
Preface

Over the past decade, the experimental ChIP-seq protocol as well as the associated computational analysis methods evolved rapidly. Researchers face a plethora of possible experimental and analytical ChIP-seq approaches, and the lack of a single perfect recipe can make use of the protocol daunting from the start. Each ChIP-seq experiment needs to be tailored to the protein or modification of interest, to the studied organism and to the biological question. Our aim is to summarise the points that need to be considered when performing such a study in order to obtain high-quality and interpretable data. In this book, we will discuss the importance of experimental and analytical choices and give advice for different scenarios. In particular, we will guide the reader through the computational analysis steps from initial quality control through peak calling to downstream analyses and visualisation. This book will thereby show a full workflow, with alternative paths that are suitable for researchers with diverse bioinformatics experience, using Unix command line and R-based solutions.

We hope that this book will help experimental biologists to design their ChIP-seq experiments with the analysis in mind, and to perform the first analysis steps themselves; moreover, it will support bioinformaticians to understand how the data is generated, what the sources of biases are and which methods are appropriate for the different analysis steps.