

EDITORIAL

## BIOMAP: A Home for All Biology Methods

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The moments of rapid acceleration of scientific progress have different origins. Some occur due to conceptual advances, such as the description of evolution by natural selection or the development of relativity theory. Some occur due to technological advances, and in the case of Biology, the development of new methodologies has been and is a driving force of its progress for more than 50 years. Both aspects go often together, an advance in basic knowledge leads to a tremendous advance in technology and vice versa. For example, the first DNA cloning experiments in the 1960s and 1970s were done by people investigating mechanisms underlying the ability of plasmids to acquire genes conferring antibiotic resistance and to exist separately from bacterial chromosomes and by groups that were studying enzymes that restrict and destroy foreign DNA [1]. Today, DNA cloning methods are used in multiple areas of the biological and chemical sciences. In our days, the advent of programmable and efficient gene targeting using the bacterial RNA-guided CRISPR-Cas9 system in animals and plants is transforming biology [2]. Initially, these systems were described by scientists, which were studying the immunity of some bacteria against certain bacteriophages [3].

On the other side, as an example, the advance in DNA sequencing methods has contributed to an enormous advance in our knowledge of many organisms. Certainly the most exciting of these findings was the first draft of the human genome published by the International Human Genome Sequencing Consortium in the journal *Nature* in February 2001 with some 90% sequence of the entire genome's 3 billion base pairs complete [4]. A surprising finding of this first draft was that the number of human genes appeared to be significantly fewer than previous estimates, which ranged from 50 000 genes to as many as 140 000.

Some technology developments open new avenues that right now we can only envisage but that can already predict tremendous advances in our knowledge in the next future. This is the case with the advance of proteomic and transcriptomic techniques and the single-cell RNA-seq technology. Throughout

history, doctors have prescribed certain medicines for certain conditions. Yet, sometimes a medicine does not work for a particular person. We now know that genetics may play a large role in the way people respond to certain medication. Personalized medicine techniques such as genome sequencing can reveal mutations in DNA that influence diseases. RNA-seq can show which RNA's are involved in specific diseases. Unlike DNA, levels of RNA change in response to the environment. Therefore, sequencing RNA can reveal a broader understanding of a person's state of health. Recent studies have linked genetic differences between individuals to RNA expression, translation, and protein levels. Oncogenomics is the application of genomics and personalized medicine to cancer research and treatment. High-throughput sequencing methods are used to characterize genes associated with cancer to better understand a given disease pathology and to improve a personalized drug treatment [5].

As the biological sciences advanced during the 20th century, an enormous volume of knowledge was generated and separate fields emerged as genetics, cell biology, ecology, microbiology, biochemistry, and molecular biology to tackle the complex sub-systems that together make up living systems. The increasing volume of knowledge generated in each of these subdisciplines made (and makes) it increasingly difficult for researchers specialized in one discipline to interact with those studying other. Scientists in each of these disciplines usually attend separate meetings, and publish in different journals, and the same occurs with the different methods in Biology. There is an explosion in new methodologies in Biology, but most of the publications on the topic are scattered among a large number of journals that belong to a variety of categories. However, to accelerate progress in the life sciences, researchers from different subdisciplines need to interact and collaborate to a greater extent. A recent example of the latter concerns the implementation of mathematical modeling tools to probe the pharmacokinetics and pharmacodynamics relationships of the available anticancer agents to improve personalized treatments [6]. Without the advance in both

instrumentation and image processing software, the revolution in cryo-electron microscopy that we have nowadays would have been inconceivable. Due to this collaboration of scientists working in these different disciplines, a flood of biological insight is being gained on systems traditionally refractant to structural characterization [7].

There are few journals dedicated to methods in Biology, and most of the methods published are disseminated in many specific journals. We believe that our advance in knowledge will benefit from a common forum, in which methods are shared by scientists having different backgrounds. With this philosophy we have established *Biology Methods and Protocols*. We have assembled an Editorial Board whose members have made many important contributions in the different disciplines of Biology. We hope that this new journal will grow into a successful and dynamic interdisciplinary methods journal, where the audience will not be restricted to one discipline or subdiscipline. In the tradition of other Oxford University Press journals, the manuscripts published will rely on a thorough peer-review process. We aim to publish new methods as well as modifications of established methods that may provide valuable tools for the research community. We strongly believe that small steps are also important. As an example, the tools and procedures that were the keys to the development of the recombinant DNA technology largely emerged as enhancements and extensions of existing knowledge, i.e., they were evolutionary, not revolutionary, in nature, and it is clear that they were transformational in its impact [8].

Published manuscripts are expected to present valid and reproducible results in sufficient detail to assess the validity of the inferences drawn and enable readers to implement these

new methods. Published papers will be available to read by all under an Open Access Model and accepted manuscripts will be visible online in the shortest possible time after acceptance. We hope to become a journal whose quality will make it rewarding for the scientist to publish their methods, and one of the references to link users with new tools.

## References

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