

## Supplemental Information for:

### Tree-sequence recording in SLiM opens new horizons for forward-time simulation of whole genomes

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Table S1. Mean coalescence time, in generations, for a simple neutral model (Example 1; see text for model description). The mean, standard deviation (SD), standard error of the mean (SEM), and relative standard error (SE%) are shown across 500 replicates for each value of  $L$  simulated. Note that the relative standard error of the mean is below 2.5% in all cases, and below 1% for the largest values of  $L$ , so any error in the estimated mean coalescence times should not substantially affect the results shown in Figure 2. (It might seem simpler to have used SLiM's coalescence-detection feature to terminate the timing comparison runs directly; however, coalescence detection requires tree-sequence recording to be enabled, making it unusable in the SLiM runs that did not use tree-sequence recording. Also, coalescence detection entails additional performance costs that would have skewed the comparison; we expect that many models will not use coalescence detection, so its overhead should not be included in the timing comparison.)

<u><math>L</math></u>	<u>mean</u>	<u>SD</u>	<u>SEM</u>	<u>SE%</u>
$10^5$	2708.8	1497.7	67.0	2.47%
$10^6$	4743.0	1672.6	74.8	1.58%
$10^7$	7897.6	1597.5	71.4	0.90%
$10^8$	10647.4	1485.5	66.4	0.62%
$10^9$	13310.4	1379.4	61.7	0.46%
$10^{10}$	15771.0	1354.3	60.6	0.38%