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Phylogenetic models of bacterial genome evolution incorporating gene insertion and deletion and horizontal gene transfer

The gene content of bacterial genomes differ significantly, even for closely related genomes. This illustrates that non-essential genes have high rates of insertion and deletion. Nevertheless, other genes can be found that have arisen only once in a phylogenetic tree and are signatures of monophyletic groups of genomes. There is thus a wide range of time scales involved in gene gain and loss. We analyse the presence-absence patterns of all genes in a specified group of related genomes using maximum likelihood methods. Each gene is assigned to one of three different scenarios. Scenario 0 genes are inferred to be present at the root and may have been deleted subsequently in some species. Scenario 1 genes are inferred to be absent at the root, have arisen only once within the tree, and may have been subsequently deleted. Scenario 2 genes have arisen more than once. Scenario 2 requires the occurrence of horizontal transfer, whereas scenario 1 can be explained either by origin of a new gene within the group studied or by horizontal transfer from outside the group. Preliminary results using Cyanobacteria and Archaea indicate that a majority of genes fall into scenarios 0 and 1, which means that their presence-absence pattern is consistent with the underlying genome tree. A significant number of scenario 2 genes are observed, but these do not obscure the strong tree-like signature in the evolution of the complete sets of genes.