Parallel Session

Cancer I

# KINETIC-BASED MODELS FOR TUMOR-IMMUNE SYSTEM COMPETITION

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Joint work with Maria Groppi and Giampiero Spiga (University of Parma).

*Keywords*: Kinetic models, Macroscopic closures, Asymptotically autonomous systems, Stability, Forward and backward bifurcations.

A mathematical model, based on a mesoscopic approach, describing the competition between tumor cells and immune system in terms of kinetic integro-differential equations is presented. Four interacting populations are considered, representing, respectively, tumors cells, cells of the host environment, cells of the immune system, and interleukins, which are capable to modify the tumor-immune system interaction and to contribute to destroy tumor cells. A closed set of autonomous ODEs is then derived by a moment procedure; two three-dimensional reduced systems of ODEs are obtained in some partial quasi-steady state approximation and their qualitative analysis is performed.

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# TRAVELLING WAVES IN MODELLING CHEMOTHERAPY FOR LOW GRADE GLIOMAS

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*Keywords*: Gliomas, Porous medium equation, Travelling waves.

The phenomena modeled by means of reaction-diffusion equations occur naturally in chemistry and biology, but also in medicine. The simplest one-dimensional versions of the reaction-diffusion equation were investigated by Kolmogorow, Petrowski and Piskun and also Fisher (biological models of population spread) in the first half of the 20th century. Alan Turing began the study of two-dimensional reaction-diffusion systems in the second half of the 20th century. He first observed that a stable steady state in a system without diffusion may lose its stability after considering the diffusion component. On the other hand, solutions of reaction-diffusion equations reveal a wide range of behaviors, including the formation of travelling waves.

We are going to study the possibility of the existence of the travelling ways in the Fisher-Kolmogorov type model describing evolution in time of low grade glioma cells proposed by [1]. Low grade gliomas are primary brain tumours which evolve very slowly in time, however inevitably cause patient death. In system is coupled with a function describing the effect of the irreversible damage by chemotherapy treatment of proposed by functionally alive tumour cells.

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# PROBABILISTIC MODELS OF CANCER: AN ESTIMATE FOR THE TIME TO RELAPSE

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*Keywords*: Luria-Delbrück, Poisson process, Cancer models, Metastases, Recurrence.

Despite improvements in treatment and therapy of primary tumours, disease recurrence is still a major cause of death for cancer-diagnosed patients. In particular, even when a primary cancer is successfully and completely resected, its ability to generate distant metastases often lead to tumour recurrence.

Mathematically, the initiation and growth of metastases can be described through different generalizations of the famous Luria-Delbrück model. In this talk I will first introduce one of these generalizations, which models the initiations of distant metastases as a non-homogeneous Poisson process and their growth as independent branching birth-death processes. The rate of metastases occurrences thus depends on the deterministic primary growth function $n(t)$: I will consider the cases of constant and exponential functions, and argue that in some specific parameters regimes they can well approximate the logistic growth case as well.

Within this framework I will then discuss different features of the model, focussing in particular on the probability distribution of the time to cancer relapse. Finally, time permitting, I will compare some of the mathematical results provided by this model with real estimates collected from relevant literature on colorectal cancer.

# GENOME WIDE STUDY OF GLUCOCORTICOID RECEPTORS' ROLE IN ESTROGEN RECEPTORS REGULATED ENHANCERS IN BREAST CANCER

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*Keywords*: Transcription, Bioinformatics.

The estrogen receptor a (ERa)-regulated enhancers characterization in breast cancer transcriptional program and the molecular mechanisms underlying the repressive functions of glucocorticoid receptors (GRs) in ERa regulated breast cancer development remain poorly understood. Here I analyze and integrate the ChIP-seqs/GRO-seq sequencing data to study the genome-wide characterization of ERa-regulated enhancers and report the repressive role of GR on these enhancers and their cognate target genes by inhibiting binding of MegaTrans complex. GR SUMOlation plays the role of leading stable trans-recruitment of the GR-N-CoR/SMRT-HDAC3 co-repressor complex on these enhancers. Together, these results delineate active enhancers in a transcriptional program and uncover a mechanism that DNA-binding nuclear receptors recruitment in trans act effectively repressive role in regulation of target enhancers' biological function, with clear implications for breast cancer and other diseases.

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