Progressive Pathways

Evolution requires progression, not merely moving from any one genome to any other genome. In this case, then, we need a progressive series of genomes to form a valid pathway.

If all the k permutations of a genome can be ordered according to fitness, we will have k levels of fitness through which progression is possible. (Of course, there may be many groups of permutations at the same level, but for now we'll assume k levels to keep it simple.) Here we'll use the same type of analysis as before with points g_0 and g_k.

In this case, g_0 has the lowest fitness of all the permutations and g_k has the highest. The number of levels remaining is therefore $k-2$. If we only use points g_0 and g_k, there will be exactly one pathway possible: $g_0 \rightarrow g_k$. If we take the point that has the greatest fitness remaining, (i.e. not used as either g_0 or g_k,) and call this point g_{k-1}, there are two recombination possibilities created: either we include g_{k-1} in the series between g_0 and g_k, or we exclude it. In this case, we get two pathways possible: $g_0 \rightarrow g_k$ and $g_0 \rightarrow g_{k-1} \rightarrow g_k$.

Now, if we take the next most-fit genome, g_{k-2}, we have the same situation as before: either we include it between g_0 and the next-lowest genome already used (in this case this would be g_{k-1}), or we exclude it. Then, we will have four pathways: $g_0 \rightarrow g_k$, $g_0 \rightarrow g_{k-1} \rightarrow g_k$, $g_0 \rightarrow g_{k-2} \rightarrow g_k$, and $g_0 \rightarrow g_{k-2} \rightarrow g_{k-1} \rightarrow g_k$.

If we continue to work backwards in this manner, we will continue to double the number of pathways that are possible, until there are no genomes left to use. Thus, the number of progressive mutational pathways through k possible permutations of a genome with k levels of fitness is:

$$n_p(k) = 2^{k-2}$$