Programm of the two lectures : **Modelisations of the tumor growth**

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The goal of the course is to present two possible modelling of the tumor growth. The first one is based on Markov chains and the second one makes use of a diffusion process, solution of a stochastic differential equation.

Lecture 1

We describe in detail our model where a tumor is considered as a collection of N independent and non-interacting cells. Once a treatment of radiotherapy is applied, the damages caused at each cell are heterogeneous and are measured by an integer between 0 and m. The state 0 (resp. m) corresponds to a cell in good health (resp. death). Between two applications of radiotherapy, a repair phase can also occur. Finally, the changing states of a given malignant cell is given by a Markov chain (Z_k) valued in the set $\{0, 1, \cdots, m\}$. We express the transition matrix in terms of the parameters of the model. One goal is to define the efficiency of the treatment. We calculate the probability that the tumor is completely destroyed after n applications of fractions dose.

[BKV2011] T. BASTOGNE, R. KEINJ et P. VALLOIS : *Multinomial model-based formulations of TCP and NTCP for radiotherapy treatment planning.* Journal of Theoretical Biology 279, 55-62, (2011).

A second way to take into consideration efficiency of the treatment is to consider the expectation of the lifetime of the tumor, where the lifetime T_N of the tumor is defined as the maximum of all the N individual lifetimes. We determine the mean and the variance of this random variable. We also show that $N \mapsto E(T_N)$ has a logarithmic behavior.

T. BASTOGNE, R. KEINJ and P. VALLOIS : *Tumor growth modeling based on cell and tumor lifespans.* Journal of Theoretical Biology 312, 76-86 (2012).

Lecture 2

We begin with a discrete setting. We consider as above a treatment which is applied to a population of cancer cells which evolve independently from each other. This aggregate of cells constitutes the tumor and its size corresponds to the number of all the elements. We take into account two antagonist forces. The first one is the natural duplication of cells. The second has two parts, the first one is the effect of the treatment and the second results from the self-limitation of the tumor (for instance a maximal possible volume).
We denote by $X_N(t)$ the size of the tumor at time t. Obviously, $N := X(0)$ is its initial size. We suppose that $\big(X_n(t)\big)$ is a birth and death process, i.e. a Markov chain in continuous time valued in $\mathbb{N}$ and with jumps equal to ± 1. It can be proved, that the proportion of cancer cells $\big(\frac{X_N(t)}{N}\big)$ converges in distribution as $N \to \infty$ to the diffusion process $V(t)$ solution of the following SDE :

$$\begin{cases} dV_t = V_t\ (a - b\,V_t)\,dt + \beta\,V_t\,dB_t \\ \\ V_0 = v > 0 \end{cases} \tag{0.1}$$

where $(B_t)_{t\geq 0}$ a standard Brownian motion starting from zero and a, β are real parameters

and $b > 0$. Note that if $\beta = 0$, then (0.1) equals the Verhulst-Voltera equation. This ordinary differential equation is often used to model the evolution in time of the size $V(t)$ of a population which is auto-limited.
We give qualitative properties of the diffusion process (V_t), solving (0.1).

J-S. GIET, S. WANTZ-MEZIÈRES and P. VALLOIS : *The Logistic SDE*. Submitted to Theory of Stochastic Processes on December 2014.