

Sickle Cell Alleles Simbio Answers

Environmental Safety of Genetically Engineered Crops Robust Methods for Estimating Allele Frequencies *Rebecca Grumet*

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since the mid 1990s when the technology was first introduced the cultivation of genetically engineered ge crops has grown exponentially in the u s alone adoption rates for transgenic cotton corn and soybeans are between 70 90 across the globe 14 million farmers grow ge crops in more than twenty countries yet many countries are discussing and debating the use and adoption of ge technology because of concerns about their impact on the environment and human health now in this comprehensive handbook a team of international experts present the scientific basis for ge crops placing them in the context of current agricultural systems and examining the potential environmental risks posed by their deployment an integrated approach to an increasingly hot and globally debated topic the book considers the past present and future of ge crops and offers an invaluable perspective for regulation and policy development

the distribution of allele frequencies has been a major focus in population genetics classical approaches using stochastic arguments depend highly on the choice of mutation model unfortunately it is hard to justify which

mutation model is suitable for a particular sample we propose two methods to estimate allele frequencies especially for rare alleles without assuming a mutation model the first method achieves its goal through two steps first it estimates the number of alleles in a population using a sample coverage method and then models ranked frequencies for these alleles using the stretched exponential weibull distribution simulation studies have shown that both steps are robust to different mutation models the second method uses bayesian approach to estimate both the number of alleles and their frequencies simultaneously by assuming a non informative prior distribution the bayesian approach is also robust to mutation models questions concerning the probability of finding a new allele and the possible highest or lowest probability for a new found allele can be answered by both methods the advantages of our approaches include robustness to mutation model and ability to be easily extended to genotypic haploid and protein structure data

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