

S1 Table. Relative difference in mean number of singletons, doubletons, and tripletons under the Wright-Fisher (N_{WF}) and Hudson (N_H) models.

Frequency	$\frac{N_{WF}-N_H}{N_{WF}}$
Singletons	0.099131
Doubletons	-0.047253
Tripletons	0.010092

From data shown in S1 Figure. These results closely match those presented in [1, 2].

References

- [1] A. Bhaskar, A. G. Clark, and Y. S. Song. “Distortion of genealogical properties when the sample is very large.” In: *Proceedings of the National Academy of Sciences of the United States of America* 111.6 (2014), pp. 2385–90.
- [2] P. F. Palamara. “ARGON: fast, whole-genome simulation of the discrete time Wright-fisher process”. In: *Bioinformatics* 32.19 (June 2016), pp. 3032–3034.