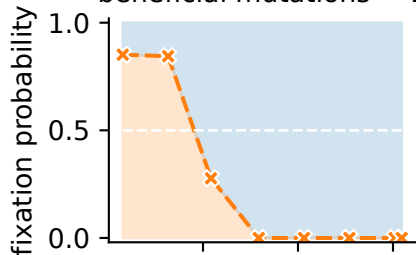
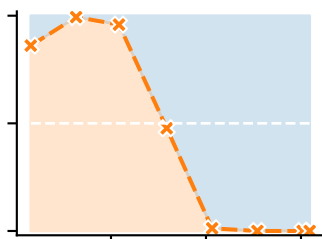


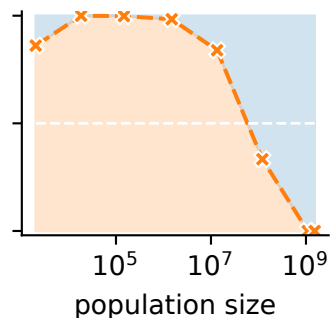
available
beneficial mutations = 1



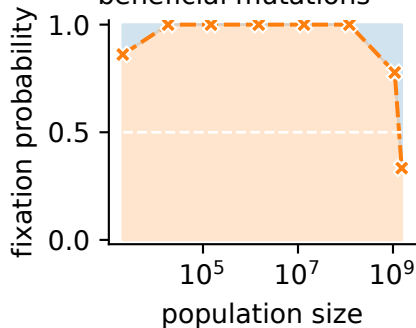
available
beneficial mutations = 2



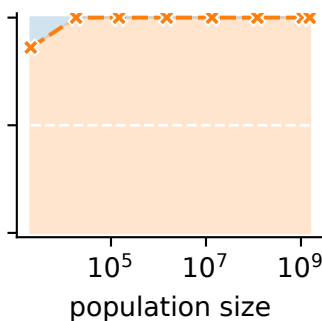
available
beneficial mutations = 3



available
beneficial mutations = 4



available
beneficial mutations = 5



genotype
—●— normomutator
- - x - - hypermutator