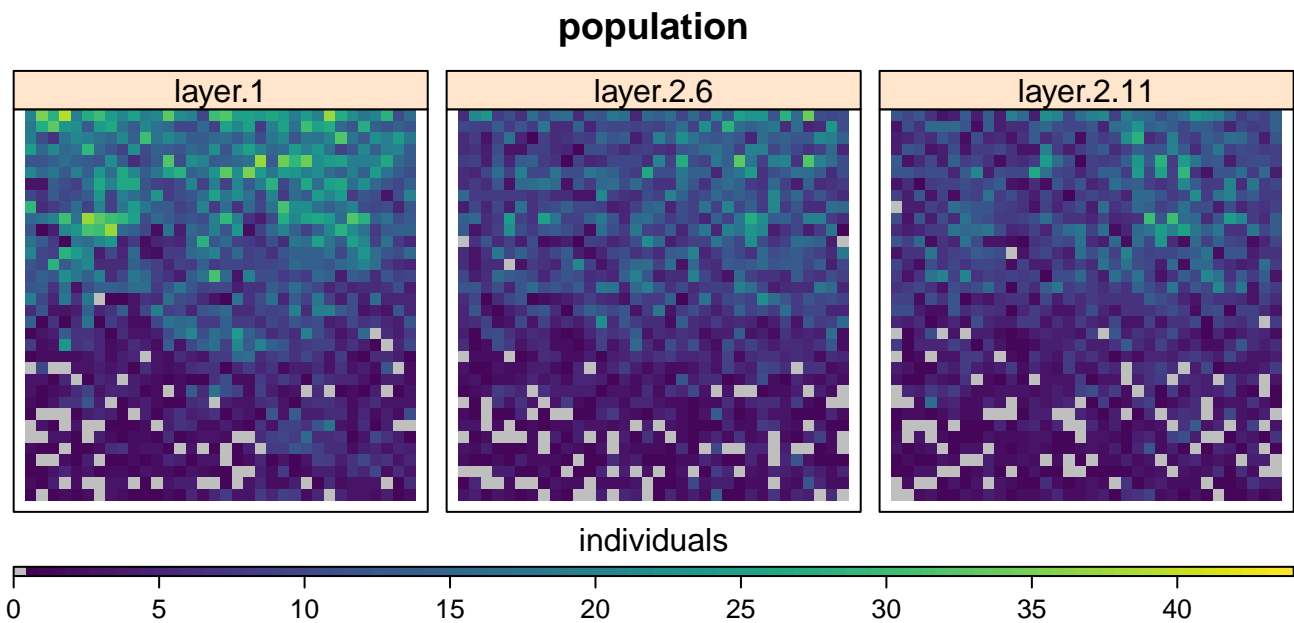
The proportion of individuals dispersing can also be specified in the dispersal functions. If dispersal proportions are not specified, the default behaviour is to disperse all individuals in all life-stages. If proportions are specified as a single number, then all life-stages disperse with that proportion, however, a vector of proportions (equal in length to the number of life-stages) can also be specified. Note, if a vector of numbers is specified that has fewer elements than life stages, than the vector will be recycled to match its number of elements to life stages (i.e. dispersal_proportion = c(0, 0.5, 1) with five life-stages will become 0, 0.5, 1, 0, 0.5). In the example below, no juveniles (stage 1) disperse, only fifty-percent of subadults (stage 2) disperse, and all adults (stage 3) disperse:

```r
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k)

egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = kernel_dispersal(arrival_probability = "suitability",
                               dispersal_distance = 5000,
                               dispersal_kernel = exponential_dispersal_kernel(distance_decay = 5000),
                               dispersal_proportion = c(0, 0.5, 1)),
  modification = NULL,
  density_dependence = ceiling_density(stages = 3))
```

```
## distance_decay:
##
## [1] 5000
##
## normalize:
##
## [1] FALSE
```

```r
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results)
```
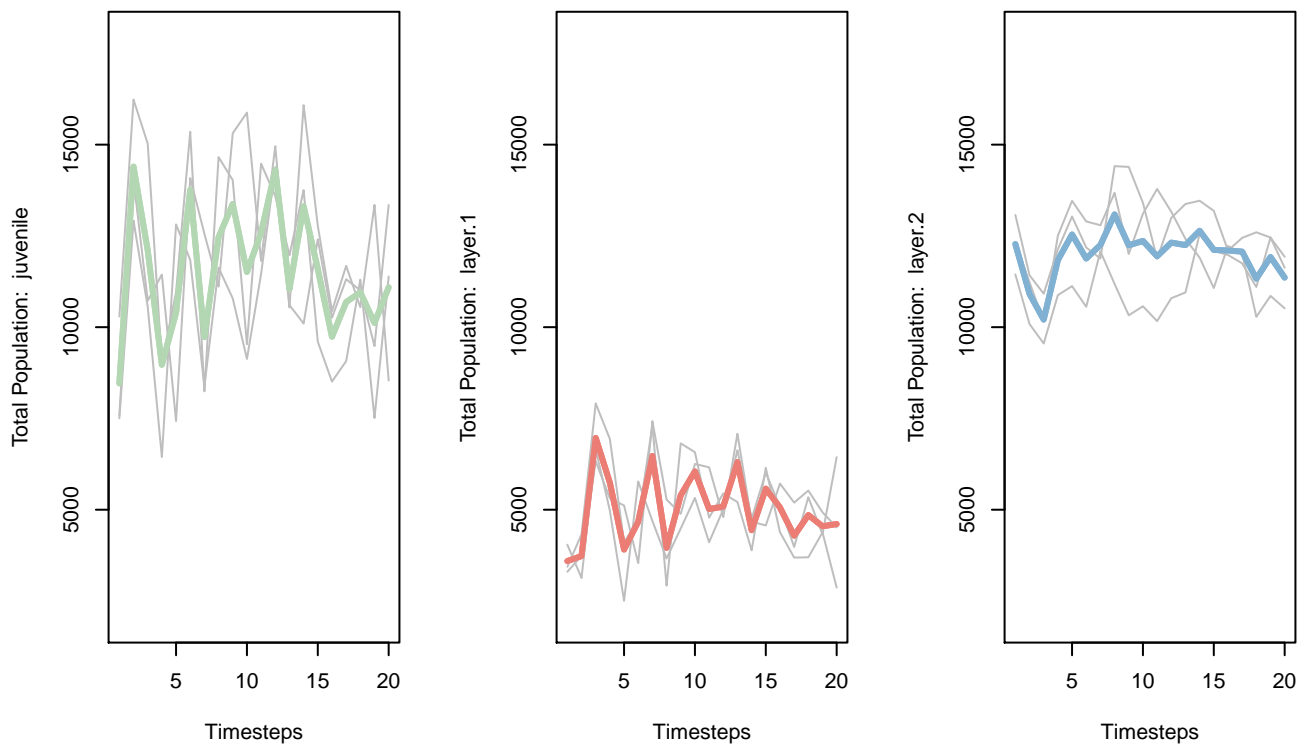
Maximum dispersal distances can also be specified for one of the alternative dispersal functions, cellular automata. Distances are expressed as spatial units (in this case meters). Maximum distances are explicitly defined for the cellular automata dispersal function. In the cellular automata dispersal function, individuals move horizontally or vertically but not diagonally.

As with the proportions, a single number will indicate maximum dispersal distances for all life-stages whilst a vector of distances (equal in length to the number of life-stages) can also be specified. In the example below, no juveniles (stage 1) disperse, subadults (stage 2) only disperse up to 2500 meters (5 cells) , and adults (stage 3) disperse up to 5000 meters (10 cells):

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k)


egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = cellular_automata_dispersal(dispersal_distance = c(0, 2500, 5000),
                                          dispersal_proportion = c(0, 0.5, 1)),
  modification = NULL,
  density_dependence = ceiling_density(stages = 3))
```

```
## distance_decay:
##
## [1] 1
##
## normalize:
##
## [1] FALSE
```
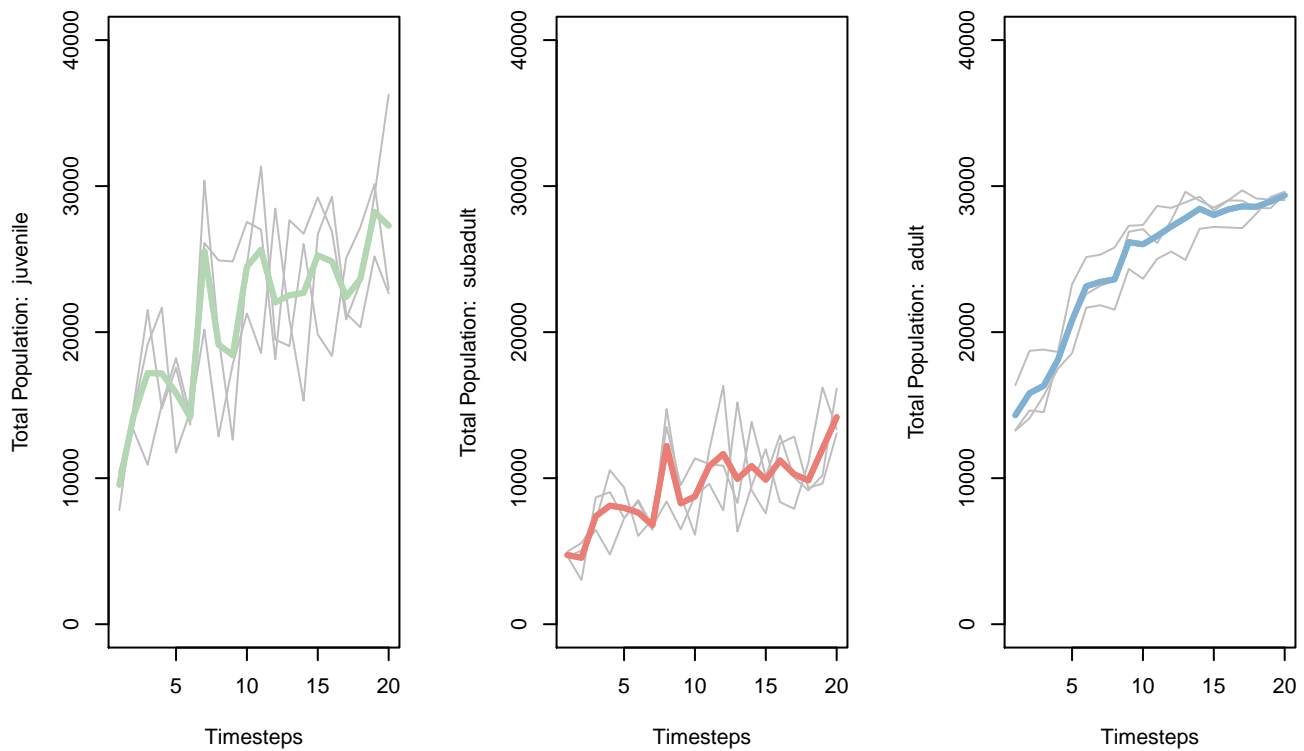
```
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
```

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```
                        replicates = 3,
                        verbose = FALSE)
```

```
plot(egk_results)
```


The 'number of cells' representation of distance should be carefully considered when specifying custom distance kernel functions. For example, below we have specified an exponential distance decay function where "r" represents spatial units - in this case 5000 meters (10 cells). How we specify the function will depend on the ecology of the species and known dispersal distances. The function should return a vlue close to zero when the maximum dispersal distances is specified for "r":

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k)


egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = kernel_dispersal(arrival_probability = "suitability",
                               dispersal_distance = 5000,
                               dispersal_kernel = function (r) exp(-r / 2000),
                               dispersal_proportion = c(0, 0.5, 1)),
  modification = NULL,
  density_dependence = ceiling_density(stages = 3))
```

```
## function (r) exp(-r / 2000)
```

```
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = NULL,
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)
```

```
plot(egk_results)
```
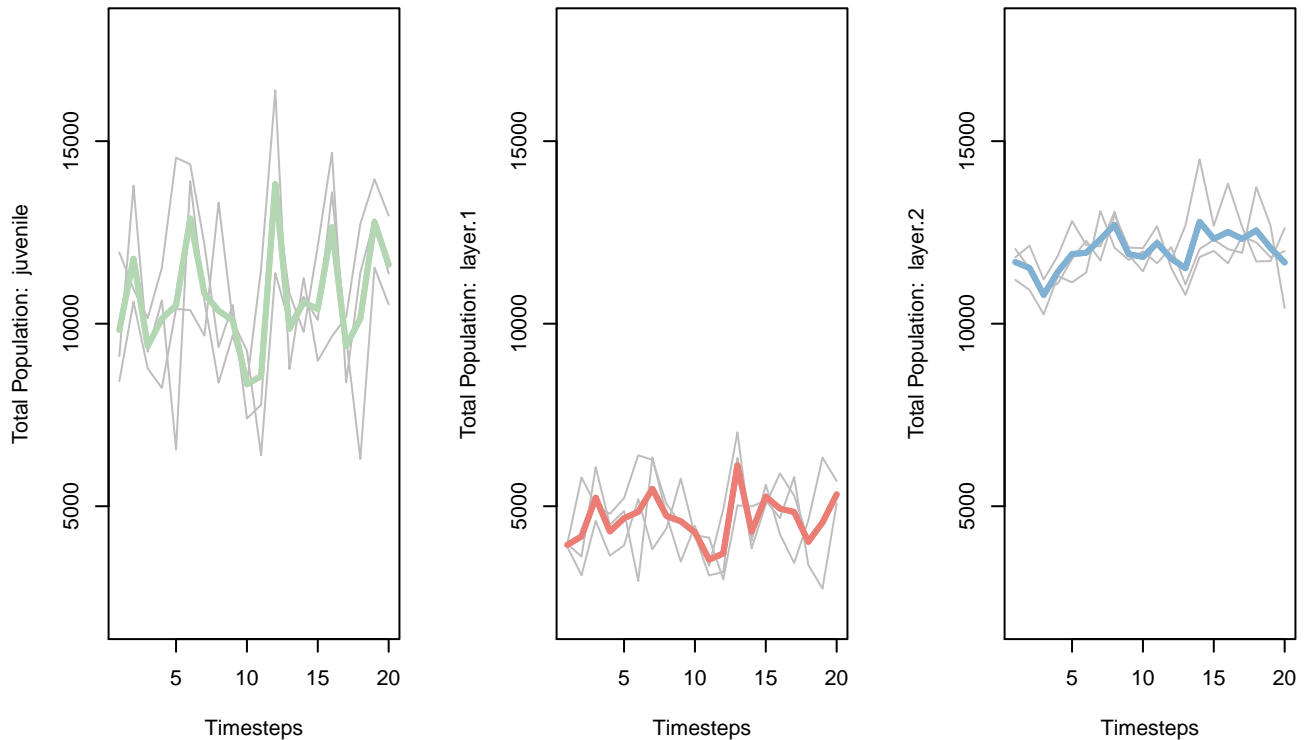

So far the kangaroo population is the only thing to be dynamically changing in the landscape, however, often habitat suitability also changes due to disturbances. To characterise habitat disturbance, we can use a series of raster layers that map the locations and severity of disturbances. Each disturbance raster will be multiplied with the original habitat suitability layer and thus contain values that represent appropriate values - zero representing the maximum disturbance and one representing no disturbance. Note, the number of disturbance layers must match the intended number of timesteps in a single simulation. There is an existing spatial dataset of fires in the steps package ("egk_fire") which we store in the landscape object. We use a pre-defined fire effects function to modify the habitat suitability in the simulation at each timestep. The function requires the name of fire layers stored in the landscape object, and an lag time which specifies the number of timesteps that each disturbance layer acts on the habitat suitability. The effect of fires can be cumulative, so if there are two fires in the same cell in succession (i.e. in a shorter space of time than the effect time) then the habitat suitability will equal suitability multiplied by both the first and second disturbance effects. A function can be specified to control the regeneration of the landscape. In this example, we provide the kangaroo fire disturbance input name ("fires"), and an lag time of five - meaning each fire layer will affect the habitat suitability (in linear decreasing intensity based on the regeneration function) for five timesteps in each simulation replicate. All functions that act on the habitat must be passed in as a list in the simulation call:

```
egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = egk_k,
                           fires = egk_fire)


egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = kernel_dispersal(arrival_probability = "suitability",
                               dispersal_distance = 5000,
                               dispersal_kernel = exponential_dispersal_kernel(distance_decay = 5000),
                               dispersal_proportion = 0.5),
  modification = NULL,
  density_dependence = ceiling_density(stages = 3))
```

```
egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = list(fire_effects(fire_layers = "fires",
                                                               lag = 5,
                                                               regeneration_function = function (time) {-ti
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results)
```
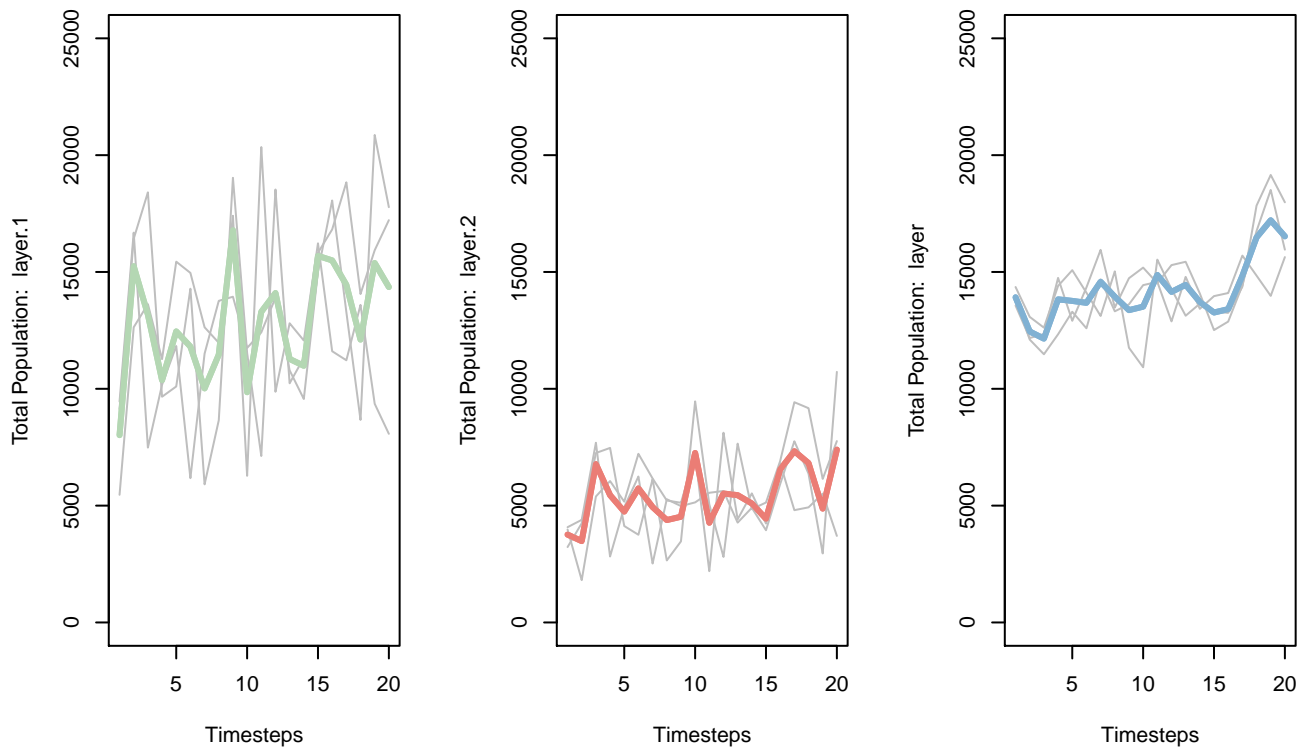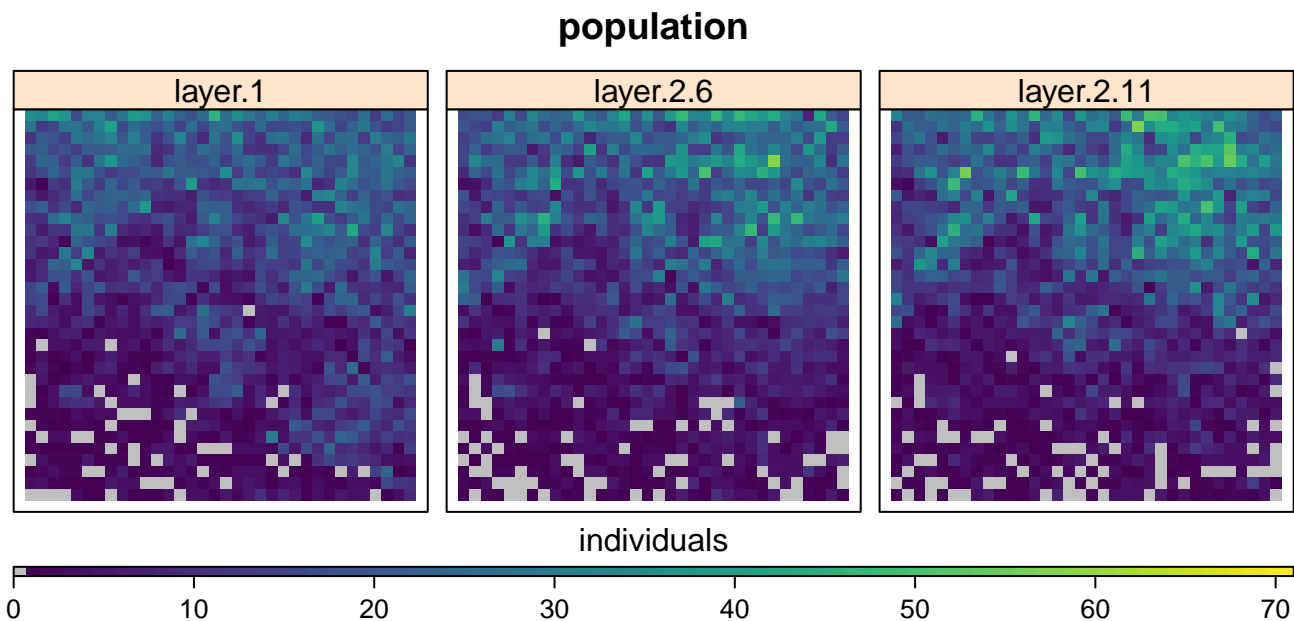

And now let's have a look at how the adult population is changing with fires occurring in the landscape:

```
plot(egk_results[1], type = "raster", stage = 3, timesteps = c(1, 10, 20), panels = c(3, 1))
```

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population

individuals

Since we are using habitat dynamics we may want to have a look at how the habitat suitability changes in a landscape. Similar to carrying capacity - as shown earlier - it is possible to view the habitat suitability throughout a single simulation:

```
plot(egk_results[1], object = "suitability", timesteps = c(1, 10, 20), panels = c(3, 1))
```

habitat
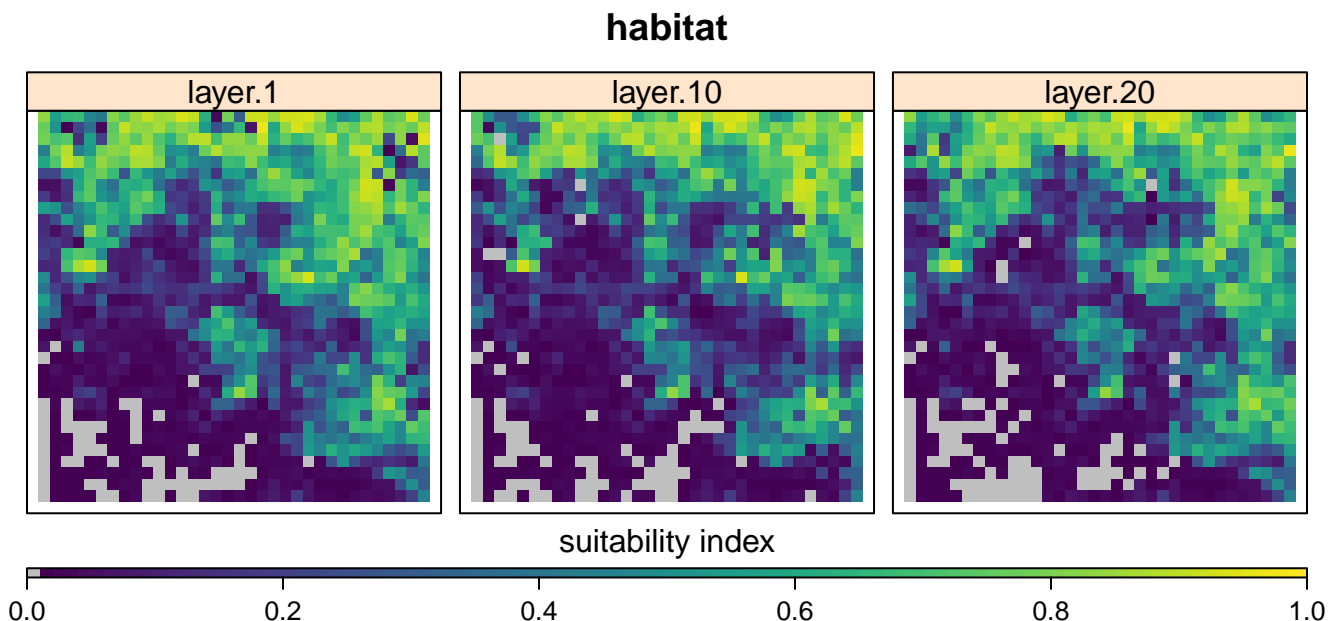
suitability index

In all of the examples above, carrying capacity has remained unchanged throughout a simulation. However, carrying capacity is often derived from dynamically changing habitat suitabilities. A function of this relationship can be specified in place of the carrying_capacity raster layer when constructing the landscape object. Internally, the carrying capacity raster will be constructed by applying the function to the habitat suitability raster at each timestep. Here we have created a function that produces descending integers from our hypothetical maximum carrying capacity population of 75 based on decreasing values of habitat suitability (one to zero):

```
carrying_cap_fun <- function (landscape, timestep) {

  fun <- function(suitability) {
    75 - round(75 * dlogis(suitability, scale = 0.25))
  }
```

```
  suit <- landscape$suitability
  if (raster::nlayers(suit) > 1) {
    suit <- suit[[timestep]]
  }

  calc(suit, fun)

}

egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = carrying_cap_fun,
                           fires = egk_fire)

egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = kernel_dispersal(arrival_probability = "suitability",
                               dispersal_distance = 5000,
                               dispersal_kernel = exponential_dispersal_kernel(distance_decay = 5000),
                               dispersal_proportion = 0.5),
  modification = NULL,
  density_dependence = ceiling_density(stages = 3))

egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = list(fire_effects(fire_layers = "fires",
                                                               lag = 5,
                                                               regeneration_function =
                                                                 function (time) {-time})),
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results[1], object = "carrying_capacity", timesteps = c(1, 10, 20), panels = c(3, 1))
```
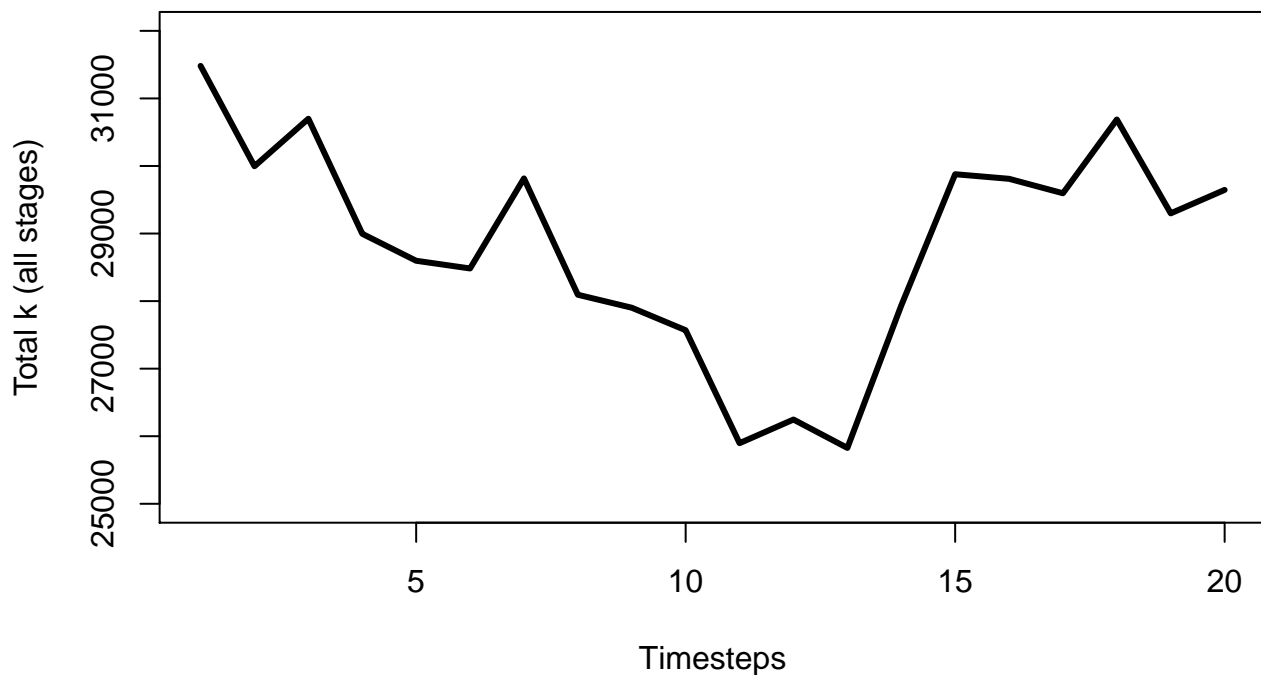
One may specify multiple disturbances affecting the habitat throughout a simulation. To do so, simply add habitat dynamic functions to the list in the simulation function - note, these will be executed in the order that they are listed. To demonstrate this functionality, we have added another disturbance - a road being constructed through the landscape over five years. There is an existing spatial dataset of a road in the steps package ("egk_road") which we store in the landscape object. Since we have already accomodated the movement of the road construction across the landscape, and the vegetation will not regenerate, we specify the effect time as one.

```r
carrying_cap_fun <- function (landscape, timestep) {

  fun <- function(suitability) {
    75 - round(75 * dlogis(suitability, scale = 0.25))
  }

  suit <- landscape$suitability
  if (raster::nlayers(suit) > 1) {
    suit <- suit[[timestep]]
  }

  calc(suit, fun)

}

egk_landscape <- landscape(population = egk_pop,
                           suitability = egk_hab,
                           carrying_capacity = carrying_cap_fun,
                           fires = egk_fire,
                           roads = egk_road)

egk_pop_dynamics <- population_dynamics(
  change = growth(transition_matrix = egk_mat,
                  global_stochasticity = egk_mat_stoch),
  dispersal = kernel_dispersal(arrival_probability = "suitability",
                               dispersal_distance = 5000,
                               dispersal_kernel = exponential_dispersal_kernel(distance_decay = 5000),
                               dispersal_proportion = 0.5),
```
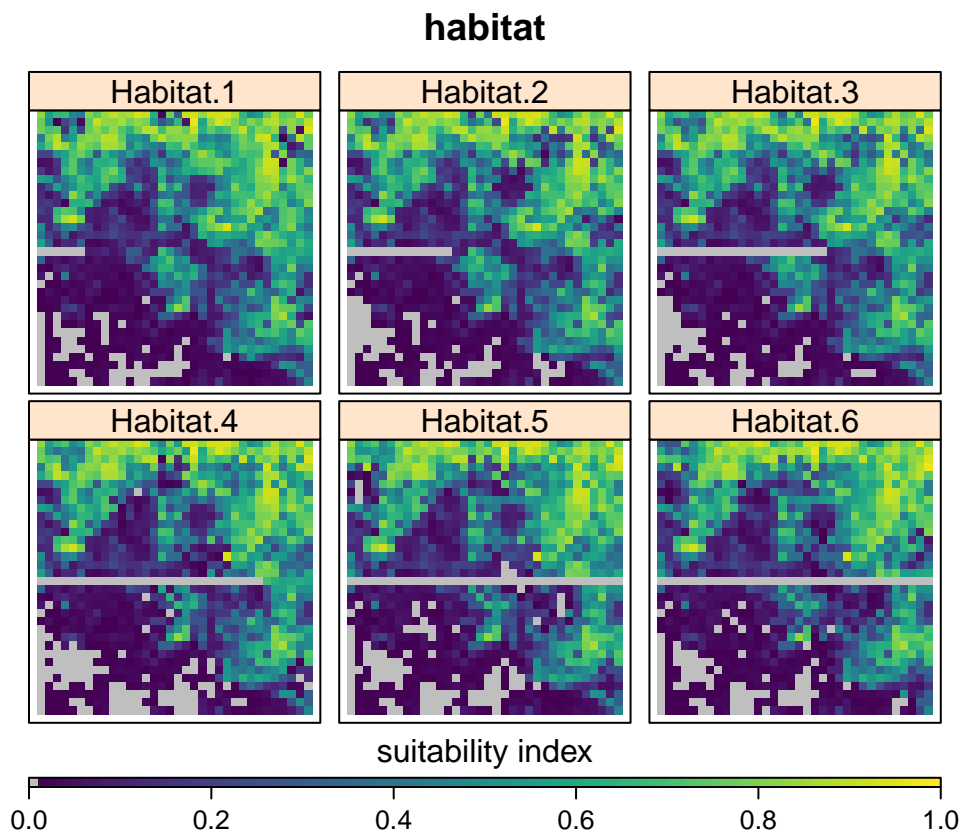
```
  modification = NULL,
  density_dependence = ceiling_density(stages = 3))

egk_results <- simulation(landscape = egk_landscape,
                          population_dynamics = egk_pop_dynamics,
                          habitat_dynamics = list(fire_effects(fire_layers = "fires",
                                                               lag = 5,
                                                               regeneration_function = function (time) {-ti
                                                  disturbance(disturbance_layers = "roads",
                                                              effect_time = 1)),
                          timesteps = 20,
                          replicates = 3,
                          verbose = FALSE)

plot(egk_results[1], object = "suitability", timesteps = c(1:6), panels = c(3, 2))
```

habitat

suitability index

0.0   0.2   0.4   0.6   0.8   1.0

```
plot(egk_results)
```