

1.) Create and edit a parameters file

parameters file:

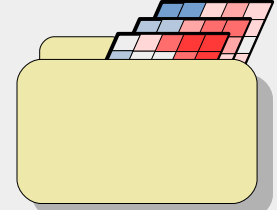
```
parameters:{
  landscape: {
    :
  }
  community: {
    species: {
      :
      genomic_arch: {
        :
      }
    }
  }
  model: {
    :
  }
}
```

Optional: Include paths to raster files and/or directories of environmental-change rasters

raster file:



raster directory:



Optional: include path to a genomic architecture file (.csv)

genomic architecture file:

loc,	p,	dom,	r,	trait,	alpha,
1,	0.5,	0,	0.5,	,	,
1,	0.5,	0,	0.5,	,	,
1,	0.5,	0,	0.01,	0,	0.5,
1,	0.5,	0,	0.01,	1,	0.5,
1,	0.5,	0,	0.01,	2,	0.5,
1,	0.5,	0,	0.5,	,	,
1,	0.5,	0,	0.5,	,	,
:	:	:	:	:	:

2.) Use the parameters file to create a model

Landscape

Characteristics:
- dimensions
- number of layers
- layers' rasters
- environmental change events

Species

Characteristics:
- carrying capacity layer
- life-history parameters
- genomic architecture
- demographic change events

Individual

Characteristics:
- genome
 $\begin{bmatrix} 0,0 \\ 1,0 \\ \vdots \\ 0,1 \end{bmatrix}$
- phenotype

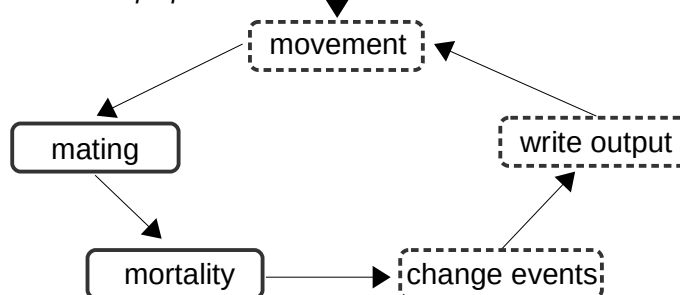
3.) Run the model

Model:

Characteristics:
- number of runs
- timesteps per run
- statistics to calculate
- data to collect

for n runs:

for t timesteps per run:



output directory:

