

# Preface

High-throughput sequencing (HTS), also named next-generation sequencing (NGS) or massive parallel sequencing (MPS), is an amazingly speedy evolving world. Since 2005, when the first HTS equipment was released to the market by 454 Life Sciences, there have been dozens of companies developing a variety of methods that offer distinct characteristics, and therefore, each protocol should be applied wisely. Being aware of the wide range and complexity of the reported HTS strategies, we observed that there is a lack of bibliographic support when scientists need to choose the most suitable methodology or combination of platforms and to define their experimental designs to achieve unambiguous aims.

Genomics core facilities can give limited advice on which technology fits one's purposes and the number of cloud-based HTS data analysis pipelines, to process output raw data in a standard mode, is rapidly increasing. Ideally, scientists that request this sort of services should have clear clue questions concerning wet-lab procedures and data analysis. Thus, the purpose of this guideline is to collect in a single volume all aspects that should be taken into account and the reasons behind when HTS technologies are being incorporated into a scientific research project, and it is directed to both, specialist, but primarily to newcomers.

Accordingly, the book encloses a brief introduction on HTS technologies challenges, followed by 14 chapters with proficient discussions and recommendations to select the best among all the available workflows for sample processing, alignment of results, algorithms at downstream data analysis, etc., and the minimum number of samples that should be characterized in each assay for accurately sequencing and interpreting genomes, sets of RNA molecules, DNA methylated regions, nucleic acids interacting with targeted proteins, metagenomes, metatranscriptomes, and/or single-cell contents. Moreover, examples of several successful strategies are analyzed to make the point of the crucial features.

Whole genome sequencing (WGS) wet-lab procedures and data analyses are portrayed in Chap. 2, followed by a description of how to face the characterization of partial genomes (i.e., genes of interest) in a number of samples in Chap. 3. In addition, a detailed variety of sequencing library preparation approaches and results examination pipelines to catalogue transcriptomes, sets of noncoding RNAs and

small RNAs as well as ribosome networking RNAs under singular conditions, are depicted within Chaps. 4–8. Furthermore, ways of studying epigenetic events such as DNA methylation and interactions of DNAs or RNAs with targeted proteins are illustrated in Chaps. 9, 10, and 11, respectively. Chapters 12 and 13 discuss the appealing world of classifying environmental (e.g., microbial communities) genomes and transcriptomes by means of metagenomics and metatranscriptomics. Likewise, the hot topic of single-cell DNA and RNA content characterization is considered in Chaps. 14 and 15. The last chapter of the book, Chap. 16, is a detailed protocol on how to submit HTS data to public repositories as required when this sort of results are being published.

As a special feature, this book includes a sort of quick reference guide as appendix for each chapter, where readers can, at a glance, access a figure representing the main steps of the wet-lab and bioinformatic workflows as well as a table that gathers information about the experimental design recommendations for the techniques described and another one referred to the bioinformatic recommended analysis software together with the results yielded by each program. The intention of this section is to grant rapid access to a summary of the principles of each of the methodologies described.

Considering that HTS technologies can be applied to a vast variety of biological questions and are used by scientists working in unlike fields such as biology, medicine, or ecology, and in a wide range of taxonomical levels (mammals, plants, bacteria, viruses, etc.), we hope that this book will be a precious resource for all scientist that lack skills in HTS and pretend to incorporate such technologies into their research.

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Field Guidelines for Genetic Experimental Designs in  
High-Throughput Sequencing

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2016, XI, 399 p. 72 illus., 42 illus. in color., Hardcover

ISBN: 978-3-319-31348-1