
Preface

For a few years, the scientific community has acknowledged that environmental DNA contains a huge amount of information about all types of organisms found in ecosystems. It is thus very attractive to try to at least partially read this information encoded in DNA molecules. The development of next-generation DNA sequencing boosted this research area, and opened the possibility of high-throughput data acquisition. However, implementing an eDNA study is not as simple as carrying out a DNA analysis on a single species. It also requires putting together many different skills, including obviously all the classical corpus of knowledge in ecology, but also skills in the field for sampling, skills at the bench for producing the sequence results, and skills in bioinformatics for dealing with massive amounts of sequence data.

As for any emerging scientific area, many preliminary or pilot experiments have been published thus far, as well as many reviews highlighting the potential of eDNA in ecology, paleoecology, archaeology, forensics, and biodiversity management. Unfortunately, despite this literature, extracting pertinent information stored in eDNA is not straightforward, and not exempt from biases. There are many potential traps in eDNA studies. The experiments must be designed very carefully, taking into account all the problems likely to occur at any step of the analysis, and include appropriate controls to ensure accurate final results. In light of these observations, we decided a few years ago to organize DNA metabarcoding schools, with now at least one session per year. Seven editions have occurred since 2012. At the beginning, the number of applicants was reasonable, however it is no longer the case due to the recent increasing interest in eDNA. The number of applicants is now far more than our teaching

capacities, and we do not feel comfortable rejecting applications from many motivated young scientists. This book is an attempt to cope with the high demand from ecologists for developing research involving eDNA.

Our aim was to write a book for ecologists, who do not necessarily have a strong background in molecular genetics. As a result, some parts might look naive to experienced molecular ecologists. Moreover, it was our wish not to give very precise protocols, but to provide the background information that will ultimately enable the design of sound experiments. This book is technically oriented, as the difficulties in eDNA studies mainly derive from the technical aspects, with which ecologists are usually not familiar. When working with eDNA in ecology, the questions and concepts remain the same as in any ecological study, and we did not emphasize these aspects, as many excellent ecological textbooks are already available. Incidentally, it is interesting to note that eDNA now allows a few questions that could not be previously addressed to be tackled. Another objective of this book was to deliver a relatively comprehensive bibliographic orientation, allowing the readers to refer to the primary literature. However, due to the recent burst of eDNA studies, it becomes very difficult to be complete, and clearly, we did not cite all pertinent papers.

Finally, we must also recognize that this book reflects our view of eDNA analysis, and does not necessarily represent all the different opinions expressed in the scientific community. Globally, our objective was to favor simple and robust solutions that might not be optimal in terms of accuracy, but which can be implemented at large scales for analyzing hundreds or thousands of environmental samples.