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# An analysis of beneficially mutated alleles

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**Abstract**

In this thesis the aim is to get a mathematical understanding of how individuals of varying reproductive fitness propagate through time. We analyze this using the Wright-Fisher model where every generation is of the same population size. Using this model we assume at first that the whole population is equally fit and obtain some interesting results. Thereafter we assume that the population can be divided into two sets where one is more fit in a reproductive sense than the other. In other words the more fit individuals carry mutated alleles and are therefore better adapted to their environment. From this we get the mathematical results needed to find the expected number of mutants for any given generation. At last we briefly discuss a growing population size.

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