

## **Abstract**

We created the first relative age estimation technique for protein folds. The method is based on fold occurrence patterns predicted by fold recognition methods on a set of completed genomes. The highest gain of a fold, in a precalculated phylogeny of the genomes, estimates the age of that fold; gain and loss events are assigned by a Parsimony method.

The ages presented show correlation with other protein age estimators and are used to investigate evolutionary pressure on fold topology. This shows for example that alpha/beta folds have different age patterns when compared to other fold categories.

We then go on to consider the relationships in structure space of folds. In particular the sharing of structural fragments between folds. Here we found that folds, in general, tend to have more structural overlap with older folds than with younger folds. The ability to create evolutionary relevant links between fold topologies, such as sharing of fragments, would have important consequences for structural classification, structure prediction and homology modeling.