

This article presents the first analysis of the joint effect of *selective sweeps* and so-called *weak seed bank* dynamics, in which organisms are able to enter a reversible state of metabolic dormancy lasting a small number of generations. Seed banks are known to slow down genetic drift, elongate branches in ancestral trees, and increase the effective rate of recombination. The findings of the article are consistent with these intuitions: fixation probabilities decline, and the signatures of selective sweeps become narrower but are persist for longer. On the other hand, predictions derived from deterministic or otherwise simplified models have shown that the effect of seed banks on the efficiency of selection is subtle [1, 2]. This article presents a scalable, `tskit`-based simulation tool for whole genome data under the joint effect of weak seed banks and selective sweeps, clarifying the applicability of the various predictions to more realistic models, and shedding light on the nonlinearities involved in the joint effect of dormancy and selection. The simulation model is a natural extension of the classical Wright–Fisher model. Given the universality of coalescent models, it is likely that findings are robust to other choices of individual-based models (at least when suitably rescaled).

The `tskit` framework is natural for neutral evolution, but more cumbersome for non-neutral processes since genotypes need to be tracked in addition to ancestral relations. The paper avoids this issue by tracking genotypes outside the main simulation data structure. Simulation parameters are well-chosen, and span a biologically plausible range while remaining computationally feasible.

The authors have provided their simulator as a GitHub repository `sleepy`, with brief installation instructions which I was able to follow. They have also provided an analysis repository, `sleepy-analysis`, which I was able to clone. However, despite the installation of the `sleepy` package running without errors, the Jupyter scripts in `sleepy-analysis` were not able to locate the `sleepy` method. I am by no means an experienced Jupyter user so may be missing something obvious, but expanding the installation instructions to include details on how to run the provided minimal code example would be a good way to improve the accessibility of the code.

The simulation outputs consist of a collection of standard population genetic statistics (linkage disequilibrium, time to most recent common ancestor, etc.), as well as the time until fixation and an estimator of the fixation probability. The last two are estimated by repeatedly introducing a selective mutation at a given site until it fixates (rather than goes extinct), and storing the number of generations until fixation and the number of trials. The latter amounts to estimating the success probability p of a geometric distribution from iid replicates, which is known to have a $p(1-p)/n$ bias, but the authors have performed $n = 1000$ replicates to render the bias negligible. The simulator is validated using a neutral scenario, for which many expected values are known analytically.

Overall, the simulations are an interesting catalogue of the joint, nonlinear impact of dormancy and selection on genetic diversity, and of the prospect of detecting sweeps in the presence of dormancy. I agree with the authors that their results are of applied importance in the analysis of many biologically important species, particularly among plants and fungi for which the weak seed bank is a natural model. The main limitations of the results are the assumptions of a constant population size, and that mutations occur in dormant individuals at the same rate as in active ones. Both assumptions are discussed and justified by the authors, but the mapping of diversity patterns arising from dormancy and selection without these assumptions remains an open task.

I have two aesthetic comments on the figures:

1. The neutral line in Figure 3c is effectively invisible. I'm guessing it overlaps almost exactly with the $s = 0.01$ line, but it would be useful to say so, or to reformat the plots to make it obvious.

2. The colour scheme in Figure 4 also makes it hard to distinguish the different trajectories, particularly the two blue-hued ones.

References

- [1] L Heinrich, J Müller, A Tellier and D Živković. Effects of population- and seed bank size fluctuations on neutral evolution and efficacy of natural selection. *Theor Popul Biol* 123:45–69, 2018.
- [2] D Živković and A Tellier. All but sleeping? Consequences of soil seed banks on neutral and selective diversity in plant species. In *Mathematical Modelling in Plant Biology*, R J Morris (ed), Springer, Cham, 2018.