Background selection (BGS), the effect that purifying selection exerts on evolution at linked sites, is expected to be ubiquitous across eukaryotic genomes. BGS effects reflect the interplay of fitness effects and rates of deleterious mutations with the recombination rate. Leveraging the theory of BGS to analyse patterns of nucleotide diversity has shed light on central issues in evolutionary biology. Fundamental to theoretical models of BGS are recombination rate estimates and an assumption that recombination rates are invariant over time. However, in some lineages recombination rates evolve very rapidly violating this central assumption. Here, we investigate the effect that recombination rate evolution can have on BGS. We show that recombination rate evolution may have localised effects and cause analyses to underestimate the effects genome-wide effects of BGS. Indeed, we find evidence that rapid recombination rate evolution in the recent history of the house mouse may impact inferences of selection in that species.

Different modes of selection (e.g. positive, purifying and balancing) can all affect variation at linked sites (REFs). In the case of purifying selection, the removal of deleterious mutations occur can cause linked neutral variants to be lost along with them through a process referred to as background selection (BGS; Charlesworth et al 1993). Of the mutations that affect fitness, the vast majority are likely deleterious with a comparatively small proportion that are beneficial (Keightley and Eyre-Walker review). For those reasons, it has been proposed that BGS be thought of as the null expectation in population genomics (REFs), providing evolutionary biologists with a framework for understanding natural selection through the analysis of genome-wide patterns of nucleotide diversity.

The first empirical evidence that selection at linked sites influences genetic variation across the genome came from studies in \textit{Drosophila}. AguadÃ© et al (1989) measured genetic variability in the \textit{yellow-achaete-scute} regions located at the tip of the X-chromosome in \textit{D. melanogaster}. The \textit{yellow-achaete-scute} regions experience restricted crossing-over and AguadÃ© et al (1989) found that they harbour far less genetic variation than had been reported for more highly recombining regions of the genome. Subsequent studies demonstrated a positive correlation between nucleotide diversity and recombination rate genome-wide in \textit{D. melanogaster} (Begun and Aquadro 1993; REFs) and similar patterns have been reported in numerous other species (Cutter and Payseur 2012).

Interpreting genome-wide patterns of genetic variability in terms of selection at linked sites accurate estimates of population genetic parameters. For example, for a give region under BGS, the expected reduction in nucleotide diversity ($\pi$) is proportional to the ratio of the local deleterious mutation rate and the local recombination rate (REFS). Empirical estimates of the recombination rate can be obtained by examining the inheritance of genetic markers through known pedigrees, as in traditional genetic mapping, or by directly comparing an individual's genome to that of its gametes (REF). Both methods directly observe recombination events over one or a small number of generations, and thus provide estimates of recombination rates for contemporary populations. The use of such recombination rate estimates when analysing genome-wide variation in $\pi$ in terms of BGS implicitly assumes that recombination rates have not changed over the time in which patterns of diversity have been established under BGS. \\

However, recombination rate landscapes evolve rapidly in some lineages. In the house mouse (\textit{Mus musculus}), for example, there has been extensive evolution of recombination rates at broad and fine scales in the last five million years. In the last 5 million years, the lineage leading to \textit{M. musculus} (2\textit{n}=40) has experienced large chromosomal rearrangements (Thybert et al 2018). Due to the requirement of at least one cross-over per chromosome per meiosis in mammals, karyotype evolution likely influences recombination rate landscapes at broad scales. Indeed, there are differences in recombination rate among populations of \textit{Mus musculus domesticus} with different karyotypes (Vara et al 2021) as well as recombination rate differences between sub-species (Dumont and Payseur 2012). Recombination in mice is typically restricted to narrow windows of the genome (on the order of 5-10 Kbp), referred to as hotspots (REFS). The locations of recombination hotspots in mice, as in humans and several other mammals (REF), are determined by the binding of a protein encoded by the PRDM9 gene to specific DNA motifs (REFS). Natural populations of \textit{M. musculus spp.} harbour various PRDM9 alleles corresponding to diffent suites of recombination hotspots (Smagulova et al 2015), there is evidence that PRDM9 has undergone recurrent bouts of positive selection in mice (Kono et al 201X). Overall, there is clear evidence that recombination rates have evolved at broad and fine scales in mice in the relatively recent past. \\

After recombination rate landscapes evolve, there will be a lag period where patterns of genetic variability more closely reflect ancestral recombination rates than the derived recombination rates. Depending on how recombination rate landscapes evolve, analysis of BGS lineages that are still within the lag period may be obscured. For example, the hallmark signature of selection at linked sites, a positive correlation between nucleotide diversity and recombination rate may not be clearly observed. In this letter, we examine how patterns of neutral genetic variability under background selection respond to evolution of the recombination rate. \\