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## Notes

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1. Investigation of the migration/proliferation dichotomy and its impact on glioma invasion

Gliomas are highly invasive brain tumors that exhibit high (and spatially heterogeneous) cell proliferation and motility rates. Our work is motivated by the migration/proliferation dichotomy (go-or-grow) hypothesis, i.e. cells proliferate only when they do not move, which may play a central role in these tumors. We introduce a lattice-gas cellular automaton (LGCA) model based on the go-or-grow mechanism. We study the effects of the migration/proliferation dichotomy mechanism on glioma invasion by means of parameter investigation and derive a macroscopic description of the LGCA model for proliferation and migration. Our analysis aims at predicting the velocity of the traveling invasion front, which depends upon fluctuations that arise from the motion of the discrete cells at the front.

BÖTTGER, KATRIN
Technische Universität Dresden
Germany

2. Large time asymptotics for a modified coagulation model

We study the large time asymptotics of a simplified two species model for particles (typically molecules or cells). The particles can be in two states: A “free” state where they simply move with a given velocity or an aggregated state where they do not move anymore. We show that depending only on the strength of the interaction between particles, either all of them eventually coagulate or some may escape.

CALVO, JUAN
Universidad de Granada
Spain

3. A nonlinear flux limited reaction-diffusion equation with applications in biology: analysis of travelling waves

We study the existence and qualitative properties of travelling waves associated to a nonlinear flux limited partial differential equation coupled to a Fisher-Kolmogorov-Petrovskii-Piskunov type reaction term. We prove the existence and uniqueness of finite speed moving fronts of \( C^2 \) classical regularity, but also the existence of discontinuous entropy travelling wave solutions. The resulting reaction flux limited diffusion system exhibits new properties compared to the classical reaction coupled to the linear diffusion equation, such as the existence of singular travelling waves which opens new perspectives of application to biology or traffic flow frameworks. We find singular profiles for the travelling waves of this equation which to a certain extent constitute the equivalent notion of shock waves in hyperbolic models for traffic flow. On the other hand, there is a wide variety and significant differences for the possible choices
of the velocity for the travelling wave solutions to the nonlinear reaction–diffusion equations with respect to those associated with linear diffusion type.

GUERRERO, PILAR
Centre de Recerca Matemàtica
Spain

4. Cluster Reverberation: A Mechanism for Robust Short-Term Memory without Synaptic Learning

Short-term memory cannot in general be explained the way long-term memory can – as a gradual modification of synaptic conductances – since it takes place too quickly. Theories based on some form of cellular bistability, however, do not seem to be able to account for the fact that noisy neurons can collectively store information in a robust manner. We show how a sufficiently clustered network of simple model neurons can be instantly induced into metastable states capable of retaining information for a short time. This could constitute a viable means available to the brain for robust short-term memory with no need of synaptic learning. Relevant phenomena described by neurobiology and psychology, such as power-law statistics of forgetting avalanches, emerge naturally from this mechanism.

JOHNSON, SAMUEL
Universidad de Oxford
United Kingdom

5. A model involving matrix-binding of paracrine signals reproduces early vascular patterning in avian embryos

During embryonic vasculogenesis, the earliest mechanism of blood vessel morphogenesis, isolated vascular cell progenitors called angioblasts assemble into a characteristic network-like pattern. So far, however, the mechanisms underlying the coalescence and patterning of angioblasts remain unclear.

We consider a hybrid cell-based approach consisting of two different modules. One one hand, angioblasts are represented as discrete and geometrically extended objects while relevant chemicals are modelled as continuous fields through a system of differential equations. Contrary to previous mathematical models that assume chemotaxis towards an autocrine signal, we favour an alternative mechanism based on matrix-binding of paracrine signals. Detailed morphometric analysis of in silico vascular networks and confocal microscopy images obtained from in vivo quail embryos reveals our model can reproduce the vascular patterns with high accuracy.

The work to be reported has been made in collaboration with W. de Back, J. Starrußand A. Deutsch (Center for High Performance Computing, Technische Universität Dresden), M. A. Herrero (Department of Applied Mathematics and IMI, Universidad
6. An optimization problem in radiotherapy

Selecting a suitable radiation strategy, in terms of radiation dose and its distribution over the selected planning target volume (PTV), is a key issue in clinical practice. To this day, this choice relies largely on the personal experience of specialists. For this reason, the development of tools that help in such decision making process would be useful for clinical purposes.

In this work we present a mathematical tool based on the Linear Quadratic (LQ) model to select the dose distribution over a PTV. To this end, we consider a tumor region where hypoxic, proliferating and healthy tissues may coexist. Our model is formulated as a variational problem where suitable constraints are included to account for clinical requirements. Under appropriate assumptions on the radiobiological parameters involved, the model thus obtained is shown to possess a unique solution, whose numerical simulation is discussed in terms of the decision-making process previously mentioned above.

López Alfonso, Juan Carlos
Universidad Complutense de Madrid
Spain

7. Microbes answer to Santa Rosalia: reconsidering the importance of aggregation in ecological networks

Homage to Santa Rosalia or Why are so many kinds of animals? With this question has opened Hutchinson in 1959 the seminal work that aimed to reconsider the niche conception that was taking place at that time after the foundation of the competitive exclusion principle [1]. Hutchinsons question has probably in the microbial world one of its most interesting challenges. Microorganisms represent an amount of biomass at least as big as that of plants with an amazing diversity, and have a key role in the evolution of the biosphere.

An increasing number of available data coming from high-throughput experiments has boosted the efforts to find ecological trends, and there is an increasing evidence pointing to a qualitative similar picture between the patterns found in macro and microorganisms [2]. Some progress have been made identifying important trends as taxa-area and distance decay relationships [3], or the influence of environmental and geographic variables as depth or salinity. These progresses have been possible in part
thanks to the reemergence of prokaryotic biogeography, but little attention have been
made to the methodological differences that microbiological data impose over classical
analysis methods of absence presence matrices.

In this talk we will discuss a null model [4] that handle these particularities and
from which we exactly compute single pairwise scores of either aggregation or segrega-
tion between any pair of operative taxonomic units. The evaluation of the significance
of single pairwise associations is still an open question, and whole community metrics
as nestedness or the C-Score are usually computed instead [5].

The comparison between the observed data and the respective randomizations,
leads to a striking result: aggregation is as frequent as segregation, a result that
is apparently in opposition to the macroscopic observed behavior where segregation
rather than aggregation have been found [5]. This result is also consistent with a
recently proposed Lotka-Volterra model [6] for plant- pollinator networks, where it is
shown how mutualistic interactions allow to the system to host a higher biodiversity,
as these interactions increase the structural stability of the network. This model,
together with the results presented here, suggest that the importance of aggregation
should be (re)considered to address Santa Rosalia’s question: Why are so many kinds
of animals in there?

[1] Hutchinson, G. E., Homage to Santa Rosalia or Why Are There So Many


[5] Gotelli, Nicholas J., Null Model Analysis of Species Co-Occurrence Patterns,

[6] Ugo Bastolla, Miguel A Fortuna, Alberto Pascual-García, Antonio Ferrera, Bar-
tolo Luque, Jordi Bascompte, The architecture of mutualistic networks mini-

PASCUAL GARCÍA, ALBERTO
Universidad Autónoma de Madrid
Spain

8. **A force dipole model for semi-dilute suspensions of swim-
ming bacteria**

We discuss results on suspensions of self-propelled bacteria where hydrodynamic in-
teractions between particles are taken into account [1]. Bacteria are modeled as point
force dipoles subject to two types of interactions: hydrodynamic interactions and
excluded volume type interactions introduced through the use of the Lennard-Jones potential. The alignment of asymmetrical particles and the presence of self-propulsion gives rise to a drastic reduction in the effective viscosity of the suspension. An explicit asymptotic formula for the effective viscosity in terms of known physical parameters is derived using a kinetic approach. This model allows for numerical simulations of a large number of particles, which are in agreement with the analytical results and experiment [2] through a full range of concentrations. This work is part of a doctoral thesis under the direction of Professor Leonid Berlyand.


**Ryan, Shawn**
Pennsylvania State University
USA