

RESEARCH

A sample article title

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available at the end of the article[†]Equal contributor**Abstract****First part title:** Text for this section.**Second part title:** Text for this section.**Keywords:** sample; article; author**Content**

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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

$$\begin{aligned} E[Z_1(vT_x)] &= \frac{\mu}{r} \log x \int_0^{v \wedge 1} x^{1-u} x^{(\lambda_1/r)(v-u)} du \\ &= \frac{\mu}{r} x^{1-\lambda_1/\lambda_0 v} \log x \int_0^{v \wedge 1} x^{-u(1+\lambda_1/r)} du \\ &= \frac{\mu}{\lambda_1 - \lambda_0} x^{1+\lambda_1/rv} \left(1 - \exp\left[-(v \wedge 1) \left(1 + \frac{\lambda_1}{r}\right) \log x\right]\right). \quad (1) \end{aligned}$$

Thus we observe that this expected value is finite for all $v > 0$ (also see [1, 3, 4, 5, 9]).

Competing interests

The authors declare that they have no competing interests.

Author's contributions

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Figures

Figure 1 Detailed steps for running stitch.pl. BNG CMAPs (blue) are shown aligned to *in silico* CMAPs (green). Alignments are indicated with grey lines. CMAP orientation for *in silico* CMAPs is indicated with a "+" or "-" for positive or negative orientation respectively. (a) The *in silico* CMAP is aligned as the reference. (b) The alignment is inverted and used as input for stitch.pl. (c) The alignments are filtered based on alignment length (purple) relative to total possible alignment length (black) and confidence. Here assuming all alignments have a high confidence score and the minimum percent aligned is 30% two alignments fail for aligning over less than 30% of the potential alignment length for that alignment. (d) Filtering produces an XMAP of high quality alignments with short (local) alignments removed. (e) High quality scaffolding alignments are filtered for longest and highest confidence alignment for each *in silico* CMAP. Third alignment (unshaded) is filtered because the second alignment is the longest alignment for in silico CMAP 2. (f) Passing alignments are used to super scaffold (captured gaps indicated in dark green). (g) Stitch is iterated and additional super scaffolding alignments are found using second best scaffolding alignments. (h) Iteration takes advantage of cases where *in silico* CMAPs scaffold BNG CMAPs as *in silico* CMAP 2 does. Stitch is run iteratively until super scaffolding alignments are found.

Figure 2 Histogram of gap lengths. Positive and negative gaps lengths for the automated output of stitch.pl. The majority of gap lengths, 66, were positive (red). The remaining 26 gaps had negative lengths (purple).

Figure 3 Putative haplotypes assembled as BNG CMAPs. Two BNG CMAPs (blue with molecule coverage shown in dark blue) align to the *in silico* CMAP of scaffold 131 (green with contigs overlaid as translucent colored squares) (left). Both BNG CMAPs are shown (blue) with molecule pileups (yellow) (right) Both BNG CMAPs have similar label patterns except within the lower coverage region indicated with a black square.

Figure 4 Extremely small negative gap length for in silico CMAP of scaffold 81. Two XMAP alignments for *in silico* CMAP of scaffold 81 are shown. BNG CMAPs (blue with molecule coverage shown in dark blue) align to the *in silico* CMAPs of scaffolds (green with contigs overlaid as translucent colored squares). Scaffolds 79-83 were placed within ChLG 5 and scaffolds 99-103 were placed with ChLG 7 by the *Tribolium* genetic map. However half of scaffold 81 aligns with its assigned ChLG and the other half with ChLG 7.

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Tables

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