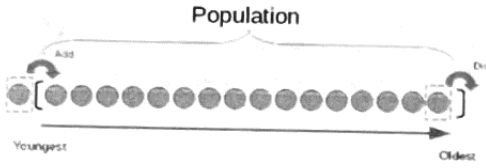

Is this a caption

Figure 2: Ageing tournament selection. This method takes the same approach as tournament selection however, rather than discarding the lowest performing model in the sample, the oldest network on the right of the age array is discarded. This promotes exploration by preferring younger networks in the population, helping to reduce the chances of the system becoming stuck in a local maxima early in the search process.

2.2 Speciation

NeuroEvolution of Augmenting Topologies (NEAT) [4] describes a framework for evolving neural networks which addresses many of the issues faced by GA, such as a formalised system for crossover, genetic encoding, the permutation problem and the protection of innovation (This is discussed in Section 2.4). While NEATs success is limited to smaller networks, however, there have been several extensions to NEAT, adapting it for larger, deeper networks [5][25]. One of the important contributions of NEAT was the use of Speciation. This method is used as a way to protect innovation in evolutionary systems by dividing the population into species which compete internally rather than with the population at large. This protects innovation by allowing new solutions to be explored and reach maturity without having to compete with older, more optimised networks. In practice this creates a less greedy algorithm supporting a greater diversity of solutions and, in theory, improving performance on highly multi-modal fitness functions. Models are divided into species based on genetic distance, δ. Equation 1 describes the process for finding the genetic distance. E and D refer to *Excess* and *Disjointed* genes respectively, which is a component of the NEAT encoding system which is explained in Section 2.6. These are connections which are not common to both of the networks being compared, with C_1 and C_2 being weight hyperparameters that can be used adjust the impact of these attributes. $\bar{w}$ denotes the difference in the parameter weights across common connections, with C_3 again a coefficient controlling the importance. (N) is simply a normalisation factor equal to the number of genes in the larger network. Using this metric, networks are placed into species based on a defined compatibility threshold, δ_t. At each iteration, a network is chosen at random from each species to represent the genotype of that species. New networks are