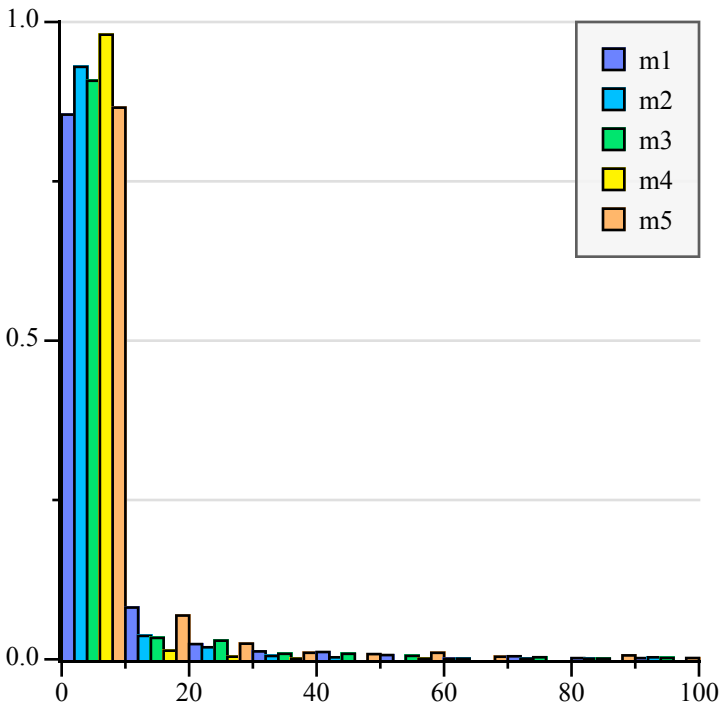


Proportion of lost mutations

m1  
m2  
m3  
m4  
m5



Mutation loss time