



ACCUEIL -> News -> Abstracts

ACCUEIL

A research group

Algorithms

Collaborators

Experimental data

News

Scientific Mediations

Some dynamical systems

Qui Fait Quoi

Rechercher



Autres Articles de :

Abstracts

Analysis of a four-state (...)

Characterization of the (...)

Classical mathematical (...)

Comparison of three modeling

DEs, DCs and Doses : Mathemati

Graph-based mathematical (...)

How the growth rate of (...)

Mathematical modeling of (...)

Modeling gene networks : (...)

Predicting lung tumor evolutio

Quantitative models of (...)

Spatial avascular growth (...)

Survival in a phase III (...)

Vascular remodeling during

Wavelet-based multifractal

MUTLI-SCALE MODELING AND OXYGEN IMPACT SIMULATION ON TEMPORAL EVOLUTION OF RECTUM CANCER TREATMENT BY RADIOTHERAPY

30/11/2015

Séna Apeke, Pascal Redou, Laurent Gaubert,
Nicolas Bousson, Dimitris Visvikis and Vincent Rodin

In the context of tumor growth, we build a multiscale stochastic model to predict cancer evolution during treatment by radiotherapy. Biological data are collected at the macroscopic scale, as PET images. We make use of microscopic model, at the cellular level, based on phase transfer probabilities in the cellular cycle. Both models are used by an intermediate model at the mesoscopic scale, which represents populations of cells in the different phases in a PET image voxel. The computations are performed at this mesoscopic scale, and we define functions to manage the interactions between these three scales. The main goal of this application is to simulate the effect of oxygen on tumor evolution during treatment by radiotherapy. For this purpose, we input various oxygen concentration values in the model and for each of them, we compare the clinical results at 8 days of treatment to those provided by the model, by using mutual information criterion. Finally, we use the best fitted oxygen value to predict tumor evolution in the following of the treatment. We highlight that it is useful, for clinical applications, to model tumor growth at our mesoscopic scale if the data are FDG images. This is more realistic, beyond a certain threshold, than working at the cellular scale. We also prove, by comparing the complexity orders of the algorithms used at cellular and population scales, that it is drastically more efficient in terms of computation time.



Voir ce site : [Séna Apeke - ResearchGate](#)