Design and Analysis Methods for Fish Survival Experiments Based on Release-Recapture

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American Fisheries Society

Monograph 5

Publication and Funding of this Monograph
were made possible by a grant from

Chelan County Public Utility District

Wenatchee, Washington 98801

American Fisheries Society Monographs: ISSN 0362-1715
Library of Congress Catalog Card Number: 87-070785
ISBN 0-913235-41-5

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Bethesda, Maryland 20814

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Preface

This monograph presents design and analysis methods for a large class of survival experiments based on release-recapture of marked populations. We developed the underlying theory primarily to address fishery issues involving spillways, hydroelectric turbines, bypass systems, and related structures on the Columbia River in the northwestern United States. Many other applications exist, however. Treatment might include dosing of lead or various pesticides to determine the chronic effect of a contaminant on survival. The general theory is for the analysis of multiple interrelated release-recapture data sets; the methods presented herein apply to any experiments involving treatment and control groups of marked animals.

During the past 20 to 25 years, much literature has appeared on the estimation of population parameters based on capture-recapture sampling. One branch of the literature includes bird-banding and fish-tagging studies where the data are from a single, terminal, harvest-related recovery, as synthesized by Brownie et al. (1985). During the same time period, other literature appeared on studies dealing with multiple recaptures of marked animals, often referred to as capture-recapture sampling for open populations, or "Jolly-Seber models" after two of the leading contributors. Seber (1982) reviewed this literature. The links between these two major developments were outlined by Brownie et al. (1985) and Brownie and Pollock (1985).

A general theory for ecological experiments and studies in which marked animals are used relies on both of the above bodies of literature plus other developments (e.g., White et al. 1982). Overall, this subject and the literature on which it is based are fairly complex and diverse. Until recently, the separate approaches and models were developed in isolation, usually using different literature, notation, and context. In the past 10 years a coalescing of this work has led to the recognition that most "capture-recapture" models are special cases of a more general theory. Today, the entire area of capture-recapture is being unified under one umbrella of theory, which provides the context for the developments we present here.

As an example of progress in the theory and computation for capture-recapture sampling, one might consider the analysis done by Hammersley (1953), who presented a method for estimating the death rate in open-population models and applied it to data on the alpine swift *Apus melba* banded in Switzerland during 1920-1950. His estimation method involved a 28 x 28 matrix and a complex iterative process. Minor iterative cycles were embedded in major cycles and were done on a desk calculator. Approximately six major cycles were required for the swift data, and each required about 10 days of hand computation. The inversion of the matrix required about 4 hours of SEAC computer time (at the U.S. National Bureau of Standards). Hammersley estimated that this inversion could have been done in "about 2 months" on a desk calculator. In summary, Hammersley's method required about

100 person-days of computation on desk calculators of the day for this large data set.

Biologists now enjoy the sophisticated formalism of the Jolly-Seber model and the many extensions and restrictions that have been published in the past 21 years. The Jolly-Seber method itself also benefited from the work of Hammersley (see Cormack 1968). Many Jolly-Seber models have parameter estimators in closed form, and estimates can be computed in a few minutes on a calculator if the data are summarized in a suitable form. Monte Carlo studies have investigated the small-sample properties of the Jolly-Seber class of models, and much is now known about the analysis theory of capture-recapture sampling data. The improved models and theory are accompanied by tremendous advances in computer technology. Commonly available desktop computers now can fully analyze the alpine swift data in about 20 seconds of computer time.

Program RELEASE, which can be run on IBM-compatible microcomputers, was developed to allow biologists to focus on design, data collection, analysis, and inference, rather than on computational details. This software is powerful and easy to use, but it can be misused if the material in this monograph is not understood. To avoid potential misuse, we encourage understanding and careful consideration of the material in this monograph (the Reader's Guide in Section 1.1.5 should prove useful). We hope readers will examine the theory and examples to gain familiarity with the basis of the methods presented. Practice running program RELEASE with example data sets would be helpful in understanding some of the issues covered. Readers are encouraged to compare theory and application and gain familiarity with the Monte Carlo features of the software.

Additional research and applications should be stimulated by this monograph. Biologists and statisticians need to work together more closely to ensure that additional well-designed, empirical studies result. We hope to see the various research findings published in refereed, primary journals. The lack of publication in primary journals has been a problem in the past (e.g., Fletcher 1985), as much of the fisheries research on the Columbia River has appeared in the gray literature.

The material in this monograph can be understood by persons with two or three upper division courses in statistics and some elementary computer skills. The less background one has in these subjects, the more one may have to struggle. The main prerequisites are an interest in the topic, an interest in science and experimentation, and a curiosity about sound and thorough inference procedures.

We express our sincere thanks to the Chelan County Public Utility District, Wenatchee, Washington, for funding the research that led to the publication of this monograph. The District was both unselfish and extremely farsighted in allocating funds to develop rigorous design and analysis methods for this class of experiments.