Preface

In the broad panorama of academic publishing regarding next-generation sequencing, there is scarcity—if not a lack—of textbooks that tackle experimental issues, rationale of data analysis, and biological interpretation of genome-level data simultaneously.

The current textbook is not intended to be a cookbook of quantitative approaches in Biology, nor is it a rigorous collection of theorems. It aims to create a common language that can be useful to experimental biologists and data analysts: the former would be able to read papers critically based on transcriptomics and to judge independently whether conclusions are appropriate, to design their own transcriptomic experiments, and to create a dialogue with data-analysts to determine together the most appropriate approaches for the specific questions answered. The latter would have a glimpse of the experimental biologist's point of view, with numerous examples of how techniques that are familiar to an analyst have answered specific biological questions.

The target audience of this book are graduate students with a background in the Natural Sciences (for example, Cellular and Molecular Biology, Neurobiology, Evolutionary Biology, Applied Mathematics, Physics, or Chemistry) who are interested in acquiring the bases of next-generation RNA sequencing and transcriptome analysis and learning how these techniques can be used to derive new knowledge about the functional organisation of the nervous system. It is beyond the scope of this book to include a detailed review of RNA and neuron biology, or of the needed mathematical tools. So we will take for granted some basic knowledge in Molecular Biology, Neurobiology, Linear Algebra, and Calculus. Throughout the book, we made our best effort to complement the basics of quantitative analysis with relevant practical examples of how we used these tools to tackle specific questions in real laboratory life. This approach may seem too simplified for students trained in the quantitative sciences and still difficult to digest for 'wet-lab' biologists but represents—in our opinion—the best possible compromise.

The book is based mainly on notes for the Neurogenomics course that was held in 2015 at Scuola Normale Superiore in Pisa with some later integrations.

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