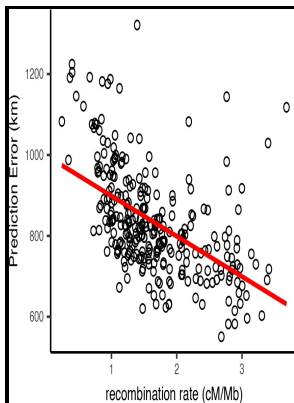


Recombination variability and evolution - algorithms of estimation and population-genetic models

Chapman & Hall - Recombination, Variability and Evolution : Algorithms of Estimation and Population Genetics by S. I. Preigel and A. B. Korol (1994, Hardcover) for sale online

Description: Using an interdisciplinary approach, the authors provide an adaptationist interpretation of the basic features of recombination, its evolutionary significance as a key process in reproduction and its importance in genetic mapping. The book synthesizes much recent information in the fields of evolutionary genetics of recombination, the analysis of genetic markers and breeding applications. The authors analyse recombination through a consideration of computer models, large *Drosophila* populations and an empirical approach to current theories. Practically-orientated readers will be interested in the discussion of a wide spectrum of mapping methods and the new algorithms proposed for genetic mapping of quantitative loci.



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Recombination variability and evolution - algorithms of estimation and population-genetic models
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Notes: Includes bibliographical references (p. [294]-354) and index.
This edition was published in 1994

Tags: #From #molecules #to #populations:
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Recombination Variability and Evolution: Algorithms of estimation and population

APPENDIX A: CALCULATIONS Let gen 0 represent the current generation, gen 1 represent the generation being simulated and gen 2, gen 3, gen 4, ..., etc.

Exploring Population Genetic Models



Filesize: 35.43 MB

With Recombination Using Efficient Forward

Fine-scale recombination rate differences between sexes, populations and individuals. In fact, it has been shown that recombination can also lead to the spurious inference of selection ;. Recombination rate evolution and the origin of species.

From molecules to populations: appreciating and estimating recombination rate variation

This article presents the theory describing the behaviour of two linked loci under selection. In order to study the effect of noncontemporary sequences on the recombination estimate, we also analyzed 10 samples of P1 consisting of a mixture of two randomly chosen sequences from each time point.

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