Parallel Session

# Mathematical Methods in Biology I

## REACTION-DIFFUSION AND INDIVIDUAL-BASED MODELS FOR ANT MOVEMENT

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Joint work with Ricardo Alonso (PUC-Rio), Thierry Goudon (U.Nice, INRIA) and Fernando Peruani (U. Nice).

*Keywords*: Reaction-diffusion euqations, Individual-based models, Ant navigation, Pheromones.

We develop two distinct approaches to modeling, simulation, and mathematical analysis of ant movement. In the first approach, we consider a system of reaction-diffusion equations of chemotaxis type modeling ant foraging dynamics. Although this model reproduces some observed behavior, such as concentration along trails, we argue that it is incomplete as a model of ant movement. Nonetheless, we present a thorough mathematical analysis of the system. In the second approach, we present and discuss an individual based model for ant movement which takes into account the rules for individual response to pheromones. For this model, we present stability results for the underlying system of nonlocal ODEs, and discuss the emergence of collective behavior, including spontaneous trail formation.

**Monday, July 23rd, 12:00** **Room: C8.2.19**

Parallel Session

# Mathematical Methods in Biology I

## AN INTEGRO-DIFFERENTIAL EQUATION MODEL FOR URBAN POPULATION DYNAMICS PREDICTING EMERGENT PATTERN FORMATION

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*Keywords*: Integro-differential, Urban, Population, Dynamic, Pattern.

Urban population distributions in large cities can show structure such as patchy patterning that may relate to important properties such as journey times, quality of life and sustainability. We use integro-differential equations to model the spatio-temporal dynamics of urban populations and services, under the assumption that they benefit from proximity to one another, as captured via spatial weight kernels. The system may tend towards a homogeneous state or a spatial pattern. With Gaussian kernels, linear stability of the spatially homogeneous steady state depends on a key function in the model, the carrying capacity for services given a local population density. In particular, patterning occurs only where the carrying capacity is convex with respect to population density. Furthermore, this spatial instability can only occur for perturbations with a sufficiently long lengthscale. Numerical continuation shows how multiple steady states corresponding to different spatial wavelengths can coexist and state transitions may occur as carrying capacity grows. Lastly, in urban centres, competition for space may cause services and population to be out of phase with one other. To generate such patterning in our model requires kernels with Fourier transforms that are negative for some wavelengths. With box and off-centre kernels, such out of phase patterning can occur and we show that this patterning occurs at a higher density and of a shorter lengthscale than in phase patterning.

Parallel Session

# Mathematical Methods in Biology I

## HYDRODYNAMIC MODELLING OF HUMAN SPERM CLUSTERING

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Joint work with Eamonn A. Gaffney (University of Oxford).

*Keywords*: Low-Reynolds-number flow, Sperm, Collective dynamics.

A fertile human male ejaculates more than 100 million sperms, which are self-propelled cells with a bending flagellum. The whip-like movement of the appendage generates fluid flow, and, in turn, the interactions between cells could be complicated, requiring coarse-grained modelling for studies of sperm collective behaviours. We have used high-speed videomicroscopic images of swimming human sperm to analyse the flow around a single cell [1]. With the aid of the direct numerical computation via the boundary element method, we have found that the time-averaged flow field is that of a pusher as frequently assumed. The temporal flow pattern is, however, more complicated, and core parts of the flow fields can be well represented by blinking Stokeslet triplets.

In this talk, we will present our multi-scale modelling for the collective behaviours of human sperm, using the Stokeslet representations obtained from the microscopic images, and will discuss how the finer-scale details of swimming dynamics impact on the population level.

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## References

[1] K. Ishimoto, H. Gadêlha, E. A. Gaffney, D. J. Smith, J. Kirkman-Brown. (2017). *Coarse-graining the flow around a human sperm.* Phys. Rev. Lett. 118, 124501.

Parallel Session

# Mathematical Methods in Biology I

## A MATHEMATICAL MODEL OF COLLECTIVE CELL MIGRATIONS BASED ON CELL POLARITY

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Joint work with Takamichi Sushida (Research Institute for Electronic Science, Hokkaido University), Hitomi Mori(Division of Life Science, Graduate School of Life Science, Hokkaido University), Sumire Ishida(Division of Life Science, Graduate School of Life Science, Hokkaido University) and Hisashi Haga (Transdisciplinary Life Science Course, Faculty of Advanced Life Science, Hokkaido University).

*Keywords*: Mathematical Model, Morphogenesis, Cell Migrations, Numerical Simulation.

Collective cell migration has been investigated as a self organization phenomenon in life activities. Recently, rotational phenomena of collective cell migrations observed in morphogenesis are focused. For example, they are observed in the elongation process of the fruiting body formation of *Dictyostelium Discoideum*. In contrast, in experiments using Madin-Darby canine kidney cells and cancer cells (a kind of epithelial cells), several migration modes which contain rotational migration are observed. Our goal is to extract essential mechanisms of collective cell migrations in morphogenesis from mathematical modeling. In this talk, we select the self-propelled particle method [1], propose a new model focusing on cell polarity, and explore mechanisms of which each migration mode occurs robustly for the parameters and the initial conditions. As a numerical result, we show a phase diagram for the parameters of a driving force by the cell polarity and the cell-cell adhesive force. In the phase diagram[2], migration modes are classified as follows:

(i) Rigid rotational migration,

(ii) Non-rigid rotational migration,

(iii) Switch rotational migration and

(iv) Uniformly directional migration.

(i), (ii), and (iv) are observed in known migration modes for some cell species. On the other hand, (iii) of which clockwise and counterclockwise rotational directions are repeated has not been observed as a typical migration mode. However, by changing cell culture environment referring to our numerical result, (iii) is observed in experiments using the esophageal cancer cells. This suggests that our model gives a standard framework for understanding collective cell migrations.

# References

[1] Camley, Brian A and Zimmermann, Juliane and Levine, Herbert and Rappel, Wouter-Jan. (2016). Collective signal processing in cluster chemotaxis: Roles of adaptation, amplification, and co-attraction in collective guidance, PLoS Comput Biol, volume 12, number 7, e1005008.

[2] M. Akiyama, T. Sushida, S. Ishida and H. Haga. (2017). Mathematical model of collective cell migrations based on cell polarity, Dev Growth Differ, Number of 2017, doi: 10.1111/dgd.12381.