

# Lab Retriever's Drop-in Model

summarized by Ken Cheng

Lab Retriever uses the same drop-in model proposed in Balding and Buckleton, 2009 [1]. The drop-in parameter  $C$  is used to calculate the probabilities of drop-in events (or lack of), as follows:

For a specific locus  $L$  that has  $n$  possible alleles, the probability that exactly  $k$  alleles drop in, for  $k > 0$ , is:

$$P(\text{exactly } k \text{ alleles drop in}) = C^k$$

To calculate the probability that no alleles drop in, we simply subtract the probability that *any* number of alleles drop in from 1. The maximum number of alleles that can drop in is limited by the locus, which has  $n$  possible alleles. Thus, at most  $n$  alleles can drop in.

$$\begin{aligned} P(\text{some allele drops in}) &= \sum_{k=1}^n P(\text{exactly } k \text{ alleles drop in}) \\ &= \sum_{k=1}^n C^k \\ &= \frac{C - C^{n+1}}{1 - C} \quad (\text{sum of geometric series}) \end{aligned}$$

$$\begin{aligned} P(\text{no allele drops in}) &= 1 - P(\text{some allele drops in}) \\ &= 1 - \frac{C - C^{n+1}}{1 - C} \\ &= \frac{(1 - C) - (C - C^{n+1})}{1 - C} \\ &= \frac{1 - C - C + C^{n+1}}{1 - C} \\ &= \frac{1 - 2C + C^{n+1}}{1 - C} \end{aligned}$$

Since the probability of no drop-in must be non-negative, this places a restriction on the value of  $C$ . That is,  $C$  must be such that the probability of no drop-in is still a valid probability. This limit occurs at roughly  $C = 0.5$ , but is dependent on  $n$ , the number of alleles in locus  $L$ . For the worst case (namely, when  $n$  approaches infinity):

$$\begin{aligned}
 P(\text{no allele drops in}) &= \lim_{n \rightarrow \infty} \frac{1 - 2C + C^{n+1}}{1 - C} \geq 0 \\
 &\frac{1 - 2C}{1 - C} \geq 0 \\
 &1 - 2C \geq 0 \\
 &C \leq 0.5
 \end{aligned}$$

Thus, we restrict the values of  $C$  to be within  $[0, 0.5]$ . Practically, however, we expect the value of  $C$ , the probability that exactly one allele drops in, to be far less than 0.5.

## References

- [1] Balding, D.J., Buckleton J., Interpreting low template DNA profiles, *Forensic Science International: Genetics* 4 (2009) 1–10.