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SI_Simupop.py
# 2 loci model of SA variation with selection, epistasis and recombination
# Written by Göran Arnqvist / Nikolas Vellnow

import simuOpt, os, sys, types, time, random
import simuPOP as sim

# note stating time of script run
start_time = time.time()

# Clear previous textfile
fileHandle = open ( 'epi.txt', 'w' )
# Write header for output
fileHandle.write ( 'r\t' + 'h_m\t' + 'h_f\t' + 's_m\t' + 's_f\t' + 'E_m\t' + 'E_f\t'
)
fileHandle.close()

runNum=0
# Make loop to repeat simulation a certain number of times set by (0,max)
for i in range (0,3000):
    popSize=5000
    replications=1
    p1=random.uniform(0.05, 0.95)
    p2=random.uniform(0.05, 0.95)
    s_m=random.uniform(0.0, 0.3)
    s_f=random.uniform(0.0, 0.3)
    h_m=0.5
    h_f=0.5
    c=-0.167
    E_m=c*s_m
    E_f=c*s_f
    r=0.05
    generations=5000
    runNum=runNum+1
    print 'Run number: ' + str(runNum)

    # Go to the next row in the output file
    fileHandle = open ( 'epi.txt', 'a' )
    fileHandle.write ( '\n' )
    selection_m=str(s_m)
    selection_f=str(s_f)
    hetero_m=str(h_m)
    hetero_f=str(h_f)
    epi_m=str(E_m)
    epi_f=str(E_f)
    rec=str(r)
    fileHandle.write ( rec + '\t' + hetero_m + '\t' + hetero_f + '\t' + selection_m
+ '\t' + selection_f + '\t' + epi_m + '\t' + epi_f + '\t' )
    fileHandle.close()

    pop = sim.Population(size=popSize, loci=2, infoFields='fitness')
    pop.setVirtualSplitter(sim.SexSplitter())
    simu=sim.Simulator(pop, rep=replications)

    simu.evolve(
        initOps=[
            sim.InitSex(),
            sim.InitGenotype(loci=0, freq=[p1, 1-p1]),
            sim.InitGenotype(loci=1, freq=[p2, 1-p2])
        ],
        #before mating selection among parents - males and females (in essence
relative fitness)
        preOps=[
            sim.MaSelector(loci=[0,1], fitness=[1, 1-(h_m*s_m), 1-s_m, 1-(h_m*s_m),
((1-(h_m*s_m))*(1-(h_m*s_m)))+E_m, ((1-(h_m*s_m))*(1-s_m))+(2*E_m), 1-s_m,

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((1-s_m)*(1-(h_m*s_m)))+(2*E_m), ((1-s_m)*(1-s_m))+(4*E_m)],
subPops=[[0, 0]],
sim.MaSelector(loci=[0,1], fitness=[((1-s_f)*(1-s_f))+(4*E_f),
((1-s_f)*(1-(h_f*s_f)))+(2*E_f), 1-s_f, ((1-(h_f*s_f))*(1-s_f))+(2*E_f),
((1-(h_f*s_f))*(1-(h_f*s_f)))+E_f, 1-(h_f*s_f), 1-s_f, 1-(h_f*s_f), 1],
subPops=[[0, 1]]],
matingScheme=sim.RandomMating(ops=[
sim.Recombinator(rates=r),
]),
),
postOps=[
sim.Stat(alleleFreq=0, step=generations-1),
sim.PyEval(r"'%.3f\t' % alleleFreq[0][0]", begin=generations-1,
output='>>>epi.txt'),
sim.PyEval(r"'%.3f\t' % alleleFreq[0][1]", begin=generations-1,
output='>>>epi.txt'),
sim.Stat(alleleFreq=1, step=generations-1),
sim.PyEval(r"'%.3f\t' % alleleFreq[1][0]", begin=generations-1,
output='>>>epi.txt'),
sim.PyEval(r"'%.3f\t' % alleleFreq[1][1]", begin=generations-1,
output='>>>epi.txt'),
],
gen = generations
)

elapsed_time = time.time() - start_time
elapsed_time = elapsed_time / 60
print 'Elapsed time: ' + str(elapsed_time) + ' mins'

print "done"

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