# Optimizing sampling design for landscape genomics: Geonomics parameters

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# This is a parameters file generated by Geonomics

# (by the gnx.make\_parameters\_file() function).

# parameters with levels specified in [brackets] are varied in the simulations

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# GGGGG :EEEE: OOOOO NN NN OOOOO MM MM IIIIII CCCCC SSSSS #

# GG EE OO OO NNN NN OO OO MM MM II CC SS #

# GG EE OO OO NN N NN OO OO MMM MMM II CC SSSSSS #

# GG GGG EEEE OO OO NN NNN OO OO MM M MM II CC SS #

# GG G EE OO OO NN NN OO OO MM MM II CC SSS #

# GGGGG :EEEE: OOOOO NN NN OOOOO MM MM IIIIII CCCCC SSSSS #

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params = {

# --------------------------------------------------------------------------#

# -----------------#

# --- LANDSCAPE ---#

# -----------------#

'landscape': {

# ------------#

# --- main ---#

# ------------#

'main': {

# x,y (a.k.a. j,i) dimensions of the Landscape

'dim': (100, 100),

# 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!)

'lyr\_0': {

# -------------------------------------#

# --- 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': [UNIFORM ENVIRONMENTAL LAYER],

# point coordinates

'pts': None,

# point values

'vals': None,

# interpolation method {None, 'linear', 'cubic',

# 'nearest'}

'interp\_method': None,

}, # <END> 'defined'

}, # <END> 'init'

}, # <END> layer num. 0

# layer name (LAYER NAMES MUST BE UNIQUE!)

'lyr\_1': {

# -------------------------------------#

# --- 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': [NLM LAYER],

# 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!)

'lyr\_2': {

# -------------------------------------#

# --- 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': [NLM LAYER],

# 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

#### 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': 10000,

# carrying-capacity Layer name

'K\_layer': 'lyr\_0',

# multiplicative factor for carrying-capacity layer

'K\_factor': [VARIED TO CONTROL POPULATION SIZE],

}, # <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': 1,

# intrinsic birth rate (MUST BE 0<=b<=1)

'b': 0.8,

# expectation of distr of n offspring per mating pair

'n\_births\_distr\_lambda': 2,

# whether n births should be fixed at n\_births\_dist\_lambda

'n\_births\_fixed': True,

# ADDED BY AB: choose nearest mate

'choose\_nearest\_mate': False,

# ADDED BY AB: choose nearest mate

'inverse\_dist\_mating': False,

# radius of mate-search area

'mating\_radius': 2,

}, # <END> 'mating'

# ----------------------------------------#

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

# ----------------------------------------#

'mortality': {

# maximum age

'max\_age': 3,

# 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': 1,

# concentration of distr of movement direction

'direction\_distr\_kappa': 0,

# 1st param of distr of movement distance

'movement\_distance\_distr\_param1': 0,

# 2nd param of distr of movement distance

'movement\_distance\_distr\_param2': [VARIED TO CONTROL MIGRATION],

# movement distance distr to use

'movement\_distance\_distr': 'lognormal',

# 1st param of distr of dispersal distance

'dispersal\_distance\_distr\_param1': 0,

# 2nd param of distr of dispersal distance

'dispersal\_distance\_distr\_param2': [VARIED TO CONTROL MIGRATION],

# dispersal distance distr to use

'dispersal\_distance\_distr': 'lognormal',

'move\_surf': {

# move-surf Layer name

'layer': 'lyr\_0',

# whether to use mixture distrs

'mixture': True,

# concentration of distrs

'vm\_distr\_kappa': 12,

# length of approximation vectors for distrs

'approx\_len': 5000,

}, # <END> 'move\_surf'

}, # <END> 'movement'

# ---------------------------------------------------#

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

# ---------------------------------------------------#

'gen\_arch': {

# whether to use tskit (to record full spatial pedigree)

'use\_tskit': False,

# time step interval for simplication of tskit tables

'tskit\_simp\_interval': 25, # changed from 100

# whether to jitter recomb bps, only needed to correctly track num\_trees

'jitter\_breakpoints': False,

# file defining custom genomic arch

# found here /p1\_gnxsims/gnx/

'gen\_arch\_file': "genomic\_architecture.csv",

# num of loci

'L': 10000,

# num of chromosomes (doesn't matter when there is no linkage)

'l\_c': [1],

# starting allele frequency (None to draw freqs randomly)

'start\_p\_fixed': 0.5,

# whether to start neutral locus freqs at 0

'start\_neut\_zero': False,

# 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,

# alpha of distr of recomb rates (default = 0.5 = unlinked)

'r\_distr\_alpha': 0.5,

# beta of distr of recomb rates

'r\_distr\_beta': None,

# whether loci should be dominant (for allele '1')

'dom': False,

# 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': 10000,

# whether to generate recombination paths at each timestep

'allow\_ad\_hoc\_recomb': False,

# whether to save mutation logs

'mut\_log': False,

'traits': {

# --------------------------#

# --- trait 1 parameters ---#

# --------------------------#

# trait name (TRAIT NAMES MUST BE UNIQUE!)

'trait\_1': {

# trait-selection Layer name

'layer': 'lyr\_1',

# polygenic selection coefficient

'phi': [VARIED TO CONTROL SELECTION STRENGTH],

# number of loci underlying trait

'n\_loci': 4,

# mutation rate at loci underlying trait

'mu': 0,

# mean of distr of effect sizes

'alpha\_distr\_mu': 0.25,

# 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 1

# --------------------------#

# --- trait 2 parameters ---#

# --------------------------#

# trait name (TRAIT NAMES MUST BE UNIQUE!)

'trait\_2': {

# trait-selection Layer name

'layer': 'lyr\_2',

# polygenic selection coefficient

'phi': [VARIED TO CONTROL SELECTION STRENGTH],

# number of loci underlying trait

'n\_loci': 4,

# mutation rate at loci underlying trait

'mu': 0,

# mean of distr of effect sizes

'alpha\_distr\_mu': 0.25,

# 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 2

#### 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': {

# total Model runtime (in timesteps)

'T': 1001,

# min burn-in runtime (in timesteps)

'burn\_T': 100,

# seed number

'num': 42,

# -----------------------------#

# --- iterations parameters ---#

# -----------------------------#

'its': {

# num iterations

'n\_its': 10,

# whether to randomize Landscape each iteration

'rand\_landscape': False,

# whether to randomize Community each iteration

'rand\_comm': False,

# whether to burn in each iteration

'repeat\_burn': False,

#whether to randomize GenomicArchitectures each iteration

'rand\_genarch': True,

}, # <END> 'iterations'

# -----------------------------------#

# --- data-collection parameters ---#

# -----------------------------------#

'data': {

'sampling': {

# sampling scheme {'all', 'random', 'point', 'transect'}

'scheme': 'all',

# when to collect data

'when': 1000,

# 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'

# -----------------------------------#

# --- stats-collection parameters ---#

# -----------------------------------#

'stats': {

# number of individs at time t

'Nt': {

# whether to calculate

'calc': True,

# calculation frequency (in timesteps)

'freq': 1,

},

# heterozgosity

'het': {

# whether to calculate

'calc': True,

# calculation frequency (in timesteps)

'freq': 10,

# whether to mean across sampled individs

'mean': False,

},

# minor allele freq

'maf': {

# whether to calculate

'calc': True,

# calculation frequency (in timesteps)

'freq': 10,

},

# mean fitness

'mean\_fit': {

# whether to calculate

'calc': True,

# calculation frequency (in timesteps)

'freq': 10,

},

# linkage disequilibirum

'ld': {

# whether to calculate

'calc': False,

# calculation frequency (in timesteps)

'freq': 100,

},

}, # <END> 'stats'

} # <END> 'model'

} # <END> params