

The development of genome sequencing revolutionised the study of bacterial genetics. It helped scientists catalogue the gene content of various clinically and industrially important bacteria and opened up the field of comparative genomics. The research findings on bacterial genetics were further enhanced by the development of allied techniques that helped in examining the interactions and functions of many components of genome. Such developments were accelerated with the widespread adoption of quantitative deep-sequencing approaches.

This book presents the application of genomic tools to examine bacterial adaptation. Aswin introduces the concepts to explain the generation and analysis of multiple types of genome-scale data. The emphasis is on data analysis and interpretation. In the context of data analysis, the author has deliberately not provided the tables of software that can be applied to a particular type of data. However, he has discussed the fundamental principles that underlie some of these software. Much of the material is drawn from recent primary literature, which is the most powerful tool in the cutting-edge and fast-growing field of bacterial research.

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