Using phylogenetic trees to measure the impact of background selection on population diversity

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If a species has a large, fragile, important genetic network, there will be many possible mutations that break it. Each time one of these mutations appears, the organism carrying it is much less likely to reproduce successfully, resulting in a loss of genetic diversity in the population. A way of measuring this loss is through the construction of weighted phylogenetic trees. I will present an artificial life simulation of a species tasked with transmitting information across a narrow synapse. The species must evolve a relatively large gene network to perform this task, and many of the possible mutations cause it to malfunction. Eventually a complete solution evolves and reaches fixation. That root population is then branched. The branches continue to evolve, and genetic distances between branches are measured. From those distances, a weighted phylogenetic tree is constructed. For reference, a second copy of the root population is branched, but continues evolving without the transmission task, so it experiences almost no selection. This second branched population shows more genetic diversity, and the branch weights on the phylogenetic tree are longer. Comparing the results of the population evolving under these two conditions yields an estimate of how strongly the nearly-neutral drift of unrelated genes is disturbed by selective pressure not to break the information-processing genetic network. This phenomenon may affect human genetics. Humans are less genetically diverse than other great apes. Based on this simulation, it is at least plausible that weak selection not to break the genetic network responsible for language may have contributed to that reduction in genetic diversity.