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Title: Computation of marginal distributions of peak-heights in electropherograms for analysing single source and mixture STR DNA samples

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Computation of marginal distributions of peak-heights in electropherograms for analysing single source and mixture STR DNA samples.

Abstract

Current models for single source and mixture samples, and probabilistic genotyping software based on them used for analyzing STR electropherogram data, assume simple probability distributions, such as the gamma distribution, to model the allelic peak height variability given the initial amount of DNA prior to PCR amplification. Here we illustrate how amplicon number distributions, for a model of the process of sample DNA collection and PCR amplification, may be efficiently computed by evaluating probability generating functions using discrete Fourier transforms.

Key words: Peak height distribution, electropherogram,, probability generating function, discrete Fourier transform, DNA mixtures

1. Introduction

2 A number of continuous peak height models and associated probabilistic
3 genotyping software implementations are available for analyzing single source
4 and mixture DNA sample base on STR loci. All the models make simpli-
5 fying assumptions regarding the distribution of peak heights of an electro-
6 pherogram given the DNA composition of the sample subject to PCR. [1]
7 introduced the use of gamma distributions, and this is used in a number of
8 other models including [2, 3, 4, 5], but truncated normal [6] and lognormal [7]
9 are also used. It is probably fair to say that a major reason for using these
10 distributions is mathematical convenience. In this paper it is shown how
11 probability distributions may be obtained for the number of amplicons aris-

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