MULTISCALE MODELLING OF RANDOM GEOMETRIC PROCESSES, FOR MULTI-PHYSICS PROBLEMS OCCURRING IN BIOMEDICINE.

V. Capasso[1,2]

[1] Department of Mathematics
University of Milan
Via Saldini, 50
20133 MILANO,Italy
vincenzo.capasso@unimi.it

[2] CIMAB
(Interuniversity Centre for Mathematics
Applied to Biology, Environment, and
Medicine)
http://www.uniurb.it/biomat/CIMAB/

Key Words: *Multiscale, Multiphysics Problems, Tumours, Angiogenesis, Stochastic Geometry, Statistics.*

ABSTRACT

Nucleation (branching) and growth processes arise in a variety of natural systems, such as e.g. biomineralization (shell growth), tumor growth, vasculogenesis, DNA replication. All these processes may be modelled as birth-and-growth processes (germ-grain models), which are composed of two processes, birth (nucleation, branching, etc.) and subsequent growth of spatial structures (vessel networks, etc), which, in general, are both stochastic in time and space.

In Biology it is well known that "there is an important relationship between the form or shape of a biological structure and his function" [D'Arcy Thomson, 1917]. In Medicine, the understanding of the principles and the dominant mechanisms underlying processes like tumour growth or angiogenesis is an essential prerequisite for prevention and treatment. Thus with respect to all fields of applications, predictive mathematical models which are capable of producing quantitative morphological features can contribute to the solution of diagnosis or optimal control problems in medical treatment.

A quantitative description of the evolution of the resulting random sets can be obtained in terms of stochastic distributions à la Dirac-Schwartz, and local geometric mean densities, at various Hausdorff dimensions with respect to the standard Lebesgue measure [1,2,3].

A non trivial difficulty arises from the strong coupling of the kinetic

parameters of the relevant birth-and-growth (or branching-and-growth) process with underlying fields, such as biochemical signals, and the geometric spatial densities of the evolving random geometric structures. Methods for reducing complexity include homogenization at mesoscales, thus leading to hybrid models (deterministic at the larger scale, and stochastic at lower scales); for example in tumour driven angiogenesis we bridge the two scales by introducing a mesoscale at which we may locally average the microscopic birth (branching)-and-growth model in presence of a large number of vessels (fibers) [1,3].

The proposed approach, also suggests methods of statistical analysis for the estimation of mean geometric densities that characterize the morphology of a real network system [1,2].

REFERENCES

[1] V. Capasso, E. Dejana, and A. Micheletti, "Methods of stochastic geometry, and related statistical problems in the analysis and therapy of tumour growth and tumour-driven angiogenesis". In: *Selected Topics on Cancer Modelling. Genesis-Evolution-Immune Competition-Therapy*" (N. Bellomo, M. Chaplain, E. De Angelis,Eds),Birkhauser, Boston,2007.

[2] V. Capasso, A. Micheletti, and D. Morale, "Stochastic geometric models, and related statistical issues in tumour-induced angiogenesis", *Math. Biosciences* (2008). In press.

[3] V. Capasso, and D. Morale, "Stochastic Modelling of Tumour-induced Angiogenesis", *J. Math. Biology* (2008). In press.