



Genetic Mapping in Experimental Populations

By J. W. Van Ooijen, J. Jansen

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Genetic linkage maps are an increasingly important tool in both fundamental and applied research, enabling the study and deployment of genes that determine important biological traits. This concise introduction to genetic mapping in species with disomic inheritance enables life science graduate students and researchers to use mapping software to produce more reliable results. After a brief refresher on meiosis and genetic recombination, the steps in the map construction procedure are described, with explanations of the computations involved. The emphasis throughout is on the practical application of the methods described; detailed mathematical formulae are avoided and exercises are included to help readers consolidate their understanding. A chapter on recognising and solving problems provides valuable guidance for dealing with real-life situations. An extensive chapter dedicated to the more complex situation of outbreeding species offers a unique insight into the approach required for many economically important and model species, both plants and animals.

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Editorial Review

About the Author

Dr J. W. (Johan) Van Ooijen has worked in the field of genetic linkage analysis for more than 20 years. He developed the QTL analysis software MapQTL® and was also involved in the development of JoinMap®, Piet Stam's genetic linkage mapping software. He continues the development of both software packages in his company, Kyazma B.V., and regularly teaches courses on genetic mapping and QTL analysis.

Dr J. (Hans) Jansen is a senior member of the Biometris group at Wageningen University and Research Centre. He is involved in research projects on various applications of molecular markers, including genetic diversity studies, the construction of genetic linkage maps, and QTL analysis involving multiple pedigree-related populations.

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