

# **Final Assignment: On the effect of phytoplankton heterogeneity on mussel spatial patterns formation**

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# 1 Introduction

Individual mussels by themselves do not have a complex behaviour. However, when a significant number of individuals interacts the emergent property of spatial self-organization appears. Van de Koppel et al. [3] demonstrated experimentally the self-organized pattern formation on mussel beds, discovering how it can affect some ecosystem processes such as the improvement of resilience to perturbation or environmental change.

Because of their reduced dimensions and high movement velocity, mussels are quite easy to be studied in their movement using an agent-based model, and be able to have results in a short time.

In their study, Van de Koppel et al. point out the characteristics that regulate mussel movement. When they are alone, mussels move at higher speed. On the other hand, when they find a dense neighbourhood they tend to slow down and form clusters, to lower the risk of predation. These properties lead to the development of regular patterns starting from an initial random disposition.

In the Mussel Assignment, it has been simulated what Van de Koppel et al. [3] studied. The effect of the number of mussels present in the arena was analysed, and it was found that it affects the cluster formation: the more mussels are present, the more and bigger the clusters. In conformity with the paper, cluster formation strongly depends on local density.

Another factor influencing movement is food: when a big cluster is formed, the available food per each mussel decreases. This leads the mussel to take longer steps. Thus, the movement of each individual is driven by two balancing factors: moving towards a big group and being more protected against predators, or stay in smaller groups or even by itself and have the possibility to eat more.

In this assignment we investigate if and how heterogeneity in the food concentration affects the spatial pattern formation in mussel beds.

# 2 Methods

In order to answer the research question, a model in Matlab is built. The model is structured in the following way. It starts with the definition of all the relevant control constants, system parameters and system variables. Next, a main `for` loop simulating the time evolution of the system is implemented. The loop is divided conceptually in 2 blocks. The first block calculates how the phytoplankton concentration is distributed over the space, while the second is responsible for the mussels movement within the arena.

## 2.1 Block 1: Phytoplankton distribution

Neglecting the interaction with zooplankton and the phytoplankton regeneration, two factors affect the phytoplankton concentration: the presence of mussels, which eat food at a certain rate, and the diffusion process from high concentration areas to lower ones. Therefore, the time evolution of phytoplankton distribution can be described by the following differential equation, where  $P$  represents the phytoplankton concentration:

$$\frac{\partial P}{\partial t} = -nF\alpha + D\Delta P \quad (1)$$

The first term  $-nF\alpha$  reflects the food eaten by mussels. The parameters used are the following:

- $n$  is the number of mussels present in the cell
- $F = 24.26 \times 10^3 \text{ cell/ml}$  is the average amount of phytoplankton eaten by one mussel. The value of  $F$  is obtained from a linearisation of the concentration profile (with medium concentration) experimentally found by Okumuş et Al. [1] and shown in Figure 1

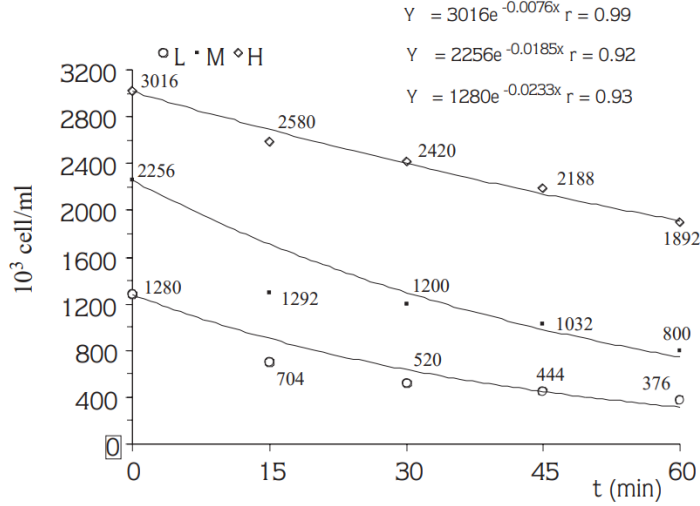


Figure 1: Concentration profiles from Okumuş et Al. [1]

- $\alpha = \frac{\text{Phytoplankton}[i,j]}{\text{Average Phytoplankton}}$  is a factor which takes into account the experimental fact that mussels tend to eat at a lower rate when the concentration is lower

The second term  $D\Delta P$  is the diffusion term. The diffusivity  $D = 0.03 \text{ m}^2/\text{day} = 0.21 \text{ cm}^2/\text{min}$  is taken from the work of Mukhopadhyay et Al. [2].

In order to calculate the spatial distribution of  $P$ , the arena in which the mussels move is divided in cells using a  $50 \times 50$  grid. The distribution is initialised to be equally spread over the entire area at a value of  $P = 2256 \times 10^3 \text{ cell/ml}$ . To update the matrix  $P$  within the temporal (for) loop, it is first necessary to calculate a matrix  $n$  containing the number of mussels in each cell. Then, for every cell the diffusion is calculated taking into account the fluxes in the x-direction and in the y-direction. Next, the matrix  $P$  is updated according to Equation 1.

## 2.2 Block 2: Mussel movement

The mussels are modelled using an agent based model, in the very same way as we did in the Mussel Assignment. Each mussel performs a random walk described by an exponential distribution:

$$F(x) = \frac{\exp \frac{-x}{\beta}}{\beta} \quad (2)$$

where  $\beta$  is given by

$$\beta = \frac{1}{P1V1 - 0.34(80 + \frac{10*P}{\text{Average } P}) + P3} \quad (3)$$

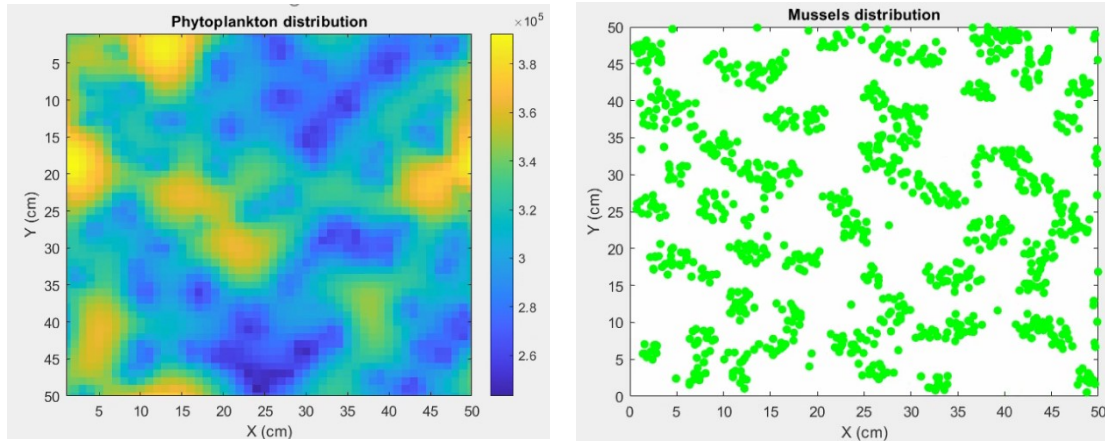
Here,  $V1$  is the number of mussels per  $\text{cm}^2$ ,  $P1$  is conversion constant (in  $\text{cm}^2$  per number) and  $P3$  is a dimensionless number that sets mussel movement when a mussel is entirely

alone. The factor  $-0.34(80 + \frac{10*P}{Average\ P})$  is responsible for the interaction between mussels and food. When the concentration of phytoplankton is low, the mussel is taking greater steps. For the sake of comparability, this factor has been scaled so that, on average, it is similar to the value of  $P2V2$  used in the Mussel Assignment.

### 3 Results

Figure 2a represents the phytoplankton distribution after 500 minutes. Starting with an initial uniform concentration, during the simulation it decreased and the areas with highest reduction are found to be near those where mussels have formed groups.

In Figure 2b the mussel distribution after 500 minutes is reported. It can be noticed that patterns are formed.



(a) Phytoplankton distribution after 500 minutes (values in cell/ml). (b) Spatial organisation of mussels after 500 minutes.

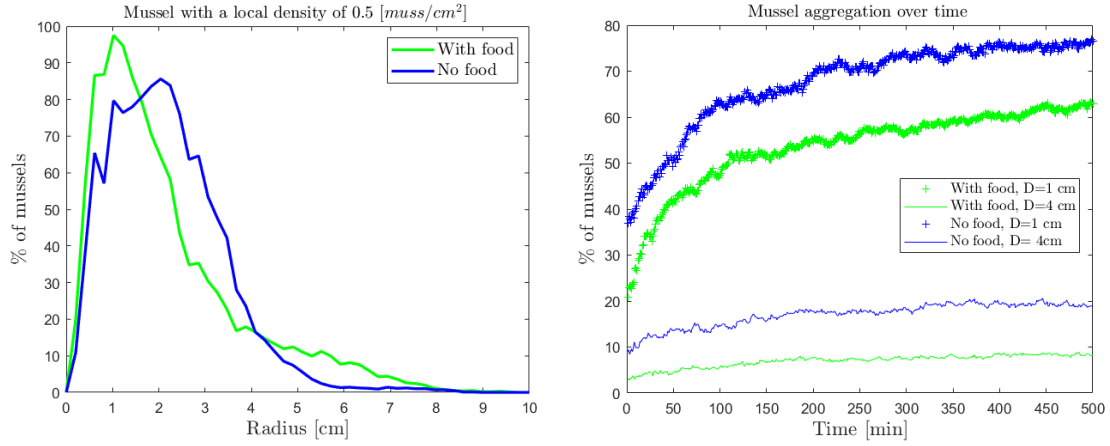
Figure 2

The results shown in Figure 3 allow only a qualitative analysis of the model. In order to better understand the difference between the original mussel model and this, two methods are used.

The first method is to calculate the number of mussels with a local density greater than  $0.5 \text{ mussel}/\text{cm}^2$  for every radius ranging from 0 to 10 cm. The result is reported in Figure 3a. This figure allows to make 2 observations. The first one concerns the size of the clusters: in the new model clusters tend to be smaller. It is clear how the line correspondent to the model with food reaches a higher percentage of mussels and decreases steeper until a radius of 4 cm, to then decrease more gently than the original model.

	Model with food heterogeneity	Mussel Assignment model
Maximum size (cm)	2.8	3.5
Average size (cm)	1.4	2.3

The second observation is that the clusters are less frequent. This is justified observing the tails of the two distributions. The green one (new model) presents a fatter tail. This means that there are more isolated mussels compared to the Mussel Assignment model.



(a) Percentage of mussels with local density of maximum 0.5 mussels/cm<sup>2</sup> as a function of different radii.

(b) Aggregation of mussels over time.

Figure 3

In Figure 3b it is represented time distribution of mussel aggregation. To do that, we considered the number of mussels that have a local density greater than 0.5 *mussel/cm*<sup>2</sup> for the different radii: 1cm and 4 cm.

As it can be noticed, the time evolution of the two models is really similar. However, the percentage of mussels within 1 cm distance is lower in the model with food of about 30%. This result attests the presence of smaller clusters by comparing the percentage of mussels within 4 cm: more than 60% of the population is pretty close to other individuals (1 cm) but only 10% of it still have neighbours within a higher radius (4 cm). However, a distance of 4 cm could also imply that the two individuals are positioned in the external part of different clusters. This is the reason why a short distance and a higher one have to be considered together to gain some information about clustering.

## 4 Discussion

The model confirmed what was experimented in the article published by Van de Koppel et al. [3]: the trade-off mussels have between moving towards a high density to create a group and continuing to stay in a low density area, by itself or in a small group where food is enough for everyone.

The heterogeneity in phytoplankton distribution seems to affect the size and the number of the clusters, which are found to be smaller and less frequent. On the other hand, the time evolution of the individuals is really similar to the time evolution found using the Mussel Assignment model.

Thus, this model shows some interesting results. However, it also presents some weaknesses. The first one concerns the value of some relevant parameters. For example, the initial phytoplankton distribution can vary greatly when different locations are considered. Moreover, the eating rate of mussels depends on other external factors such as the mussel size and the temperature of water.

The second weakness is that the term for the food-mussel interaction in Equation 3 is not backed by literature. Therefore, experimental validation is probably needed.

Finally, the regeneration of phytoplankton and its interaction with zooplankton are

neglected. However, these factors have a major influence on the evolution of phytoplankton concentration.

## References

- [1] Banibrata Mukhopadhyay and Rakhi Bhattacharyya. A delay-diffusion model of marine plankton ecosystem exhibiting cyclic nature of blooms. *Journal of biological physics*, 31:3–22, 01 2005. doi:10.1007/s10867-005-2306-x.
- [2] Ibrahim Okumuş, Nadir Başçınar, and Mükerrerrem Özkan. The effects of phytoplankton concentration, size of mussel and water temperature on feed consumption and filtration rate of the mediterranean mussel (*mytilus galloprovincialis* lmk). *Turkish Journal of Zoology*, 26:167–172, 01 2002.
- [3] Johan van de Koppel, Joanna Gascoigne, Guy Theraulaz, Max Rietkerk, Wolf Mooij, and Peter Herman. Experimental evidence for spatial self-organization and its emergent effects in mussel bed ecosystems. *Science (New York, N.Y.)*, 322:739–42, 11 2008. doi:10.1126/science.1163952.

## Appendix

```

% Parameters
N = 1000; % Number of mussels
Length = 50; % Length of the Arena, in cm
EndTime = 500; % Number of minutes
dT = 1; % minute
DeltaX = 1;
DeltaY = 1;
% Declaring the parameters that describe movement speed
P1 = 100;
Rescale = 40*10−6;
P3 = 3;
D1 = 2; % cm, mussels within this distance are considered neighbors
D2 = 6; % cm, mussels within this distance are considered as "within
% cluster distance", in cm.

% Parameters related to phytoplankton
% massPhyto = 2.4; % microg
% gamma = 0.1; % per minute 0.3/60/24
% k = 108; %micro g per minute 108*10−6
D = 2.1*10−5*10000; % per minute 0.03/60/24
F = 24.26*103; % (cell/ml) average phytoplankton eaten by 1 mussel per
% timestep
AveragePhytoDensity = 2256*103; % average phytoplankton density in
% sea water [cell/ml] source: Average-phytoplankton-biomass-chlorophyll-
% a-concentration-chl-a-Secchi-depth-total_tbl3-225653264

% Constant and variable declaration, used below
Diagonal=diag(ones(N,1)); % Used below
Distance=zeros(N,N); % Assigning the array
Beta = zeros(N,1);
StepSize = zeros(N,1);
Angle = zeros(N,1);

% Initial distribution
X = rand(N,1)*50;
Y = rand(N,1)*50;
X_int = X;
Y_int = Y;
% Initial phytoplankton concertation distribution

P = ones(Length, Length)*AveragePhytoDensity;
dP = zeros(Length, Length);
NetP = zeros(Length, Length);

```

```

%% Main loop

vidfilePhytoplankton = VideoWriter('Phytomovie.mp4','MPEG-4');
vidfileMussel = VideoWriter('Musselmovie.mp4','MPEG-4');
open(vidfilePhytoplankton);
open(vidfileMussel);

for Time=1:EndTime

DistributionMussels =zeros(Length,Length);

X_int = round(X);
Y_int = round(Y);

    % Finding the amount of mussels in each cell
    for m = 1:Length
        for n= 1:Length
            for s=1:N
                if X_int(s)+1==m && Y_int(s)+1==n
                    DistributionMussels(m,n) = DistributionMussels(m,n) + 1;
                end
            end
        end
    end

    % calculate the reaction term
    dP = -DistributionMussels*F;

    % Calculate the diffusion flows
    FXP (1:Length,2:Length) = -D * (P(1:Length,2:Length) - ...
        ...P(1:Length,1:Length-1))/DeltaX;

    FYP (2:Length,1:Length) = -D * (P(2:Length,1:Length) - ...
        ...P(1:Length-1,1:Length))/DeltaY;

    FXP(1:Length,1) = -D * (P(1:Length,1)- P(1:Length,Length))/DeltaX;
    % Boundaries conditions for the flows
    FYP(1, 1:Length) = -D * (P(1,1:Length)- P(Length,1:Length))/DeltaY;

    for i=1:Length
        for j=1:Length
            % boundaries conditions

```



```

    if i~=Length && j==Length
        NetP(i,j) = FXP(i,j)-FXP(i,1)+FYP(i,j) - FYP(i+1,j);
    elseif i==Length && j==Length
        NetP(i,j) = FXP(i,j)-FXP(i,1)+FYP(i,j) - FYP(1,j);
    elseif i==Length && j~=Length
        NetP(i,j) = FXP(i,j)-FXP(i,j+1)+FYP(i,j) - FYP(1,j);
    % regular flow
    else
        NetP(i,j)= FXP(i,j)-FXP(i,j+1)+ FYP(i,j)-FYP(i+1,j);
    end

end

end

% Updating the phytoplankton population

P = P+NetP*dT+dP*dT.*P/AveragePhytoDensity; % *

% MUSSEL MOVEMENT CALCULATIONS

for i=1:N
    for j=1:N
        Distance(i,j)= sqrt((X(i)-X(j))^2+(Y(i)-Y(j))^2);
    end
end

Nr_In_Dist1 = (Distance<D1)-Diagonal;
Nr_In_Dist2 = (Distance<D2)-Diagonal;

% Calculating densities of mussels
V1 = sum(Nr_In_Dist1)/(D1.^2*pi()); % sum/surface

for m = 1:Length
    for n= 1:Length
        for s=1:N
            if X_int(s)+1==m && Y_int(s)+1==n
                Beta(s)=1/(max(0.001,P1*V1(s)-...
                ...0.34*(80+10*mean(mean(P))/P(m,n))+P3));
                % Setting a random step size
                StepSize(s)= -Beta(s)* log(rand());
            end
        end
    end
end

end

% setting a random stepsize
Angle = rand(N,1)*360;

```

```

%Implementing the steps
X = X + StepSize.*cos(Angle);
Y = Y + StepSize.*sin(Angle);

% Periodic boundary conditions
for i = 1:N
    if X(i)>Length
        X(i) = X(i) - Length;
    end

    if X(i)<0
        X(i) = X(i) + Length;
    end

    if Y(i)>Length
        Y(i) = Y(i) - Length;
    end

    if Y(i)<0
        Y(i) = Y(i) + Length;
    end
end

% Mussel distribution
figure(1)
plot(X,Y, 'g. ', 'MarkerSize',20)
title('Mussels_distribution')
ylabel('Y_(cm)')
xlabel('X_(cm)')
ylim([0 50])
xlim([0 50])
drawnow
FilmMussel(Time) = getframe(gcf);
writeVideo(vidfileMussel ,FilmMussel(Time));

% food distribution
figure(2)
imagesc(P)
colorbar()
title('Phytoplankton_distribution')
ylabel('Y_(cm)')
xlabel('X_(cm)')
ylim([1 50])
xlim([1 50])
h = colorbar;
ylabel(h, 'cell/ml')

```

```
FilmPhytoplankton(Time) = getframe(gcf);  
writeVideo(vidfilePhytoplankton ,FilmPhytoplankton(Time));  
  
%      % Mussel and food distribution  
%      figure(3)  
%      imagesc(P)  
%      colorbar()  
%      hold on  
%      plot(X,Y, 'g. ', 'MarkerSize',20)  
%      title('Mussels and food distribution , N=1000')  
%      ylabel('Y (cm)')  
%      xlabel('X (cm)')  
%      ylim([0 50])  
%      xlim([0 50])  
%      drawnow  
  
end  
  
close(vidfilePhytoplankton)  
close(vidfileMussel)
```