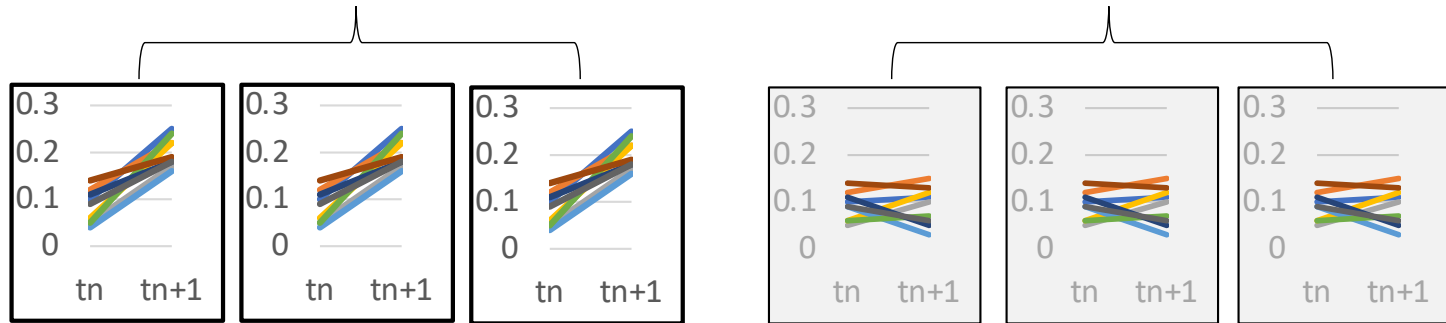
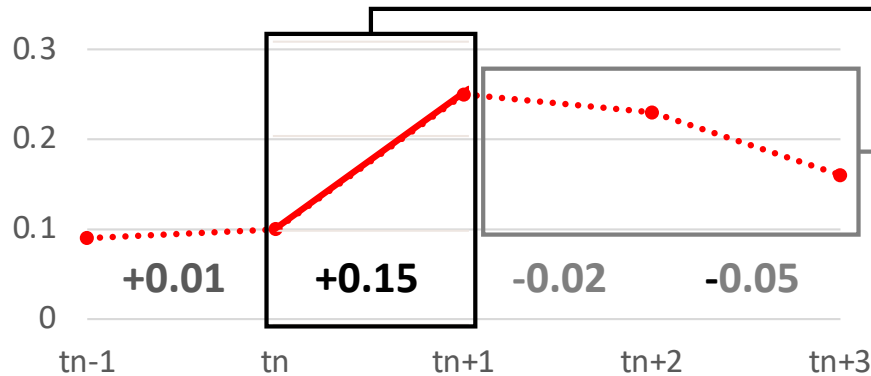
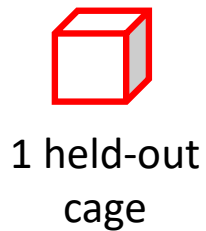


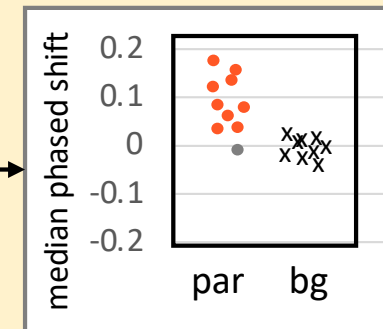
1. At each time segment, examine allele frequencies in 9 cages to identify **SNPs that shift in parallel** and matched background SNPs



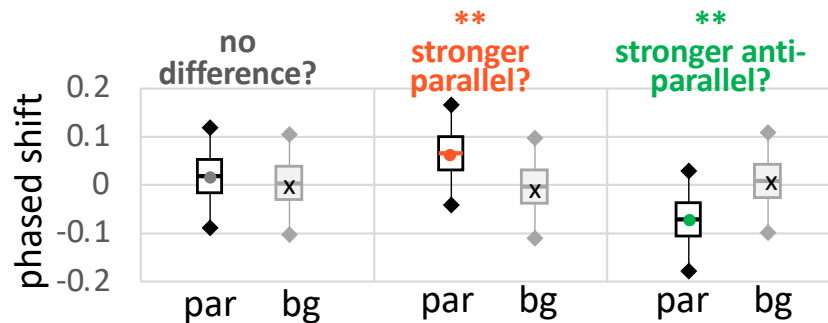
2. Record shift in held-out cage at each SNP



4. Repeat for each left-out cage



3. Compare held-out shift sets at parallel SNPs to background SNPs



5. Repeat for other time segments

