Introduction

Sequence comparison methods have proven essential for elucidating the mechanisms that govern gene function and regulation, as well as for inferring evolutionary relationships. The underlying paradigm is that selection lowers the rate of mutation in functional DNA, and hence such regions tend to be resistant to evolutionary drift.

Pairwise sequence alignments show regions of high similarity between two species, and thus have been used as reliable guides for locating regions of homology, such as protein-coding genes common to the two organisms. When the two species are relatively distant (*e.g.*, mouse and human), strong local similarities in non-coding regions may indicate elements with some role in regulation (*e.g.*, promoters and binding sites for regulatory proteins).

Multiple alignments of sequences from related species are more reliable than pairwise alignments, since the chance of a random match in a column decreases considerably. Thus, conserved regions in multiple alignments are likely to be functional.

Insights revealed by visual inspection of the alignments can be correlated with the existing experimental evidence for validation or can prompt further laboratory investigation. Combining computational and experimental methods could ultimately be the key for the automatic analysis of uncharacterized data.

We describe three web-based tools for visualizing alignments of bacterial genomes: the ***Enteric*** and ***Menteric*** web servers, and the ***Maj*** viewer.

A set of seven enteric bacterial species (Table 1) was chosen as the genetic system for our comparative views. This choice was prompted by the availability of sequence and annotation data.