



```

#####
#### LANDSCAPE ####
#####
'landscape': {

#####
#### main ####
#####
'main': {
    #x,y (a.k.a. j,i) dimensions of the Landscape
    'dim': (50,50),
    #x,y resolution of the Landscape
    'res': (1,1),
    #x,y coords of upper-left corner of the Landscape
    'ulc': (0,0),
    #projection of the Landscape
    'prj': None,
}, # <END> 'main'

#####
#### layers ####
#####
'layers': {

    #layer name (LAYER NAMES MUST BE UNIQUE!)
    'shift': {

#-----#
#--- layer num. 0: init parameters ---#
#-----#

        #initiating parameters for this layer
        'init': {

            #parameters for a 'defined'-type Layer
            'defined': {
                #raster to use for the Layer
                'rast': b4,
                #point coordinates
                'pts': None,
                #point values
                'vals': None,
                #interpolation method {None, 'linear', 'cubic',
                #'nearest'}
                'interp_method': None,

            }, # <END> 'defined'

        }, # <END> 'init'

#-----#
#--- layer num. 0: change parameters ---#
#-----#

        #landscape-change events for this Layer
        'change': {

            0: {
                #array or file for final raster of event, or directory
                #of files for each stepwise change in event
                'change_rast': af,
                #starting timestep of event
                'start_t': change_T,
                #ending timestep of event
                'end_t': T,
                #number of stepwise changes in event
                'n_steps': T-change_T,
            }, # <END> event 0

        }, # <END> 'change'

    }, # <END> layer num. 0

```

```

#layer name (LAYER NAMES MUST BE UNIQUE!)
'stable': {

#-----#
#--- layer num. 1: init parameters ---#
#-----#

#initiating parameters for this layer
'init': {

#parameters for a 'defined'-type Layer
'defined': {
#raster to use for the Layer
'rast': stable,
#point coordinates
'pts': None,
#point values
'vals': None,
#interpolation method {None, 'linear', 'cubic',
#'nearest'}
'interp_method': None,

}, # <END> 'defined'

}, # <END> 'init'

}, # <END> layer num. 1

#layer name (LAYER NAMES MUST BE UNIQUE!)
'K': {

#-----#
#--- layer num. 2: init parameters ---#
#-----#

#initiating parameters for this layer
'init': {

#parameters for a 'defined'-type Layer
'defined': {
#raster to use for the Layer
'rast': K,
#point coordinates
'pts': None,
#point values
'vals': None,
#interpolation method {None, 'linear', 'cubic',
#'nearest'}
'interp_method': None,

}, # <END> 'defined'

}, # <END> 'init'

}, # <END> layer num. 2

#layer name (LAYER NAMES MUST BE UNIQUE!)
'move': {

#-----#
#--- layer num. 2: init parameters ---#
#-----#

#initiating parameters for this layer
'init': {

#parameters for a 'defined'-type Layer
'defined': {
#raster to use for the Layer
'rast': np.ones((50,50)),
#point coordinates
'pts': None,

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        #point values
        'vals':          None,
        #interpolation method {None, 'linear', 'cubic',
        #'nearest'}
        'interp_method':  None,

        }, # <END> 'defined'

    }, # <END> 'init'

}

```

#### NOTE: Individual Layers' sections can be copy-and-pasted (and  
 #### assigned distinct keys and names), to create additional Layers.

```

    } # <END> 'layers'

}, # <END> 'landscape'

```

#####

```

#####
#### COMMUNITY ####
#####

```

```

'comm': {

    'species': {

        #species name (SPECIES NAMES MUST BE UNIQUE!)
        'spp_0': {

            #-----#
            #--- spp num. 0: init parameters ---#
            #-----#

            'init': {
                #starting number of individs
                'N':          1000,
                #carrying-capacity Layer name
                'K_layer':    'K',
                #multiplicative factor for carrying-capacity layer
                'K_factor':   2.5,
                }, # <END> 'init'

            #-----#
            #--- spp num. 0: mating parameters ---#
            #-----#

            'mating' : {
                #age(s) at sexual maturity (if tuple, female first)
                'repro_age':  0,
                #whether to assign sexes
                'sex':        False,
                #ratio of males to females
                'sex_ratio':  1/1,
                #whether P(birth) should be weighted by parental dist
                'dist_weighted_birth': False,
                #intrinsic growth rate
                'R':          0.5,
                #intrinsic birth rate (MUST BE 0<=b<=1)
                'b':          0.5,
                #expectation of distr of n offspring per mating pair
                'n_births_distr_lambda': 1,
                #whether n births should be fixed at n_births_dist_lambda
                'n_births_fixed': True,
                #radius of mate-search area
                'mating_radius': 5,
                #whether individs should choose nearest neighs as mates
                'choose_nearest_mate': False,
                #whether mate-choice should be inverse distance-weighted
                'inverse_dist_mating': False,
            }
        }
    }
}

```

```

    }, # <END> 'mating'

#-----#
#--- spp num. 0: mortality parameters ---#
#-----#

'mortality' : {
  #maximum age
  'max_age': None,
  #min P(death) (MUST BE 0<=d_min<=1)
  'd_min': 0,
  #max P(death) (MUST BE 0<=d_max<=1)
  'd_max': 1,
  #width of window used to estimate local pop density
  'density_grid_window_width': None,
}, # <END> 'mortality'

#-----#
#--- spp num. 0: movement parameters ---#
#-----#

'movement': {
  #whether or not the species is mobile
  'move': True,
  #mode of distr of movement direction
  'direction_distr_mu': 0,
  #concentration of distr of movement direction
  'direction_distr_kappa': 0,
  #mean of distr of movement distance
  'movement_distance_distr_param1': 0.25,
  #variance of distr of movement distance
  'movement_distance_distr_param2': 0.5,
  #movement distance distr to use ('lognormal','levy','wald')
  'movement_distance_distr': 'wald',
  #mean of distr of dispersal distance
  'dispersal_distance_distr_param1': 0.5,
  #variance of distr of dispersal distance
  'dispersal_distance_distr_param2': 0.5,
  #dispersal distance distr to use ('lognormal','levy','wald')
  'dispersal_distance_distr': 'wald',
}, # <END> 'movement'

#-----#
#--- spp num. 0: genomic architecture parameters ---#
#-----#

'gen_arch': {
  #file defining custom genomic arch
  'gen_arch_file': None,
  #num of loci
  'L': 1000,
  #value to use for fixed starting allele freqs (None to draw)
  'start_p_fixed': 0.5,
  #whether to start neutral locus freqs at 0
  'start_neut_zero': True,
  #genome-wide per-base neutral mut rate (0 to disable)
  'mu_neut': 0,
  #genome-wide per-base deleterious mut rate (0 to disable)
  'mu_delet': 0,
  #shape of distr of deleterious effect sizes
  'delet_alpha_distr_shape': 0.2,
  #scale of distr of deleterious effect sizes
  'delet_alpha_distr_scale': 0.2,
  #NOTE: MAIN SCRIPT OVERRIDES THE FOLLOWING TWO PARAMS
  #TO SET RECOMBINATION RATES TO A FIXED VALUE OF
  #0.5, 0.05, OR 0.005 FOR INDEPENDENT,
  #WEAK, OR STRONG LINKAGE VALUES
  #alpha of distr of recomb rates
  'r_distr_alpha': 1000,
  #beta of distr of recomb rates
  'r_distr_beta': 1e3,
  #whether loci should be dominant (for allele '1')
  'dom': False,

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#whether to allow pleiotropy
'pleiotropy': False,
#custom fn for drawing recomb rates
'recomb_rate_custom_fn': None,
#number of recomb paths to hold in memory
'n_recomb_paths_mem': int(1e4),
#total number of recomb paths to simulate
'n_recomb_paths_tot': int(1e5),
#num of crossing-over events (i.e. recombs) to simulate
'n_recomb_sims': 100_000,
#whether to generate recombination paths at each timestep
'allow_ad_hoc_recomb': False,
#whether to save mutation logs
'mut_log': False,
#whether to jitter recomb bps, to correctly track num_trees
'jitter_breakpoints': False,
#whether to use tskit (to record full spatial pedigree)
'use_tskit': True,
#time step interval for simplification of tskit tables
'tskit_simp_interval': 100,

'traits': {

#-----#
#---trait 0 parameters ---#
#-----#
#trait name (TRAIT NAMES MUST BE UNIQUE!)
'trait_0': {
#trait-selection Layer name
'layer': 'shift',
#polygenic selection coefficient
'phi': 1,
#NOTE: MAIN SCRIPT CHANGES NEXT PARAM TO 4, 20, OR 100
#FOR LOW-REDUNDANCY SCENARIOS OF DIFF. POLYGENICITY,
#OR 8, 40, OR 200 FOR HIGH-REDUNDANCY SCENARIOS
#number of loci underlying trait
'n_loci': 50,
#mutation rate at loci underlying trait
'mu': 0,
#mean of distr of effect sizes
'alpha_distr_mu' : 0,
#variance of distr of effect size
'alpha_distr_sigma': 0,
#max allowed magnitude for an alpha value
'max_alpha_mag': None,
#curvature of fitness function
'gamma': 1,
#whether the trait is universally advantageous
'univ_adv': False
}, # <END> trait 0

#-----#
#---trait 1 parameters ---#
#-----#
#trait name (TRAIT NAMES MUST BE UNIQUE!)
'trait_1': {
#trait-selection Layer name
'layer': 'stable',
#polygenic selection coefficient
'phi': 1,
#NOTE: MAIN SCRIPT CHANGES NEXT PARAM TO 4, 20, OR 100
#FOR LOW-REDUNDANCY SCENARIOS OF DIFF. POLYGENICITY,
#OR 8, 40, OR 200 FOR HIGH-REDUNDANCY SCENARIOS
#number of loci underlying trait
'n_loci': 50,
#mutation rate at loci underlying trait
'mu': 0,
#mean of distr of effect sizes
'alpha_distr_mu' : 0,
#variance of distr of effect size
'alpha_distr_sigma': 0,
#max allowed magnitude for an alpha value
'max_alpha_mag': None,
#curvature of fitness function

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```

        'gamma':                1,
        #whether the trait is universally advantageous
        'univ_adv':              False
    }, # <END> trait 1

```

#### NOTE: Individual Traits' sections can be copy-and-pasted (and  
 #### assigned distinct keys and names), to create additional Traits.

```

        }, # <END> 'traits'

    }, # <END> 'gen_arch'

}, # <END> spp num. 0

```

#### NOTE: individual Species' sections can be copy-and-pasted (and  
 #### assigned distinct keys and names), to create additional Species.

```

    }, # <END> 'species'

}, # <END> 'comm'

```

#####

```

#####
#### MODEL ####
#####

```

```

'model': {
    # NOTE: NEXT PARAM OVERRIDDEN BY MAIN SCRIPT
    #total Model runtime (in timesteps)
    'T':                100000,
    #min burn-in runtime (in timesteps)
    'burn_T':           30,
    #seed number
    'num':               None,

```

```

#####
#### iterations parameters ####
#####
'its': {
    #num iterations
    'n_its':            1,
    #whether to randomize Landscape each iteration
    'rand_landscape':   False,
    #whether to randomize Community each iteration
    'rand_comm':        False,
    #whether to randomize GenomicArchitectures each iteration
    'rand_genarch':     True,
    #whether to burn in each iteration
    'repeat_burn':      False,
    }, # <END> 'iterations'

```

```

#####
#### data-collection parameters ####
#####
'data': {
    'sampling': {
        #sampling scheme {'all', 'random', 'point', 'transect'}
        'scheme':        'all',
        #sample size at each point, for point & transect sampling
        'n':              1000,
        #coords of collection points, for point sampling
        'points':         None,
        #coords of transect endpoints, for transect sampling
        'transect_endpoints': None,
        #num points along transect, for transect sampling
        'n_transect_points': None,
    }

```

```

#collection radius around points, for point & transect sampling
'radius':          None,
#when to collect data
'when':            [change_T-1,
                    int((change_T-1+T-1)/2),
                    T-1],
#whether to save current Layers when data is collected
'include_landscape': False,
#whether to include fixed loci in VCF files
'include_fixed_sites': True,
},
'format': {
  #format for genetic data {'vcf', 'fasta'}
  'gen_format':      ['vcf'],
  #format for vector geodata {'csv', 'shapefile', 'geojson'}
  'geo_vect_format': 'csv',
  #format for raster geodata {'geotiff', 'txt'}
  'geo_rast_format': 'geotiff',
  #format for files containing non-neutral loci
  'nonneut_loc_format': 'csv',
},
}, #<END> 'data'

} # <END> 'model'

} # <END> params

```