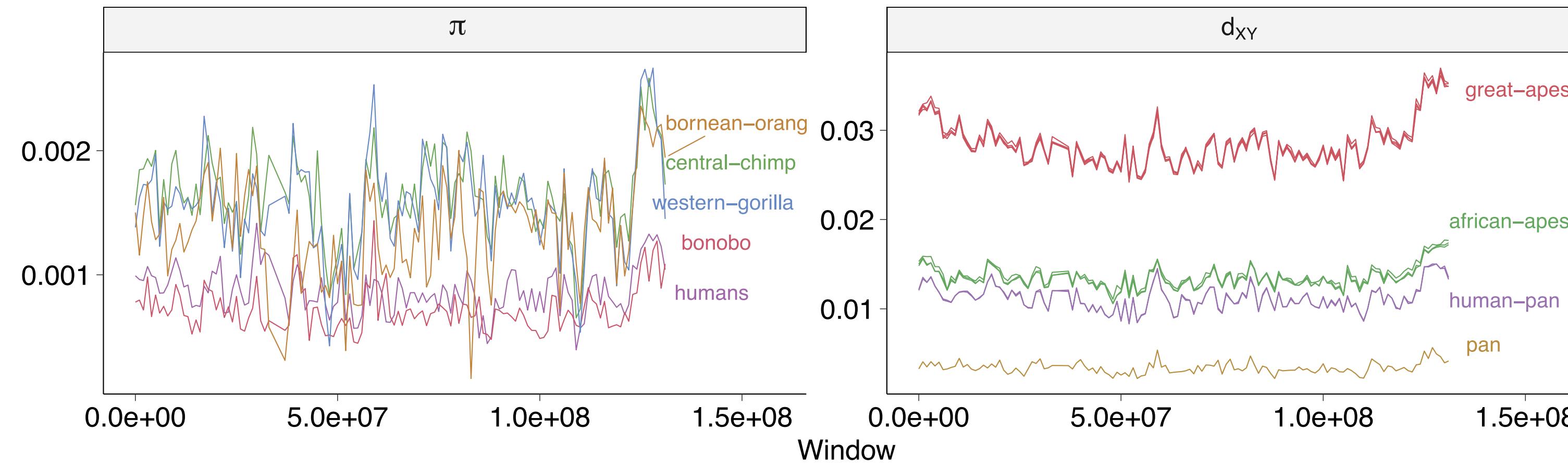


Why are landscapes of diversity correlated among great apes?

1 Landscapes of diversity and divergence are correlated among great apes

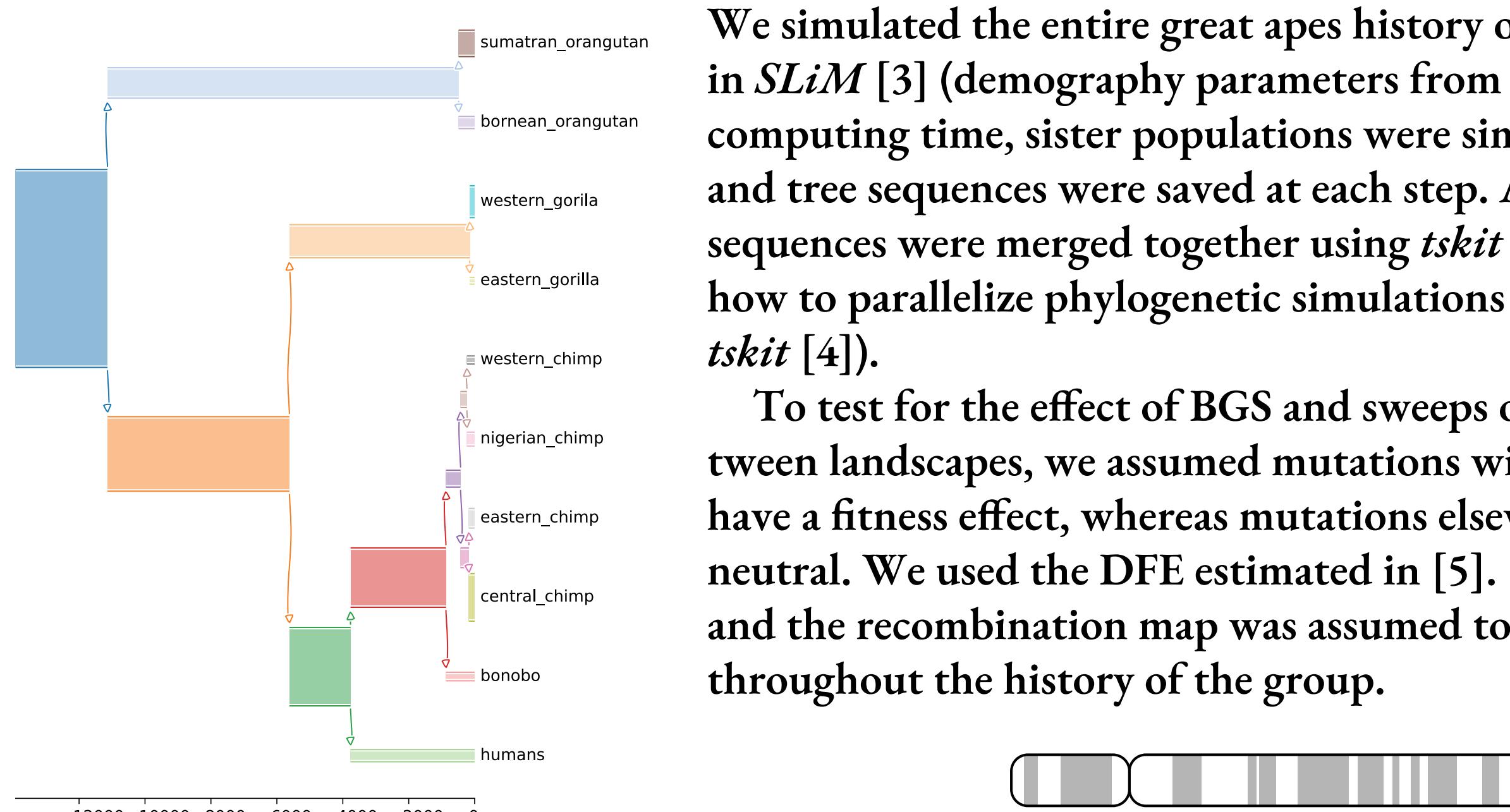
Levels of genetic diversity (and divergence) along chromosomes seem to be correlated across the great apes. Which processes could be maintaining these correlations over such long time scales?

- Selection
- Direct effects
- Indirect effects (linked selection)
- Shared ancestral variation
- Local variation in mutation rates
- GC-biased gene conversion



Data from [1]. Levels of diversity along chromosome 12 computed in 1Mb windows using *scikit-allel* [2].

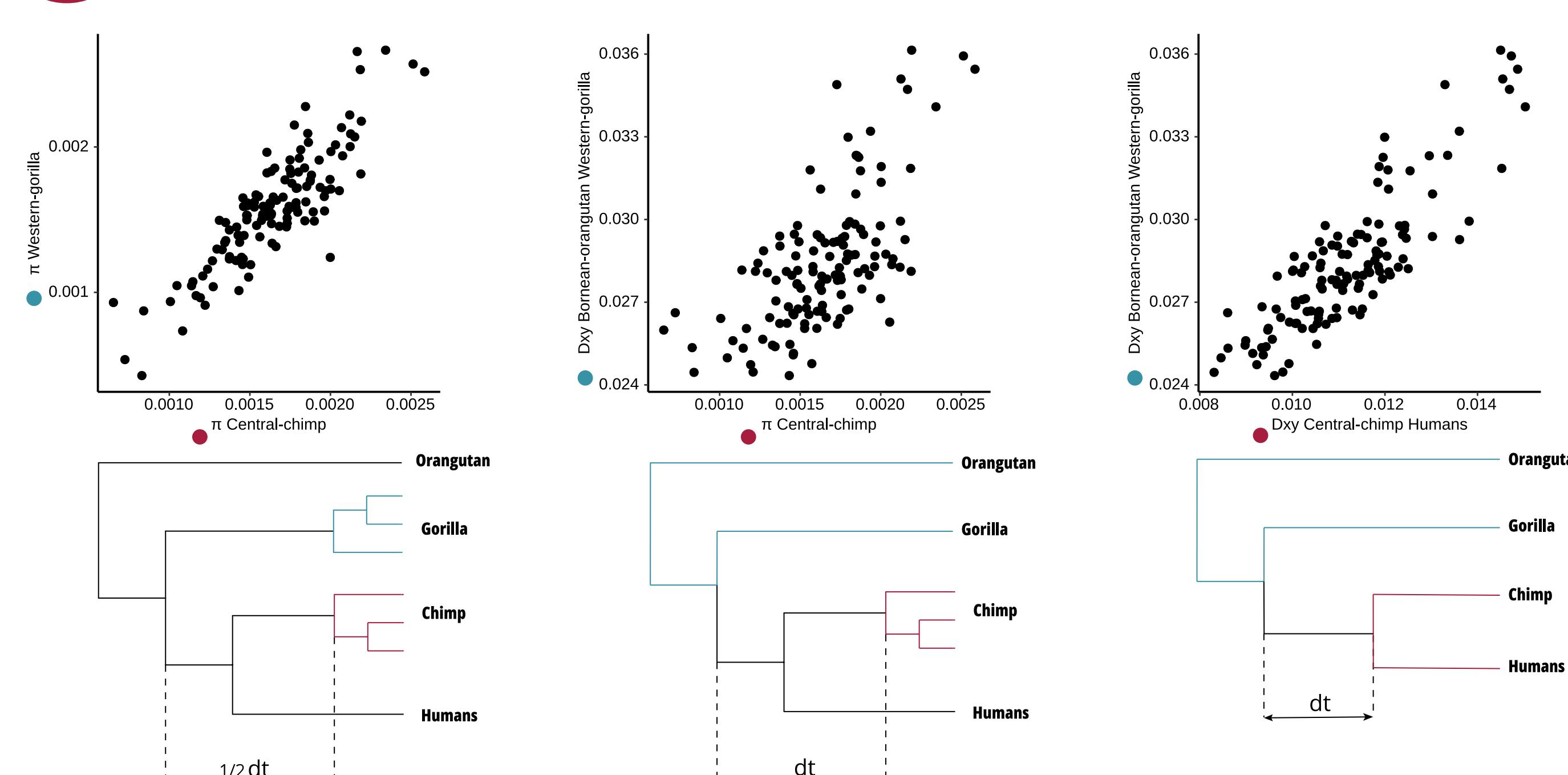
2 Whole-chromosome SLiMulations of the entire great apes history



We simulated the entire great apes history of chromosome 12 in *SLiM* [3] (demography parameters from [1]). To minimize computing time, sister populations were simulated in parallel and tree sequences were saved at each step. At the end, the tree sequences were merged together using *tskit* (see the vignette on how to parallelize phylogenetic simulations using *SLiM* and *tskit* [4]).

To test for the effect of BGS and sweeps on correlations between landscapes, we assumed mutations within exons could have a fitness effect, whereas mutations elsewhere were always neutral. We used the DFE estimated in [5]. Exon annotations and the recombination map was assumed to be the same throughout the history of the group.

3 How to quantify relationships between landscapes?



Murillo F. Rodrigues¹,
✉ mufernando_murillor@uoregon.edu

Andrew D. Kern¹, Peter L. Ralph^{*1,2}

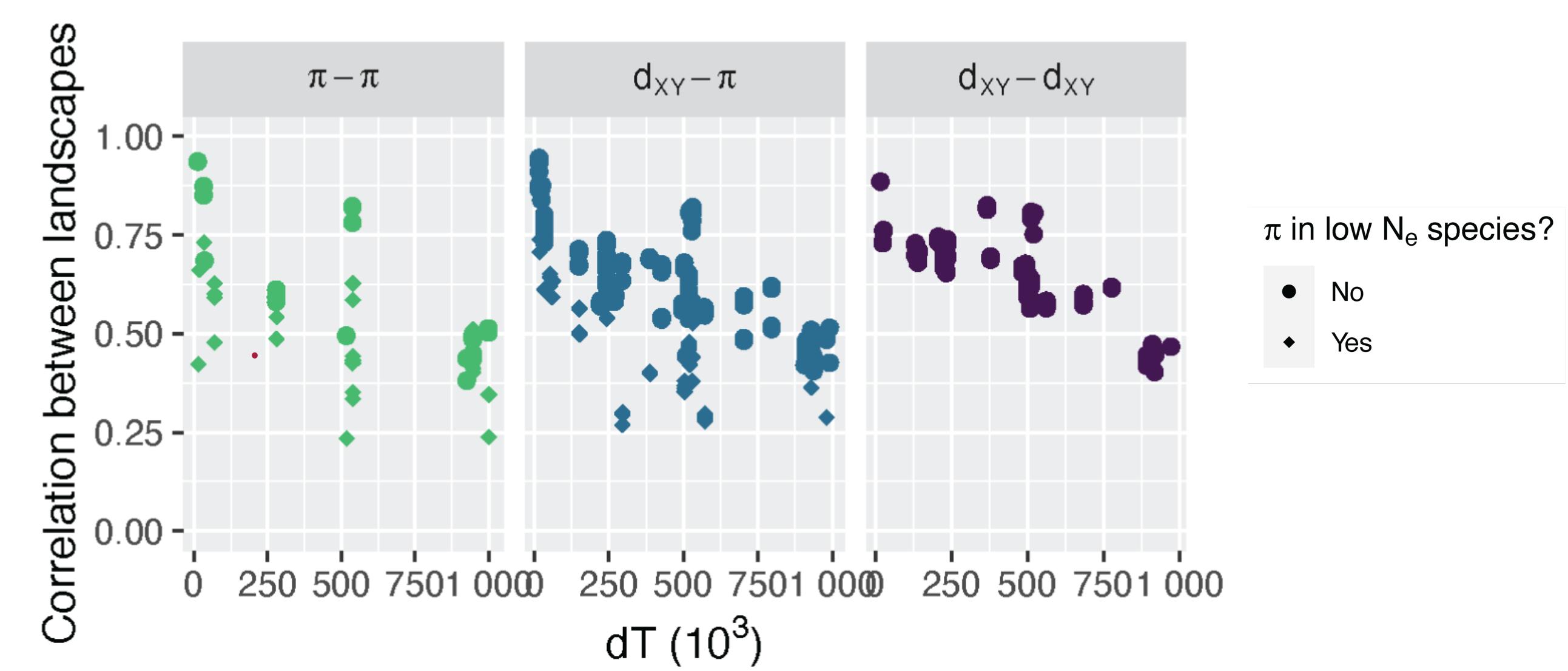
¹ Institute of Ecology and Evolution, University of Oregon

² Department of Mathematics, University of Oregon

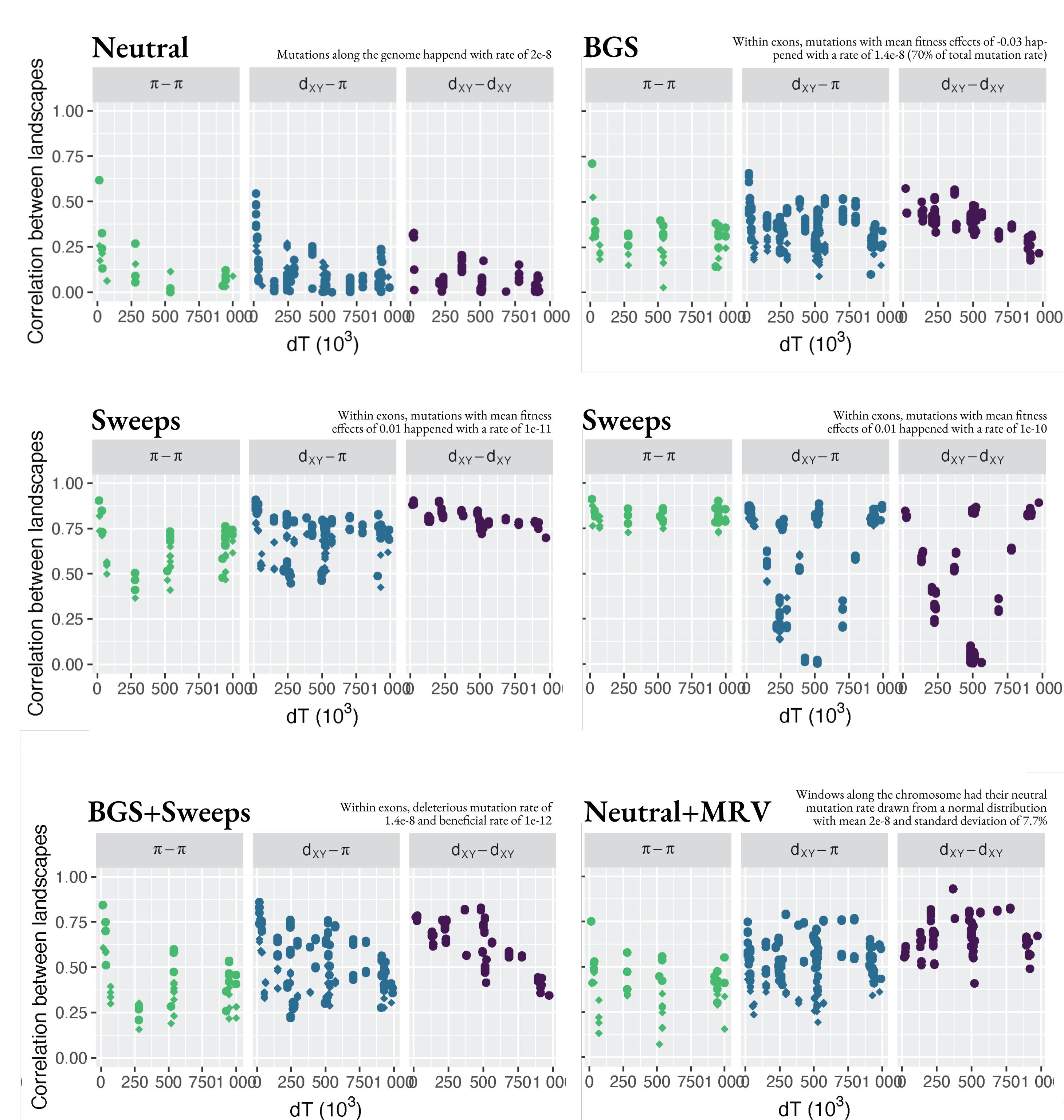
* Contributed equally

4 Positive and negative selection can maintain landscapes correlated

Empirical data

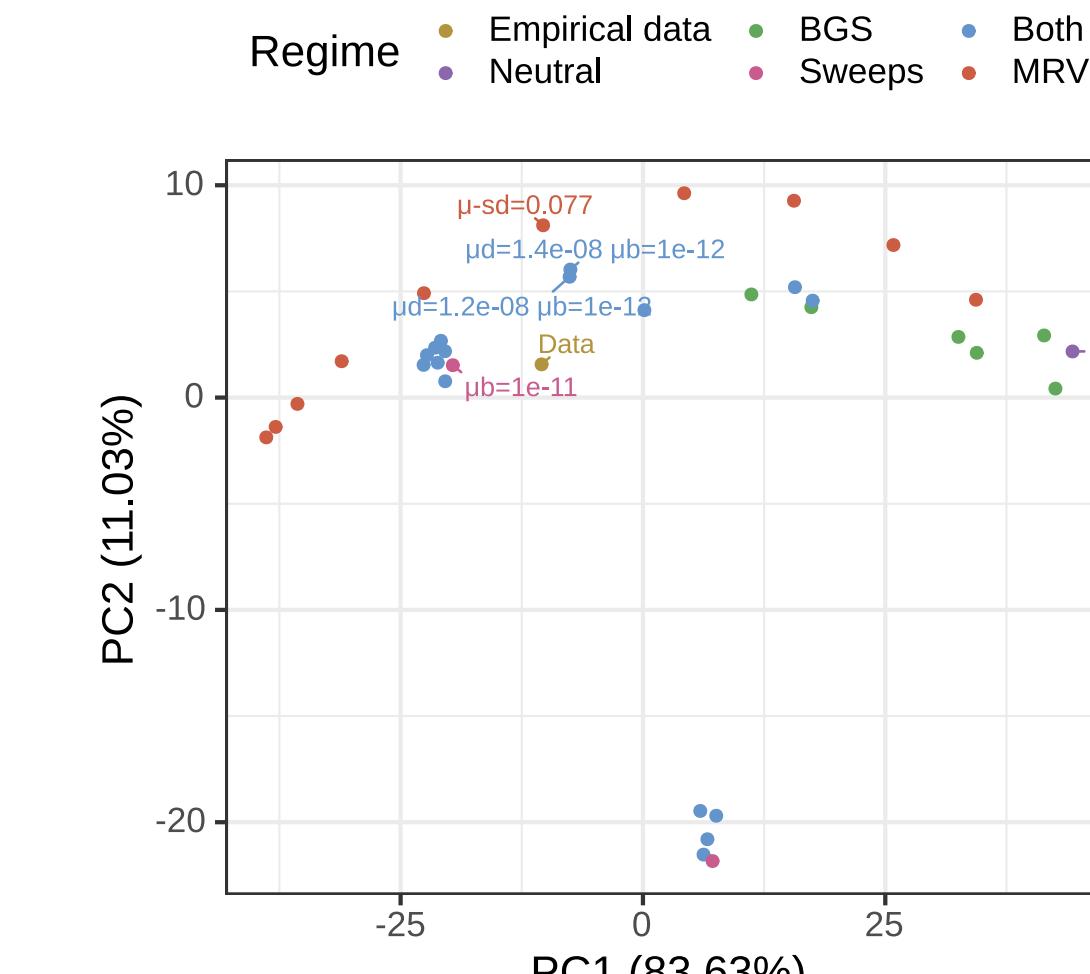


Simulations



5 Conclusions

- Shared ancestral variation cannot explain correlations (see Neutral simulations)
- Background selection increases correlations, but not to the same extent as seen in the data
- Both **background selection and sweeps seem to be needed**
- Mutation rate variation could in principle maintain correlations (but ask me why I don't think that is the main process shaping levels of diversity and divergence in the great apes)



References

- [1] Prado-Martinez, Javier, et al. "Great ape genetic diversity and population history." *Nature* 499.7459 (2013): 471-475.
- [2] Miles, Alistair, and N. J. Harding. "scikit-allel: A Python package for exploring and analysing genetic variation data." (2017).
- [3] Haller, Benjamin C., and Philipp W. Messer. "SLiM 3: forward genetic simulations beyond the Wright–Fisher model." *Molecular biology and evolution* 36.3 (2019): 632-637.
- [4] https://tskit.dev/pyslim/docs/stable/vignette_parallel_phylo.html

github.com/mufernando/peqg22



For more info and a high definition copy of this poster