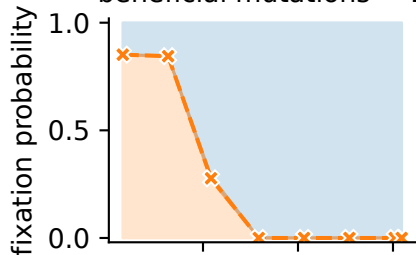
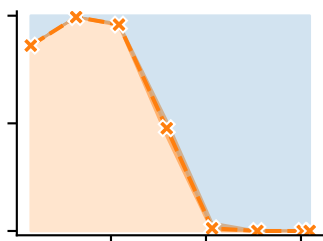


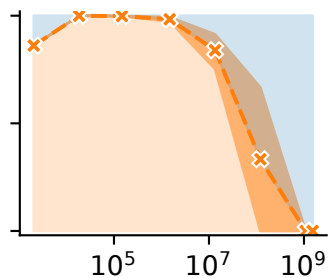
available  
beneficial mutations = 1



available  
beneficial mutations = 2



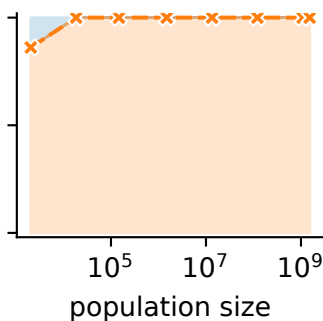
available  
beneficial mutations = 3



available  
beneficial mutations = 4



available  
beneficial mutations = 5



genotype  
—●— normomutator  
- - x - hypermutator