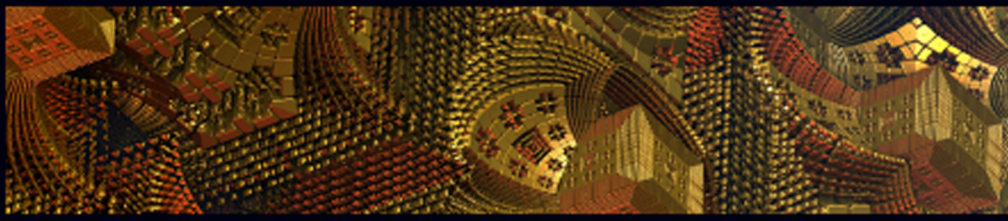
CRC FOCUS



PRACTICAL GUIDE TO CHIP-SEQ DATA ANALYSIS

Borbala Mifsud
Kathi Zarnack
Anaïs F Bardet

CRC Press
Taylor & Francis Group

A CHAPMAN & HALL BOOK

Practical Guide to ChIP-seq Data Analysis

Focus Computational Biology Series

This series aims to capture new developments in computational biology and bioinformatics in concise form. It seeks to encourage the rapid and wide dissemination of material for emerging topics and areas that are evolving quickly. The titles included in the series are meant to appeal to students, researchers, and professionals involved in the field. The inclusion of concrete examples and applications, and programming techniques and examples, is highly encouraged.

Systems-Level Understanding of Microbial Communities

Theory and Practice

Aarthi Ravikrishnan and Karthik Raman

Practical Guide to ChIP-seq Data Analysis

Borbala Mifsud, Kathi Zarnack, Anaïs F Bardet

Practical Guide to ChIP-seq Data Analysis

Borbala Mifsud

Kathi Zarnack

Anaïs F Bardet

CRC Press
Taylor & Francis Group
Boca Raton London New York

CRC Press is an imprint of the
Taylor & Francis Group, an **informa** business

CRC Press
Taylor & Francis Group
6000 Broken Sound Parkway NW, Suite 300
Boca Raton, FL 33487-2742

Printed on acid-free paper
Version Date: 20181008

International Standard Book Number-13: 978-1-138-59652-8 (Hardback)

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.

Taylor & Francis
Taylor & Francis Group
http://taylorandfrancis.com

Authors

Borbala Mifsud obtained a PhD in molecular biology at the Institute of Molecular Pathology (IMP) in Vienna, Austria. In the laboratory of Thomas Jenuwein, she worked on epigenetic profiling of a histone methyltrasferase mutant mouse, using ChIP-seq. In 2010, she started her postdoctoral work at the EMBL European Bioinformatics Institute (EBI) in the laboratory of Nicholas Luscombe. She is currently an assistant professor at Hamad Bin Khalifa University, Doha, Qatar and honorary lecturer at Queen Mary University London, UK, working on 3D chromatin conformation and the integration of epigenomic data.

Kathi Zarnack earned a PhD in molecular biology at the Max-Planck Institute for Terrestrial Microbiology in Marburg, Germany, working on the impact of posttranslational modifications on transcription factor specificity. Moving into bioinformatics, she then joined the EMBL European Bioinformatics Institute (EBI) in Hinxton, UK, as a postdoctoral researcher in the group of Nicholas Luscombe. Since 2014, she leads a research group on Computational RNA Biology at the Buchmann Institute for Molecular Life Sciences (BMLS), Goethe University Frankfurt, Germany.

Anaïs F. Bardet completed a PhD in computational biology in the laboratory of Alexander Stark at the Institute of Molecular Pathology (IMP) in Vienna, Austria. She studied the conservation of transcription factor binding sites in different *Drosophila* species and developed tools and pipelines for the comparative analysis of ChIP-seq data. She then worked as a postdoctoral researcher in the laboratory of Dirk Schübeler at the Friedrich Miescher Institute for Biomedical Research (FMI) in Basel, Switzerland, where she investigated the sensitivity of transcription factors to DNA methylation. Since 2017, she is a tenured researcher at the National Center for Scientific Research (CNRS) at the University of Strasbourg, France, where she develops projects exploring the regulation of transcription factor binding.

Taylor & Francis
Taylor & Francis Group
http://taylorandfrancis.com

Contents