Navigating Phylogenetic Trees using Graphing Algorithms

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So...What’s the problem?

The solution to our problems?

A Graph, a starting node in the Graph and goal node in the Graph.

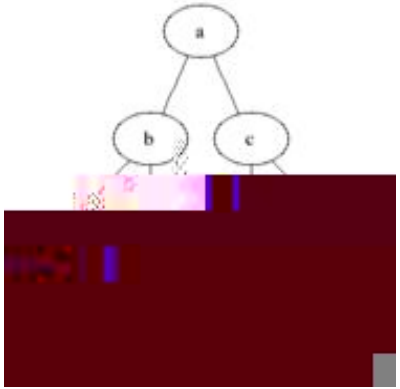
Goal node. The shortest path back to starting node.

*Making this function was hard.

So how does it work?

-Visits neighbor nodes first before moving on to next level neighbors. As opposed to simply going the full depth(Depth first search).

Here’s a nice gif to demonstrate exactly how it works:



Gif source: https://en.wikipedia.org/wiki/Breadth-first_search

Data and Formatting

-Works on data sets presented in the Newick format:

Example:

Results

-The program can:

-Trace the path taken between species.

-Calculate number of edges.

-Find the distance between species.

-Good news: Program works on practice Data Set. And creates nice graph in GraphSpace.

-Bad news: Wasn’t able to find a Newick Tree format database to download loads of data directly from. So Data-wise the program is very limited. And I had to build all of the test graphs and corresponding dictionaries.