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Editorial

It is my pleasure to announce the launching of a new series of issues of Discrete Applied Mathematics on Computational Molecular Biology. The rapid progress of molecular biology with the stimulus of the "Big Science" initiative of the Human Genome Project has generated tremendous challenges for mathematicians and computer scientists. During the last decade, a new discipline of computational molecular biology has emerged, with its own conferences and with a need for adequate publication venues. Discrete Applied Mathematics has been a natural host for some of these studies. Two volumes of high-quality papers of Discrete Applied Mathematics on Computational Molecular Biology (including this one) have already been published as special volumes. It is time to turn this temporary hostel into a long-term settlement. Future issues or volumes will from now on be part of an ongoing series within the journal.

The new series will emphasize within the computational molecular biology spectrum rigorous study and analysis of discrete models and structures arising in the field. Such models are both invaluable tools for solving practical problems in molecular biology and biotechnology, and are also a source of novel fascinating combinatorial structures. Historically, it is interesting to note that biology has been a source and an inspiration for the invention and study of discrete structures for at least forty years: Interval graphs are arguably the graph family that inspired the study of many specially structured graph families, and definitely that of all intersection graphs. They were invented independently in the late 1950s by the Hungarian Mathematician Hajos and in the pioneering studies on the linear structure of genes, by the biologist and later Nobel laureate Seymour Benzer.

The two first special issues of Discrete Applied Mathematics on Computational Molecular Biology have been a tremendous success. They resulted in two full volumes containing very high-quality papers, which were all thoroughly refereed according to the standards of the journal. I am grateful to the editors of the special volumes, Sorin Istrail, Pavel Pevzner and Ron Shamir, for their vision in the launching of these volumes, for the impressive collections already produced, and for their continued dedication and ongoing success. I also express my sincere thanks to all the anonymous referees for their essential contributions to this community effort. I am most thankful to editors of the special volumes for having now agreed to take on themselves edit a regular series within Discrete Applied Mathematics dedicated to Computational Molecular Biology. I am sure this will be continue to be a source of exciting problems, fascinating discrete mathematics, and important applications.

Peter L. Hammer
Editor-in-Chief