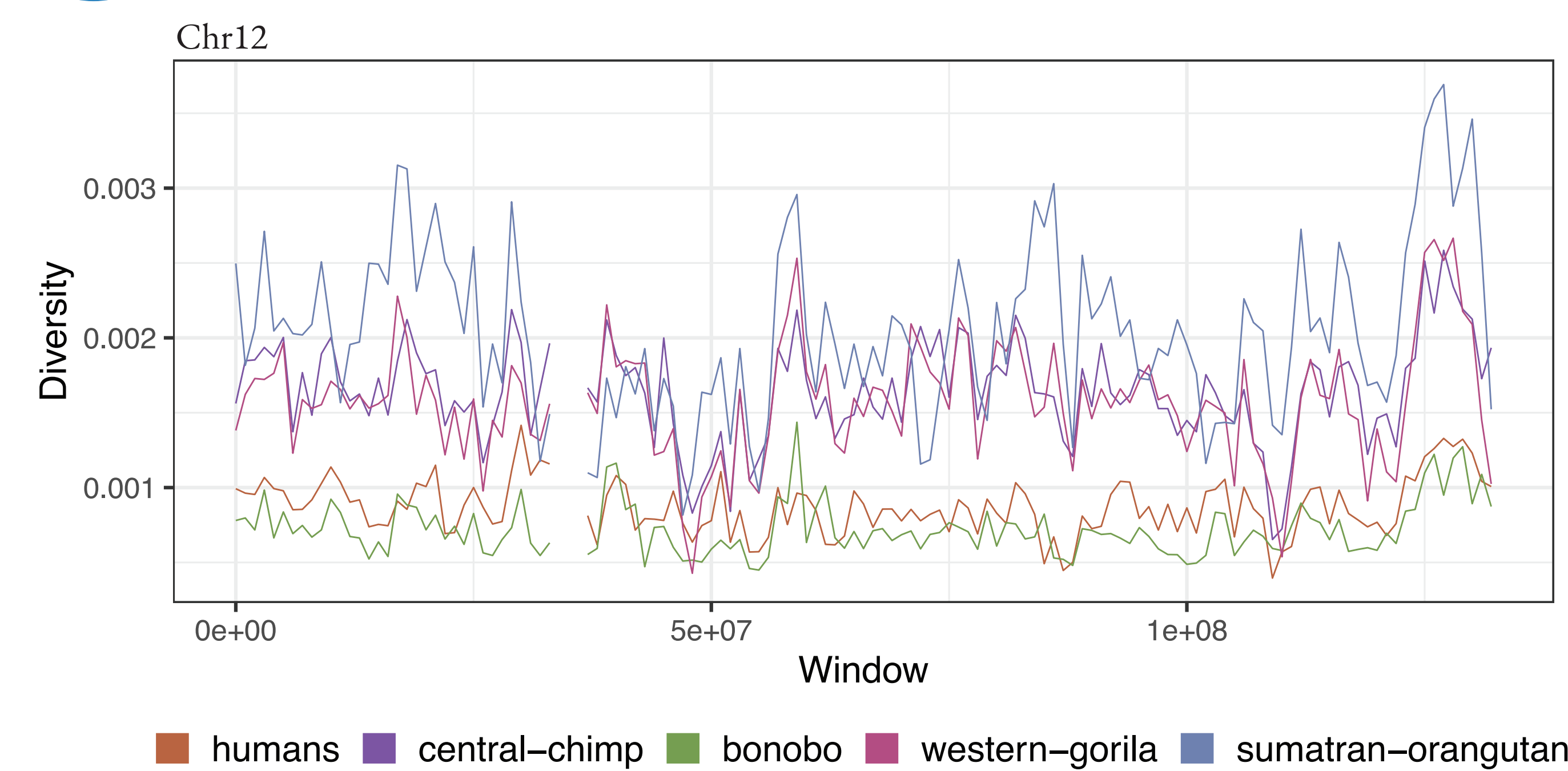


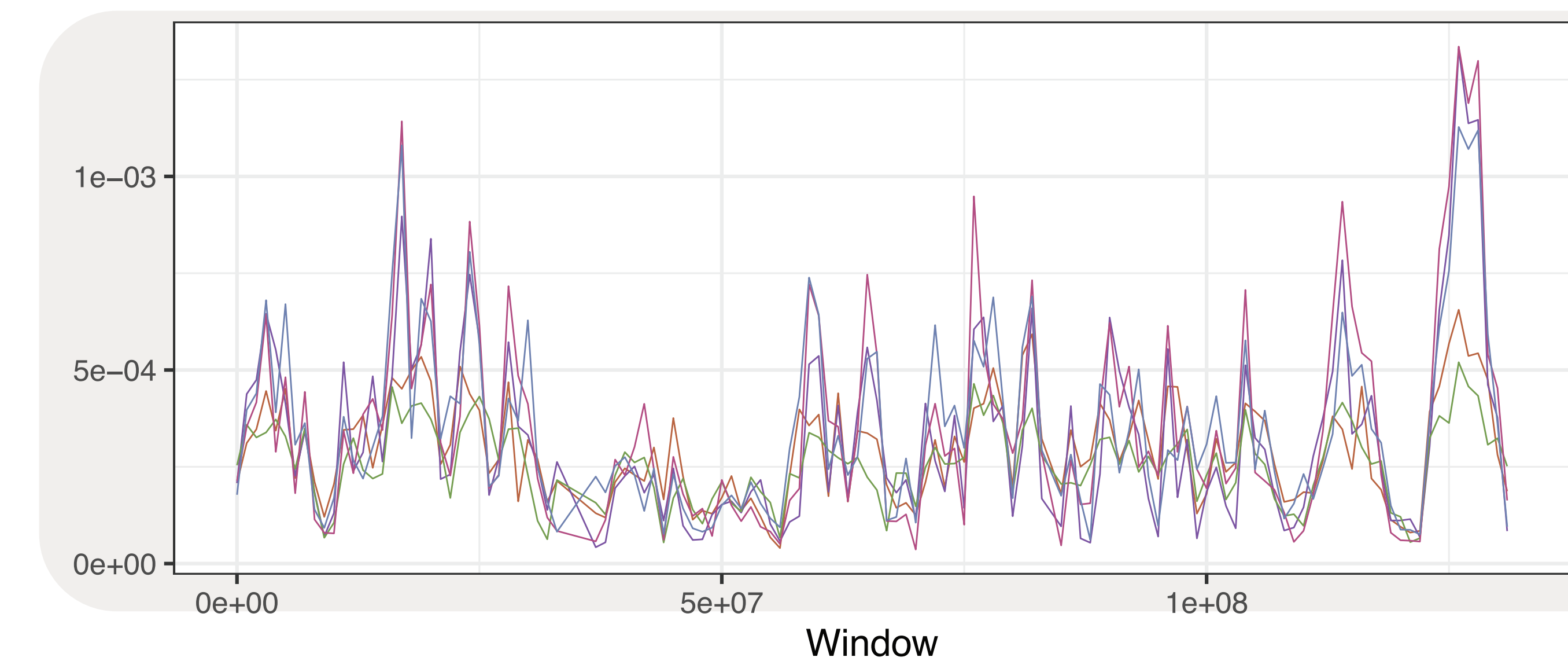
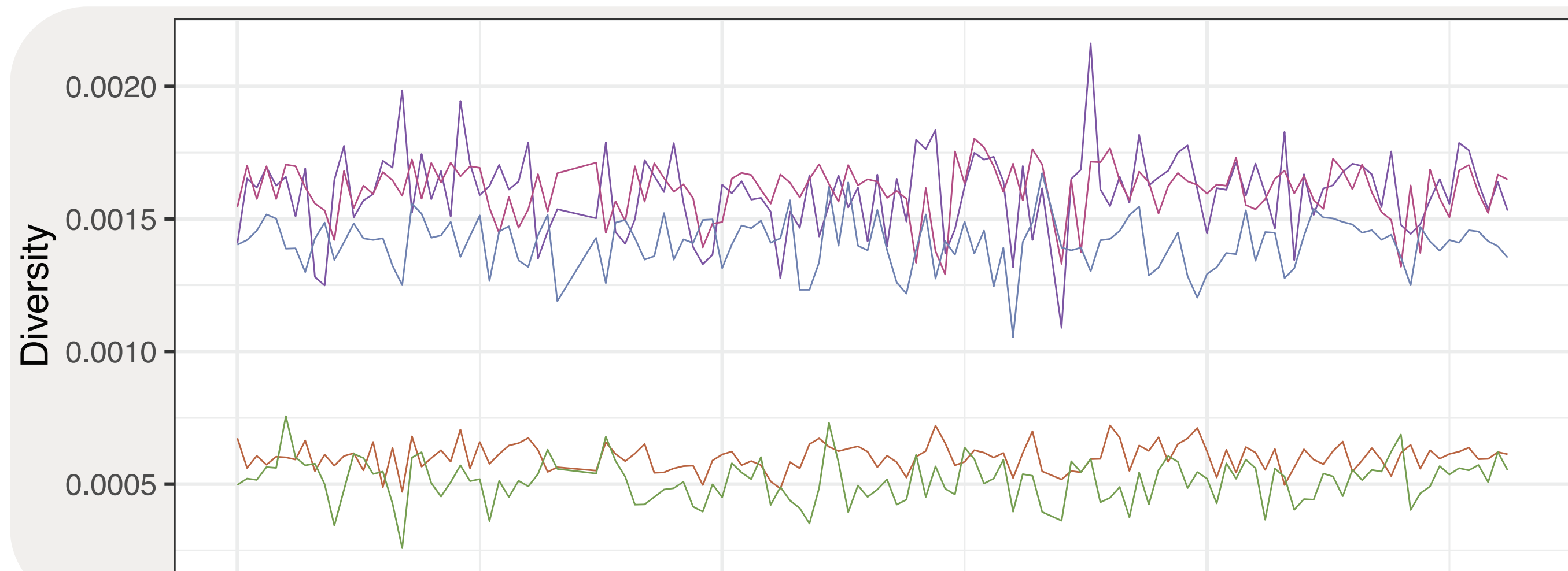
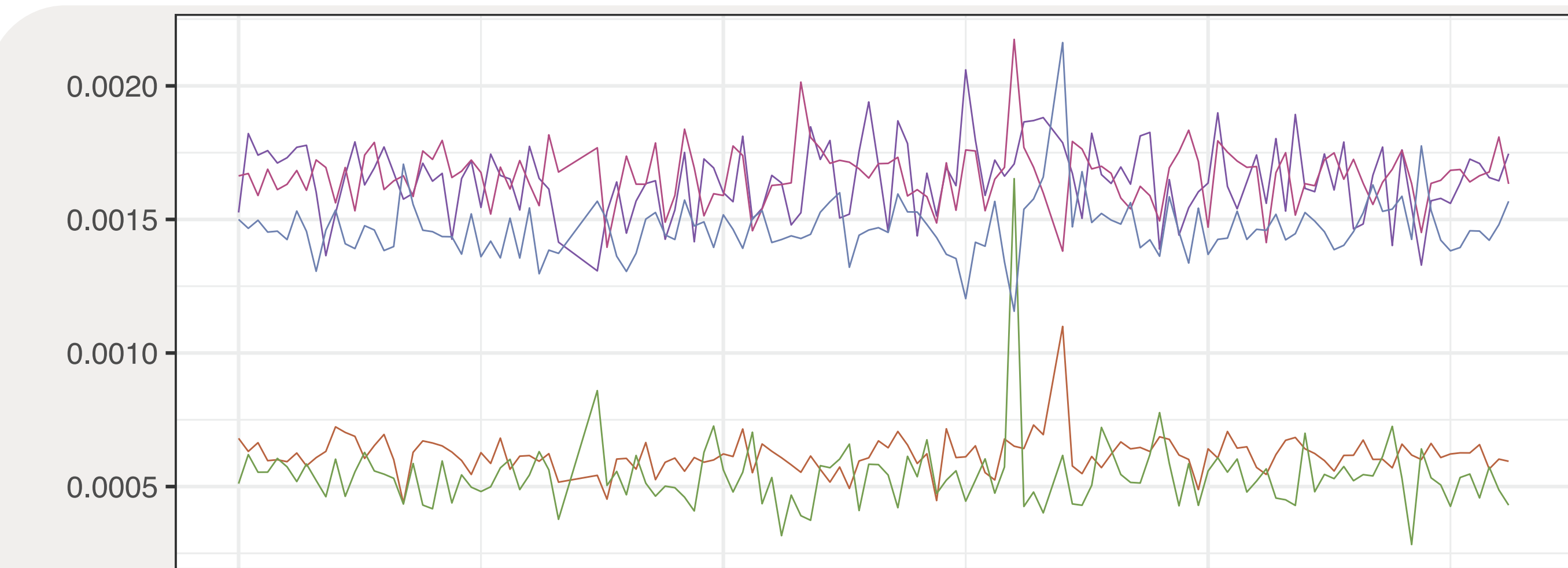
Natural selection and landscapes of diversity in the great apes

1 What causes variation in diversity along the genome?



Data from [1]. Diversity computed in 1Mb windows using *scikit-allel* [2].

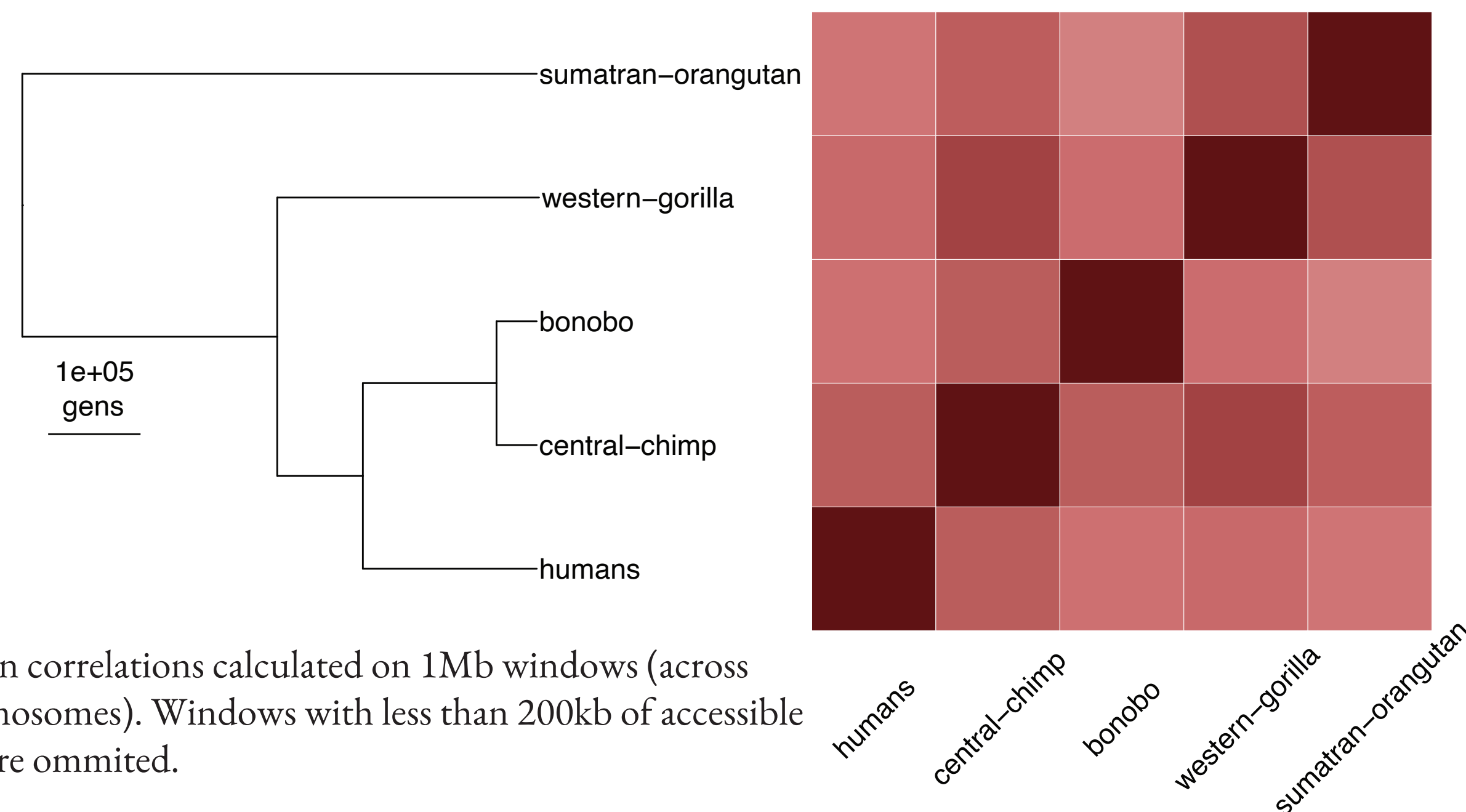
4 Can we get realistic looking landscapes in SLiMulations^[3]?



2 Why are the landscapes of different species correlated? (i.e., why do they share their ups and downs?)

Which processes could maintain genome-wide levels of diversity correlated over such long time scales?

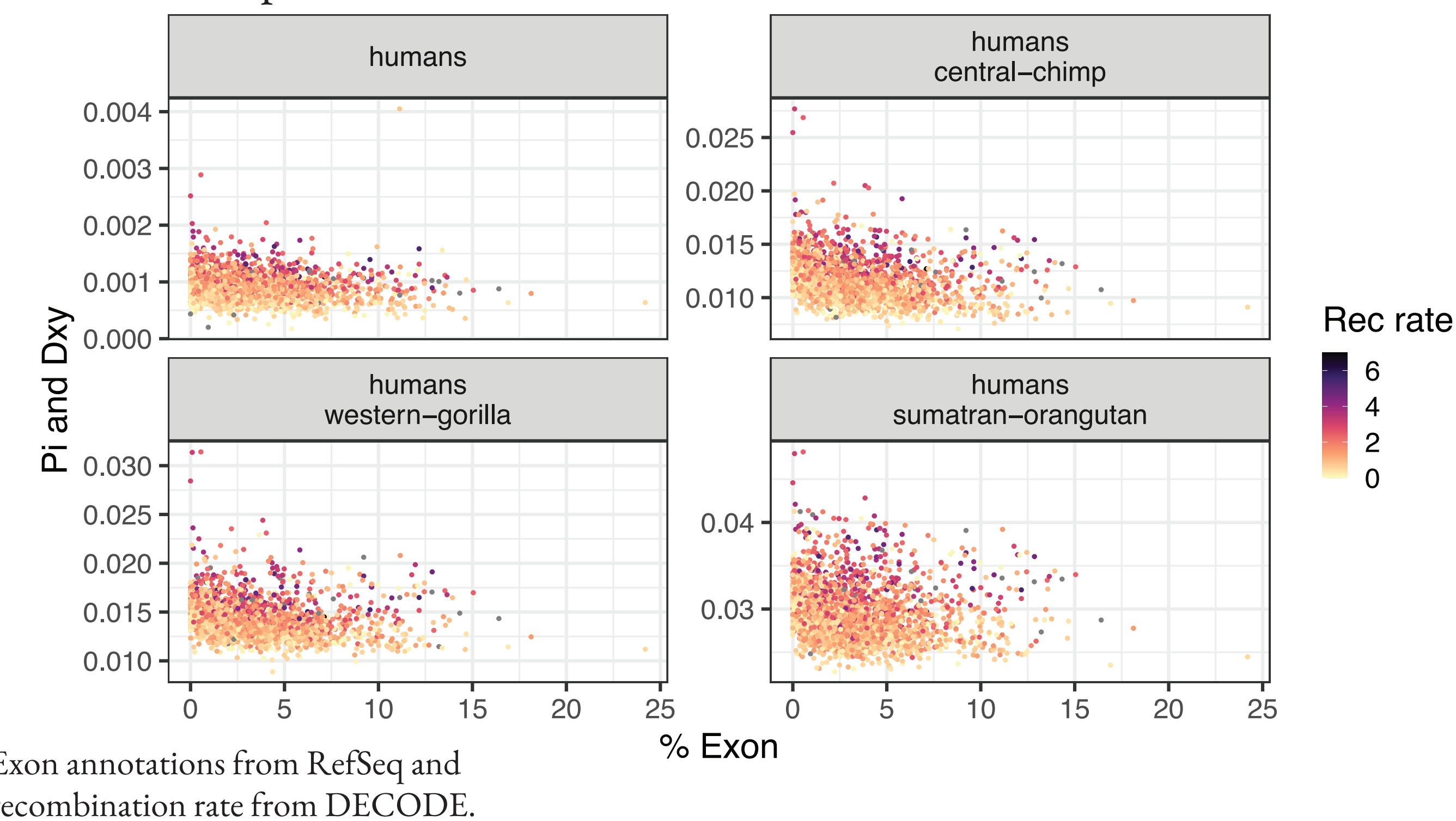
Under neutrality, the correlations should decay with time. Can constraint maintain correlations? How much constraint would we need for that?



Spearman correlations calculated on 1Mb windows (across all chromosomes). Windows with less than 200kb of accessible bases were omitted.

3 Can genomic features explain some of this variation?

Patterns of diversity (and divergence) are correlated with the proportion of exonic bases in a window. But why does the correlation decay in more distant comparisons?



Exon annotations from RefSeq and recombination rate from DECODE.

Neutral simulation reveals landscapes that are (1) less heterogeneous, (2) not correlated between species and (3) not correlated with exon density.

Rec rate
1 2 3 4 5

Simulation of the great apes history for Chromosome 12. Each edge in the great apes tree has population size as estimated in [1]. Neutral mutations happen with constant rate of $2e-8$.

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Simulation with deleterious mutations reveals landscapes that are (1) less heterogeneous, (2) slightly correlated between species and (3) weakly correlated with exon density.

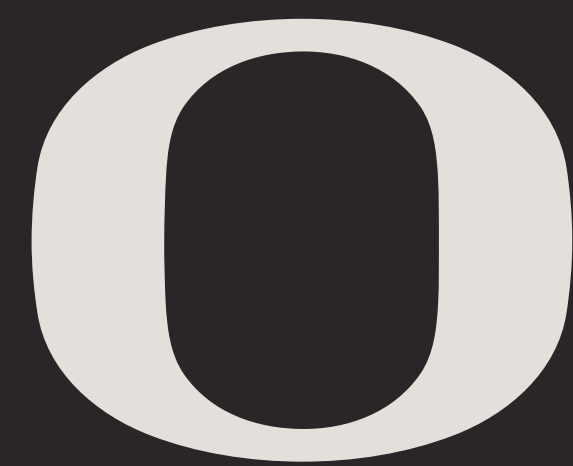
Mutations happen with constant rate of $2e-8$, but in exons 30% of them had fitness effect drawn from a distribution with mean -0.03.

B
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Simulation with deleterious and beneficial mutations reveals landscapes that are (1) highly heterogeneous, (2) highly correlated between species and (3) strongly correlated with exon density.

Mutations happen with constant rate of $2e-8$, but in exons 30% of them had fitness effect drawn from a distribution with mean -0.03 and 0.5% of the mutations had their fitness effect drawn from a distribution with mean 0.01.

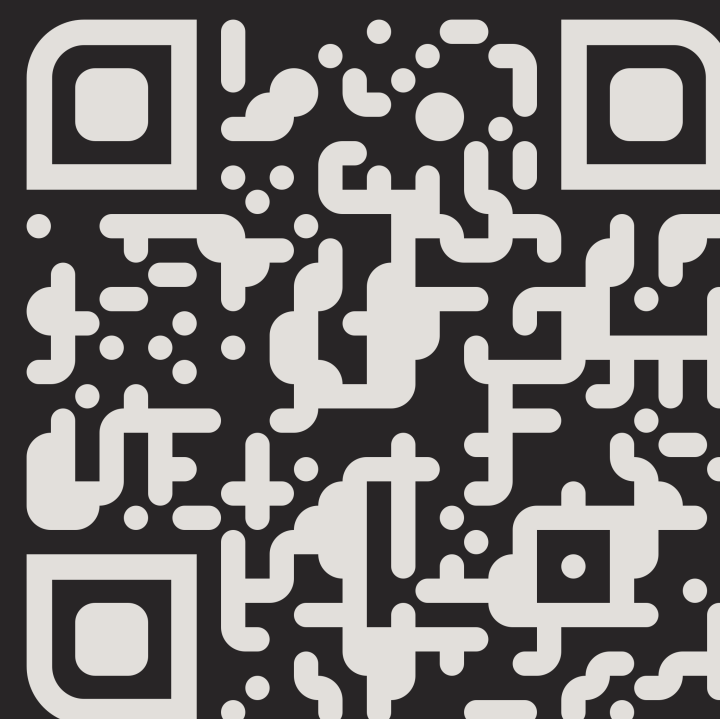
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github.com/mufernando/probgen21



For more info and a high definition copy of this poster

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.