

## HW 8: Clades of Spiders

Your job is to create a program to trace the descent of a family of monstrous descent. Given a small list of spiders, you must determine the most recent common ancestor, and then print out every spider in the smallest clade which contains them all. Your notebook should be called `clade-finder.ipynb`.

Start by downloading the file `spiders.tree`. This file contains species names of many monstrous spiders. Each line contains many species, separated by tabs. The first name represents an ancestral species, while the names that come after it are its direct descendants. One species (*M. ungoliant*) is the root of the tree, and ancestor to all the rest. It is specially marked as having the ancestor (`root`).

Your program will start by asking the user which file to open. It will then ask the user for a comma-separated list of one or more species. It will find the most recent common ancestor of all those species, and print it out. Then it will print out every descendant species of the common ancestor (direct or indirect). This is the smallest *clade* to which the given species belong.

For example:

```
Please enter a tree file: spiders.tree
For which species do you wish to find a clade: M. zahadum, M. anubarakus
Thank you.

The most recent common ancestor is M. ilwrathius.
The smallest clade containing these consists of M. ilwrathius,
M. frostbitus, M. nerubianus, M. anubarakus, M. anubrekanus, M. zahadum
```

Remember that you may be given three or more species, for which to find the clade. Also remember that this will be tested on another `.tree` file, which you will not be given. (However, it is guaranteed that the tree will be well-formed, with only one root and no cycles.)

