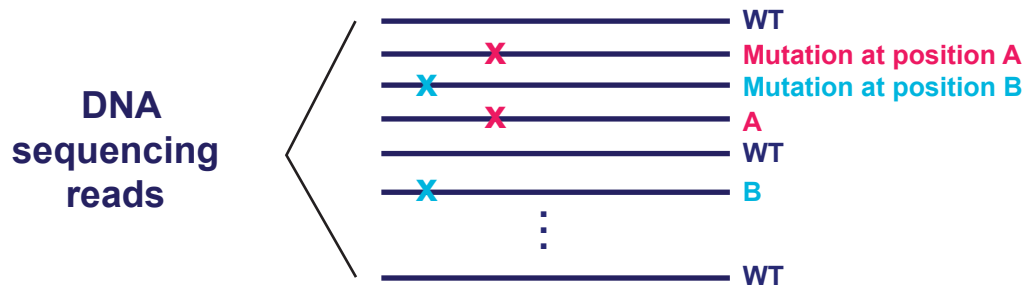


The results of the experiment come in the form millions of DNA sequencing reads. My goal is to identify if each sequence is the natural one (wild-type) or a mutant.

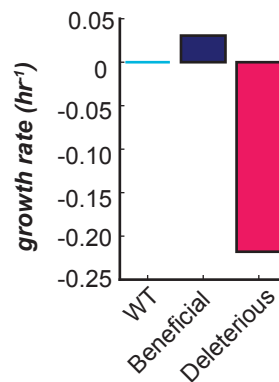
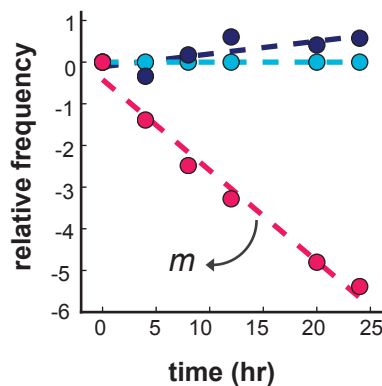
1. determine identity of each sequence as a mutant or wild-type (WT)



2. Count reads for each mutant. In this experiment, I am collecting counts for 3,180 unique mutants. For simplicity, I am showing an example with two hypothetical mutants, A and B.

N_{WT}
 N_A
 N_B

3. Mutant counts from each time point taken during the experiment are used to calculate an allelic frequency normalized by the wild-type. The slope (m) is the growth rate relative to the naturally sequence.



The growth rate effects of all of the mutants in this experiment can be summarized in a heatmap for each TYMS background.

