

# Summary of the class discussion and conclusions for TreeGeneBrowser: phylogenetic data mining of gene sequences from public databases

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- ✍ Basically the method provided by this paper is useful to gene searching where the database contains phylogenetic information, especially when the user focuses on the small species of the taxonomy. Otherwise, BLAST is more efficient.
- ✍ Combing this method with BLAST might be a good choice. Searching the gene in BLAST and show the results in tree might be a better solution.
- ✍ The visualization of the results into tree and gene score is a good way to help users to compare the results both from the row and column directions.
- ✍ There are total 10M species in total, that is, the level of the tree could be very deep. So how do you decide the levels of the depth when searching?
- ✍ There are no normalizations for five ad hoc scoring methods. It is not so clear what we really measure there.
- ✍ We are not sure about the difference between first database and third database generated from GOBASE databases.