

## Enabling the Use of Externally-built alignments and trees in ARB for Evolutionary Analysis

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In order to investigate gene evolution, gene sequences from various organisms are commonly aligned to form a phylogenetic tree. Besides viewing the taxonomic information on the tree, a user may want to visually inspect how the gene product and KEGG pathway with the associated sequence has evolved, giving greater power to evolutionary hypothesis testing. A software package, such as ARB, has the power to pool this information from Genbank records, but ARB uses the local computer resources to perform the alignment. Therefore, a user may want to use external resources (such as the CIPRES portal on Terragrid), to perform the alignment and tree construction, and then import and link that information back into ARB to manipulate the data.

To accomplish this, we have created a pipeline that integrates external alignment and de novo tree construction for an arbitrary protein family (even one that contains over 10,000 member sequences). We have developed custom python scripts and an ARB import filter to extract metadata from Genbank records and import this info with an externally-built alignment and phylogenetic tree. Using our scripts, a custom database, that includes all of the sequences and associated meta-data in the study, is imported into an ARB database using uniqueIDs. The user can then use the ARB suite of tools to manipulate the phylogenetic tree and display the associated metadata.

We demonstrate the use of our tool by examining a protein family of interest to the "Tracking down the cheaters" project. All code will be made available on our website that will allow other groups to view custom fields extracted from Genbank records on phylogenetic trees using externally-built trees and alignments.