

Notes on facultative parthenogenesis metapopulation model started 21-July 2024

29-July 2024 note: Alleles promoting parthenogenesis in this model will be neutral unless there is a pleiotropic penalty. This can be a viability or fertility penalty. Here, will try the fertility penalty.

Use will enter number between 0 and 1 which represents the % fertility penalty for parthenogenetically reproducing females.

Locus 3 will be converted to a neutral allele and Locus 2 will be the locus controlling parthenogenesis. If parthenogenesis is affected by natural selection, its allele frequency should behave significantly differently from an otherwise identical, independently evolving, neutral locus.

Individual based Monte Carlo simulation

Diploid model with 3 loci (can vary linkage)

Only Gamete Duplication mode of parthenogenesis is able to be easily simulated:

Gamete Duplication (diploid embryo forms by duplication of a single gamete followed by cell fusion)

Sister Meiotic Cell Fusion (two daughter haploid cells from the same meiosis fuse) involves four different possible tetrad types: non-recombinant, single crossover in first interval, single crossover in second interval, double recombinant

Within each tetrad types there are 6 possible fusions: (12, 13, 14, 23, 24, 34)

Locus 1 – fitness; has two alleles 1 and 0

Two options (user chooses):

(1) Large value dominant

Genotypes 11 and 10 survive; genotype 00 dies

Initial genotype 11 over entire metapopulation

(2) Fitness overdominance

Genotype 10 survives; genotypes 11 and 00 die

Initial genotype 10 over entire metapopulation

Locus 2 – parthenogenetic abilities

Additive

$(\text{Sum of alleles})/2$ represents probability of parthenogenetic reproduction in the event of no males encountered

Initial value 0.0 across entire metapopulation. Maximum allele value 0.5.

If a female has mated with no males, then if $\text{RNG}(0.1)$ is less than the sum of alleles at this locus, the female will produce parthenogenetic offspring.

Locus 3 – neutral locus with same allelic value range and mutational rules as Locus 2 – internal negative control for detecting natural selection on Locus 2

Metapopulation structure

PopSize individuals in main population

SubPopSize individuals in subpopulation (initial value 0)

Generational procedure

1. Encounter phase – each individual encounters C individuals in their environment (main pop or sub pop)
2. Reproductive phase
 - a. If female has encountered ≥ 1 male; N sexual offspring are produced
 - b. If female has not encountered any males AND if $\text{RNG}(0,1) < (\text{Locus 2 determined phenotype})$ AND $\text{RNG}(0,1) < (\text{Locus 3 determined phenotype})$ then MaxRepro parthenogenetic offspring are produced
3. Mutation phase – each allele in population has MutRate probability of mutating to a different value (0,1)
4. Migration and maturation phase – For every offspring produced, the program will determine whether individuals stay where they are produced or move. Then a new generation of adults is drawn for both the main population and subpopulation, based on the pop sizes of those two populations. The number of offspring in the subpopulation will have to be counted to determine how many subpopulation adults will need to be drawn. In early generations, the number of offspring produced in the subpopulation will likely be less than the maximum.

Determine:

Are non-zero values of Loci 2 and 3 able to invade metapopulation?

If so, what are the equilibrium allele frequencies at Loci 2 and 3?

Under what conditions wrt fitness locus and metapopulation structure is parthenogenesis able to invade?

Collect from user at beginning of run:

PopSize = total number of individuals in metapopulation

There is a large main population and a small subpopulation
MaxSubSize = maximum number of individuals in subpopulation
MaxRepro = maximum number of offspring per female
Migration = migration rate
Mutation = mutation rate
Rec1 = recombination rate between Locus 1 and Locus 2
Rec2 = recombination rate between Locus 2 and Locus 3
NumInds = number of individuals each female encounters prior to mating
NumGens = number of generations in the run

Keep track of for every individual
Sex = sex of individual (each newly produced individual is 50% male/female based on RNG); 0=male, 1=female
Location = 0 in main population, 1 in subpopulation
Loc1Allele1
Loc1Allele2
Loc2Allele1
Loc2Allele2
Loc3Allele1
Loc1Allele2
Number of offspring produced (important for females)
Subarray of all info on NumInds individuals the focal individual has encountered prior to mating

A further implementation of this model should test the prediction that lethal mutations should be purged out of a subpopulation with a high mean parthenogenetic capability. This could be tested with the current dominance mutational mode, but it might be more efficient to start the frequency of the 0 mutation at something like 0.25 and watch it go down. Locus 2 could also be started at a mean of 0.5. The prediction should be that if the number of individuals encountered subpopulation is low enough, mean parthenogenetic capability should go up while the lethal allele frequency in the subpopulation should go down and equilibrate at a level lower than the level in the main population (given a small enough subpopulation and a low enough migration rate)

Code:

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100 rem Facultative Parthenogenesis Metapopulation model v1

200 rem get run parameters from user
300 ? "enter size of metapopulation"
400 input PopSize
401 rem PopSize=100
500 ? "enter maximum size of subpopulation"
600 input MaxSubSize
601 rem MaxSubSize=50
700 ? "enter reciprocal of migration rate [enter 0 for no migration; i.e. no subpopulation]"
800 input migRecip
801 rem migRecip=1000
810 if migRecip = 0 then migration = 0 else migration = 1/migrecip
900 Migration = 1/migRecip
1000 ? "enter reciprocal of mutation rate"
1100 input mutRecip
1101 rem mutRecip=1000
1200 Mutation = 1/mutRecip
1300 rem ? "enter recombination rate between Locus 1 and Locus 2"
1400 rem input Rec1
1401 Rec1=0.5
1500 rem ? "enter recombination rate between Locus 2 and Locus 3"
1600 rem input Rec2
1601 Rec2=0.5
1700 ? "enter number of individuals encountered in main population"
1800 input NumInds
1801 rem NumInds=4
1802 ? "enter number of individuals encountered in sub population"
1803 input NumIndsSub
1810 ? "enter number of offspring per female"
1820 input MaxRepro
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1821 rem MaxRepro=10
1830 ? "choose fitness dominance [1] or fitness overdominance [2]"
1840 input f
1841 rem f=1
1850 if f=1 then OverDom=0 else OverDom=1
1900 ? "enter number of generations in the run"
2000 input NumGens
2001 rem NumGens=5
2100 ? "enter name of output file"
2200 input Outfile$
2201 rem Outfile$="outfile"
2210 rem ? "enter random seed"
2220 rem input RandomSeed
2230 RandomSeed=rnd(5000)
2260 randomize RandomSeed

2270 ? "enter % reproduction of Parthenogenesis vs. sexual reproduction"
2280 input ParthReduction
2290 ParthRepro=int(ParthReduction*MaxRepro+0.5)
2300 ? "Sexual reproduction produces ";MaxRepro; " offspring. Parthenogenetic reproduction produces ";ParthRepro; " offspring."
2310 ? "Enter % reproduction for parthenogenetic-capable females reproducing sexually"
2320 input x
2325 ParthPenalty=1-x
2330 ? "Hit any key followed by <return> to continue"
2380 input continue
2390 rem dimensioning
2400 dim Sex(PopSize*2)
2500 dim Location(PopSize)
2600 dim Loc1Allele1(PopSize)
2700 dim Loc1Allele2(PopSize)
2800 dim Loc2Allele1(PopSize)
2900 dim Loc2Allele2(PopSize)
3000 dim Loc3Allele1(PopSize)

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3100 dim Loc3Allele2(PopSize)
3200 dim OffspringAlive(MaxRepro*PopSize)
3400 dim OffspringSex(MaxRepro*PopSize)
3500 dim OffspringLocation(MaxRepro*PopSize)
3600 dim OffspringLoc1Allele1(MaxRepro*PopSize)
3700 dim OffspringLoc1Allele2(MaxRepro*PopSize)
3800 dim OffspringLoc2Allele1(MaxRepro*PopSize)
3900 dim OffspringLoc2Allele2(MaxRepro*PopSize)
4000 dim OffspringLoc3Allele1(MaxRepro*PopSize)
4100 dim OffspringLoc3Allele2(MaxRepro*PopSize)
4200 dim PopInds(PopSize)
4300 dim SubInds(PopSize)
4400 dim Meeting(PopSize,NumInds)
4500 dim SexMothers(PopSize)
4600 dim SexFathers(PopSize)
4700 dim ParthMothers(PopSize)
4710 dim score(MaxRepro*PopSize)
4720 dim OriginalIndex(MaxRepro*PopSize)

4730 dim NewOffspringAlive(MaxRepro*PopSize)
4740 dim NewOffspringSex(MaxRepro*PopSize)
4750 dim NewOffspringLocation(MaxRepro*PopSize)
4760 dim NewOffspringLoc1Allele1(MaxRepro*PopSize)
4770 dim NewOffspringLoc1Allele2(MaxRepro*PopSize)
4780 dim NewOffspringLoc2Allele1(MaxRepro*PopSize)
4790 dim NewOffspringLoc2Allele2(MaxRepro*PopSize)
4800 dim NewOffspringLoc3Allele1(MaxRepro*PopSize)
4810 dim NewOffspringLoc3Allele2(MaxRepro*PopSize)
4815 dim Loc1Freq(2*numGens)
4820 dim Loc2Freq(2*numGens)
4830 dim Loc3Freq(2*numGens)
4840 dim MainPopCount(2*numGens)
4850 dim SubPopCount(2*numGens)

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4860 dim SexualOffspring(2*numGens)
4870 dim ParthOffspring(2*numGens)
4880 dim Sexuals(2*numGens)
4890 dim Parths(2*numGens)
4895 dim ParthMode(2*numGens)
4896 dim frequency(2*PopSize)
4897 dim ModeFreq(2*numGens)

4900 rem keep track of the maximum value of locus 2 allele that has appeared
4910 MaxParth=0

5000 rem set initial arrays
5100 for a = 1 to PopSize
5200 aa=rnd(1)
5300 if aa<0.5 then Sex(a)=1 else Sex(a)=0
5400 Location(a)=0
5500 Loc1Allele1(a)=1
5600 if OverDom=1 then Loc1Allele2(a)=0 else Loc1Allele2(a)=1
5700 Loc2Allele1(a)=0
5800 Loc2Allele2(a)=0
5900 Loc3Allele1(a)=0
6000 Loc3Allele2(a)=0
6100 next a

6200 rem start main loop

6300 for main = 1 to NumGens

6400 rem mutation phase
6500 for a = 1 to PopSize
6600 rem locus 1 allele 1
6700 z=rnd(1)
6800 if z< Mutation then loc1Allele1(a)=abs(loc1Allele1(a)-1)

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6900 rem locus 1 allele 2
7000 z=rnd(1)
7100 if z<Mutation then loc1Allele2(a)=abs(loc1Allele2(a)-1)
7200 rem locus 2 allele 1
7300 z=rnd(1)
7400 if z<Mutation then loc2Allele1(a)=rnd(1)/2
7410 if loc2Allele1(a)>MaxParth then MaxParth=loc2Allele1(a)
7500 rem locus 2 allele 2
7600 z=rnd(1)
7700 if z<Mutation then loc2Allele2(a)=rnd(1)/2
7710 if loc2Allele2(a)>MaxParth then MaxParth=loc2Allele2(a)
7800 rem locus 3 allele 1
7900 z=rnd(1)
8000 if z<Mutation then loc3Allele1(a)=rnd(1)/2
8100 rem locus 3 allele 2
8200 if z<Mutation then loc3Allele2(a)=rnd(1)/2
8300 next a

10000 rem encounter phase
10010 rem each individual encounters NumInds or NumIndsSub individuals depending on its environment
10020 rem for programming simplicity, self-encounters and duplicate encounters count (bad luck)
10030 rem values of the Meeting variable are the subscripts of the encountered individual
10100 for a = 1 to PopSize
10150 if Location(a)=0 then x=NumInds else x=NumIndsSub
10200 for b = 1 to x
10300 zz=rnd(PopSize+1)
10500 if Location(a)=Location(zz) then goto 10600 else goto 10300
10600 Meeting(a,b)=zz
10700 next b
10800 next a

11000 rem encounters check
11100 rem for a = 1 to PopSize

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11200 rem if Sex(a)=1 then goto 11300 else goto 11800
11300 rem ? "female ";a; "meets ";
11400 rem for b = 1 to NumInds
11500 rem if Sex(Meeting(a,b))=1 then ? "female ";Meeting(a,b);" ";
11600 rem if Sex(Meeting(a,b))=0 then ? "male ";Meeting(a,b);" ";
11700 rem next b
11750 rem ?
11800 rem next a

13900 SexualMatingsCount=1
13950 ParthMatingsCount=0

14000 rem find male that each female mates with
14050 rem for computational simplicity, each female will mate with the last male she encountered
14100 for a = 1 to PopSize-1
14110 MatingFlag=0
14150 if Sex(a)=1 then goto 14200 else goto 15100
14200 rem focal individual is female
14250 for b = 1 to NumInds
14400 if Sex(Meeting(a,b))=0 then
14450   MatingFlag=1
14500   SexMothers(SexualMatingsCount)=a
14600   SexFathers(SexualMatingsCount)=Meeting(a,b)
14650 end if
15000 next b
15010 if MatingFlag=1 then goto 15070 else goto 15050
15050 ParthMatingsCount=ParthMatingsCount+1
15060 ParthMothers(ParthMatingsCount)=a
15065 goto 15100
15070 SexualMatingsCount=SexualMatingsCount+1
15100 next a

15110 rem record number of sexual and parthenogenetic reproducing females this generation

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15120 Sexuals(main)=SexualMatingsCount-1

15130 Parths(main)=ParthMatingsCount

15200 rem check matings

15300 rem for a = 1 to SexualMatingsCount-1

15400 rem ? "female ";SexMothers(a); " mates with male ";SexFathers(a)

15500 rem next a

15600 rem for a = 1 to ParthMatingsCount

15700 rem ? "female ";ParthMothers(a); " attempts parthenogenesis"

15800 rem next a

16000 rem reproduction phase

16100 rem sexual reproduction

16200 OffspringCount=0

16300 for a = 1 to SexualMatingsCount-1

16400 if Loc2Allele1(SexMothers(a))+Loc2Allele2(SexMothers(a))=0 then max=MaxRepro else max=int(MaxRepro*(1-ParthPenalty)+.5)

16410 for b=1 to max

16450 OffspringCount=OffspringCount+1

16500 rem determine maternal haplotype

16600 x = rnd(2)

16700 y = rnd(1)

16800 z = rnd(1)

16900 if x=0 and y>Rec1 and z>Rec2 then mhaplotype =1

17000 if x=0 and y>Rec1 and z<Rec2 then mhaplotype =2

17100 if x=0 and y<Rec1 and z>Rec2 then mhaplotype =3

17200 if x=0 and y<Rec1 and z<Rec2 then mhaplotype =4

17300 if x=1 and y>Rec1 and z>Rec2 then mhaplotype =5

17400 if x=1 and y>Rec1 and z<Rec2 then mhaplotype =6

17500 if x=1 and y<Rec1 and z>Rec2 then mhaplotype =7

17600 if x=1 and y<Rec1 and z<Rec2 then mhaplotype =8

17700 if mhaplotype =1 then

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17710  OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(SexMothers(a))
17720  OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(SexMothers(a))
17730  OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(SexMothers(a))
17740  end if
18000  if mhaplotype =2 then
18010   OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(SexMothers(a))
18020   OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(SexMothers(a))
18030   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(SexMothers(a))
18040  end if
18300  if mhaplotype =3 then
18310   OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(SexMothers(a))
18320   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(SexMothers(a))
18330   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(SexMothers(a))
18340  end if
18600  if mhaplotype =4 then
18610   OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(SexMothers(a))
18620   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(SexMothers(a))
18630   OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(SexMothers(a))
18640  end if
18900  if mhaplotype =5 then
18910   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(SexMothers(a))
18920   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(SexMothers(a))
18930   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(SexMothers(a))
18940  end if
19200  if mhaplotype =6 then
19210   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(SexMothers(a))
19220   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(SexMothers(a))
19230   OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(SexMothers(a))
19240  end if
19500  if mhaplotype =7 then
19510   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(SexMothers(a))
19520   OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(SexMothers(a))
19530   OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(SexMothers(a))
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19540 end if
19800 if mhaplotype =8 then
19810   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(SexMothers(a))
19820   OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(SexMothers(a))
19830   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(SexMothers(a))
19840 end if
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20100 rem determine paternal haplotype
20200 x = rnd(2)
20300 y = rnd(1)
20400 z = rnd(1)
20500 if x=0 and y>Rec1 and z>Rec2 then phaplotype=1
20600 if x=0 and y>Rec1 and z<Rec2 then phaplotype =2
20700 if x=0 and y<Rec1 and z>Rec2 then phaplotype =3
20800 if x=0 and y<Rec1 and z<Rec2 then phaplotype =4
20900 if x=1 and y>Rec1 and z>Rec2 then phaplotype =5
21000 if x=1 and y>Rec1 and z<Rec2 then phaplotype =6
21100 if x=1 and y<Rec1 and z>Rec2 then phaplotype =7
21200 if x=1 and y<Rec1 and z<Rec2 then phaplotype =8
21300 if phaplotype =1 then
21310   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(SexFathers(a))
21320   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(SexFathers(a))
21330   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(SexFathers(a))
21340 end if
21600 if phaplotype =2 then
21610   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(SexFathers(a))
21620   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(SexFathers(a))
21630   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(SexFathers(a))
21640 end if
21900 if phaplotype =3 then
21910   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(SexFathers(a))
21920   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(SexFathers(a))
21930   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(SexFathers(a))
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21940 end if
22200 if phaploptype =4 then
22210   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(SexFathers(a))
22220   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(SexFathers(a))
22230   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(SexFathers(a))
22240 end if
22500 if phaploptype =5 then
22510   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(SexFathers(a))
22520   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(SexFathers(a))
22530   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(SexFathers(a))
22540 end if
22800 if phaploptype =6 then
22810   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(SexFathers(a))
22820   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(SexFathers(a))
22830   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(SexFathers(a))
22840 end if
23100 if phaploptype =7 then
23110   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(SexFathers(a))
23120   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(SexFathers(a))
23130   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(SexFathers(a))
23140 end if
23400 if phaploptype =8 then
23410   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(SexFathers(a))
23420   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(SexFathers(a))
23430   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(SexFathers(a))
23440 end if

23700 rem set other offspring parameters
23800 OffspringAlive(OffspringCount)=1
23900 zz=rnd(1)
24000 if zz<0.5 then OffspringSex(OffspringCount)=1 else OffspringSex(OffspringCount)=0
24100 if Location(SexMothers(a))=1 then OffspringLocation(OffspringCount)=1 else OffspringLocation(OffspringCount)=0
24200 next b

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24300 next a

24350 rem save current OffspringCount number as the number of offspring produced by sexual reproduction this generation

24360 SexualOffspring(main)=OffspringCount

24400 rem parthenogenic reproduction

24500 rem produce parthogenetic offspring by gamete cell duplication

24510 for a = 1 to ParthMatingsCount

24600 zz=rnd(1)

24700 if zz<(Loc2Allele1(ParthMothers(a))+Loc2Allele2(ParthMothers(a))) then goto 25000 else goto 31900

25000 rem female will reproduce parthenogenetic offspring

25100 for b = 1 to ParthRepro

25150 OffspringCount=OffspringCount+1

25200 rem determine maternal haplotype

25300 x = rnd(2)

25400 y = rnd(1)

25500 z = rnd(1)

25600 if x=0 and y>Rec1 and z>Rec2 then mhaplotype=1

25700 if x=0 and y>Rec1 and z<Rec2 then mhaplotype =2

25800 if x=0 and y<Rec1 and z>Rec2 then mhaplotype =3

25900 if x=0 and y<Rec1 and z<Rec2 then mhaplotype =4

26000 if x=1 and y>Rec1 and z>Rec2 then mhaplotype =5

26100 if x=1 and y>Rec1 and z<Rec2 then mhaplotype =6

26200 if x=1 and y<Rec1 and z>Rec2 then mhaplotype =7

26300 if x=1 and y<Rec1 and z<Rec2 then mhaplotype =8

26400 rem parthenogenetic offspring represent duplicated maternal meiotic haplotypes

26500 if mhaplotype =1 then

26510 OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(ParthMothers(a))

26520 OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(ParthMothers(a))

26530 OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(ParthMothers(a))

26540 OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(ParthMothers(a))

26550 OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(ParthMothers(a))

26560 OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(ParthMothers(a))

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26570 end if
27100 if mhaplotype =2 then
27110   OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(ParthMothers(a))
27120   OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(ParthMothers(a))
27130   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(ParthMothers(a))
27140   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(ParthMothers(a))
27150   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(ParthMothers(a))
27160   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(ParthMothers(a))
27170 end if
27700 if mhaplotype =3 then
27710   OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(ParthMothers(a))
27720   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(ParthMothers(a))
27730   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(ParthMothers(a))
27740   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(ParthMothers(a))
27750   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(ParthMothers(a))
27760   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(ParthMothers(a))
27770 end if
28300 if mhaplotype =4 then
28310   OffspringLoc1Allele1(OffspringCount)=Loc1Allele1(ParthMothers(a))
28320   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(ParthMothers(a))
28330   OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(ParthMothers(a))
28340   OffspringLoc1Allele2(OffspringCount)=Loc1Allele1(ParthMothers(a))
28350   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(ParthMothers(a))
28360   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(ParthMothers(a))
28370 end if
28900 if mhaplotype =5 then
28910   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(ParthMothers(a))
28920   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(ParthMothers(a))
28930   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(ParthMothers(a))
28940   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(ParthMothers(a))
28950   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(ParthMothers(a))
28960   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(ParthMothers(a))
28970 end if
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29500 if mhaplotype =6 then
29510   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(ParthMothers(a))
29520   OffspringLoc2Allele1(OffspringCount)=Loc2Allele2(ParthMothers(a))
29530   OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(ParthMothers(a))
29540   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(ParthMothers(a))
29550   OffspringLoc2Allele2(OffspringCount)=Loc2Allele2(ParthMothers(a))
29560   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(ParthMothers(a))
29570 end if
30100 if mhaplotype =7 then
30110   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(ParthMothers(a))
30120   OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(ParthMothers(a))
30130   OffspringLoc3Allele1(OffspringCount)=Loc3Allele1(ParthMothers(a))
30140   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(ParthMothers(a))
30150   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(ParthMothers(a))
30160   OffspringLoc3Allele2(OffspringCount)=Loc3Allele1(ParthMothers(a))
30170 end if
30200 if mhaplotype =8 then
30210   OffspringLoc1Allele1(OffspringCount)=Loc1Allele2(ParthMothers(a))
30220   OffspringLoc2Allele1(OffspringCount)=Loc2Allele1(ParthMothers(a))
30230   OffspringLoc3Allele1(OffspringCount)=Loc3Allele2(ParthMothers(a))
30240   OffspringLoc1Allele2(OffspringCount)=Loc1Allele2(ParthMothers(a))
30250   OffspringLoc2Allele2(OffspringCount)=Loc2Allele1(ParthMothers(a))
30260   OffspringLoc3Allele2(OffspringCount)=Loc3Allele2(ParthMothers(a))
30270 end if

31300 rem set other offspring parameters
31400 OffspringAlive(OffspringCount)=1
31500 zz=rnd(1)
31600 if zz<0.5 then OffspringSex(OffspringCount)=1 else OffspringSex(OffspringCount)=0
31700 if Location(ParthMothers(a))=1 then OffspringLocation(OffspringCount)=1 else OffspringLocation(OffspringCount)=0

31800 next b
31900 next a

```


31950 rem set number of offspring produced in parthenogenetic loop as the number of parthenogenetic offspring produced this generation

31960 ParthOffspring(main)=OffspringCount-SexualOffspring(main)

41000 rem randomly sort offspring pool

41050 rem assign RND (0,1) to each member of OffspringCount

41100 for a = 1 to OffspringCount

41200 score(a)=rnd(1)

41250 OriginalIndex(a)=a

41300 next a

41400 rem sort OffspringCount subscripts by the random number and get new subscript for each member

41500 REM Bubble Sort Algorithm

41600 FOR i = 1 TO OffspringCount - 1

41700 FOR j = 1 TO OffspringCount - i

41800 IF score(j) > score(j + 1) THEN

41900 REM Swap the elements in score array

42000 temp = score(j)

42100 score(j) = score(j + 1)

42200 score(j + 1) = temp

42300 REM Swap the corresponding indices in originalIndex array

42400 TempIndex = OriginalIndex(j)

42500 OriginalIndex(j) = OriginalIndex(j + 1)

42600 OriginalIndex(j + 1) = TempIndex

42700 END IF

42800 NEXT j

42900 NEXT i

43000 REM Print the sorted array and original indices

43100 rem PRINT "Sorted Scores and Original Indices:"

```
43200 rem FOR i = 1 TO OffspringCount
43300 rem  PRINT "Score: "; score(i); " Original Index: "; originalIndex(i)
43400 rem NEXT i
```

```
43500 rem set new reordered offspring array
43600 for a = 1 to OffspringCount
43700 NewOffspringAlive(a)=OffspringAlive(OriginalIndex(a))
43800 NewOffspringSex(a)=OffspringSex(OriginalIndex(a))
43900 NewOffspringLocation(a)=OffspringLocation(OriginalIndex(a))
44000 NewOffspringLoc1Allele1(a)=OffspringLoc1Allele1(OriginalIndex(a))
44100 NewOffspringLoc1Allele2(a)=OffspringLoc1Allele2(OriginalIndex(a))
44200 NewOffspringLoc2Allele1(a)=OffspringLoc2Allele1(OriginalIndex(a))
44300 NewOffspringLoc2Allele2(a)=OffspringLoc2Allele2(OriginalIndex(a))
44400 NewOffspringLoc3Allele1(a)=OffspringLoc3Allele1(OriginalIndex(a))
44500 NewOffspringLoc3Allele2(a)=OffspringLoc3Allele2(OriginalIndex(a))
44600 next a
```

```
45000 rem selection phase
45100 for a = 1 to OffspringCount
45200 if OverDom=0 then goto 45300 else goto 46000
45300 rem fitness dominance
45400 if NewOffspringLoc1Allele1(a)+NewOffspringLoc1Allele2(a)=0 then NewOffspringAlive(a)=0
45500 goto 47000
46000 rem fitness overdominance
46100 if NewOffspringLoc1Allele1(a)+NewOffspringLoc1Allele2(a)=0 then NewOffspringAlive(a)=0
46200 if NewOffspringLoc1Allele1(a)+NewOffspringLoc1Allele2(a)=2 then NewOffspringAlive(a)=0
47000 next a
```

```
48000 rem simultaneously determine migration and send living offspring into adult pool for next generation
48100 rem need to keep count of number of individuals in the main and sub populations
48200 mainCount=0
48300 subCount=0
48350 OffspringCounter=0
```

```

48400 for a = 1 to PopSize
48450 OffspringCounter=OffspringCounter+1
48460 if NewOffspringAlive(OffspringCounter)=0 then goto 48470 else goto 48500
48470 OffspringCounter=OffspringCounter+1
48480 goto 48460
48500 z=rnd(1)
48600 if z< Migration then NewOffspringLocation(OffspringCounter)=abs(NewOffspringLocation(OffspringCounter)-1)
48700 if NewOffspringLocation(OffspringCounter)=0 then mainCount=mainCount+1 else subCount=subCount+1
48900 if subCount> MaxSubSize then NewOffspringLocation(OffspringCounter)=0
49000 rem Migration determination is complete; now the individual goes into the adult pool for the next generation
49100 Sex(a)=NewOffspringSex(OffspringCounter)
49200 Location(a)=NewOffspringLocation(OffspringCounter)
49300 Loc1Allele1(a)=NewOffspringLoc1Allele1(OffspringCounter)
49400 Loc1Allele2(a)=NewOffspringLoc1Allele2(OffspringCounter)
49500 Loc2Allele1(a)=NewOffspringLoc2Allele1(OffspringCounter)
49600 Loc2Allele2(a)=NewOffspringLoc2Allele2(OffspringCounter)
49700 Loc3Allele1(a)=NewOffspringLoc3Allele1(OffspringCounter)
49800 Loc3Allele2(a)=NewOffspringLoc3Allele2(OffspringCounter)
49900 next a

49910 rem check genotypes
49920 rem for a = 1 to PopSize
49930 rem ? "ind# ";a;" ";
49940 rem ? "sex ";Sex(a);" ";
49950 rem ? "loc ";Location(a);" ";
49960 rem ? "genotype ";Loc1Allele1(a);Loc1Allele2(a);" ";Loc2Allele1(a);Loc2Allele2(a);" ";Loc3Allele1(a);Loc3Allele2(a)
49965 rem next a
49970 rem ? "hit any key then [return] to continue"
49980 rem input x$

50000 rem compute and store generation data
50100 rem calculate allele frequencies at each locus for this generation
50110 cls

```

```

50112 maincount=0
50114 subcount=0
50120 ? "generation ";main
50150 Loc1Count=0
50200 Loc2Count=0
50300 Loc3Count=0
50400 for a = 1 to PopSize
50450 Loc1Count=Loc1Count+Loc1Allele1(a)+Loc1Allele2(a)
50500 Loc2Count=Loc2Count+Loc2Allele1(a)+Loc2Allele2(a)
50600 Loc3Count=Loc3Count+Loc3Allele1(a)+Loc3Allele2(a)
50610 if Location(a)=0 then maincount=maincount+1
50620 if Location(a)=1 then subcount=subcount+1
50700 next a
50750 Loc1Freq(main)=Loc1Count/(2*PopSize)
50760 ? "mean fitness (determined by Locus 1) = ";Loc1Freq(main)
50800 Loc2Freq(main)=Loc2Count/PopSize
50900 ? "Mean Parthenogenetic Capability (determined by Locus 2) = ";Loc2Freq(main)
51000 Loc3Freq(main)=Loc3Count/PopSize
51100 ? "Locus 3 mean (neutral locus) = ";Loc3Freq(main)
51110 ? "main population: ";maincount;" individuals"
51120 ? "subpopulation: ";subcount;" individuals"
51125 ? Sexuals(main); " females reproduced sexually"
51130 ? SexualOffspring(main); " sexual offspring produced"
51135 ? Parths(main);" females attempted to reproduce parthenogenetically"
51140 ? ParthOffspring(main); " parthenogenetic offspring produced ";
51142 if OverDom=1 and ParthOffspring(main)>0 then ? "(but these die due to homoz. Lethality)" else ?
51150 ? "Maximum value of parthenogenetic allele that has appeared: ";MaxParth

51160 rem every 10th generation calculate the mode of the alleles at the parthenogenesis locus
51170 if main/10 = int(main/10) then goto 51175 else goto 52200
51175 rem calculate mode of Loc2Allele1
51176 threshold=0.0000001
51177 mode=0

```

```

51178 maxFreq=0
51179 rem find the frequency of each number
51180 for i=1 to PopSize
51190 count=1
51200 if frequency(i)=0 then
51210 for j=i+1 to PopSize
51220 if abs(Loc2Allele1(i)-Loc2Allele1(j))<threshold then
51230 count=count+1
51240 frequency(j)=-1
51245 rem mark as counted
51250 end if
51260 next j
51270 frequency(i)=count
51280 end if
51290 next i
51300 rem find the mode
51310 for i=1 to PopSize
51320 IF frequency(i) > maxFreq THEN
51330 maxFreq = frequency(i)
51340 mode = Loc2Allele1(i)
51350 END IF
51360 NEXT i
51370 ParthMode(main)=mode
51380 ModeFreq(main)=maxFreq
51390 ? "most common parth allele (at locus 2 allele 1): ";mode
51400 ? "# inds with most common allele: ";maxFreq

52200 next main

52300 rem print all data to output file
52400 open outfile$ for output as #1
52500 ?#1, "metapopulation size: ";PopSize
52600 ?#1, "subpopulation size: ";MaxSubSize

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```

52700 ?#1, "sexual reproduction produces ";MaxRepro;" offspring"
52800 ?#1, "parthenogenetic reproduction produces ";ParthRepro;" offspring"
52850 ?#1, "penalty for parthenogenetic-capable females reproducing sexually: ";ParthPenalty
52900 ?#1, "migration rate: ";migration
53000 ?#1, "mutation rate: ";mutation
53100 ?#1, "recombination rate, interval 1: ";Rec1
53200 ?#1, "recombination rate, interval 2: ";Rec2
53300 ?#1, "each individual in the main population encounters ";NumInds; " individuals"
53400 ?#1, "each individual in the subpopulation encounters ";NumIndsSub; " individuals"
53500 ?#1, "fitness overdominance (0=no, 1=yes): ";OverDom
53510 ?#1, "maximum value of parthenogenetic allele that appeared: ";MaxParth
53550 ?#1, "random seed: ";RandomSeed
53600 ?#1, "generation";chr$(9);"mean Loc2"; chr$(9);"mean Loc3"; chr$(9);"Mean Loc1"; chr$(9);"f prod sexually"; chr$(9);"sexual
offspring"; chr$(9);"f prod parth"; chr$(9);"parth offspring";chr$(9)"parth mode";chr$(9);"mode freq"
53700 for a = 1 to numGens
53800 ?#1, a; chr$(9);Loc2Freq(a); chr$(9);Loc3Freq(a); chr$(9);Loc1Freq(a); chr$(9);Sexuals(a); chr$(9);SexualOffspring(a);
chr$(9);Parths(a); chr$(9);ParthOffspring(a);
53805 if a/10=int(a/10) then ? #1, ParthMode(a);chr$(9);ModeFreq(a) else ? #1,
53900 next a
54000 close #1
55000 end

```