

```

function mimicry_model(filename,link, nsteps);

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% larval trait evolution model
%
% link options:
%
% 'nolink' - no linked traits
% 'llink' - larval traits 1 & 2 linked (1 must be beneficial before 2 is)
% 'plink-' - negative parent effects on positive larval traits,no linked larval traits
% 'plink+' - positive parent effects on positive larval traits,no linked larval traits
% 'lplink+' - positive parent effects on positive larval traits, linked larval traits
% 'lplink+' - positive parent effects on positive larval traits, linked larval traits
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
tic
n=1e6; % number of larvae
m=1e3; % number of adults
survival_factor=.0000005;
mortality_rate=0.999995;
mean_trait=zeros(nsteps,2);
% first assume normal distribution of larval fish traits, say long spines
% and bulbs on spines
%define genes of initial potential parents for trait 1 & trait 2
% 2nd column is trait, 3rd column is genes for that trait
parent_genes=randn(m,2,2);
parent_age=ones(m,1);

init_parent_genes=parent_genes;

for i=1:nsteps
%assign parent mortality
parent_mort=ones(size(parent_age)).*0.025;
%mate parents and assign genes to larvae
larvae_genes=zeros(n,2,2);
if i==1
parents=[ceil(m.*rand(n,1)), ceil(m.*rand(n,1))];
else
parents=[ceil(length(parent_age).*rand(n,1)), ceil(length(parent_age).*rand(n,1))];
end
%set larvae genes for trait 1
larvae_pr=rand(n,2); %random number to determine which of parent genes larvae gets
larvae_genes(larvae_pr(:,1)<0.5,1,1)=parent_genes(parents(larvae_pr(:,1)<0.5,1),1,1);
larvae_genes(larvae_pr(:,1)>=0.5,1,1)=parent_genes(parents(larvae_pr(:,1)>=0.5,1),1,2);

larvae_genes(larvae_pr(:,2)<0.5,1,2)=parent_genes(parents(larvae_pr(:,2)<0.5,2),1,1);
larvae_genes(larvae_pr(:,2)>=0.5,1,2)=parent_genes(parents(larvae_pr(:,2)>=0.5,2),1,2);
%set larvae genes for trait 2
larvae_pr=rand(n,2); %random number to determine which of parent genes larvae gets
larvae_genes(larvae_pr(:,1)<0.5,2,1)=parent_genes(parents(larvae_pr(:,1)<0.5,1),2,1);
larvae_genes(larvae_pr(:,1)>=0.5,2,1)=parent_genes(parents(larvae_pr(:,1)>=0.5,1),2,2);
larvae_genes(larvae_pr(:,2)<0.5,2,2)=parent_genes(parents(larvae_pr(:,2)<0.5,2),2,1);
larvae_genes(larvae_pr(:,2)>=0.5,2,2)=parent_genes(parents(larvae_pr(:,2)>=0.5,2),2,2);

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%determine survival of larvae

switch link

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case 'link'
%for larval linked trait model uncomment following two lines
    larv_trait=larvae_genes(:,1,1)+larvae_genes(:,1,2);
    larv_trait(larv_trait>4)=larv_trait(larv_trait>4)+larvae_genes(larv_trait>4,2,1)+larvae_genes(larv_trait>4,2,2); %
benefit of trait 2 is dependent on a certain level of trait 1.

case 'nolink'
    larv_trait=(larvae_genes(:,1,1)+larvae_genes(:,1,2)+larvae_genes(:,2,1)+larvae_genes(:,2,2));

%larv_trait=(larvae_genes(:,1,1)>1.65)+(larvae_genes(:,1,2)>1.65)+(larvae_genes(:,2,1)>1.65)+(larvae_genes(:,2,2)>1.
65);

case 'plink-'
    larv_trait=(larvae_genes(:,1,1)+larvae_genes(:,1,2)+larvae_genes(:,2,1)+larvae_genes(:,2,2));

%larv_trait=(larvae_genes(:,1,1)>1.65)+(larvae_genes(:,1,2)>1.65)+(larvae_genes(:,2,1)>1.65)+(larvae_genes(:,2,2)>1.
65);
    parent_trait=10.*(parent_genes(:,1,1)+parent_genes(:,1,2)+parent_genes(:,2,1)+parent_genes(:,2,2));
    parent_mort=parent_mort+parent_trait.*survival_factor; %harmful to parent

case 'plink+'
    larv_trait=(larvae_genes(:,1,1)+larvae_genes(:,1,2)+larvae_genes(:,2,1)+larvae_genes(:,2,2));

%larv_trait=(larvae_genes(:,1,1)>1.65)+(larvae_genes(:,1,2)>1.65)+(larvae_genes(:,2,1)>1.65)+(larvae_genes(:,2,2)>1.
65);
    parent_trait=10.*(parent_genes(:,1,1)+parent_genes(:,1,2)+parent_genes(:,2,1)+parent_genes(:,2,2));
    parent_mort=parent_mort-parent_trait.*survival_factor; %beneficial to parent

case 'lplink-'
    larv_trait=larvae_genes(:,1,1)+larvae_genes(:,1,2);
    larv_trait(larv_trait>4)=larv_trait(larv_trait>4)+larvae_genes(larv_trait>4,2,1)+larvae_genes(larv_trait>4,2,2); %
benefit of trait 2 is dependent on a certain level of trait 1.
    parent_trait=10.*(parent_genes(:,1,1)+parent_genes(:,1,2)+parent_genes(:,2,1)+parent_genes(:,2,2));
    parent_mort=parent_mort+parent_trait.*survival_factor; %harmful to parent

case 'lplink+'
    larv_trait=larvae_genes(:,1,1)+larvae_genes(:,1,2);
    larv_trait(larv_trait>4)=larv_trait(larv_trait>4)+larvae_genes(larv_trait>4,2,1)+larvae_genes(larv_trait>4,2,2); %
benefit of trait 2 is dependent on a certain level of trait 1.
    parent_trait=10.*(parent_genes(:,1,1)+parent_genes(:,1,2)+parent_genes(:,2,1)+parent_genes(:,2,2));
    parent_mort=parent_mort-parent_trait.*survival_factor; %beneficial to parent

end

larv_mort=mortality_rate-survival_factor.*larv_trait;
lsurvive_test=rand(n,1);
larvae_genes=larvae_genes((lsurvive_test>=larv_mort)==1,:,:);

%determine survival of parents
if i==1
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    psurvive_test=rand(m,1);
else
    psurvive_test=rand(length(parent_age),1);
end
%for constant age-dependent mortality uncomment following two lines. Mortality is 0.5 and increases by 0.1 linearly
after 8 years of age.
parent_mort(parent_age>=8)=(parent_mort(parent_age>=8)+0.1.*(parent_age(parent_age>=8)-8));

%for parental linked trait model uncomment following line and one of the two after that lines
%parent_trait=1000.*(parent_genes(:,1,1)+parent_genes(:,1,2)+parent_genes(:,2,1)+parent_genes(:,2,2));
%parent_mort=parent_mort+parent_trait.*survival_factor; %harmful to parent
%parent_mort=parent_mort-parent_trait.*survival_factor; %beneficial to parent
parent_genes=parent_genes(psurvive_test>=parent_mort,:);
parent_age=parent_age(psurvive_test>=parent_mort);

%determine new parent pool assuming all larvae survive to reproduce

parent_genes=[parent_genes; larvae_genes];
parent_age=parent_age+1;
parent_age=[parent_age; ones(size(larvae_genes,1),1)];

if(rem(i,floor(nsteps./100))==0)
    fprintf('%d%s%d%s\n',100.*i./nsteps,'% done in ');
    toc;
end

mean_trait(i,:)=mean(squeeze(mean(parent_genes)));
age_dist(i,:)=hist(parent_age,[1:25]);
mean_pmort(i)=mean(parent_mort);
mean_lmort(i)=mean(larv_mort);

clear larvae_genes;

end

eval(['save -mat ',filename,'.mat parent_genes init_parent_genes mean_trait mean_pmort mean_lmort age_dist']);
end

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