

Modeling Demographic Processes In Marked Populations

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 Springer

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Foreword

Demography can be considered the key to understanding much of biology. It is the demographic processes of birth and death which govern the spread of populations through environments and the spread of genes through populations. An understanding of demography can yield not only an understanding of population size and population change, it can help us to understand the form and function of life histories; when organisms mature, when they breed, and when they die. Demographic insights allow us to see how populations function, how they interact with their changing environment, and how they adapt.

The analysis of demographic processes in free-living organisms is however no simple task and involves considerable challenges in observation and analysis. Some 20 years ago, there was a concerted effort to promote inter-disciplinary collaboration between biologists and statisticians to address these challenges and thereby to further our understanding of demographic processes in natural populations. Although many diverse organisms can be studied in the wild, birds have proved particularly amenable with large numbers being marked and followed by large networks of observers. It was no coincidence then that the European Union for Bird Ringing (EUR-ING) played a leading role in these initiatives, teaming up in the mid-1980s with the Mathematical Ecology Group of the Biometric Society, and the British Ecological Society, to bring together experts from diverse fields to address the challenges in hand. Twenty years on, progress has been considerable and we now have significant insights into demographic processes thanks to the wide range of quantitative tools and systematically collected datasets which have been built up over this period.

The biological questions and the methodological challenges are however by no means settled, indeed the field continues to progress at an ever accelerating pace. In 2003, a group of just under 100 scientists met to discuss and identify the key areas of development in which ongoing research effort should be focused. As listed in the Contents section, the group identified five areas defined by biological applications and five areas defined by statistical approaches including the issue of software with which to implement state-of-the-art analyses. Experts in each of these areas then took the lead in assembling authoritative contributions, with one or two overview- or perspectives- papers prepared by leading figures, and three to five primary research papers which reported the most significant new findings. A further open-forum was created for notable contributions which lay outside the ten targeted areas. Authors

came together to discuss their contributions at a meeting hosted by the University of Otago at the beginning of 2007.

This field continues to move rapidly, but we hope this resulting volume will stand as a definitive compilation on the state-of-the-field at the present time, and that it will steer the further development of the field over the years ahead. As reflected in this volume, we anticipate increasing emphasis on integrated approaches which combine multiple sources of information and an increasing emphasis on Bayesian approaches. In terms of biological applications, it has traditionally been the field of wildlife management which has provided the impetus for developing modern approaches, but increasingly we see the activities of evolutionary biologists and biodemographers as a driver of growth in this field. Modeling demographic processes in marked populations is a truly interdisciplinary endeavour, and we look forward to continued fruitful dialogue not just between biologists and statisticians but between these different fields of biology which are conceptually similar and which share the same need for sound quantitative approaches to demographic analysis.

This volume has been a team effort, and as well as crediting all the work of the authors themselves and the associate editors listed in the Contents section, we would like to acknowledge Prof. Richard Barker and his team for their hard work and kind hospitality in hosting a successful meeting of contributors in Dunedin. All contributions have benefited from the expert input of at least two referees, and we would of course like to thank Prof. G.P. Patil, Manjula Jude (Project Manager at Integra Software Services), Lindy Paul and the team at Springer for facilitating the publication of this volume.

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