

RESEARCH

Methods to compute the composite log-likelihood (CLL) of allelic frequencies for the detection of signatures of selection in diploid genomes

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Abstract

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Keywords: composite log-likelihood; signatures of selection; diploid genomes

Background

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Sub-sub-sub heading for section Text for this sub-sub-sub-heading ... In this section we examine the growth rate of the mean of Z_0 , Z_1 and Z_2 . In addition, we examine a common modeling assumption and note the importance of considering the tails of the extinction time T_x in studies of escape dynamics. We will first consider the expected resistant population at vT_x for some $v > 0$, (and temporarily assume $\alpha = 0$)

$$E[Z_1(vT_x)] = E\left[\mu T_x \int_0^{v \wedge 1} Z_0(uT_x) \exp(\lambda_1 T_x(v-u)) du\right].$$

If we assume that sensitive cells follow a deterministic decay $Z_0(t) = xe^{\lambda_0 t}$ and approximate their extinction time as $T_x \approx -\frac{1}{\lambda_0} \log x$, then we can heuristically estimate the expected value as

$$E[Z_1(vT_x)] = \frac{\mu}{r} \log x \int_0^{v \wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)} du$$

$$\begin{aligned} &= \frac{\mu}{r} x^{1-\lambda_1/\lambda_0 v} \log x \int_0^{v \wedge 1} x^{-u(1+\lambda_1/r)} du \\ &= \frac{\mu}{\lambda_1 - \lambda_0} x^{1+\lambda_1/rv} \left(1 - \exp \left[-(v \wedge 1) \left(1 + \frac{\lambda_1}{r} \right) \log x \right] \right). \quad (1) \end{aligned}$$

Thus we observe that this expected value is finite for all $v > 0$ (also see [1, 2, 3, 4, 5]).

Competing interests
The authors declare that they have no competing interests.

Author's contributions
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Acknowledgements
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Figures

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Figure 2 Sample figure title. Figure legend text.

Tables

Table 1 Sample table title. This is where the description of the table should go.

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