

Preface

Higher order living things consist of many key components such as the skeleton, the locomotor apparatus, the respiratory apparatus, the cardiovascular system, the digestive system, nerves, ..., and then the central nervous system, which control them all in unity. Organs, tissues, and cells form the organic hierarchy of an individual, while each of them exhibits a certain individuality. *Individuality* is thus a central factor of life.

Cells can be thought of the basic units of individuality. For example, cancer cells invade normal tissues to destroy organs, viruses invade normal cells, and immune cells attack viruses. Inside a cell are the nucleus, microsomes, Golgi apparatus, lysosomes, mitochondria, ... and various other organelles, through which proteins transmit signals.

The purpose of the present monograph is to describe some recent developments in mathematical modelling and mathematical analysis of certain problems arising from cell biology. We are particularly interested in cancer cells and their growth via several stages. To describe the event, multi-scale models are applied, involving continuously distributed environment variables and several components related to particles. Hybrid simulations are also carried out, using the discretization of environment variables and the Monte Carlo method for the principal particle variables. These modelling and simulation tools are put on rigorous mathematical foundations.

This monograph consists of four chapters. The first three chapters are concerned with modelling, while the last one is devoted to mathematical analysis. In Chap.1, we examine molecular dynamics at the early stage of cancer invasion. We construct a pathway network model based on a biological scenario, and then determine its mathematical structures. In Chap.2, we introduce the modelling over viewing several biological insights, using partial differential equations. Transport mechanics and movement via gradients are the main factors, and several models are introduced including the Keller–Segel systems. In Chap.3, we turn to the method of averaging to model the movement of particles. This is based on mean field theories, using deterministic and stochastic approaches. Then, appropriate parameters for stochastic simulations are examined. The segment model is finally proposed as an application. In Chap.4, we examine thermodynamical features of these models and how these

structures are applied in mathematical analysis, that is negative chemotaxis, parabolic systems with non-local term accounting for chemical reactions, mass-conservative reaction-diffusion systems, and competitive systems of chemotaxis. We conclude this monograph with the method of the weak scaling limit applied to the Smoluchowski–Poisson equation.

Recent developments of cell biology using mathematical modelling occur at a very fast pace. Among them are bone metabolism, drug resistance, and signal transmission. We hope to extend and summarize these studies in future work.

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