Amos, W, Nichols, HJ, Churchyard, T and Brooke, MDL

Rat eradication comes within a whisker! A case study of a failed project from the South Pacific

http://researchonline.ljmu.ac.uk/3361/

Article

Citation (please note it is advisable to refer to the publisher's version if you intend to cite from this work)


LJMU has developed LJMU Research Online for users to access the research output of the University more effectively. Copyright © and Moral Rights for the papers on this site are retained by the individual authors and/or other copyright owners. Users may download and/or print one copy of any article(s) in LJMU Research Online to facilitate their private study or for non-commercial research. You may not engage in further distribution of the material or use it for any profit-making activities or any commercial gain.

The version presented here may differ from the published version or from the version of the record. Please see the repository URL above for details on accessing the published version and note that access may require a subscription.

For more information please contact researchonline@ljmu.ac.uk

http://researchonline.ljmu.ac.uk/
Annotated Visual Basic code for simulating impact of bottlenecks of different sizes on allele frequencies assuming samples of size 50 and 82 before and after the even.

Dim Mu As Single, Het As Single, Nal As Integer, silent As Integer, none As Integer
Dim popsize As Long, Leadin As Integer, w1 As Integer, w2 As Integer
Dim A(1000, 2, 2) As Integer, counts(2, 2) As Integer, ptge As Integer
Dim Survive As Integer, Initial As Integer, n1, n2 As Long

Sub Main()
    Worksheets("nulls2").Activate
    rw = 0
    Randomize Timer
    popsize = 1000 ' set the default population size of 1000
    For Survive = 5 To 100 Step 10 ' explore a range of survivor numbers
        For ptge = 1 To 50
            rw = rw + 1
            For silent = 0 To 3
                Setup ' initialise the genotypes
                Phase1 ' two generations of reproduction at full population size
                Call Assess(1) ' calculate pre-bottleneck frequencies
                prefq1 = counts(1, 1) / (2 * (50 - none1))
                prefq2 = counts(2, 1) / (2 * (50 - none1))
                Het1 = Het: Nal1 = Nal: none1 = none ' store parameters
                bottle ' undergo a bottleneck of size survive
                Call Assess(2) ' calculate post-bottleneck frequencies
                Het2 = Het: Nal2 = Nal: none2 = none ' store post-bottleneck parameters
                postfq1 = counts(1, 2) / (2 * (82 - none2))
                postfq2 = counts(2, 2) / (2 * (82 - none2))
                If prefq1 < prefq2 Then ' store results for minor allele
                    pre = prefq1
                    Post = postfq1
                Else
                    pre = prefq2
                    Post = postfq2
                End If
                Cells(rw, 1 + 4 * silent) = Survive ' output results
                Cells(rw, 2 + 4 * silent) = pre
                Cells(rw, 3 + 4 * silent) = Post
                Cells(rw, 4 + 4 * silent) = Abs(pre - Post)
            Next silent
        Next rep
    Next Survive
    Average ' calculate average values for all pre-bottleneck frequencies across all bottleneck sizes
End Sub

Sub Assess(x As Integer) ' count allele frequencies etc.
    If x = 1 Then num = 50 Else num = 82 ' used empirical sample sizes
    Nal = 0 ' zero allele count
    Het = 1 ' set het to 1
    Erase counts ' zero allele counter
    none = 0 ' zero null genotype counter
    n = 0
    For g = 1 To num ' sample pre-number of rats
        variable 'nulls' = 1 if second allele is null and 2 if first allele is a null
        nulls = Abs(2 * (A(g, 1, w2) = 3)) + Abs(1 * (A(g, 2, w2) = 3))
    For h = 1 To 2 ' assay each allele
        If nulls = 0 Then ' standard genotype
            countsA = counts(A(g, h, w2), x) = countsA + 1
        ElseIf nulls < 3 Then ' heterozygote null
            countsA = counts(A(g, nulls, w2), x) = countsA + 1
        Else ' homozygote nulls
            none = none + 1
        End If
    Next h
Next g

For h = 1 To 2 ' scan both alleles visible
    If counts(g, x) > 0 Then
        Nal = Nal + 1 ' store allele number
        Het = Het - (counts(h, x) / (num - none * 2)) ^ 2 ' and heterozygosity
    End If
Next h
End Sub

Sub bottle()
    For f = 1 To popsize ' zero the recipient array, just to be sure
        A(f, 1, w2) = 0
        A(f, 2, w2) = 0
    Next f
For gen = 0 To 20
    n1 = Survive * 3 ^ gen ' exponential increase up to a maximum of popsize (1000)
    n2 = Survive * 3 ^ (gen + 1)
    If n1 > popsize Then n1 = popsize
    If n2 > popsize Then n2 = popsize
    fem = Int(n1 / 2) ' introduce sexes because important at small sizes
    mal = n1 - fem
    For f = 1 To n2
        Z = Int(Rnd(1) * fem) + 1 ' select first half female
        If Rnd(1) < 0.5 Then A(f, 1, w2) = A(Z, 1, w1) Else A(f, 1, w2) = A(Z, 2, w1)
        Z = Int(Rnd(1) * mal) + fem ' select second half male
        If Rnd(1) < 0.5 Then A(f, 2, w2) = A(Z, 1, w1) Else A(f, 2, w2) = A(Z, 2, w1)
    Next f
    If n1 = popsize Then Exit For ' terminate when popsize is reached (drift will be minimal afterwards)
    w1 = 3 - w1
    w2 = 3 - w2
Next gen
End Sub

Sub Phase1() ' two generations to randomize the genotypes (only 1 really necessary!)
    For f = 1 To 2
        Reproduce
        w1 = 3 - w1 ' change the array pointers
        w2 = 3 - w2
    Next f
End Sub

Sub Reproduce() ' for g = 1 To popsize
    Z = Int(Rnd(1) * popsize) + 1 ' select first half female
    If Rnd(1) < 0.5 Then A(g, 1, w2) = A(Z, 1, w1) Else A(g, 1, w2) = A(Z, 2, w1)
    Z = Int(Rnd(1) * popsize) + 1 ' select second half male
    If Rnd(1) < 0.5 Then A(g, 2, w2) = A(Z, 1, w1) Else A(g, 2, w2) = A(Z, 2, w1)
Next g
End Sub

Sub Setup() ' w1 and w2 are pointers that alternate each generation between 1 and 2. Thus, genotypes in generation x stored in w1 are used to populate generation x+1 in w2. The pointers are then reversed.
    m = Int(Rnd(1) * 20) + 1
    w1 = 1
    w2 = 2
    x = 0
    For f = 1 To popsize ' initialise all individuals with genotype 1,1
        A(f, 1, 1) = 1
        A(f, 2, 1) = 1
    Next f
    pbn = ptge * popsize / 100 ' set the initial target percentage frequency of the minor allele
    For g = 1 To pbn ' set that frequency of individuals to genotype 2,2
        A(g, 1, 1) = 2
        A(g, 2, 1) = 2
    Next g
    pbn2 = times * silent * popsize / 100 ' if null alleles are present, add these
    For g = pbn + 1 To pbn + pbn2
        A(g, 1, 1) = 3
        A(g, 2, 1) = 3
    Next g
End Sub

Sub Average() ' then output the averages
    Dim sm(20, 100, 2) As Single ' array for storing averages
    For silent = 0 To 3
        sm = 0
        For f = 1
            v1 = (Cells(f, 1 + silent * 4) + 5) / 10 ' bottleneck size
            v2 = Cells(f, 2 + silent * 4) * 100 ' minor allele frequency pre-bottleneck
            v3 = Cells(f, 4 + silent * 4) ' change in frequency
            sm(v1, v2, 1) = sm(v1, v2, 1) + v3
            sm(v1, v2, 2) = sm(v1, v2, 2) + 1
            f = f + 1
        Loop Until IsEmpty(Cells(f, 1 + silent * 4)) ' then output the averages
        For g = 1 To 10
            For h = 0 To 100
                If sm(g, h, 2) > 1 Then Cells(h + 2, g + 20 + silent * 11) = sm(g, h, 1) / sm(g, h, 2)
            Next h
        Next g
End Sub
Next silent
End Sub