

Preface

This book germinated from an earlier project examining patterns of genetic diversity retained in an isolated stand of American chestnut founded in the late 1800's (Pierson et al., 2007). The stand was initiated with 10 trees, and our interest was to find out whether the stand exhibited signs of losses of genetic diversity, or unevenness in the spread of genetic diversity, due to population genetics effects associated with small populations (drift, differential offspring or pollen productivity, spatial effects, etc.). The American chestnut was one of the most important trees of the forests of eastern North America until it came under attack from the chestnut blight threatening it with extinction. Efforts are underway to develop new strains of American chestnut that are blight resistant so that the species can be reintroduced to proliferate and regain its natural place in eastern forests. Our previous research, which is described in some detail in Chapter 16, was conducted in part to determine to what degree the introduction of small numbers of founders might be problematic in coming restoration projects to return the species to its native habitats. That study led us to ask: what are the best ways to reintroduce species to promote population growth and the retention of genetic diversity? How do founder number, founder placement geometry, and life history characteristics interact to affect population growth and genetics trajectories?

We developed the computer program NEWGARDEN to examine these questions. This book is both an instruction manual on how to use the program, and a series of examples where we have used the program to demonstrate that founder number, geometry, and varying life history characteristics can interact to affect population expansion and diversity in complex ways. Since most species are constantly throwing off small isolated populations, most threatened and endangered species likewise involve such stands, and the activities of man are creating an increasingly fragmented world, the implications of our results also take on relevance for evolutionary and ecological considerations across a wide variety of plant species. This book is in no way comprehensive with regard to the above issues. Instead, we hope it demonstrates that different species will call for different introduction strategies or evolutionary analyses, and that NEWGARDEN can contribute to examining the breadth of factors affecting establishing

populations. A disk including the NEWGARDEN program and instructions on how to use it are included with this book. Additional information may be found at: <http://math.uc.edu/~pelikan/NEWGARDEN>

We both would like to thank the University of Cincinnati and our respective Departments of Biological Sciences and Mathematical Sciences. Thanks also to the publishing team (especially R. Primlani) at Science Publishers for this opportunity and all of their assistance. We are grateful for funding provided by the Ohio Plant Biotechnology Consortium and the American Chestnut Foundation in support of the early research that acted as the stimulus for this work. Our thanks also to Theresa Culley, Brian Keane, Tom Kuehnert, Martin Lawrence, Jacky Lee, Stephen Matter, Sarah Pierson, and the Science Publishers editors, all of whom improved the manuscript through reviewing, commenting upon, and/or providing suggestions and materials. SR especially thanks Colleen Daley for her ever-inspiring support on this project: she has contributed to every page. Likewise, SP thanks Anita Buck for her encouragement and advice.

Steven Rogstad
Department of Biological Sciences
University of Cincinnati
Cincinnati, OH 45221-0006
USA
steven.rogstad@uc.edu

Stephan Pelikan
Department of Mathematical Sciences
University of Cincinnati
Cincinnati, OH 45221-0025
pelikan@math.uc.edu