Self-Organization of Bacterial and Human Populations: Same Model, Different Scale

Romas Baronas*[1], Boleslovas Dapkūnas[1] and Remigijus Šimkus[2]
Vilnius University, Vilnius, Lithuania
[1]Institute of Computer Science, [2]Institute of Biochemistry, *e-mail: romas.baronas@mif.vu.lt

Introduction

Chemotaxis denotes the movement of organisms in response to chemical gradients. In positive chemotaxis, organisms move towards the chemoattractant, and in negative chemotaxis, away from the chemorepellent [1].

The dynamics of chemotactic population and chemoattractant is usually modelled mathematically using a system of nonlinear equations of the reaction-diffusion-chemotaxis type. The chemotaxis-type models are mostly applied in biology [1].

Neto and Claeyssen have applied a chemotaxis model to describe economic growth containing capital-induced labor migration [2].

Short et al. proposed a chemotaxis-type system to describe the movement of criminals toward increasing concentrations of an attractiveness value [3,4].

In this work [5], the chemotaxis-based self-organization and patterning relationship between bacterial and human populations were investigated computationally.

The aim of this work: to investigate the chemotaxis-based self-organizing and patterning relationship between bacterial and human populations using chemotaxis-based dimensionless mathematical models and to estimate values of the corresponding dimensional model parameters [5].

Mathematical model

Keller-Segel model of chemotaxis

The dynamics of a chemotactic population and its attractant are described by a system of Keller-Segel-type reaction-diffusion-chemotaxis equations, which in the dimensionless form read

$$\frac{\partial u}{\partial t} = D\Delta u - \nabla\left(h(u,v)u\nabla v\right) + \gamma f(u,v),$$

$$\frac{\partial v}{\partial t} = \Delta v + \gamma(g_p(u,v) - g_d(u,v)v), \quad \mathrm{x} \in \Omega \subset \mathbb{R}^n,$$

$u(x, t)$ – the population density,
$v(x, t)$ – concentration of the attractant (chemical signal),
D – dimensionless diffusion coefficient,
$h(u, v)$ – chemotactic sensitivity,
$f(u, v)$ – rate of population growth and death,
$g_p(u, v)$ – production rate of the attractant,
$g_d(u, v)$ – degradation rate of the attractant,
γ – spatial and temporal scale.

1) *Bacterial self-organization* [1,6,7]

$$h(u,v) = \chi, \quad f(u,v) = \alpha u(1-u),$$

$$g_p(u,v) = \frac{u}{1+\beta u}, \quad g_d(u,v) = 1,$$

u, v – bacterial density and chemoattractant concentration.

2) *Capital-induced labor migration* [2]

$$h(u,v) = \chi, \quad f(u,v) = \alpha u(1-u),$$

$$g_p(u,v) = v^{\phi}u^{1-\phi}, \quad g_d(u,v) = 1,$$

u, v – densities of labor and capital.

3) *Urban crime propagation* [3,4]

a) [3]

$$h(u,v) = \frac{\chi}{k_2+v}, \quad f(u,v) = k_1 - (k_2+v)u,$$

$$g_p(u,v) = (k_2+v)u, \quad g_d(u,v) = 1,$$

b) [4]

$$h(u,v) = \chi, \quad f(u,v) = \kappa uv + h_1,$$

$$g_p(u,v) = \frac{u}{1+\epsilon u} + h_2, \quad g_d(u,v) = 1,$$

u, v – densities of criminals and attractiveness value.

Numerical simulation

The mathematical model was defined as an initial boundary value problem and was solved numerically by using finite difference technique.

The model was applied to 2D (a unit disk) and 1D (the circumference of the unit disk) domains.

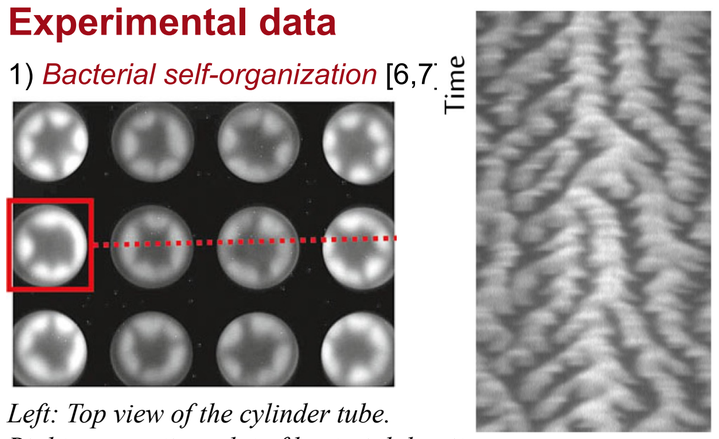
1D: 150 points in space and a step size 10^{-4} in time.

2D: 50×150 polar grid and the time step 5×10^{-8}.

The simulator was programmed in Java language.

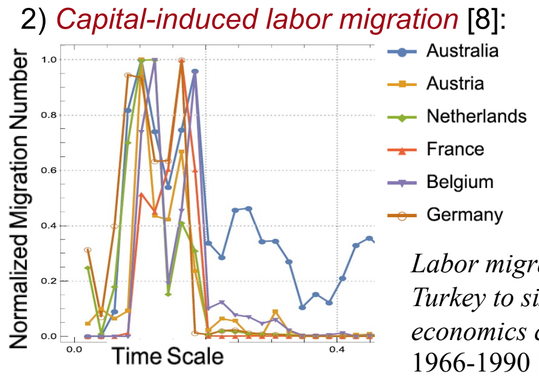
Experimental data

1) *Bacterial self-organization* [6,7]



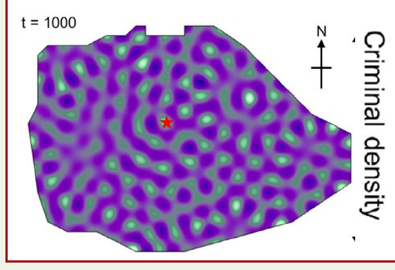
Left: Top view of the cylinder tube. Right: space–time plot of bacterial density near the circumference of the disk.

2) *Capital-induced labor migration* [8]:



Labor migration from Turkey to six western economics countries in 1966-1990 [8].

3a) *Urban crime propagation* [1]:



Distribution of criminal hotspots (density) in a spatial region approximately describing the outline of Edinburgh. Simulated by Painter [1].

Scaling the model

The parameter γ was used to simulate domains of different sizes.

The relation between dimensionless time t and space variables r (2D model) and x (1D) is invariant to γ.

$$T = \left(\frac{R}{R^*}\right)^2 D_c T^*, \; D_c = \frac{T}{T^*}R^{*2}, \; D_n = D\,D_c\,,$$

T^*, R^*, D_c, D_n are the dimensional duration, radius and diffusion coefficients of population and attractant.

Estimation of dimensional parameters

Bacterium E. Coli: using the vessel radius R^* = 4 mm and duration $T^* = 1.5\times10^4$s, the diffusion coefficients: D_c = 1.28 ×10−4 cm²/s and D_n = 1.28 ×10⁻⁵ cm²/s.

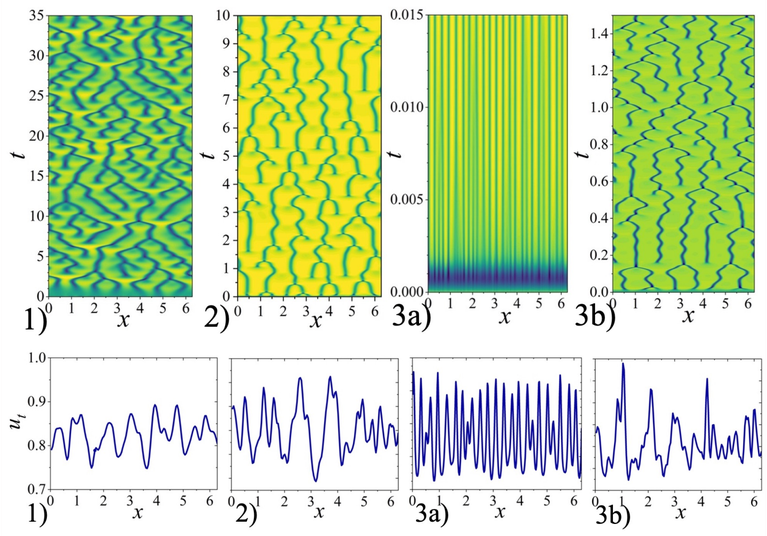
Labor migration: using the geographical radius R^* = 9000 km and duration T^* of 5 years corresponds to the dimensionless duration T of 1 unit, the diffusion coefficients $D_c = D_n \approx 16.2 \times10^6$ km²/year, i.e. the velocity of the labor force migration is 5700 km/year.

Crime hotspot formation: the time for crime hotspots to develop $T^* = (S/\pi)T/D_c$, where S – city area. For Edinburgh: S=119km, simulated dimensionless T=0.01. T^* = 3788 days (assuming D_c = 100 m²/day).
The number of hotspots equals to about 100.

Modeling a real urban area with a circle is a fairly rough approximation. However, the circle can be used to investigate the dynamics of the crime hotspot formation and to estimate values of the dimensional parameters. The simulation in a regular domain is simpler than that in a domain close to real city area.

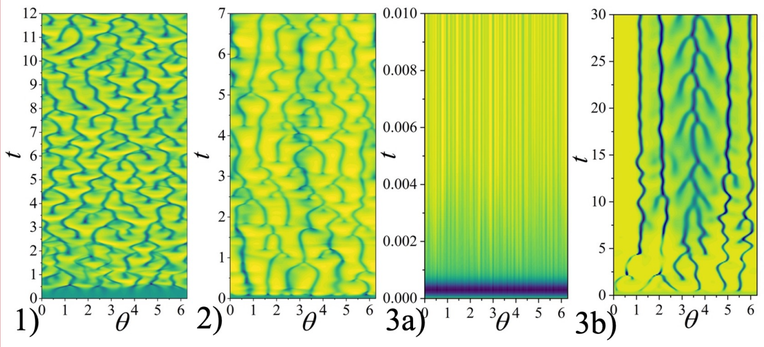
Simulation results

1D: Along the perimeter of the unit disk



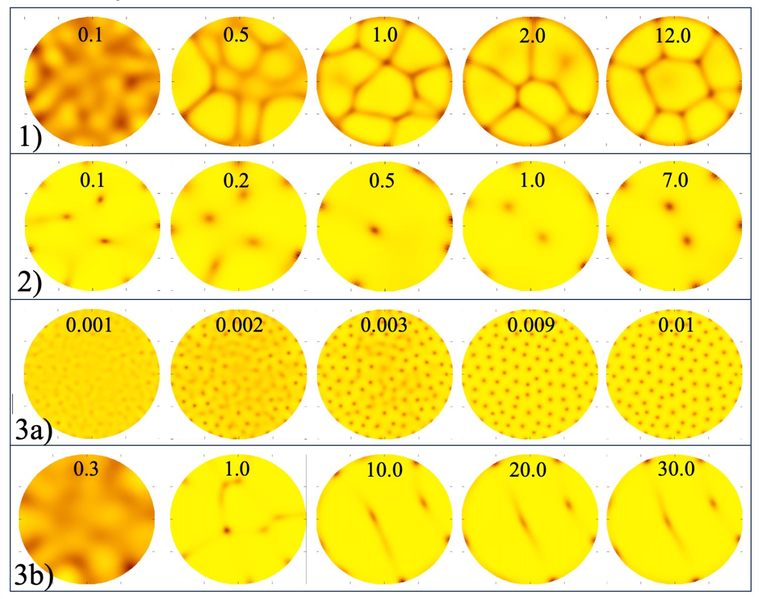
Spatiotemporal plots of the population densities and the average densities simulated in 1D *using four specific models*

2D: Along the perimeter of the unit disk



Spatiotemporal plots of the population densities simulated in 2D.

2D: Top views of the unit disk



Top views of the population densities of bacterial self-organization (1), capital-induced labour migration (2) and urban crime propagation (3) at time moments indicated inside the images.

Conclusions

The chemotaxis-type equations can be applied to study various chemotactic-like systems. The population specificity is expressed by functions h, f, g_p and g_d.

The spatial distribution of clusters of individuals in the population domain depends on the type of boundary conditions as well as on the form of specific functions.

Numerical simulation can be used to estimate dimensional parameters.

The movement toward an attractant in the human population is as similar to the movement in a bacterial population, except the significant difference in scale.

References

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