

## Sequescence

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### Introduction

*Sequescence* is a Java application that simulates the appearance of miscoding lesions as the result of post-mortem damage in ancient DNA.

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### Using Sequescence

The application can be executed on any platform provided that Java has been installed.

To execute *Sequescence*, place the .jar file and the sequence alignment in the same directory. From a command line in the directory, type the following:

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java -jar Sequescence.jar
```

The application will prompt the user for the following:

- 1) **Input file.** This is the name of the file containing the sequence alignment. The alignment should be in Fasta format. Individual sequences should not run across multiple lines.
- 2) **Number of aligned sequences.**
- 3) **Damage rate (average per base).** This is the mean damage rate for each nucleotide in the alignment. Note that *Sequescence* implements an age-independent model of sequence damage.
- 4) **Proportion of Type I damage.** The proportion of miscoding lesions that represent Type I damage ( $A \rightarrow G$  and  $T \rightarrow C$ ).
- 5) **Proportion of Type II damage.** The proportion of miscoding lesions that represent Type II damage ( $C \rightarrow T$  and  $G \rightarrow A$ ).
- 6) **Alpha parameter for among-site rate variation.** The shape parameter for gamma-distributed rates among sites. Small values of alpha indicate substantial rate variation among sites. Enter a value of 0 for homogeneous rates among sites.

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### Citation

If you use *Sequescence* in your research, please cite the following paper.

Ho SYW, Heupink TH, Rambaut A, and Shapiro B (2007) Bayesian estimation of sequence damage in ancient DNA. *Molecular Biology and Evolution*, 24: 1416-1422.