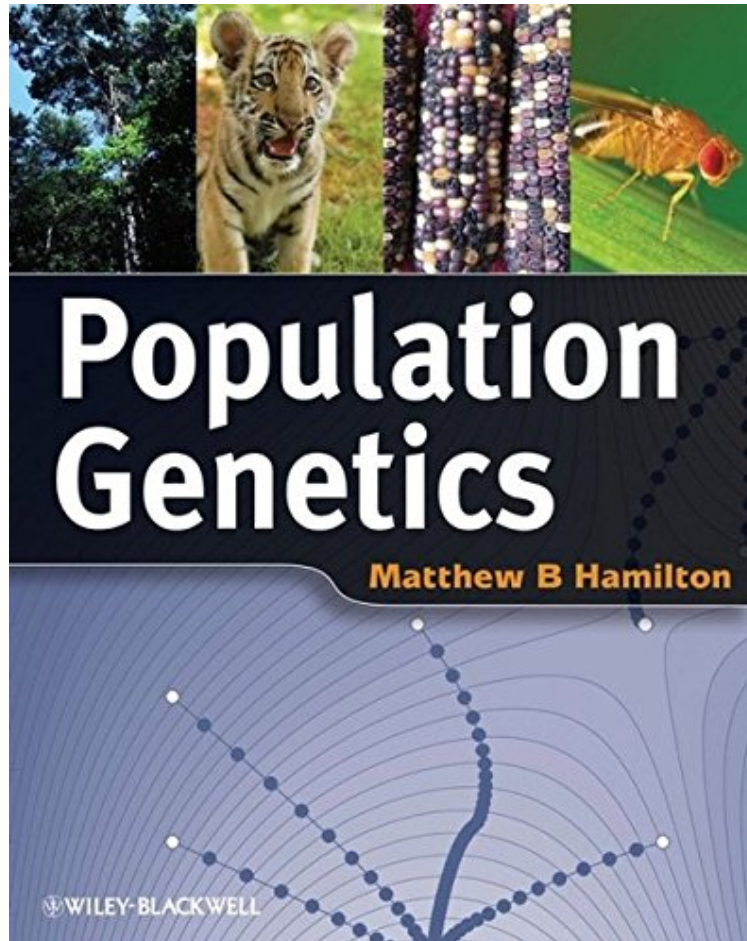


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To achieve these goals, the book design emphasizes a well explained introductions to key principles and predictions. These are augmented with case studies as well as illustrations along with introductions to classical hypotheses and debates. (Zentralblatt MATH, 2012) The most catching aspect of Hamiltons book is its extremely well thought-out structure and pedagogical concept. All sections are well motivated in the respective introduction and all chapters have reviews at the end. A large number of problems have been interspersed throughout the text for students to work on, and the solutions are provided at the end of each chapter. A very interesting and novel feature is the use of so-called interact boxes, which are essentially links to interactive learning and simulation software available on the internet. (Human Genetics, December 2009) "Hamilton's volume would be the best choice for someone seeking a thorough grounding in the subject." (The Quarterly of Biology, April 2010) "Both population biologists and upper-level biology students will appreciate the relatively clear explanations of exceptionally difficult material." (CHOICE, November 2009) From the Back CoverThe key to understanding population genetics is gaining familiarity with a set of traditional conceptual approaches along with classical hypotheses and debates. Armed with this background, many empirical studies will be readily understood because the basic hypotheses they address are understood from first principles. To achieve this goal, this book is designed to contain mostly conceptual material that is augmented with case studies as illustrations. Several outstanding pedagogical features including methods boxes and exercises to assist students in conducting simulations using public domain software will be integrated into the text.About the AuthorMatthew B. Hamilton teaches population genetics, evolutionary processes, and similar undergraduate and graduate courses at Georgetown University. He conducts research on the processes that shape genetic variation within species using molecular genetic markers as well as predictive mathematical models.